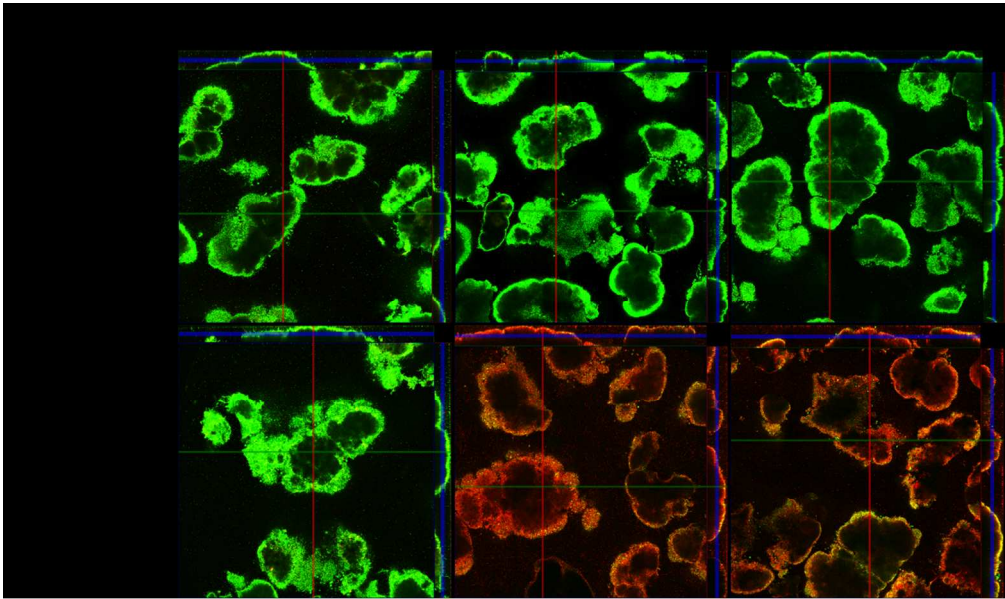


<http://mc.manuscriptcentral.com/fems>

**Predation by *Bdellovibrio bacteriovorus* significantly reduces viability and alters the microbial community composition of activated sludge flocs and granules**

Journal:	<i>FEMS Microbiology Ecology</i>
Manuscript ID:	FEMSEC-16-06-0345.R2
Manuscript Type:	Research article
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Complete List of Authors:	Feng, Shugeng; Nanyang Technological University, The Singapore Centre for Environmental Life Sciences Engineering Tan, Chuan Hao; Nanyang Technological University, The Singapore Centre for Environmental Life Sciences Engineering Constancias, Florentin; Nanyang Technological University, SCELSE Kohli, Gurjeet; Nanyang Technological University, The Singapore Centre for Environmental Life Sciences Engineering Cohen, Yehuda; Hebrew University of Jerusalem, Department of Microbial and Molecular Ecology Rice, Scott; University of New South Wales, Centre for Marine Bio-Innovation; Nanyang Technological University, The Singapore Centre on Environmental Life Sciences Engineering
Keywords:	<i>Bdellovibrio bacteriovorus</i> , predation, microbial community, activated sludge, granules, floccular sludge

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232x138mm (150 x 150 DPI)

Review



Reviewer: 1

#### Comments to the Author

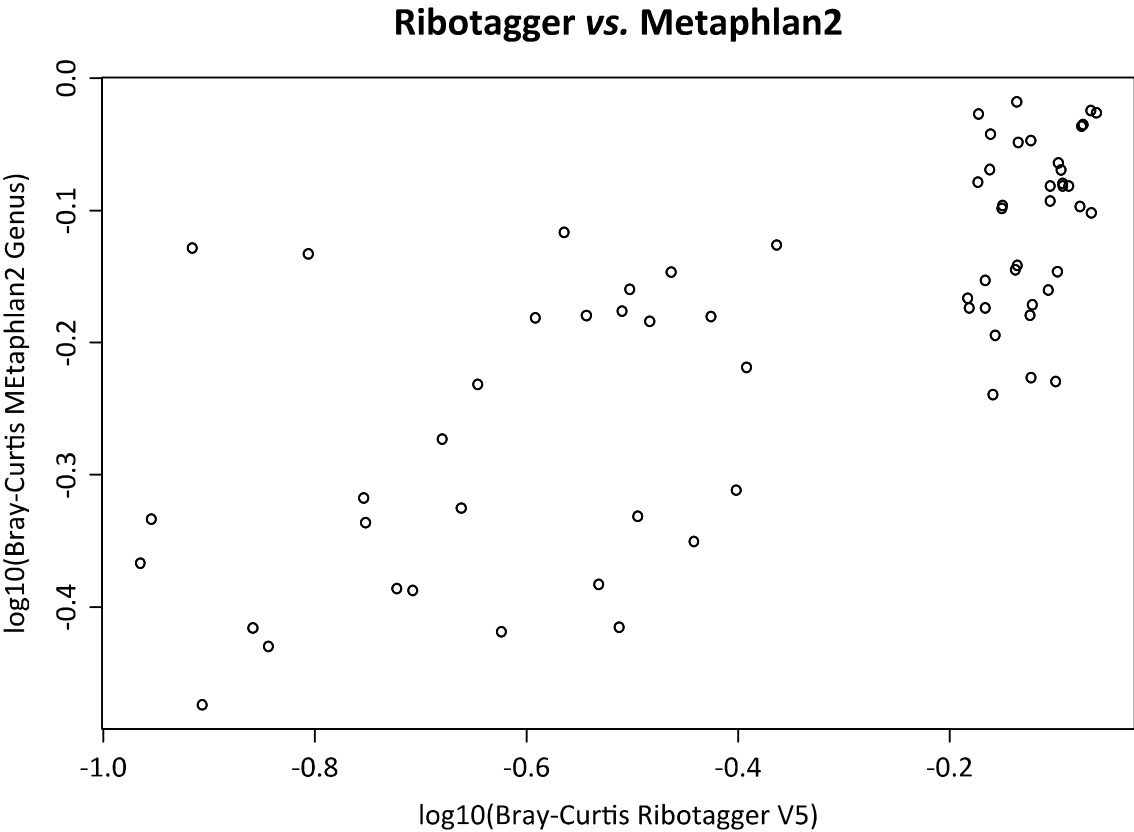
The revised manuscript by Feng et al. has many improvements, but I still have concerns mainly about the RNA sequence data analysis.

The Ribotagger method used has not been published, so it is impossible to say how well it performs. The 33 nt used for taxonomic classification is very short and probably not very reliable. There are several other methods published, that use either a set of genes or different parts of the 16S rRNA gene for taxonomic classification, for example metaxa2 or metaphlan2.

The Ribotagger method has now been accepted and published in BMC Bioinformatics (Xie *et al.*, 2016 – Attached for review purposes). The paper describes how to identify and extract taxonomically informative ribotags located in a specified variable region of the small subunit ribosomal RNA (SSU) gene in a high-throughput fashion. The Ribotagger method exhibits high sensitivity and specificity and is substantially faster than comparable programs. However, this method may exhibit limited taxonomic resolution for some reads, i.e., it may not be able to resolve some taxa at the genus or species level due to the use of the short 33 nt and stringent criteria applied. In such circumstances, we did additional BLAST searches against the NCBI-nr database to confirm the unresolved taxa and these have been highlighted in Fig. 5 (Lines 798-800).

Xie C, Goi CLW, Huson DH, Little PFR & Williams RBH (2016) RiboTagger: fast and unbiased 16S/18S profiling using whole community shotgun metagenomic or metatranscriptome surveys. *BMC Bioinformatics* 17: 277-282. DOI 10.1186/s12859-016-1378-x.

As suggested by the reviewer, we have re-analysed our RNA sequencing data using Metaphlan2 and compared the results to those using Ribotagger. We found that Metaphlan2 may not be suitable for our RNA sequencing study. This is because Metaphlan2 uses marker genes (i.e., taxa specific sequences other than rRNA) for taxonomic classification with high resolution, making it particularly useful for metagenomic based analyses. However, in our current study, we did not deplete rRNA experimentally and hence >95% of total sequences are rRNA. Therefore, our dataset has a low amount of mRNA sequences (<5% of the total RNA reads). Consequently, Metaphlan2 was able to resolve only two taxa at the species level in our study (**Table\_Metaphlan2** – Attached). Furthermore, no *Bdellovibrio* taxa were detected using Metaphlan2, even for samples spiked with the *Bdellovibrio* cultures. Hence Metaphlan2 does not appear to be suitable for the determination of community composition for our data. Nevertheless, our analysis showed that there is a strong correlation between community dissimilarities (Bray-Curtis) generated using Ribotagger (OTU level) and Methaphlan2 (genus level) (Mantel test;  $r=0.75$ ,  $p < 0.001$ ), suggesting that both methods demonstrated similar trends in terms of the overall community changes (**Figure\_Ribotagger vs. Metaphlan2** – see below). Therefore, we consider that our analysis using the Ribotagger method is rather comprehensive and reflective of the community members present based on the available short sequences. We have now included comments regarding the use of the Ribotagger vs. Metaphlan2 in the discussion (Lines 462-472).



Mantel statistic based on Pearson's product-moment correlation

Call:  
mantel(xdis = Bray-Curtis Ribotagger V5, ydis = Bray-Curtis MEtaphlan2 Genus)

Mantel statistic r: 0.7529  
Significance: 0.001

Upper quantiles of permutations (null model):  
90% 95% 97.5% 99%  
0.153 0.218 0.288 0.387  
Permutation: free  
Number of permutations: 999

Also all the sequence data should be made public, that is also the journal policy.  
[We have now submitted the sequence data to SRA, with the accession number SRP094935 and this is now included in the materials and methods section \(Lines 205-207\).](#)

The authors find big differences in the microbial community profiles, but not in the functional profiles. As noted, this might be due to the functional redundancy, but if there is a strong functional redundancy, why the performance of the community would be then reduced? The short time can't be the explanation, since the expression of the 16S rRNA has changed during this period. I think that these contradictory results have more to do with the possible biases from the 16S data analysis.  
[We agree with the reviewer that the discrepancy between community and functional profiles is more likely due to functional redundancy and is less likely due to the short exposure times. We have modified the text to indicate that this is likely to be due to the functional redundancy in the community, where the predation resistant taxa may subsequently contribute to the maintenance of](#)

1 reactor performance. As highlighted above, we are confident of the taxonomic analysis and  
2 assignment based on the Ribotagger methodology. While the amount of mRNA was not sufficient  
3 for taxonomic assignment using Metaphlan2, the amount of mRNA was nonetheless sufficient for  
4 quantification of community changes in functional genes. We have now included the changes in the  
5 discussion (Lines 506-515) as well as in the conclusions (Lines 538-544).  
6  
7

8 Minor comments:

9 1. Change also the graphical abstract, it still has the duplicated 0h image.

10 We again apologise for this oversight and have corrected the graphical abstract.  
11

12 2. use Bray-Curtis dissimilarity instead of distance.

13 We thank the reviewer for this suggestion and have made the appropriate changes at lines 248, 789,  
14 and 820.  
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17 Reviewer: 2  
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19 Comments to the Author

20 line 462, poor sentence '...that the most TAGs...'

21 The sentence has now been changed to '... that most TAGs ...' (now line 473).  
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24 line 501, reactors 'that' were.....

25 Changed (now line 518).  
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28 It is not clear in the methods that both the floc and granule reactors were performing SNDPR. Were  
29 there differences in the performance? That could relate to differences detected in the mRNA  
30 analysis that indicated significant expression differences between the floc and granule sludges.  
31 Some comment in the discussion could be made on this.

32 We thank the reviewer for highlighting this question. In fact, both the floccular and granular reactors  
33 were operated for SNDPR and showed comparable nutrient removal efficiency (i.e., >80% of  
34 phosphorus and nitrogen removal and ~100% carbon removal). When we specifically compared the  
35 mRNA profiles of genes associated with SNDPR between the two reactors, no significant  
36 differences were observed, suggesting that the communities of both reactors were expressing  
37 similar functional genes associated with SNDPR (i.e., Fig S3. carbon metabolism and nitrogen  
38 metabolism). Thus, the differentiation of flocs and granules at the mRNA level was unlikely to be a  
39 consequence of differences in SNDPR performance and were more likely due to other processes,  
40 such as genes associated with floccular vs granular biofilm formation. We have now included such  
41 comment in the discussion (Line 506-515).  
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RiboTagger: fast and unbiased 16S/18S profiling  
using whole community shotgun metagenomic or  
metatranscriptome surveys

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September 9, 2016

Abstract

Taxonomic profiling of microbial communities is often performed using  
small subunit ribosomal RNA (SSU) amplicon sequencing (16S or 18S),  
while environmental shotgun sequencing is often focused on functional anal-  
ysis. Large shotgun datasets contain a significant number of SSU sequences  
and these can be exploited to perform an unbiased SSU-based taxonomic  
analysis. Here we present a new program called RiboTagger that identi-  
fies and extracts taxonomically informative ribotags located in a specified  
variable region of the SSU gene in a high-throughput fashion. RiboTag-  
ger permits fast recovery of SSU-RNA sequences from shotgun nucleic acid  
surveys of complex microbial communities. The program targets all three  
domains of life, exhibits high sensitivity and specificity and is substantially  
faster than comparable programs.

## Background

Studying the composition and dynamics of microbial communities is a key problem in microbiome research and microbial ecology [1]. Traditionally, these studies have been based on isolating and sequencing short subunits of the 16S and 18S genes, present in bacteria or archaea, and eukaryotes, respectively. Typically most studies now make use of amplicon sequencing to obtain such data from complex microbial communities [2, 3]. The PCR amplicon technique was very useful when sequencing power was limited, however, with the increasing power and complexity of the new generation of sequencing technologies, the broad advantages of amplicon sequencing are starting to be balanced by major limitations, which include PCR primer selection and amplification bias [4, 5]. In particular, no PCR primers are able to amplify all known bacterial taxonomic groups efficiently and uniformly [5], which leads to biased rRNA profiling analysis, and the use of short read technologies, notably Illumina, results in a complex, interdependent chain of technical decisions, that can heavily influence the subsequent community profiling results [6].

Within microbiome research, there is increasing use of whole community gDNA surveys (*i.e.* shotgun metagenomics), which offer, at theoretically, a less biased view of community composition than using from amplicon based methods, by eliminating dependency on 16S primers [7]. In practice however, the interpretation of shotgun metagenome data is heavily dependent on having access to reference genomes of community members, without which substantial limitations of interpretation may arise [8]. While the intended use of these shotgun data is typically to capture functional capacity of a community [9], or to permit member genome recovery [8], it has been recognized that whole community shotgun surveys will of course contain a substantial number of reads derived from SSU-rRNA genes, and these can be exploited for the purposes of community profiling [10, 11, 12, 13, 14, 15, 16, 17]. Similarly, when using total RNA metatranscriptome sequencing, rRNA often account for 95% of reads sequenced, and thus provides coverage of SSU diversity to great depth. Within this general area, a number of examples of this approach have been undertaken and several software implementations of this approach are now available [13, 16, 17], mostly based on the use of Hidden Markov Models to capture reads of SSU-origin from the total read population [10, 11, 12, 13, 14, 16, 17].

Here we present a new open source software package, RiboTagger<sup>1</sup> to analyze rRNA data from shotgun sequencing reads. The software takes raw metagenome or metatranscriptome sequencing reads in FASTQ or FASTA files as input, and is able to process billions of Illumina HiSeq reads under an hour. RiboTagger produces a BIOM formatted files for downstream analysis in standard packages

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<sup>1</sup><https://github.com/xiechaos/ribotagger>

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like QIIME [18] or MEGAN [19]. It is equally sensitive over all known bacterial and archaeal phyla and classes, and highly specific in not classifying non-rRNA sequences as rRNA.

## Implementation

We start with genomic DNA or total RNA from a microbial community that has been sequenced, then attempt to recover sequencing reads covering a particular region on 16S rRNA gene using a short conserved *recognition sequence* (RS). A short sequence adjacent to the RS is used as the *tag sequence* (TS) to represent the origin of the 16S gene. For this strategy to be feasible with short-read sequencing technologies, by nature both RS and TS have to be short but informative and in particularly the RS must be conserved across all taxonomic branches, while the TS must be diverse with high taxonomic resolution. The boundaries of each hypervariable region are logical candidates for being RS, which we call ribotags from here on. After examining all bacterial and archaeal 16S sequences in the RDP database [20] we designed a combination of probe patterns and Position Specific Scoring Matrices (PSSM) to recognize the conserved site immediately outside a hypervariable region as RS, which we describe as a *universal recognition profile* (**Fig. 1**). The short region in the hypervariable region adjacent to the RS is then considered as a candidate tag sequence for the hypervariable region (**Fig. 1**). In this PSSM-based detection, the RS sequences are 23 n.t. in length and the TS are typically 33 n.t. in length. The lengths of both RS and TS were empirically determined so as to achieve a good trade-off between sensitivity and specificity, while maintaining a total length that is smaller than a typical sequencing read. For each of the three domains of life and each of the most commonly used variable regions, namely V4, V5, V6 and V7, we computed a universal recognition profile by analyzing the Greengenes database [21] (**Fig. 2**). To improve sensitivity, our implementation provides and can utilize a set of 17–30 supplementary taxon-specific recognition profiles for each of the variable regions.

## Results

### Validation analyses

Application of our universal profiles to the Greengenes database gave rise to a set of 90,061 ribotags. Each ribotag was assigned a taxon based on the set of SSU sequences that contain it, using the majority taxon in the case of discordance. The sensitivity of each of the profiles is over 95% percent (**Fig. 2**), as established by applying the profiles to all SSU sequences in the SILVA database [22]. To



test the false positive rate, we ran the profiles on 5.6 billion faux reads, obtained by sampling all 80nt non-overlapping fragments in the RefSeq database (release 66), calculating the false positive rate to be at most  $2 \times 10^{-6}$  in all cases (**Fig. 2**). To address the problem of the extent to which sequencing-error can generate false ribotags, RiboTagger estimates the expected frequency of each ribotag due to sequencing error, based on the observed frequencies of ribotags that differ by one letter and a simple probabilistic model.

To determine how well ribotags can differentiate between organisms at a given taxonomic rank, we computed the *concordance* of all ribotags obtained from an analysis of the Greengenes database. We consider a ribotag as fully concordant (or to have concordance 1) at a given taxonomic rank, if all database sequences that contain that ribotag have the same taxonomic assignment at the given rank. For example, the concordance is between 0.95 and 1.00 if between 95% and 100% of the database sequences that contain the ribotag all have the same taxon assignment. The percentages of V4 ribotags with a given range of concordance (*i.e.* 1, [0.95,1), [0.95,0.90), etc) for different taxonomic ranks as annotated in the Greengenes database are shown in **Figure 3A**. Approximately 80% of all ribotags are fully concordant on the species level, while practically all reads are concordant at the phylum level. Results are similar for V6 ribotags, while the number of fully concordant ribotags is about 5% lower for V5 and V7 (data not shown). We also examined the degree of concordance against de novo OTU clusters defined by Greengenes over a range of percent identity thresholds, showing that for ribotags in clusters defined at 99% similarity, over 80% show no sequence differences (**Fig. 3B**).

Due to the short length of the 16S tags, we need to consider the possible influence of sequencing errors explicitly. PCR artifacts during library generation would lead to abnormally high numbers of reads with identical starting position and sequence content. Therefore, simply counting sequencing reads with different starting position can detect possible PCR artifacts. Using stringent quality value filtering for each nucleotide that covers 16S tags can also the impact of limit potential sequencing errors, which results extremely low error probability for each sequencing read considered. For example, with quality value threshold 30, the probability of sequencing error is only 0.1%. In addition, we also calculate the number of expected number of occurrence of any 16S tag, assuming the tag is not present at all. Assuming the tag of interest is not present, given the observed average sequencing error probability at each nucleotide position along the tag and the abundance of all other tag sequences with one nucleotide difference in the data, we can calculate the expected abundance of the tag of interest by sequencing error. Firstly, for the tag under study, all tag sequences with one nucleotide difference from the tag of interest are collected. Each of the 1nt neighbors will contribute



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$E = n \times e/3$  false positive counts to the tag of interest, where  $n$  is the number of reads covering the 1nt neighbour and  $e$  is the observed error probability for the difference position on the tag of interest. The sum of  $E$  for all 1nt neighbours gives the expected false positive tag of interest due to one sequencing error. Multiple sequencing errors can be also considered in a similar fashion but due to the quality-value filtering step, we can consider the probability of observing multiple sequencing errors in ribotag sequences as negligible.

Example

To illustrate the results obtained from RiboTagger, we ran RiboTagger against a coupled DNA-Seq and RNA-Seq datasets generated from an activated sludge community of an operational wastewater treatment (Ulu Pandan Water Reclamation Plant, Northworks, Tank 3C operated by the Public Utilities Board, Republic of Singapore; samples obtained between 10/08/2012 and 17/08/2012). Genomic DNA and total RNA sequencing were each performed on a HiSeq2500 Rapid run using 250bp paired end sequencing for DNA samples, and 150 bp paired end read sequencing for RNA samples. From the DNA dataset, we observed a total of 4686 V4-region ribotags in the entire dataset. We can estimate whether the number of observed 16S tags is as expected using the following rough approximation: if we assume there are up to 5000 genes in a typical free-living bacteria [23], and if we neglect the likely variation in 16S copy number across the member species in the community, and assume that one of those is a 16S gene with roughly 9 equally sized V-regions and 10 equally sized conserved regions, then we would expect approximately  $308,505,950/(195000)=3247$  reads to originate from a single V-region in our analysis, which is a conservative underestimate to our observed number. For the RNA data, we report only results for one sample to for purposes of illustration, specifically with a total of 41,523,808 RNA reads available after QC filtering, we obtained a total of 4867 tags, of which the top 11 accounted for 20%, 80% and 95% of community membership (as described by total number of reads). Collectively there are 327 unique genera detected, 203 families, 128 orders and 51 phyla, The majority of annotated tags at kingdom level (1450) were attributable to bacteria, as expected in this community, with 34 and 40 tags being assigned to archaea and eukaryota, respectively. Approximately 3343 tags could not be assigned any annotation using SILVA v119 [22], including 1 and 41 in the top 20% and 50% of the community, respectively. These latter results highlight the substantial numbers of unknown taxa residing in complex microbial communities.

## Comparison to related programs

Using the RNA dataset described above, we compared the computational time of RiboTagger against two other existing search tools, RiboFrame [16] and SSUsearch [17], which are designed for retrieval of 16S sequences from whole metagenomic sequencing datasets. The comparison was carried out on a standalone server with the following specifications – 2 Intel Xeon X7542 (18M Cache, 2.66 GHz) CPUs, 128 GB memory, internal 146 GB HDD and external 8 TB RAID HDD. RiboTagger took approximately 90 minutes to complete, and we observed RiboTagger to be approximately 6 times faster than RiboFrame (~9 hr) and 6.6 times faster than SSUsearch (~10 hr). As RiboTagger and SSUsearch both used SILVA annotations, we compared the identity and relative abundance of detected phyla between both programs. In total 112 phyla were detected (51 with RiboTagger and 86 with SSUsearch) of which 25 were common between the two methods. The number of unclassifiable sequences differed, with 21.6% being called in SSUsearch and 47.5% in RiboTagger, however, of the 25 common phyla, 7 accounted for 95% of community composition in each set of results. The overall correlation between relative abundance was 0.99 (with 25 common phyla) and 0.88 (using all 112 phyla with non-detects set as zero). We note that while some of these differences may be accounted for by different database versions (SILVA v115 and SILVA v119 for SSUsearch and RiboTagger, respectively) and/or handling of unclassifiable sequences, these results suggest that further investigation of the differences between detection methodologies are warranted.

## Practical aspects

RiboTagger is implemented as a platform independent Perl program. It can be executed in a single command in several modes which are briefly described here, along with their respective outputs. Full details can be found on the RiboTagger project page on Github (see **Availability and Requirements**)

### Single input file mode

The most basic way to run RiboTagger is using a single FASTQ file (including with either gzip and bzip2 compression), which will generate an output file formatted as a table with the following fields:

- **tag**: the tag sequence for the variable region
- **n**: the number of reads that contains this tag

- **npos**: the number of different locations of the tag on their source reads (big value of **n** with small value of **npos** indicates the presence of duplicated reads or would be observed in the case of analysing amplicon sequencing reads).
- **fp**: the number of reads you would expect to see this tag due to sequencing errors alone
- **long.total.count**: the number of reads containing a longer sequence of this tag (see the **--long** option)
- **long1.count**, **long2.count**, **long3.count**: number of reads containing the most abundant variants of this tag's long sequences (a low value of **long1.count** to **long.total.count** ratio indicates that this tag is very likely representing a mixture of "species")
- **long1**, **long2**: the most abundant long representative sequences of this tag

**Multiple input file mode**

For multiple input files, RiboTagger can return a series of files. Data from paired end read data can also be combined into a single output. The **.tab** file returns a table of unnormalized read counts, with ribotags indexed in rows and samples indexed in columns. The **.anno** files contains QC, metadata and annotations, if available, for the same set of ribotags with the following columns fields:

- **tag**: the ribotag sequence
- **use**: "tag" or "long", whether the annotation was based on the short tag or long representative sequence
- **taxon\_level**: taxa rank of this annotation of this tag
- **taxon\_data**: taxa rank of the most specific annotation appeared in the database (SILVA or Greengenes) for this tag
- **long**: the long representative sequence of this tag
- **long\_total**: the number of samples having any long representative sequence
- **long\_this**: the number of samples having this long sequence as its major representative of this tag
- **support**: the number of database sequences having this this tag or long sequence

- **confidence**: the proportion of the database sequences agreed on this annotation
- **k, p, c, o, f, g, s**: annotation for each of the taxa ranks, namely kingdom/domain, phylum, class, order, family, genus, and species

The `.xls` file is an Excel file combining data from the `.tab` and `.anno` files. Using `biom.pl`, a `.biom` file can be subsequently used by QIIME [19]. We have implemented options for generating annotations to either SILVA [21] or Greengenes [22]. All 4 file types can automatically be generated if RiboTagger is run in batch mode.

## Conclusions

Here, we have developed software for the fast recovery of SSU-RNA sequences from shotgun nucleic acid surveys of complex microbial communities. Our code is fast, completing an analysis of about 40M reads within 1.5 hrs, and with output an annotated matrix of read counts that can be used for downstream community profiling analysis with minimal further processing. Our implementation executes in a single line, avoiding the complications and the lack of robustness inherent in combination-type pipelines and is at least 6 times faster than SSUsearch [17] and RiboFrame [16]. Additional, we also note that our approach avoids the use of OTU generation, which recent analyses suggest may carry significant advantages in resolving intra-community dynamics when using some classes of experimental designs [24].

## Availability and Requirements

Project name: RiboTagger

Project home page: <https://github.com/xiechaos/ribotagger>

Operating system(s): Platform independent

Programming language: Perl

Other requirements: None

Any restrictions to use by non-academics: currently free-for-use. RiboTagger will be released under an open source license after it is published.

## List of abbreviations

*OTU*, operational taxonomic unit; *PSSM*, Position specific scoring matrix; *RS*, recognition sequence; *TS*, tag sequence

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**Ethics approval and consent to participate**

Not applicable.

**Consent for publication**

Not applicable

**Availability of data and material**

The sequencing datasets analyzed during the current study are not yet publicly available due to their forming part of a large set of data being released as part of a primary manuscript. They are available from the corresponding author on reasonable request.

**Competing interests**

The authors declare that they have no competing interests

**Funding**

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**Author contribution statement**

C.X. conceived and designed the approach and implemented methods. C.X., W.G, R.B.H.W analyzed example data, and all authors interpreted the results. The paper was mainly written by X.C, D.H.H and R.B.H.W.

## Acknowledgements

We thank our colleagues Larry Liew, Stefan Wuertz, Yehuda Cohen, Uma Shankari d/o Chanda Segaran, Stephan C. Schuster, Daniela Moses for providing access to data they sampled and sequenced, and Siao Yun Chang, Choon Leng Lau and their colleagues from the Public Utilities Board (Republic of Singapore) for assistance with access to facilities and sampling operations.

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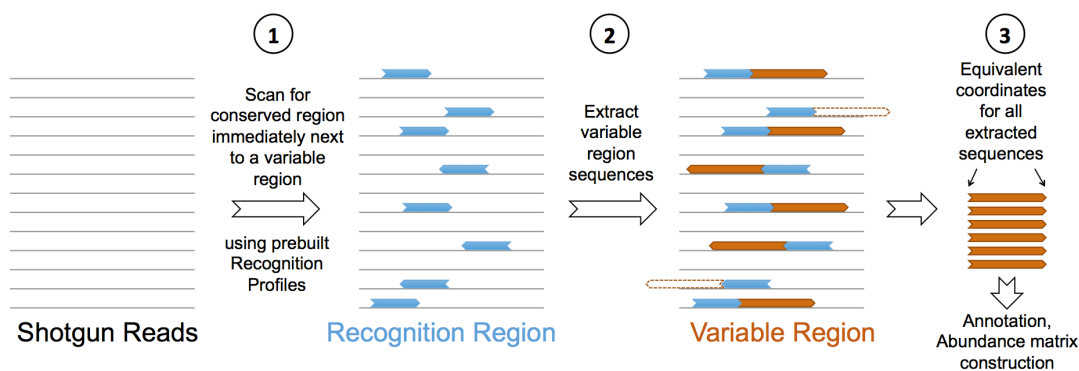


Figure 1: Schematic representation of RiboTagger detection scheme. Starting with shotgun sequencing reads from (either gDNA or cDNA) RiboTagger proceeds as follows; (1) all reads are screened using PSSMs for the presence of a conserved recognition sequence (blue arrowed rectangles) adjacent to V-regions using a cohort of pre-defined recognition profiles; (2) for reads that are positive for recognition sequences, the adjacent V-region tag sequence is extracted, assuming if sufficient length is available (dashed blue rectangles denote in sufficient length in the tag sequence); and (3) for related tag sequences, equivalent coordinates are defined, prior to counting and annotation.













		Universal Recognition Profile	Sensitivity	False Positive Rate
V4	B		96.9%	3.4E-07
	A		96.2%	1.7E-10
	E		96.9%	9.6E-07
V5	B		96.6%	1.2E-06
	A		95.6%	3.3E-08
	E		96.5%	5.1E-07
V6	B		98.3%	1.9E-07
	A		95.6%	3.1E-08
	E		97.7%	6.0E-07
V7	B		98.4%	2.0E-06
	A		95.3%	1.6E-08
	E		97.2%	4.1E-07

Figure 2: Universal recognition profiles for each of the variable regions V4–V7 used to target bacteria (B), archaea (A) and eukaryotes (E), respectively, with corresponding observed sensitivities and false positive rates.

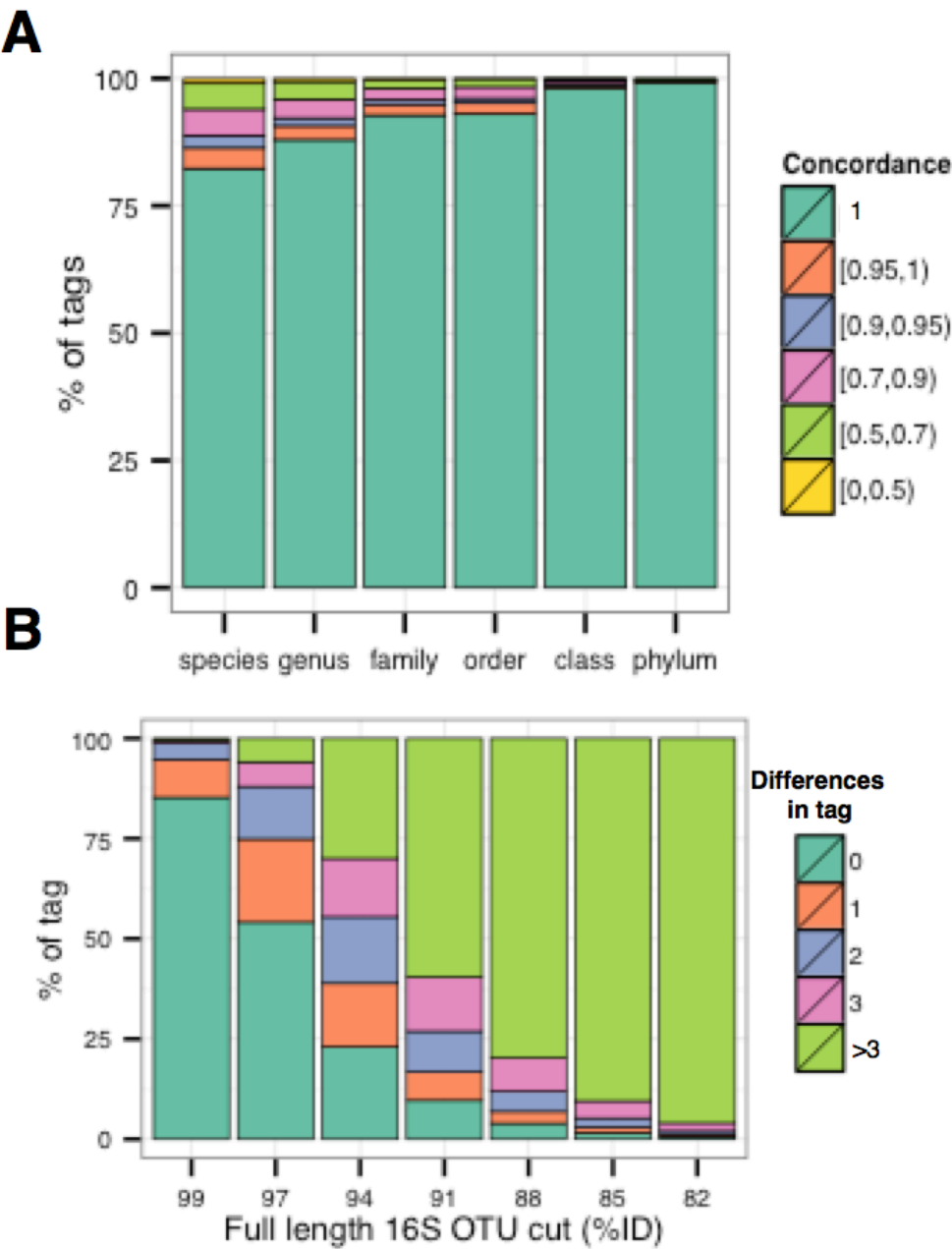


Figure 3: Percentage of V4 ribotags with a given range of concordance for different taxonomic ranks as (A) annotated in the Greengenes database and (B) as measured against Greengenes de novo OTU clusters as a function of cluster formation threshold.

**1 Predation by *Bdellovibrio bacteriovorus* significantly reduces viability**  
**2 and alters the microbial community composition of activated sludge**  
**3 flocs and granules**

4  
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13  
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15  
16 Key words: *Bdellovibrio bacteriovorus*, predation, microbial community changes,  
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22

23     **Abstract**

24     We recently isolated and characterized a predatory *Bdellovibrio bacteriovorus* strain  
25     from activated sludge (Ulu Pandan Water Reclamation Plant, Singapore), and this  
26     strain, *B. bacteriovorus* UP was able to prey upon a broad spectrum of bacterial  
27     isolates from the activated sludge when grown as planktonic cells or as biofilms. Here,  
28     we have tested the effect of *Bdellovibrio* predation on floccular and granular sludge to  
29     determine if the spatial organization, loosely or tightly aggregated communities, was  
30     protective from predation. The effect of predation was assessed using a combination  
31     of biomass quantification, cellular activity measurement and microscopic image  
32     analysis to determine community viability. Additionally, changes in the microbial  
33     communities due to predation by *B. bacteriovorus* UP were analyzed through total  
34     RNA sequencing. Predation led to a significant reduction in microbial activity and  
35     total biomass for both floccular and granular sludge communities. Predation was also  
36     associated with significant changes in the microbial community composition in both  
37     communities, with >90% of the community members reduced in relative abundance  
38     after 24 h. Of those community members, the dominant organisms, such as  
39     *Proteobacteria* and *Bacteroidetes*, were the most affected phylotypes. This suggests  
40     that predatory bacteria, which display indiscriminant feeding, could significantly shift  
41     the species composition and thus, may disturb the operational performance of  
42     wastewater treatment systems.

## 44 Introduction

45 Predation plays a significant ecological role within ecosystems, which has been well  
46 documented for higher organisms (Berryman, 1992, Godfray & Pacala, 1992,  
47 Fedriani *et al.*, 2000, Ripple & Beschta, 2004), and has also been well described with  
48 respect to the predation of microorganisms by viruses (bacteriophages) and protists in  
49 natural and engineered ecosystems (Curds, 1982, Bergh *et al.*, 1989, Gonzalez *et al.*,  
50 1990, Suttle & Chan, 1994, Ronn *et al.*, 2002, Parry, 2004, Sutherland *et al.*, 2004).  
51 Wastewater treatment plants (WWTPs) are engineered systems designed to remediate  
52 wastewater, which contain various organic materials as well as high concentrations of  
53 nutrients such as nitrogen and phosphorus (Bolong *et al.*, 2009, Wells *et al.*, 2009).  
54 The WWTP is dependent upon a highly diverse microbial community that collectively  
55 functions to remove carbon and nutrients from used water (Bitton, 2005, Ahmed *et al.*,  
56 2008, Yilmaz *et al.*, 2008). The community is typically present as a floccular biomass  
57 (known as activated sludge), where the community members are loosely held together  
58 by self-produced extracellular polymers as suspended biofilms. A relatively recent  
59 advance in wastewater treatment technology has been the conversion of floccular  
60 biomass into granules (Morgenroth *et al.*, 1997, Beun *et al.*, 1999, Wilen *et al.*, 2004,  
61 Tan *et al.*, 2014). Granules are more compact with increased biomass density and  
62 granules have distinct advantages over floccular sludge that make them attractive for  
63 application for wastewater remediation. For example, the highly dense granules settle  
64 faster than floccular biomass, which can reduce settling time and requires small  
65 settling tanks (Lin *et al.*, 2003, Yang *et al.*, 2003, Adav *et al.*, 2007). Granular  
66 biomass also is more tolerant to high strength and industrial waste (Gonzalez-Gil &  
67 Holliger, 2014).

68 The function of both floccular and granular activated sludge, e.g., degradation of  
69 organic matter as well as nitrogen and phosphorus removal (Lin *et al.*, 2003,  
70 Schwarzenbeck *et al.*, 2004), is highly dependent on the collective metabolic  
71 activities of the constituent microbial community members (Ghigliazza *et al.*, 1998,  
72 Wagner *et al.*, 2002, Ahmed *et al.*, 2008). Therefore, any environmental disturbance  
73 of the key functional microorganisms may significantly affect the performance of  
74 WWTPs. Whilst WWTPs can be impacted by chemical stresses, such as organic  
75 compounds and toxicants (Shchegolkova *et al.*, 2016), they are also subjected to  
76 biological stressors in the form of microbial predators. Indeed, the impact of



77 predators, such as bacteriophages and protozoa, has been extensively studied,  
78 particularly for their impact on the performance of wastewater treatment systems  
79 (Ewert & Paynter, 1980, Jurgens *et al.*, 1994, Jurgens & Gude, 1994, Wanner *et al.*,  
80 2000, Shapiro *et al.*, 2010). However, few studies have focused on the role of  
81 *Bdellovibrio*-and-like organisms (BALOs) and their potential influence on the  
82 structure and function of microbial communities in wastewater treatment systems.

83 *Bdellovibrio* species are a group of predatory organisms that are commonly found  
84 in natural and man-made ecosystems, which prey upon a broad range of Gram-  
85 negative bacteria (Jurkevitch *et al.*, 2000, Sockett, 2009). In a previous study, a  
86 *Bdellovibrio* species, *Bdellovibrio bacteriovorus* UP, was isolated and characterized  
87 from activated sludge (Ulu Pandan Water Reclamation Plant, Singapore) (Feng *et al.*,  
88 2016). This isolate was shown to prey on all but one of the Gram-negative isolates,  
89 irrespective of whether they were grown as biofilms or as planktonic cultures as  
90 populations or dual-species communities. As expected, none of the Gram-positive  
91 bacteria or fungi was sensitive to predation. Those experiments focused on simple  
92 pair-wise assembled communities, in contrast to the floccular and granular  
93 communities that contain high densities of much more complex communities. This  
94 exceptionally high species diversity may protect the otherwise sensitive Gram-  
95 negative bacteria in that the predation-resistant bacteria can serve as barriers  
96 protecting the sensitive bacteria. Further, it is possible that the higher density and  
97 increased structural integrity of the granules may afford the communities increased  
98 protection from predation compared to the loosely organized floccular biomass.

99 In this study, the effects of *B. bacteriovorus* UP upon both floccular and granular  
100 communities were investigated. The impact of predation on the overall microbial  
101 community composition and function was determined through total RNA sequencing  
102 analysis as well as alterations of biomass and viability of the communities. The results  
103 showed that the viability and total microbial biomass of both sludge communities  
104 were significantly reduced due to the presence of *B. bacteriovorus* UP. Additionally,  
105 while there were significant alterations in the microbial community composition,  
106 changes in functional gene expression were limited for either sludge type due to the  
107 predation by *B. bacteriovorus* UP.

108 **Materials and Methods**

### 109 Preparation of *Bdellovibrio bacteriovorus* UP

110 Frozen *B. bacteriovorus* UP stocks were thawed on ice and mixed (1:24 v/v) with  
111 *Pseudomonas protegens* suspensions in liquid DNB ('Lab-Lemco' power 0.1 g/L,  
112 yeast extract 0.2 g/L, peptone 0.5 g/L and NaCl 0.5 g/L, amended by 3 mM MgCl<sub>2</sub>  
113 and 2 mM CaCl<sub>2</sub>) medium and incubated for 24 h. The co-cultures of *B.*  
114 *bacteriovorus* UP incubated with *P. protegens* were centrifuged at 2,000 g for 10 min,  
115 and the supernatant containing *B. bacteriovorus* UP cells was inoculated (1:9 v/v)  
116 with fresh *P. protegens* suspensions. *B. bacteriovorus* UP cells were collected after 48  
117 h cultivation with *P. protegens* by centrifugation (2,000 g for 10 min). The  
118 supernatant was passed through 0.45 µm membrane filters twice to remove the prey  
119 bacteria. Part of the 0.45 µm filtrate was further passed through 0.2 µm membrane  
120 filters three times to remove the predator for use as a negative control. The  
121 *Bdellovibrio* cell numbers were presented here as plaque forming units (PFU's).  
122 PFU's was determined through counting plaques formed on a given prey species  
123 lawn. In brief, the *Bdellovibrio* cell suspension was serially diluted and the dilutions  
124 were incubated on the lawns of *P. protegens*. After 3-5 d incubation, the plaques were  
125 counted to determine the PFU.

### 126 Maintenance of floccular and granular sludge

127 Activated sludge collected from the Ulu Pandan Water Reclamation Plant was used to  
128 seed laboratory reactors in which the microbial community was maintained as  
129 floccular biomass or was converted into granular biomass. The floccular sludge (Fig.  
130 S1A) was collected from the sequencing batch reactor (SBR) undergoing stable  
131 simultaneous nitrification, denitrification and phosphorus removal (SNDPR)  
132 performance, which was fed with synthetic wastewater with organic matter, ammonia  
133 and phosphate. The organic source was a mixture of acetate and propionate of 200 mg  
134 COD/L (COD<sub>Acetate</sub> : COD<sub>Propionate</sub>, 3:1) and the ammonia and phosphate  
135 concentrations were 20 mg N-NH<sub>4</sub><sup>+</sup>/L and 10 mg P-PO<sub>4</sub><sup>3-</sup>/L, respectively. This reactor  
136 was operated with a working volume of 4 L and a cycle time of 5 h. Each cycle  
137 included stages of: 58 min anaerobic, 105 min aerobic and 25 min anoxic periods in  
138 the first phase, and 38 min anaerobic, 40 min aerobic and 20 min anoxic periods in  
139 the second phase (Zhou *et al.*, 2010).

140 The granular SBR reactor (Fig. S1B) had a volume of 4 L and used the same feed  
141 synthetic wastewater as above. The operation of the bioreactor involved a 6 h cycle

comprised of two different phases: Phase I - feeding (8 min), anaerobic (60 min), aerobic (80 min at day 0 and gradually increased to 95 min by the end of week 5) and anoxic (40 min at day 0 and gradually increased to 50 min by the end of week 5); Phase II - feeding (2 min), anaerobic (30 min), aerobic (40 min at day 0 and gradually increased to 70 min by the end of week 5) and anoxic (30 min). Each cycle was completed with a settling stage (60 min at day 0 and gradually decreased to 5 min by the end of week 5) and a 10 min decanting stage. The settling time was 5 min per cycle from week 6 onwards (Tan *et al.*, 2015).

**Predation of floccular and granular sludge**

Floccular biomass of the floccular sludge and granules of the granular sludge were both collected during the anoxic stage. The microbial biomass in the floccular and granular sludge was collected by centrifugation (5,000 g, 8 min) and the pellet was re-suspended in DNB. Both the sludge samples were incubated with *B. bacteriovorus* UP cell suspensions (final concentration, 10<sup>8</sup> PFU/mL) as the ‘Treated’ group, whilst the negative control had no predators added. At 0, 24 and 48 h, the activated sludge was collected to determine the ATP content (microbial activity) and total protein (total biomass). The experiments were repeated independently three times.

**Total biomass quantification of microbial community**

The total biomass was quantified by determining the total amount of protein, where the floccular and granular sludge samples were lysed using a probe sonicator (SM Vibracell VCX750, Sonics & Materials, Inc.), and quantified using the Bradford assay according to the manufacture’s guidelines (Bio-Rad<sup>TM</sup>) at 595 nm (TECAN, INFINITE<sup>®</sup> 200, PRO). The protein concentrations were calculated by comparing the OD<sub>595</sub> readings with a standard curve generated using bovine serum albumin. The total biomass was determined for each of the three independent experiments with three technical replicates for each sample.

**Microbial activity measurement (ATP)**

Total ATP was quantified as a proxy for microbial activity and viability to determine the predation impact on floccular and granular community. Briefly, 100 µL of the experimented floccular or granular sludge were mixed evenly with 100 µL of the ATP measurement reagent (BacTiter-Glo<sup>TM</sup>, Promega). The luminescence response was

quantified as relative luminescence unit (RLU) using a micro-plate reader (TECAN, INFINITE<sup>®</sup> 200, PRO). The ATP measured from three samples for each time point and for each treatment condition.

#### **Viability of microbial community in floccular and granular sludge**

The viability of the microbial community in sludge was additionally assessed by the Live/Dead staining assay according to the manufacture's guidelines (*BacLight*<sup>™</sup> Cell Viability Assays, Thermo Fisher Scientific Inc.). Stained samples were observed and image acquisition of sludge community was conducted by using a ZEISS LSM780 confocal microscope (Carl Zeiss Optical Co., Ltd., Germany) equipped with an argon ion laser at 488 nm (for SYTO9) and a diode laser at 561 nm (for propidium iodide) for excitation. Images were captured with the ZEISS LSM780 confocal microscopy bundled program ZEN 2010. Multiple images (two-dimensional images for floccular sludge and three-dimensional images for granular sludge) were captured randomly for quantitative image analysis using IMARIS (V7.6.4. Bitplane, Oxford Instruments).

#### **RNA extraction, library preparation and sequencing**

Total RNA was extracted from floccular and granular biomass using a RNA Clean and Concentrator<sup>™</sup>-5 kit (ZYMO Research Corporation, Singapore) according to the manufacturer's guidelines. DNA was removed using TURBO DNA-free kit (Applied Biosystems, Singapore). RNA quality was determined using Agilent 2100 Bioanalyser and reported as RNA integrity number. The quantity of total RNA and residual DNA was measured by Quant-iT RiboGreen RNA and PicoGreen DNA assays (Invitrogen, Singapore), respectively. Total RNA, 200 ng, was used for complimentary DNA (cDNA) library preparation according to the manufacturer's instructions (Illumina, Singapore). Each cDNA library was ligated with a unique adaptor sequence for sample multiplexing. A total of 12 different cDNA libraries were pooled and sequenced by Illumina Hiseq (Hiseq 2500, Illumina) and a total of 263 million raw sequencing reads with an average read length of 101 nucleotides were generated. [The RNA sequencing dataset obtained in this study is now deposited in the Sequence Read Archive \(SRA\), NCBI with an accession number of SRP094935.](#)

#### **Sequencing analysis for community structure and functions**

210 Illumina adaptors, shorter reads (-m 50) and low quality reads (-q 20) were removed  
211 using cutadapt (version 1.11)(Chen *et al.*, 2014). High quality reads (97±0.3% of the  
212 raw reads) were subjected to sortmeRNA analysis (version 2.0)(Kopylova *et al.*,  
213 2015) to extract both rRNA (92±2%) and mRNA (8±2%). In order to characterize the  
214 taxonomic composition of the microbial communities, rRNA reads were analyzed  
215 using a fast tag-based approach, the RiboTagger (Xie *et al.*, 2016). The RiboTagger  
216 scripts used in this study can be found at the following link  
217 <http://chaos.bic.nus.edu.sg/ribotagger/manual.html>. Briefly, a universal primer for  
218 each of hyper-variable regions, i.e., V4, V5, V6 and V7 of the 16S rRNA was used to  
219 scan each sequencing read to obtain 33 nt downstream of the primer, and the 33 nt  
220 sequences were defined as the tag of the 16S rRNA gene. Those universal primer  
221 sequences are conserved among bacteria, *Achaea* and eukaryotes (Xie *et al.*, 2016).  
222 Short reads that did not cover the full 33 nt region were discarded. Each different tag  
223 (TAG) was used as a signature sequence to represent one operational taxonomic unit  
224 (OTU). TAGs assigned to the *Bdellovibrionaceae* family, as well as TAGs that only  
225 occurred once (i.e., singletons) were removed from the TAG table prior to random  
226 subsampling for normalization. For functional analysis, mRNA sequences were  
227 aligned against the NCBI non-redundant (NR) protein database  
228 (<ftp.ncbi.nlm.nih.gov/blast/db/FASTA/nr.gz>, March 2016) using DIAMOND (version  
229 0.7.10.59, <http://ab.inf.uni-tuebingen.de/software/diamond>) (Buchfink *et al.*, 2015).  
230 Aligned reads were assigned to KO using GI to KEGG mapping file implemented in  
231 MEGAN (version CE\_6\_5\_5). In order to remove mRNA expressed by *Bdellovibrio*  
232 *bacteriovorus* species, the lowest common ancestor approach was used to define the  
233 taxonomic origin of mRNA reads (LCA, default parameters, MEGAN). Only genes  
234 expressed by taxa other than *Bdellovibrionaceae* family were kept for further  
235 analysis.

236

237 **Statistical analysis**

238 All statistical analyses were conducted using Prism 6 Version 6.04 (GraphPad) or R  
239 ([www.r-project.org](http://www.r-project.org)). Statistical analyses for changes of ATP content, protein  
240 concentration, quantitative image data as well as alpha diversity indices were  
241 performed using two-way ANOVA, followed by Sidak post-tests to examine  
242 differences between the ‘control’ and ‘treated’ groups. Differences in relative  
243 abundance of taxa between ‘treated’ and ‘control’ groups were tested based on the

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2  
3 244 null hypothesis that there is no difference between the two groups. Corrected *P*-values  
4 245 based on 1% false discovery rates (FDR) were reported in each case. Multivariate  
5 246 analysis was conducted to determine the overall changes of community composition  
6 247 and function between different treatments. Taxonomic and functional community data  
7 248 were clustered based on Bray-Curtis [dissimilarity](#) (at the OTU and pathway levels,  
8 249 respectively) using PCoA and dendrogram with complete linkage clustering method.  
9 250 Multivariate differences between groups were assessed using PERMANOVA.  
10 251 Multivariate analysis and plots were performed using *vegan* R package (Oksanen *et*  
11 252 *al.*, 2007). Differential gene expression was analyzed using DESeq2 R package (Love  
12 253 *et al.*, 2014), which includes standardization and normalization procedures as well as  
13 254 negative binomial model testing.  
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## 24 256 **Results**

### 257 **The microbial activity and biomass of floccular and granular sludge** 258 **communities were significantly affected by *B. bacteriovorus* UP predation**

259 The viability of floccular and granular sludge communities was determined by  
260 quantifying microbial activity and total biomass, which were represented by ATP  
261 content and total protein concentration, respectively. The ATP content of the  
262 predator-free controls for both floccular and granular sludge communities increased  
263 gradually whilst the protein content remained similarly over 48 h, indicating that the  
264 control sludge biomass stayed viable during the period of the experiment (Fig. 1). In  
265 the presence of *B. bacteriovorus* UP, the ATP content of the floccular sludge  
266 decreased significantly in the first 24 h of predation compared to the controls without  
267 *B. bacteriovorus* UP ( $P<0.0001$ ) (Fig. 1A). The ATP content of the granular sludge  
268 was also reduced significantly in the first 24 h of predation ( $P<0.0001$ ) and was  
269 further reduced at 48 h ( $P<0.0001$ ) (Fig. 1C). Similarly, the total biomass of both  
270 floccular and granular sludge communities was reduced significantly, ~50% reduction  
271 in protein concentration, when cultured in the presence of *B. bacteriovorus* UP at 24 h  
272 ( $P<0.0001$ ) (Fig. 1B and D). The protein concentration of the floccular sludge was  
273 further reduced to approximately 30% of the predator-free controls at 48 h (Fig. 1B).  
274 In contrast, there was no further biomass reduction after the first 24 h for the granular  
275 sludge incubated with *B. bacteriovorus* UP (Fig. 1D).



276

277 ***B. bacteriovorus* UP predation significantly reduced the viability of floccular and**  
278 **granular sludge communities**

279 To better understand the impact of predators on the viability of the sludge  
280 communities and structural role of biofilms (i.e., loosely aggregated flocs vs. highly  
281 compact granules) against predation, the biomass was stained with the Live/Dead  
282 reagents and quantified by image analysis. As expected, in the absence of added  
283 predators (Fig. 2A ‘-*B. b* UP’), most cells in the floccular sludge community appeared  
284 to be viable (green color) for the 48 h duration of the experiment, with only a few  
285 dead cells visible (red color). The bio-volume of the viable cells gradually increased  
286 from  $2.7 \pm 0.14 \times 10^5 \mu\text{m}^3$  to  $3.2 \pm 0.12 \times 10^5 \mu\text{m}^3$ , whilst the bio-volume of the non-  
287 viable cells,  $< 1.0 \times 10^5 \mu\text{m}^3$ , did not change significantly over the 48 h ( $P > 0.05$ ) (Fig.  
288 2B). The live/dead (L/D) ratios of the floccular sludge community in the predator-free  
289 controls fluctuated between 4-6, suggesting that most of the biomass in the predator-  
290 free controls was viable over the 48 h (Fig. 2C). In contrast, the viability of the  
291 floccular sludge community incubated with *B. bacteriovorus* UP decreased  
292 significantly from  $2.54 \pm 0.17 \times 10^5 \mu\text{m}^3$  at 0 h to  $0.28 \pm 0.03 \times 10^5 \mu\text{m}^3$  at 48 h  
293 ( $P < 0.0001$ ) (Fig. 2A and B, ‘+*B. b* UP’), whilst non-viable cells increased  
294 significantly from  $1.07 \pm 0.11 \times 10^5 \mu\text{m}^3$  at 0 h to  $3.21 \pm 0.22 \times 10^5 \mu\text{m}^3$  at 48 h  
295 ( $P < 0.0001$ ). Correspondingly, the Live/Dead ratios decreased from  $2.71 \pm 0.88$  at 0 h  
296 to  $0.10 \pm 0.05$  at 48 h (Fig. 2C). There was no distinct structural predation pattern  
297 observed where all cells in flocs were found evenly preyed upon by *B. bacteriovorus*  
298 UP (Fig. 2A).

299 Similar results were observed for the granular sludge community, where the  
300 predator-free control was composed predominantly of viable cells over the 48 h (Fig.  
301 3A and B). The bio-volume of viable cells decreased by 34% at 48 h, whilst the bio-  
302 volume of the non-viable cells did not change significantly over the 48 h ( $P > 0.05$ )  
303 (Fig. 3B). The Live/Dead ratios of the granular sludge community in the predator-free  
304 control decreased from  $19.58 \pm 5.96$  at 0 h to  $12.64 \pm 2.37$  at 24 h and eventually to  
305  $9.97 \pm 2.91$  at 48 h (Fig. 3C), suggesting that most cells of the granular sludge  
306 community in the control were viable but that the viability decreased gradually over  
307 time. In contrast, the viability of the granular sludge community incubated with *B.*  
308 *bacteriovorus* UP decreased markedly from  $2.29 \pm 0.09 \times 10^7 \mu\text{m}^3$  at 0 h to  
309  $3.92 \pm 0.28 \times 10^6 \mu\text{m}^3$  at 48 h ( $P < 0.0001$ ) (Fig. 3A and B, ‘+*B. b* UP’), whilst non-



viable cells increased significantly from  $1.47 \pm 0.06 \times 10^6 \mu\text{m}^3$  at 0 h to  $1.66 \pm 0.06 \times 10^7 \mu\text{m}^3$  at 48 h ( $P < 0.0001$ ). Thus, the Live/Dead ratios were reduced by approximately 50 fold in the presence of the predator, i.e.,  $16.04 \pm 4.02$  at 0 h to  $0.25 \pm 0.08$  at 48 h (Fig. 3C). Although most cells in both sludge samples incubated with *B. bacteriovorus* UP appeared to be non-viable, the morphological structures of the floccular and granular sludge were unaffected by predation.

### **Predation pressure results in a significant change in the microbial community composition**

Predation significantly reduced both the viability and total biomass of both floccular and granular sludge communities. Total RNA sequencing of both sludge communities indicated that predation resulted in a shift from high (no predator) to low (with predator) diversity, as determined by Shannon-Wiener diversity analysis of the communities (Fig. S2). Regardless of the sludge type (floccular and granular sludge) and 16S RNA hyper-variable regions used (V4-V7), the diversity of the microbial communities was consistently reduced after *Bdellovibrio* treatment. For example, based on the V5 hyper-variable region of 16S rRNA, the Shannon-Wiener index for the floccular sludge community decreased from  $4.15 \pm 0.34$  to  $3.67 \pm 0.06$  ( $P < 0.05$ ), whilst that of granular sludge community was reduced from  $3.57 \pm 0.11$  to  $2.75 \pm 0.15$  ( $P < 0.01$ ). Generally, the taxonomic composition of both sludge communities was found dramatically affected by predation (Table S1). A principal coordinates analysis (PCoA) indicated that not only was there a significant difference between floccular and granular sludge communities ( $P < 0.001$ ) (Fig. 4, Axis 1), but also between the control and the treated groups in the granular sludge community, where the controls were segregated from the treated cluster (Fig. 4, Axis 2; triangles). For the floccular sludge community, the treatment effect on the overall community composition was not as distinct as for the granular sludge due to the variability amongst the controls, where one control group was clearly different from the other two biological replicates (Fig. 4, Axis 2; circles-red). Despite this, the floccular sludge communities of two of the control groups were clearly separated from the predator treated reactors (Fig. 4, Axis 2; circles), demonstrating the effect of *B. bacteriovorus* UP on both floccular and granular sludge communities.

### **The impact of predation on the individual phylotype in the sludge communities**

The top 200 most abundant TAGs, making up >95% of the sludge community, were selected from the RNA sequence data to investigate the impact of predation on different phylotypes (Table S2). The results showed that members of the *Acidobacteria* (7%, 14 out of 200), *Bacteroidetes* (13%), *Planctomycetes* (4%) and *Proteobacteria* (27.5%) were the predominant groups of identifiable microorganisms in the floccular sludge community (Table S2 - Floccular sludge). Similarly, *Bacteroidetes* (12%), and *Proteobacteria* (28%) were the predominant microorganisms in granular sludge community (Table S2 - Granular sludge). It should be noted that between 35%-45% of both floccular and granular community members that comprised the top 200 most abundant TAGs could not be taxonomically assigned based on the RiboTagger due to the use of short rRNA reads (Table S2).

The relative abundance of each TAG between the ‘treated’ and the ‘control’ groups was log10 transformed. A log10 transformed ratio less than 0 indicates that the relative abundance of the community member was reduced due to the presence of *B. bacteriovorus* UP; whilst a log transformed ratio higher than 0 suggests that the relative abundance of community members increased. More than 90% of the 200 most abundant TAGs for the floccular sludge were reduced in relative abundance ( $\text{Log}_{10}<0$ ) (Table S2 - Floccular sludge). The majority of those clearly taxonomically assigned TAGs that were reduced in relative abundance were *Bacteroidetes* (15 TAGs) and *Proteobacteria* (19 TAGs), some of which were significantly reduced in abundance due to the predation by *Bdellovibrio* ( $P<0.01$ ), such as TAG238 (*Bacteroidetes*) as well as TAG134 and TAG1 (*Proteobacteria*) (Fig. 5A). The 19 *Proteobacteria* TAGs were mainly from the *Alphaproteobacteria*, *Betaproteobacteria* and *Gammaproteobacteria* clades (Fig. 5A). It should be noted that there were also many TAGs in the floccular sludge communities that could not be taxonomically assigned but that were also significantly ( $P<0.01$ ) reduced in relative abundance e.g., TAG42, TAG133 and TAG402 (Fig. 5A).

Similarly, of the 200 most dominant TAGs from the granular sludge communities, > 90% were reduced in relative abundance ( $\text{Log}_{10}<0$ ) upon predation by *B. bacteriovorus* UP (Table S2 - Granular sludge). The majority of those clearly taxonomically assigned TAGs that were greatly reduced in relative abundance were *Bacteroidetes* (21 TAGs) and *Proteobacteria* (52 TAGs) (Table S2 and Fig. 5B). Notably, those TAGs that were significantly reduced in abundance mainly belonged to the *Proteobacteria* clade ( $P<0.01$ ) (Fig. 5B). Similarly, for the granular sludge, a

great number of the TAGs that were sensitive to *B. bacteriovorus* UP could not be taxonomically assigned (Table S2).

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### 381 **The impact of predation on the microbial community function**

382 To determine the impact of predation on microbial community function, mRNA reads  
383 from both sludge communities were extracted and analysed using DESeq2 package by  
384 R. A total of  $27 \pm 1\%$  mRNA reads (randomly subsampled to 847,400 reads per  
385 sample) were mapped to the KEGG pathways, including  $39 \pm 5\%$ ,  $44 \pm 3\%$ ,  $12 \pm 3\%$  and  
386  $6 \pm 1\%$  of the reads assigned to the classes of metabolism, genetic information  
387 processing, environmental information processing and cellular processes, respectively  
388 (Fig. S3). Multivariate analysis revealed that floccular sludge was remarkably  
389 different from the granular sludge in terms of KEGG functions ( $R^2 = 0.23$ ,  $P < 0.01$ ).  
390 The differential expression of several KEGG pathways such as cAMP signaling,  
391 thiamine metabolism, two component systems, etc., distinguished the floccular from  
392 granular sludge communities. In contrast to its impact on community composition  
393 (Fig. 4 and 5), predation had no significant effect on the expression of functional  
394 genes for either the floccular or granular sludge.

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### 396 **Discussion**

397 *Bdellovibrio* species are highly active and mobile predators, which have a broad prey  
398 spectrum, mainly Gram-negative bacteria, and they can feed on planktonic cells as  
399 well as biofilms (Rice *et al.*, 1998, Kadouri & O'Toole, 2005). Whilst the formation  
400 of biofilms, such as floccular and granular sludge, is thought to protect bacteria from  
401 predation by physically excluding the predators through the production of an  
402 extracellular EPS matrix (McSwain *et al.*, 2005, Adav *et al.*, 2008). The effects of  
403 predation by *B. bacteriovorus* UP on individual microbial isolates from activated  
404 sludge were investigated and it was shown that almost all of the Gram-negative  
405 bacteria were sensitive to predation. Dual-species cultures composed of two bacterial  
406 isolates, either in planktonic or biofilm form, were also sensitive to *B. bacteriovorus*  
407 UP (Feng *et al.*, 2016). Additionally, previous work showed that *Bdellovibrio* species  
408 readily preyed upon biofilms developed by single species (Kadouri & O'Toole, 2005,  
409 Dashiff *et al.*, 2011). However, few studies have focused on more complex microbial  
410 communities, such as floccular and granular sludge and therefore, these were

investigated here to determine the impact of predation on floccular and granular sludge communities from the isolation site of *B. bacteriovorus* UP.

It has previously been suggested that the granular sludge, which is more compact and has a higher unit volume of EPS than floccular sludge, should be generally better protected bacteria from other microbial predators, such as bacteriophages and protozoa relative to floccular sludge (Weber *et al.*, 2007, Adav *et al.*, 2008). However, it has been shown that viral predation can significantly modify both microbial biomass production and granular sludge community composition and that this also affected the biomass and energy transfer in the ecosystems (Suttle, 1994, Fuhrman, 1999, Koskella & Brockhurst, 2014). Not only did bacteriophage infection alter the sludge community composition, but it also strongly affected the sludge performance (Barr *et al.*, 2010). The effects of protozoan grazing on microbial communities and their performances were also well documented (Pauli *et al.*, 2001, Huws *et al.*, 2005, Matz & Kjelleberg, 2005, Yu *et al.*, 2011). For example, protozoan predation was shown to cause a clear population shift of nitrite-oxidizing bacteria, however, the nitrification performance of the microbial community was not significantly affected and this may be due to redundancy of nitrite oxidation capacity in other community members (Yu *et al.*, 2011).

The data presented in this study showed that biofilms and microbial communities were generally not protected from the predation by *B. bacteriovorus* UP. Indeed, both floccular and granular sludge communities seemed equally sensitive to predation. This was reflected in the significant reductions in microbial biomass, ATP content and Live/Dead staining (Figs. 1-3). The ATP results at 48 h for floccular sludge seem to contrast with viability as assessed using the Live/Dead staining reagents (Fig. 1A and Fig. 2A). This could be due to the recovery of the floccular sludge community over time (Barr *et al.*, 2010). Alternatively, the increase of ATP content after 48 h could be attributed to the growth of *B. bacteriovorus* UP associated with the floccular biomass or in the liquid space surrounding the floccular sludge. ATP measurements should comprise both sludge and supernatant, and hence if there are any free-swimming *Bdellovibrio* in the supernatant, they will be captured by the ATP assay. This is supported by the RNA sequence data, which indicated that there was 46 times more *Bdellovibrio* sequencing reads associated with the floccular sludge compared to the granular biomass at the end of the experiment despite being seeded with equal numbers of the predator (Table S1). While the number of *Bdellovibrio* was not

determined at the beginning of the experiments, comparison of the treated and non-treated reactors shows a 100 fold increase in *Bdellovibrio* reads (Table S1). In contrast, the numbers of *Bdellovibrio* reads detected for the granular sludge were considerably lower than for the treated floccular biomass and this may correlated with the lower ATP concentration detected at 48 h (Table S1).

For the granular sludge, it was observed that, even for the predator-free controls, the interiors of the granules were unstained, either by the SYTO9 or propidium iodide reagents. Whilst it is possible that the granules were hollow (Ma *et al.*, 2006, Koh *et al.*, 2007), this was more likely due to limited penetration of the reagents or the excitation light into the granule interior (usually deeper than 80-130  $\mu\text{m}$ ) (Saiki *et al.*, 2002). Further work using FISH and cryo-sectioning of granules would be helpful in resolving these possibilities. Nonetheless, it was clear that the surface and near surface regions were highly susceptible to the predation by *B. bacteriovorus* UP. Therefore, compared with protozoan grazing and viral lysis of microorganisms (Matz & Kjelleberg, 2005, Kay *et al.*, 2011), *B. bacteriovorus* UP showed stronger predation effects on complex microbial communities (Figs. 4 and 5).

Total RNA sequencing analysis additionally demonstrated that predation significantly affected the sludge communities. In this study, a fast and unbiased 16S profiling method, the RiboTagger was used to determine the community composition (Xie *et al.*, 2016). Unlike Methaphlan2 that uses marker genes for taxonomic classification with high resolution and is particularly useful for metagenomic samples, the RiboTagger that based on the highly abundant 16S rRNA sequences for community profiling was found to be more suitable and reliable for our RNA sequencing study (with high rRNA and less mRNA reads). Despite the differences in taxonomic resolution, both RiboTagger and Methaphlan2 demonstrated a strong correlation between community dissimilarities (Bray-Curtis) (Mantel test;  $r=0.75$ ,  $p < 0.001$ ), suggesting that both methods detected similar trends in the community changes (Data not shown). Subsequent sequencing analysis based on the RiboTagger using the Silva rRNA database indicated that most TAGs could be identified using the V5 region, which also had the highest number of high quality reads compared to other regions (Table S1). Irrespective of the variable region used, it was observed that both floccular and granular sludge communities were significantly reduced in microbial diversity after the predation by *B. bacteriovorus* UP as shown by the Shannon-Wiener index (Fig. S2). Therefore, the V5 region was used for subsequent analyses.



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The reductions in the granular community diversity were more striking than for the floccular communities (Table S1 and Fig S2). This might be related to the inherent differences in community composition between flocs and granules in that communities with more diverse compositions (i.e., floccular sludge) might better withstand predation pressure (McCann, 2000, Girvan *et al.*, 2005, Erkus *et al.*, 2013). It was shown here that most TAGs were primarily assigned to the classes of *Proteobacteria* and *Bacteroidetes*, which were also consistent with bacterial groups identified in other activated sludge communities (Wagner *et al.*, 2002, Kong *et al.*, 2007, Mahendran *et al.*, 2012). Within these classes, many bacterial groups, such as ammonia-oxidizing bacteria, nitrite-oxidizing bacteria, phosphate accumulating bacteria, as well as bacteria that hydrolyze diverse organic matter in wastewater, are responsible for essential functions, including nutrient and carbon removal (Wagner *et al.*, 2006, Kong *et al.*, 2007). Some members of these functional bacterial groups in the activated sludge communities in this study, such as *Nitrospira* (containing nitrite-oxidizing bacteria) and *Acinetobacter* (containing phosphate accumulating bacteria) (Daims *et al.*, 2006), were dramatically reduced in their relative abundance due to predation by *B. bacteriovorus* UP. Therefore, the biological removal of nitrogen and phosphate by activated sludge community may potentially be reduced correspondingly. To address this question, the mRNA data was extracted from the total RNA sequencing reads and analysed to determine if predation had significant impact on reactor performance, as indicated by changes in gene expression. Unlike the dramatic changes in sludge community diversity after predation (Fig. S2), there was very little difference in the community level expression of functional genes between the controls and treated samples for either floccular or granular sludge (Fig. S3). A detailed analysis on specific community functions, such as carbon and nitrogen metabolism, also showed no significant difference between control and treated sludge samples (Fig. S3). Further, when we compared the expression profiles of genes involved in SNDPR (i.e., carbon, nitrogen and phosphorus metabolism) between the floccular and granular communities, we observed no differences in gene expression between the two sludge types, even though they have distinct taxonomic profiles. This may not be surprising since many different organisms may contribute to carbon or nutrient removal, the genetically encoded functional redundancy of these diverse communities may mask the effect of *Bdellovibrio* predation on individual species and



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3 513 therefore retaining the sludge functions for nutrient removal. Finally, low numbers of  
4 514 *Bdellovibrio* sequencing reads, representing less than 0.02% of the community, were  
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6 515 observed in the control reactors and reflects their natural abundance levels. Given that  
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8 516 these were 1000 fold lower than the reactors that were seeded exogenously with the  
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10 517 predator, it is possible that there is also an important density or predator-prey ratio  
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12 518 that is required for the predator to impact the community dramatically, which should  
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14 519 be investigated in subsequent experiments.

15 520 *Bdellovibrio* predation upon both floccular and granular activated sludge can  
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17 521 significantly alter microbial community composition. Even so, the effects of predation  
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19 522 by *Bdellovibrio* on the performance of sludge community in more complex systems,  
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21 523 such as sequencing batch reactors and even full-scale systems are largely unknown.  
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23 524 Additionally, the operational conditions for both floccular and granular sludge may  
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25 525 not favor the proliferation of *Bdellovibrio* species. For example, such systems include  
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27 526 periods of anoxic or anaerobic incubation, which are unfavourable to *Bdellovibrio*  
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29 527 spp. Therefore, further studies on the impact of *Bdellovibrio* on waste-water systems  
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31 528 might sample the different incubation tanks or stages as well as quantify the predators  
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33 529 numbers and activity in those stages as well as undertaking such experiments over a  
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35 530 much longer time frame.

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37 531 In this study, the effects of predation by *B. bacteriovorus* UP on highly complex  
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39 532 microbial community that formed both floccular and granular activated sludge were  
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41 533 studied. It was shown that *B. bacteriovorus* UP exerted a significant impact on these  
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43 534 microbial communities, in terms of biomass, viability and community composition.  
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45 535 This shows that *B. bacteriovorus* UP is a generalist predator that can have broad  
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47 536 impact on the microbial communities (Jurkevitch *et al.*, 2000). Interestingly, while the  
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49 537 community composition was dramatically altered by *Bdellovibrio* predation, there  
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51 538 were limited changes in community functions based on mRNA expression, suggesting  
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53 539 functional redundancy and high levels of resilience within sludge communities under  
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55 540 predation pressure. It will be interesting to determine if longer-term predation  
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57 541 experiments may alter the community functions and responses and if the community  
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59 542 was able to recover from such perturbations.  
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For Peer Review



## Figure Legends

**Fig. 1** Effects of predation by *B. bacteriovorus* UP on microbial activity and total biomass of communities in floccular and granular sludge. Microbial activity was represented as ATP relative luminescence unit for (A) floccular and (C) granular sludge, respectively; and total biomass was represented as protein concentration in (B) floccular and (D) granular sludge, respectively. Sludge was incubated in the absence (negative control, ■) and presence (treatment, □) of *B. bacteriovorus* UP. Data represent the means of three independent replicates. Error bars represent the standard deviation. Two-way ANOVA was performed and Sidak post-tests were conducted to compare each treatment to the negative control where significant differences were indicated as follows: \*  $P < 0.05$ , \*\*\*\*  $P < 0.0001$ .

**Fig. 2** Effects of predation by *B. bacteriovorus* UP on the viability of floccular sludge. **A.** Floccular sludge was incubated over 48 h in the absence and presence of *B. bacteriovorus* UP. Viable cells were shown in green (SYTO9 stained), whilst non-viable cells were shown in red (PI stained). Confocal microscopy images were taken at 200× magnification. Scale bars represent 500 µm. **B.** Bio-volumes of viable (live) and non-viable (dead) communities in floccular sludge incubated in the absence (negative control, ■ and □ respectively) and presence (treatment, ■ and ■, respectively) of *B. bacteriovorus* UP. **C.** The ratio of live/dead communities in predator-free controls (■) and *Bdellovibrio*-treated groups (□). Data represent the means of multiple replicates (n=30). Error bars represent the standard deviation. Two-way ANOVA was performed and Sidak post-tests were conducted to compare each treatment to the negative control where significant differences were indicated as follows: \*  $P < 0.05$ , \*\*\*\*  $P < 0.0001$ .

**Fig. 3** Effects of predation by *B. bacteriovorus* UP on the viability of granular sludge. **A.** Granular sludge was incubated over 48 h in the absence and presence of *B. bacteriovorus* UP. Viable cells were green (SYTO9 stained), whilst non-viable cells were red (PI stained). Confocal microscopy images were taken at 200× magnification. Scale bars represent 500 µm. **B.** Bio-volumes of viable (live) and non-viable (dead) communities in granular sludge incubated in the absence (negative control, ■ and □ respectively) and presence (treatment, ■ and ■, respectively) of *B. bacteriovorus* UP. **C.** The ratio of live/dead communities in predator-free controls (■) and *Bdellovibrio*-

774 treated groups ( $\square$ ). Data represent the means of multiple replicates (n=20). Error bars  
775 represent the standard deviation. Two-way ANOVA was performed and Sidak post-  
776 tests were conducted to compare each treatment to the negative control where  
777 significant differences were indicated as follows: \*  $P<0.05$ , \*\*\*\*  $P<0.0001$ .

778 **Fig. 4** Principal coordinates analysis (PCoA) showing the alterations of microbial  
779 communities in floccular (circle) and granular (triangle) sludge incubated in the  
780 absence (control; cyan) and presence (treatment; red) of *B. bacteriovorus* UP. The  
781 data were square root transformed and similarities among communities were  
782 computed based on the Bray-Curtis [dissimilarity](#). Data represented three independent  
783 replicates. PERMANOVA was performed using R. Factors including type of sludge  
784 (floccular vs. granular sludge) and *B. bacteriovorus* UP treatment (control vs.  
785 treatment) contributing to the community differences were indicated as follows: the  
786 interaction between type and treatment ( $R^2 = 0.07$ ;  $P<0.01$ ), the main effect for type  
787 ( $R^2 = 0.81$ ;  $P<0.001$ ) and for treatment ( $R^2 = 0.04$ ;  $P>0.05$ ).

788 **Fig. 5** Effects of predation by *B. bacteriovorus* UP on the dominant microbial taxa in  
789 (A) floccular and (B) granular sludge. The  $\text{Log}_{10}$  of the ratios of sequencing reads of  
790 *Bdellovibrio*-treatment group to negative control were calculated for each TAG.  
791 [TAGs that were unidentified by the RiboTagger were subjected to comparison against](#)  
792 [NCBI-nr database and the closest relative with > 97% sequence identity are shown](#)  
793 [where applicable](#). Data represent the means of three biological replicates, with error  
794 bars representing the standard deviation. Multiple *t*-test was performed with 1% false  
795 discovery rate to compare each treatment to the negative control where significant  
796 differences were marked with ‘\*’.

797 **Supporting Information**

798 **Fig. S1** The activated sludge samples used in this study. Floccular sludge (A) and  
799 granular sludge (B) were observed with stereotypic microscopy (Stereo V8, ZEISS).  
800 Images were taken at 10 $\times$  magnification. Scale bars represent 500  $\mu\text{m}$ .

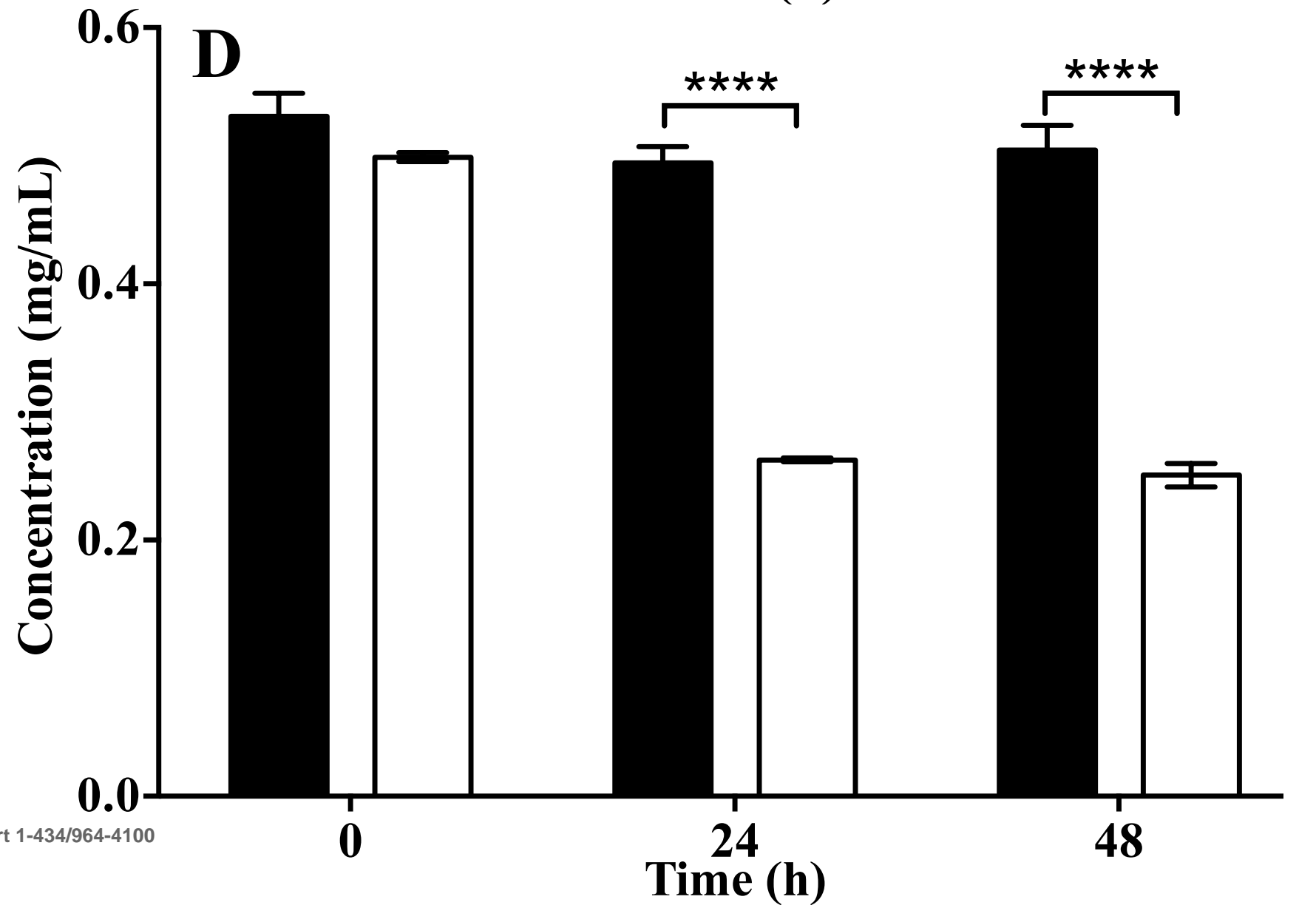
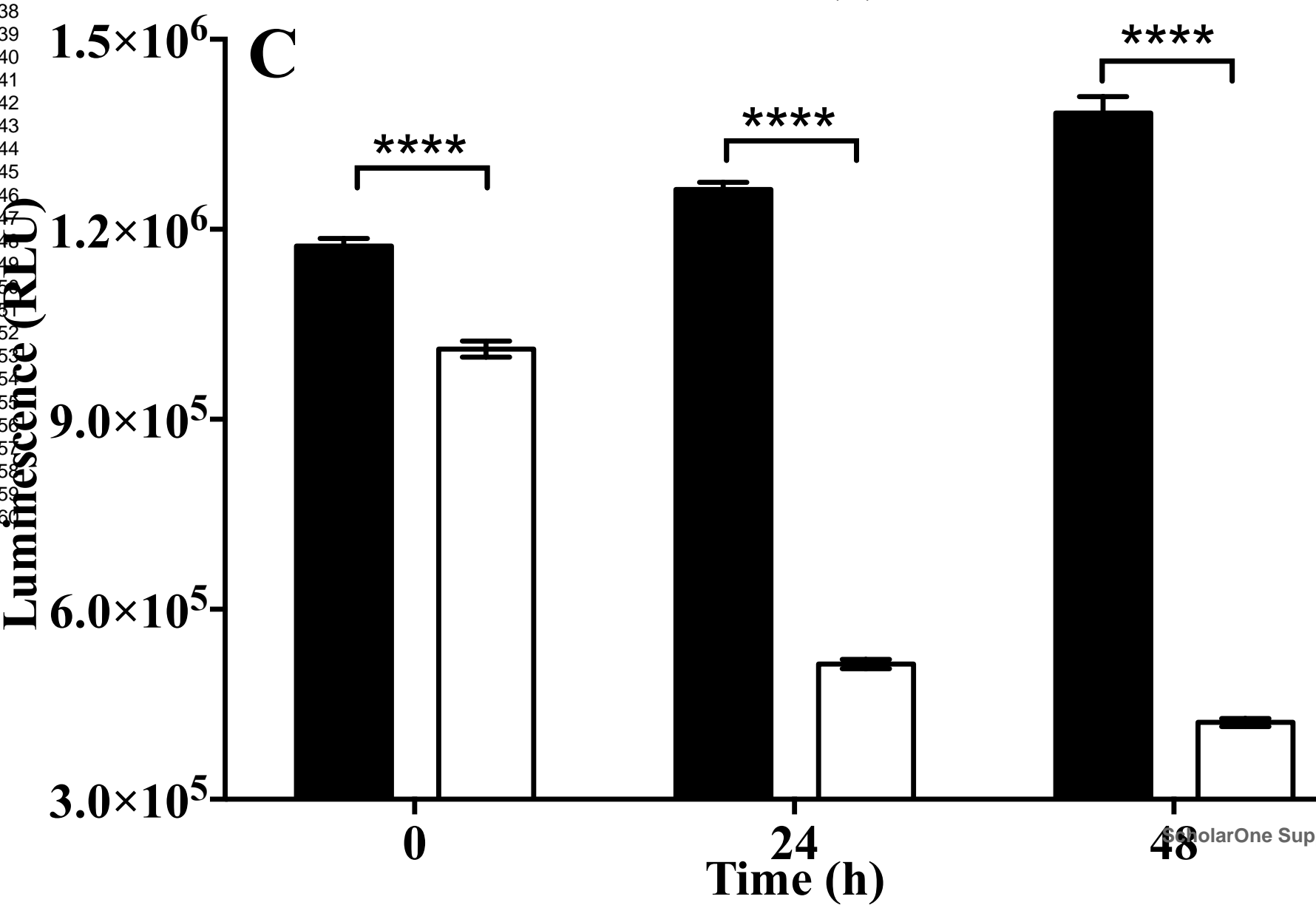
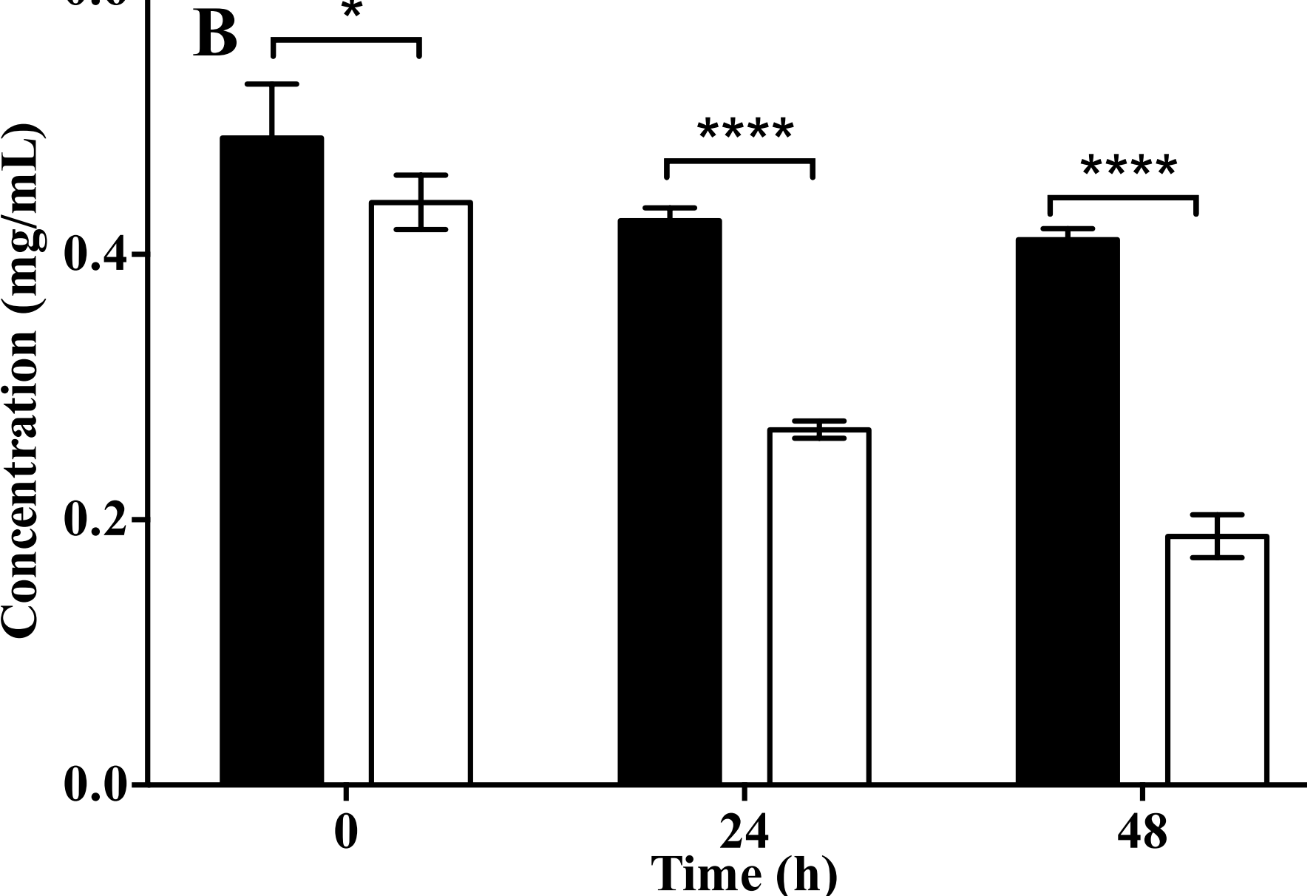
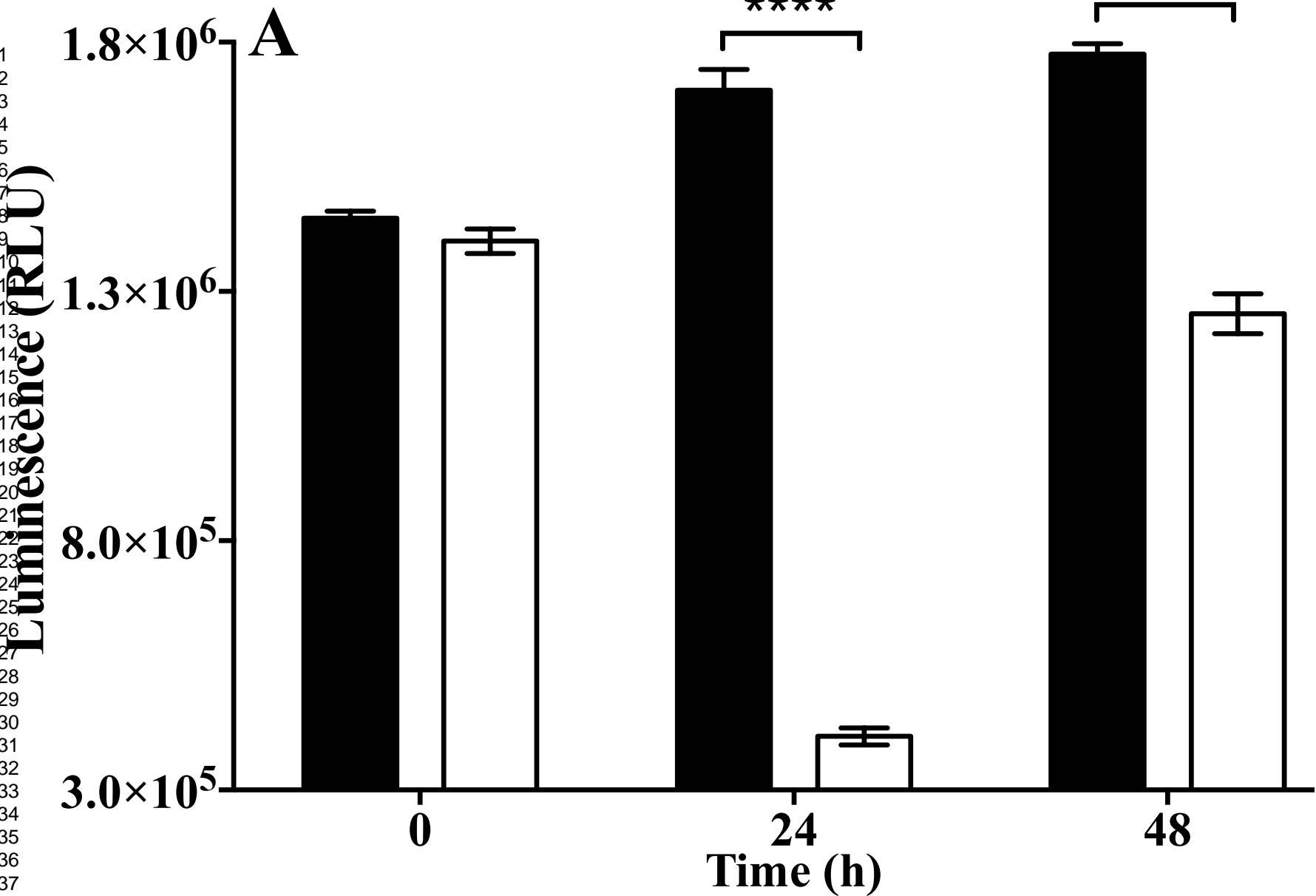
801 **Fig. S2** Comparison of alpha diversities of floccular and granular sludge community  
802 in the absence and presence of *B. bacteriovorus* UP. The alterations of community  
803 diversity were investigated into each hyper-variable region V4-V7. Diversity was  
804 measured by Shannon-Wiener index. The top and bottom boundaries represented the  
805 75<sup>th</sup> and 25<sup>th</sup> quartile values. Two-way ANOVA was performed, followed by Sidak

post-tests to examine differences between ‘control’ and ‘treated’ groups, where significant differences were indicated as follows: \*  $P < 0.05$ , \*\*  $P < 0.01$ .

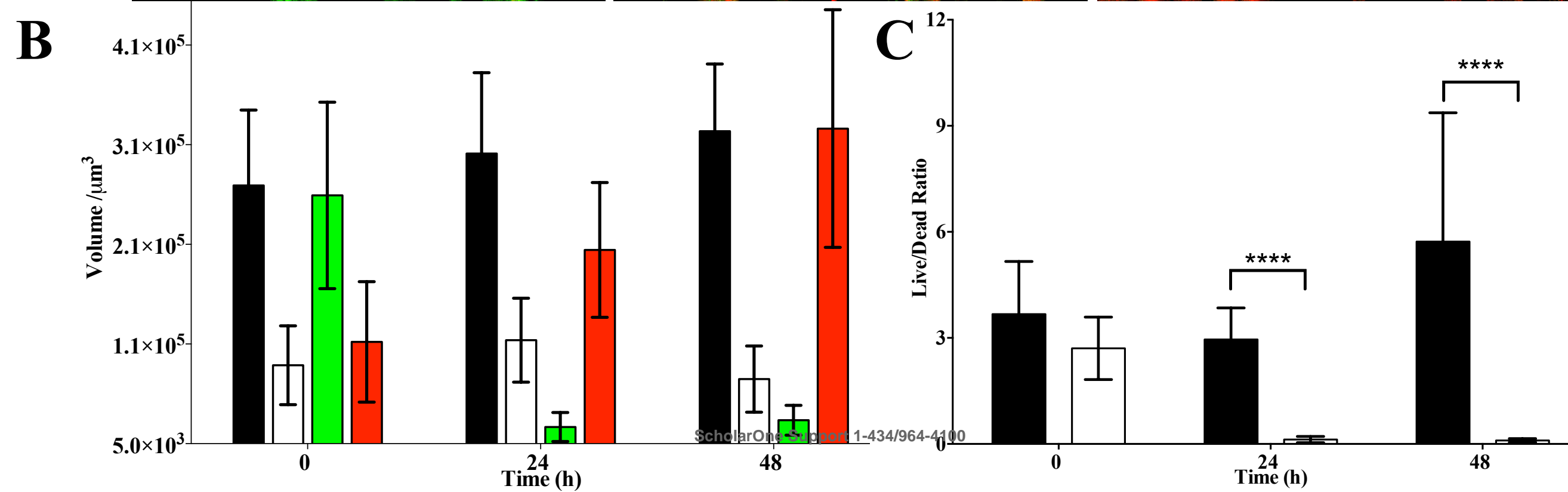
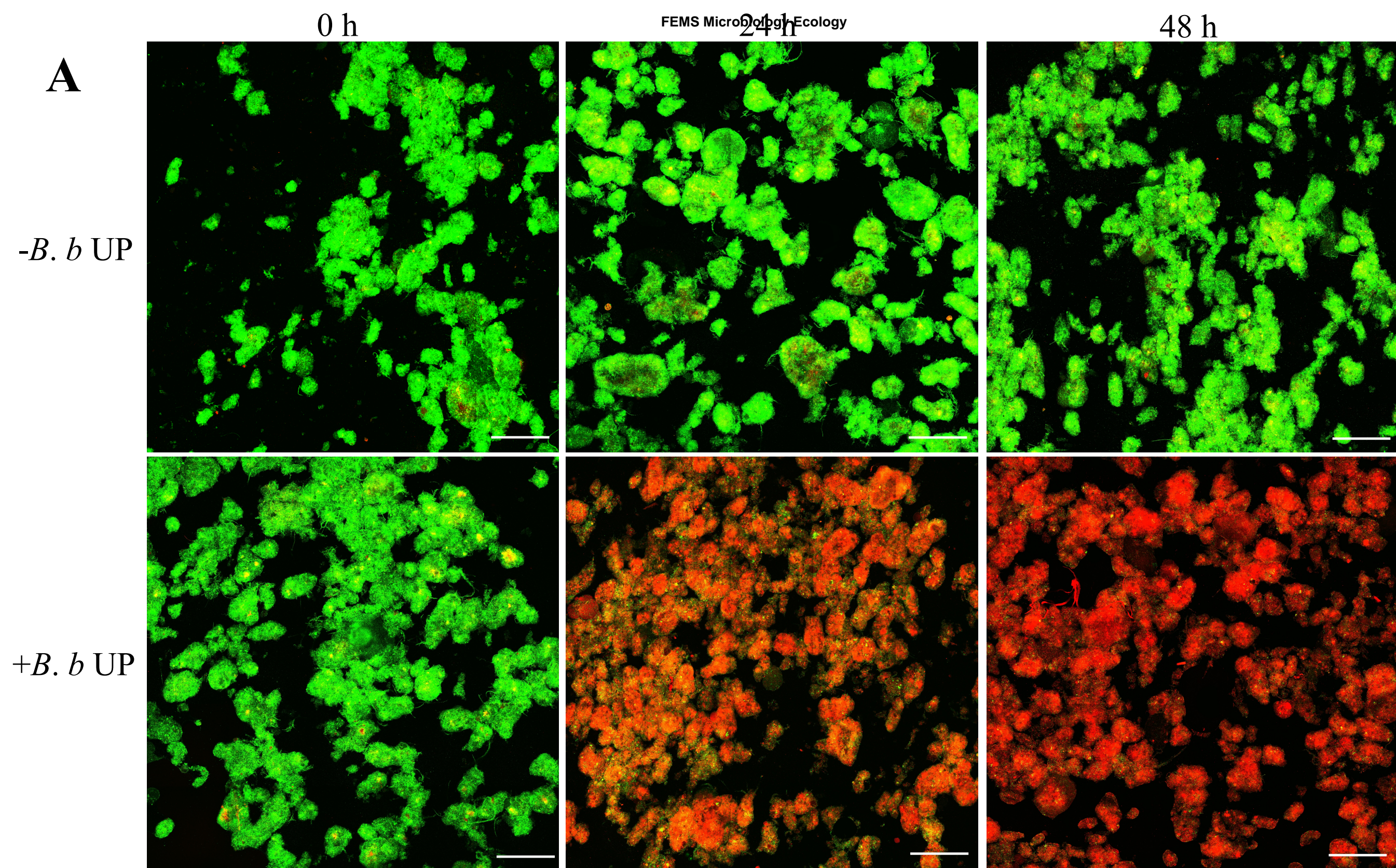
**Fig. S3** Unsupervised clustering of the sludge samples based on the KEGG pathway expression. Similarities among samples were computed based on the Bray-Curtis dissimilarity and clustered using complete linkage. Log10Mean indicates the overall relative abundance of the reads assigned to a particular pathway. As differential expression tests only reported significant differences between sludge and granules samples, the Log2 fold change (log2FC) sign was reported to highlight those pathways that were significantly differentially expressed between Granules vs. Floccular sludge samples ( $p < 0.05$ ). Data represented three independent biological replicates.

**Table S1** 16S rRNA sequence data including hyper-variable regions V4-V7 extracted by RiboTagger scripts.

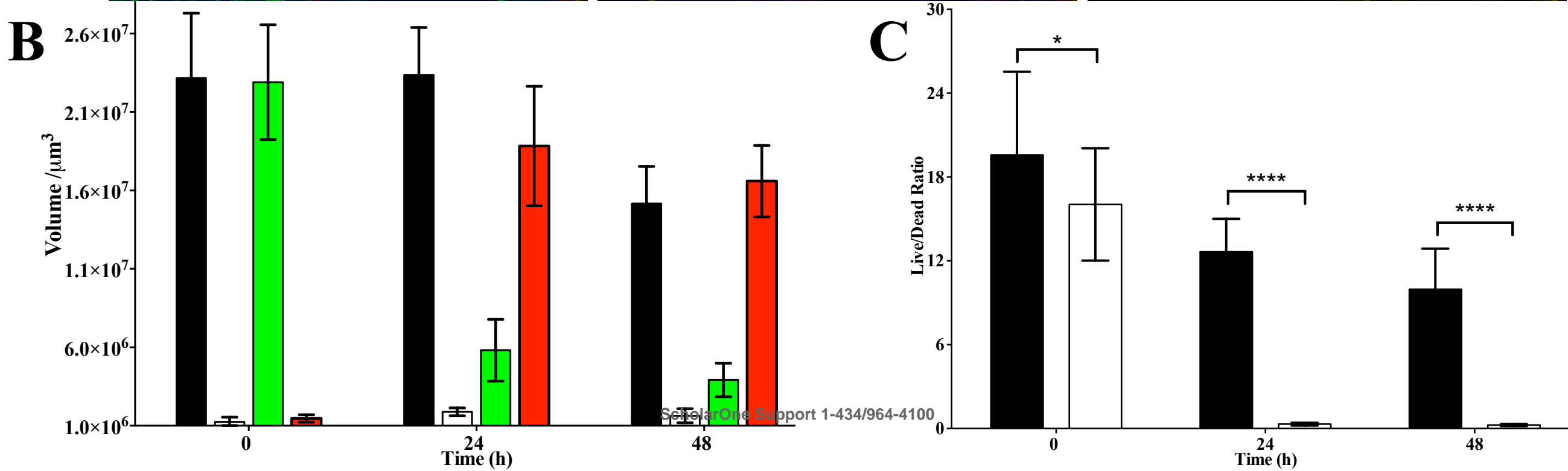
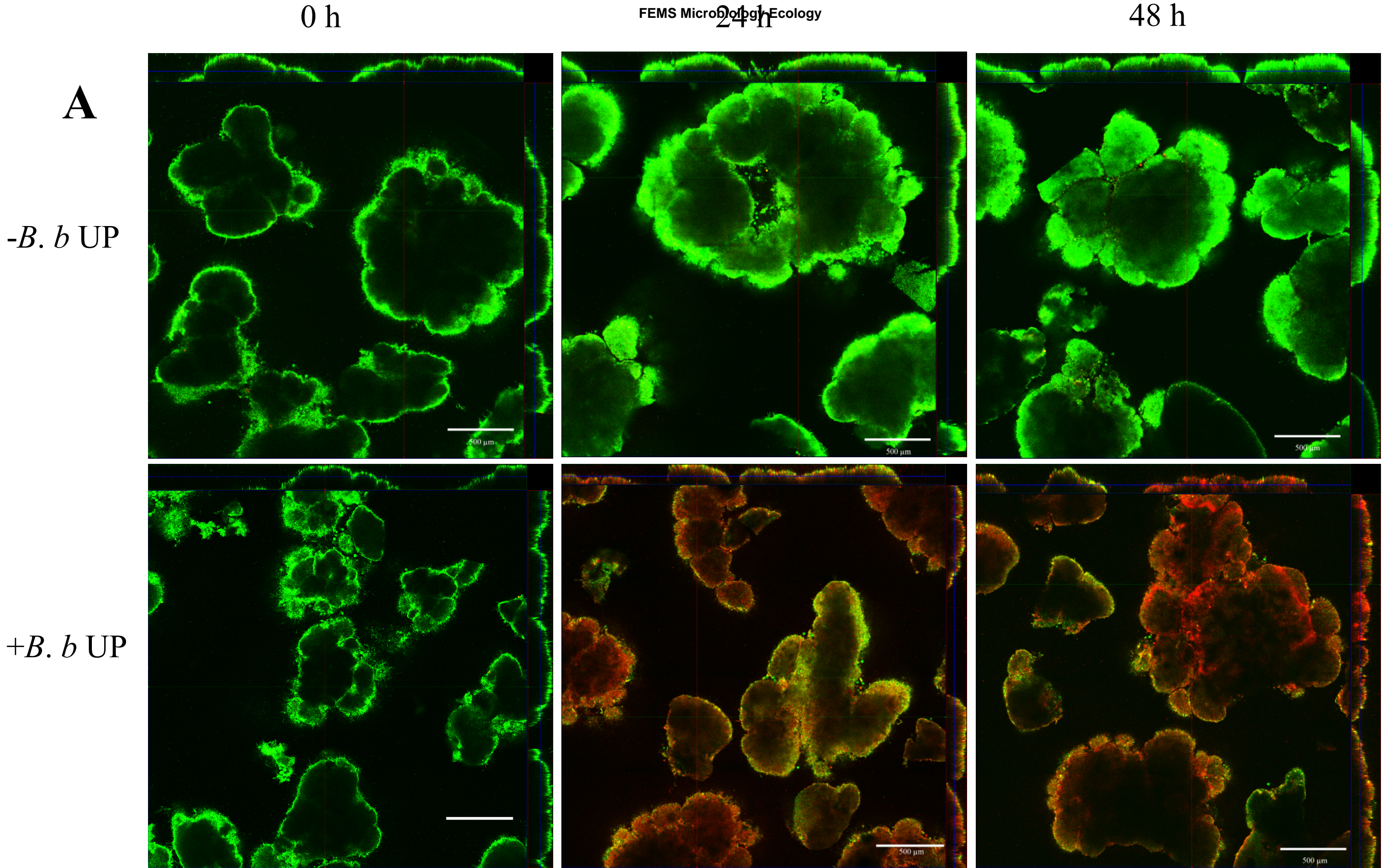
**Table S2** The top 200 TAGs of microorganisms making up >95% of the microbial community in both floccular and granular sludge.



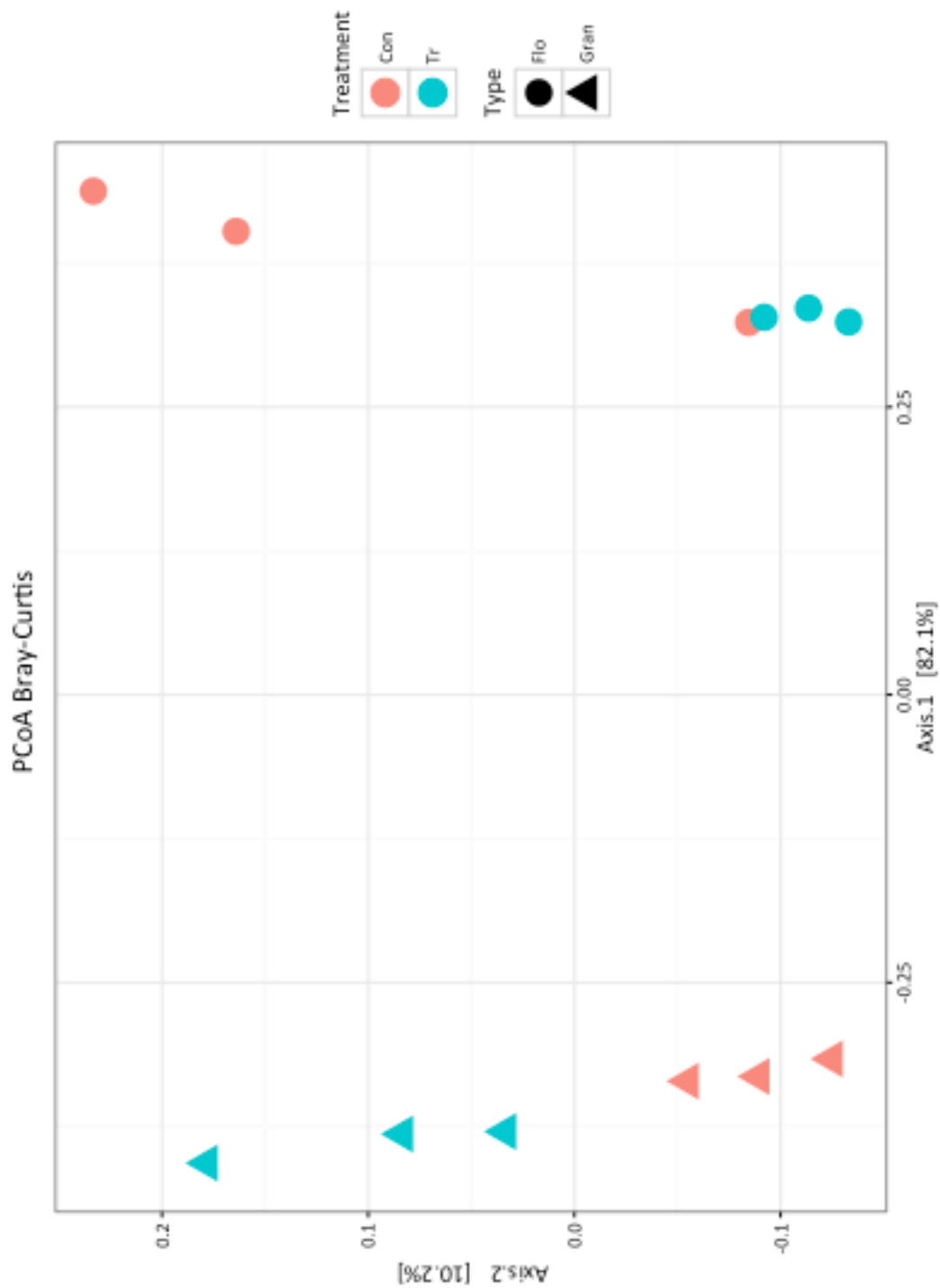








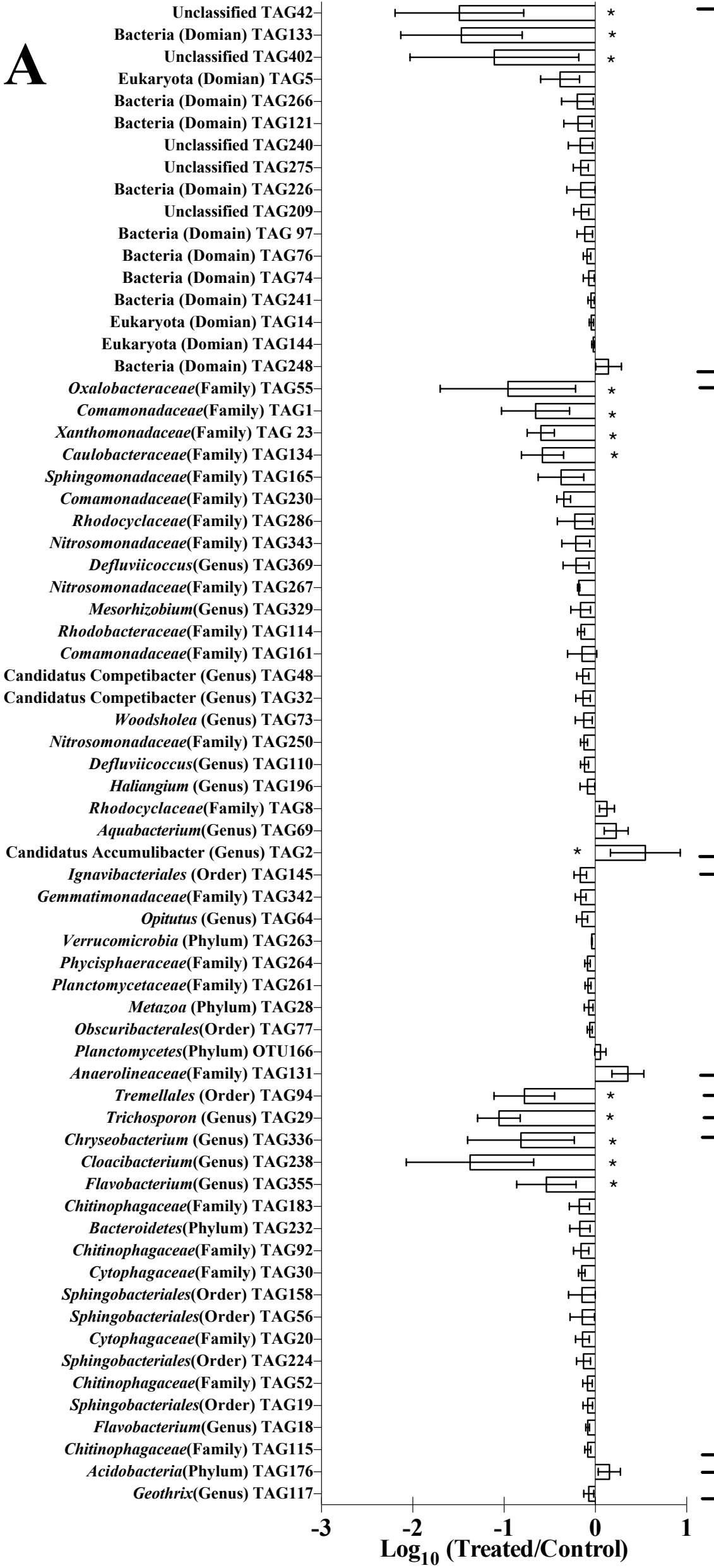






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FEMS Microbiology Ecology

Unidentified  
TAGs

Proteobacteria

Other  
Bacteria

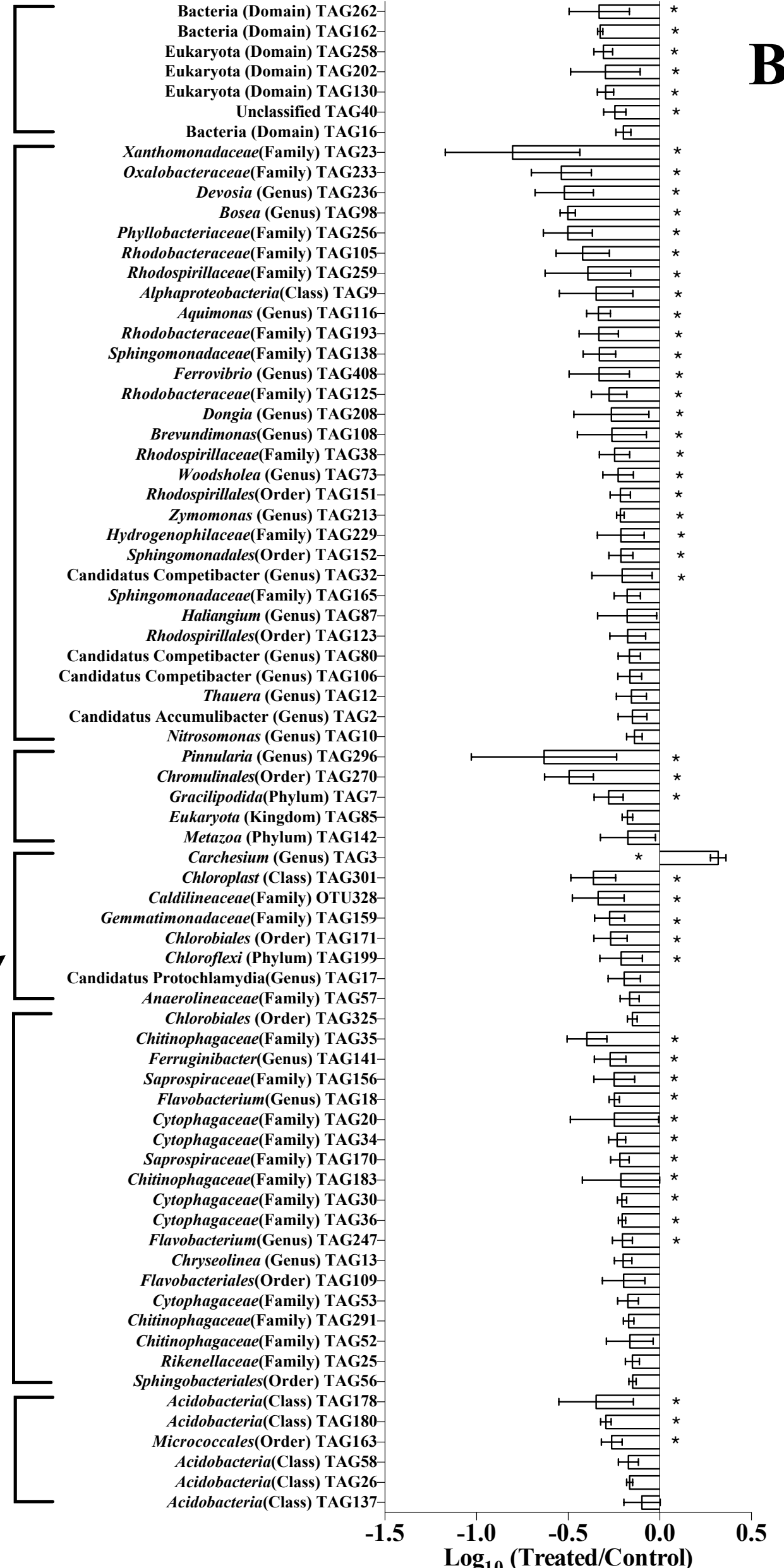
Eukaryota

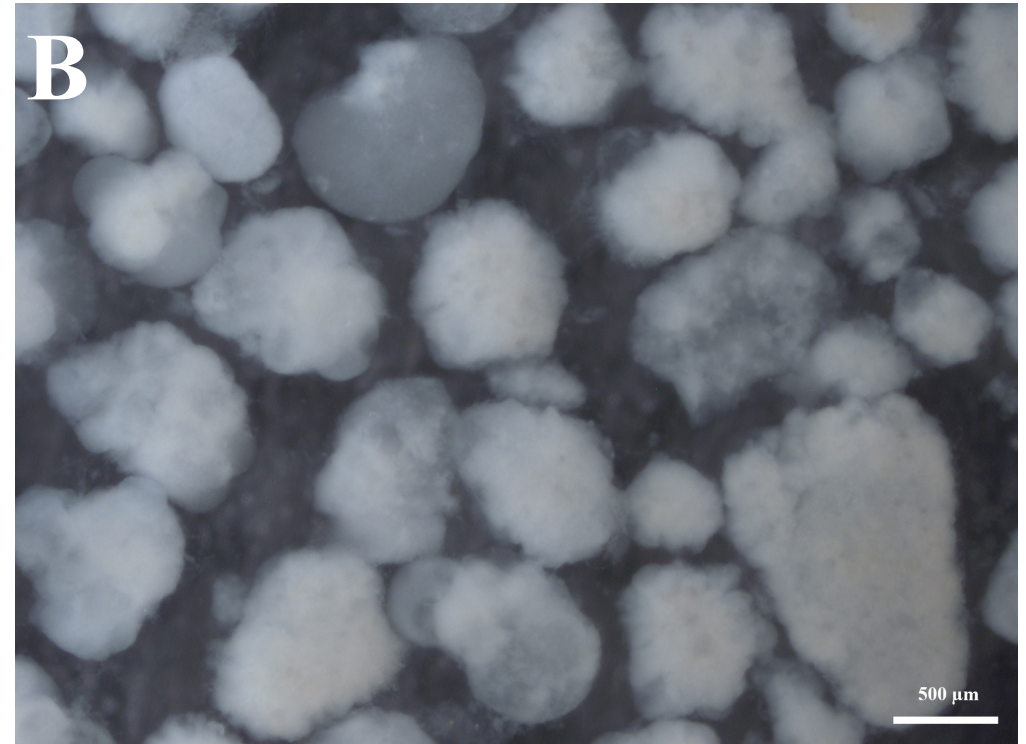
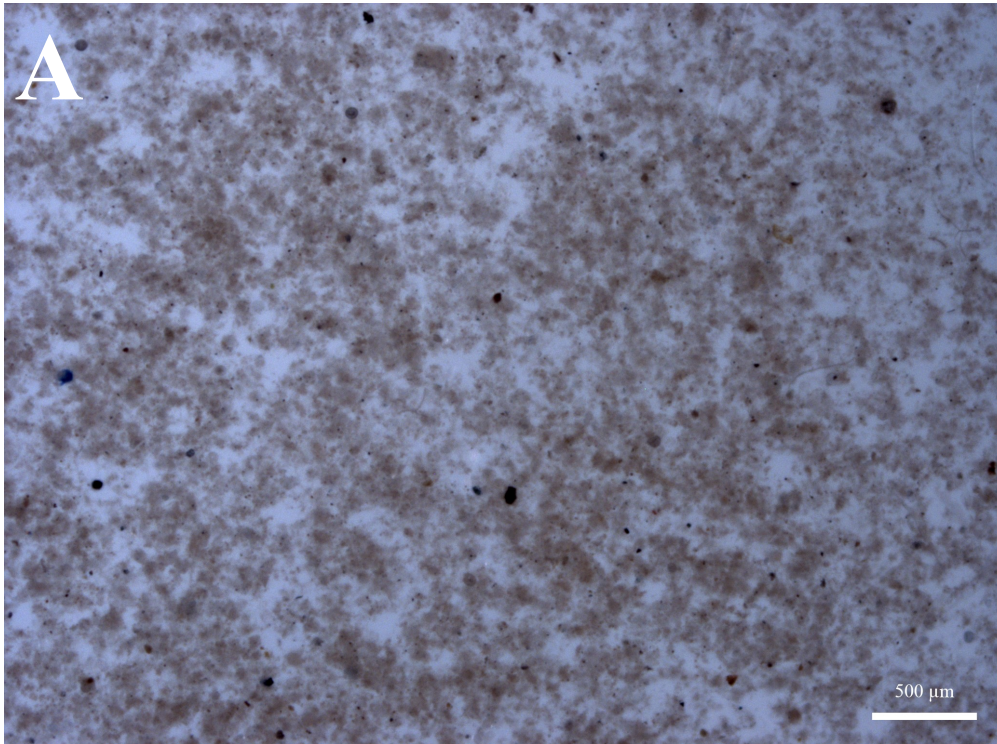
Bacteroidetes

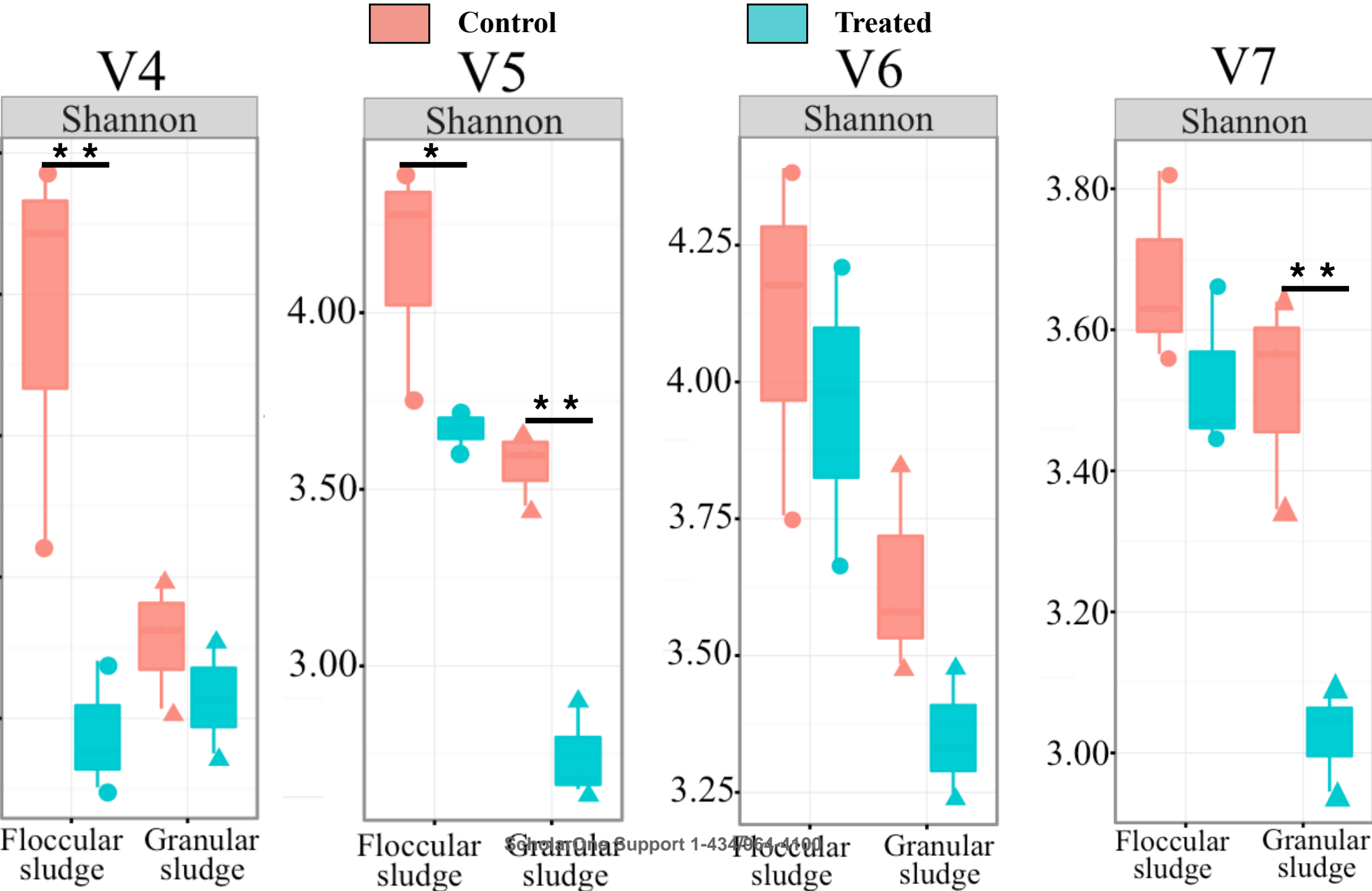
Acidobacteria

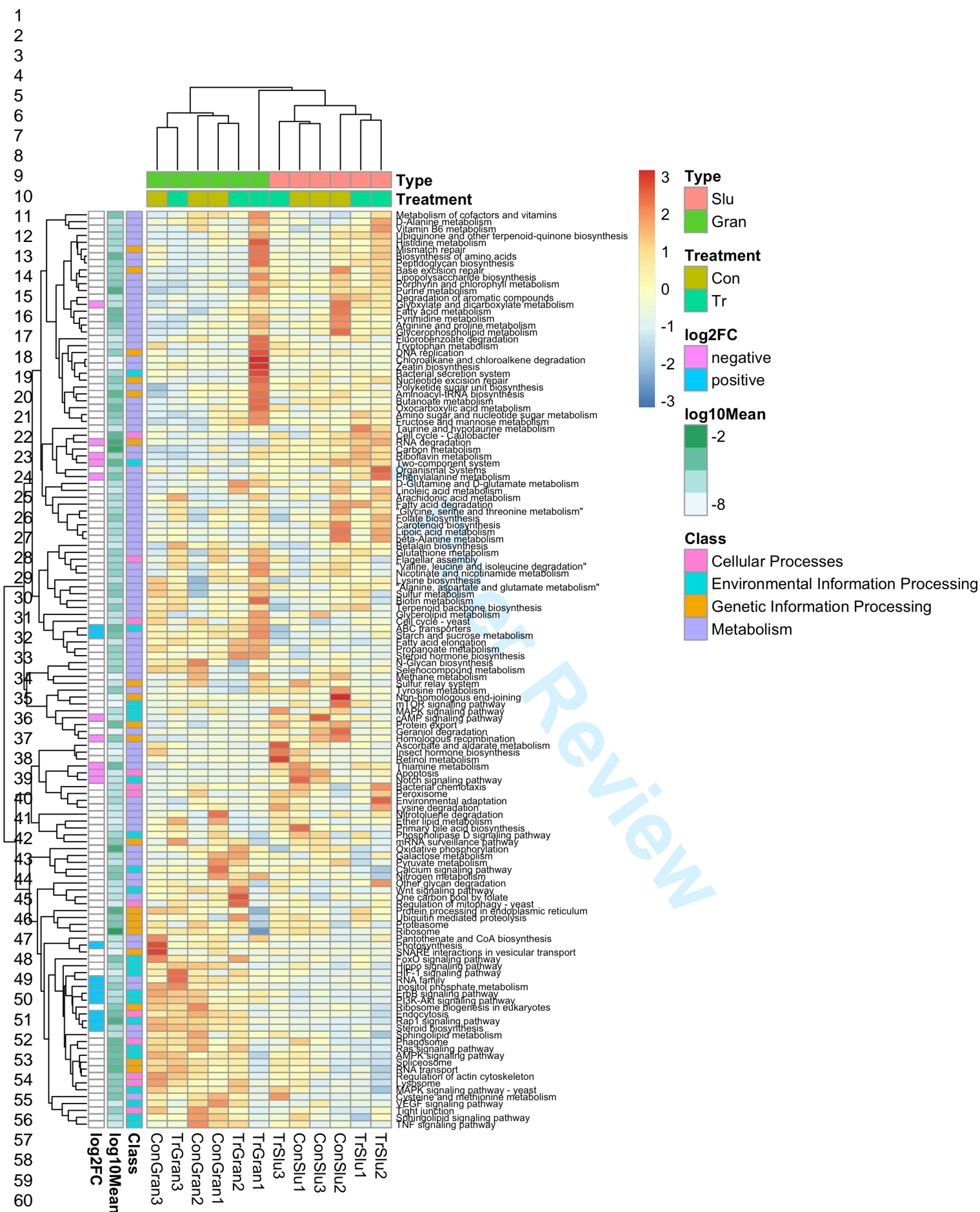
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tag	Flocs Control 1	Flocs Control 2
TTTTGTAAGACAGTGGTGAAATCCCCGGGCTCA	0	3
TTGGGTAAGTCAGATGTGAAATCCCCGGGCTCA	13218	1695
CTTTGTAAGTCAGGTGTGAAAGCCTGGGGCTCA	208	55
CCTGACAAGTCTGATGTGAAAGACCTGGGCTTA	0	4
TGATGTAAGACAGATGTGAAATCCCCGGGCTCA	5759	5986
TTTTTTAAGACAGGCGTGAAATCCCCGGGCTTA	3044	2481
CTCGAAAAGCGTTCCTGTGAAATCCCCCGGCTCA	241	426
CTTGCCAAGTGCTTTGTGAAATCCCACGGCTCA	6237	3502
TTTTGTAAGACAGATGTGAAATCCCCGGGCTTA	1534	828
AACATCTCACACATTGATGTGAGACGGAGGCGG	2	0
AACAACCTCACACATTGATGTGAGACGGAGGCGG	0	0
AACAACCTCATTCAAGTCAATTGATTGAGACGGAG	0	0
TTTGGTCAGTCAGCCGTGAAAGCCCCGGGCTTA	128	253
TTTGGTAAGTCAGATGTGAAATCCCCGGGCTCA	1152	1473
AACAACCTCATTCAATGAGTGAGACGGAGG	0	0
TTCGTTAAGTCTGATGTGAAAGCCCTGGGCTCA	1163	2044
AACAACCTCATTGTAAAAGATGAGACGGAGGCGG	0	0
TCAGACTAAGTCGAATGTAAAATACCAAGGCTT	8	0
GAATGTAAGTCAGACGTGAAATCCCGGAGCTCA	0	0
CCCTGTAAGTCAGTGGTGAAATATCTCAGCTTA	0	0
TGCTGTAAGTCAGATGTGAAATCCCCGGGCTTA	869	592
TTTGATAAGTCAGATGTGAAATCCCCGGGCTCA	909	1316
TTTGGTAAGTCAGATGTGAAAGCCCCGGGCTCA	297	221
TCTTTCAAGCGTCTGTGAAAGCCTCCGGCTCA	701	1730
TTTTGTAAGTCAGATGTGAAATCCCCGGGCTTA	561	558
TTTGGTAAGACAGGCGTGAAATCCCCGGGCTCA	1090	1357
TTTGGTAAGCCTTCTGTAAAGCTTCGGGCCCA	489	888
TTTCGGGCTGAGCTGTGAAGGCTCACCGCAAGG	118	149
TTATGCAAGACAGATGTGAAATCCCCGGGCTCA	379	1939
TTATGTAAGACAGATGTGAAATCCCCGGGCTCA	1131	792
CTTGGCAAGTCAGATGTGAAAGCCCATGGCTTA	456	496
TTTGTAAGACAGTGGTGAAATCCCCGGGCTCAA	0	0
TAATATAAGTTGGGCGTGAAACCTCTGAGCTTA	0	0
TTTGTCGCGTCTGCTGTGAAAACCTCGGGGCTTA	431	884
TTCGGTCAGTCAGCCGTGAAAGCCCCGGGCTCA	154	170
TATGATAAGTCAGGTGTGAAATCCCGGGGCTCA	0	0
TCGTGCAAGACAGATGTGAAATCCCCGGGCTTA	841	484

TTTGCCAAGTTTGGTGTGAAATCTCCCGGCTTA	793	1099
TTTTCCAAGTTGGATGTGAAAGCCTTGAGCTCA	936	1039
CCCTGTAAGTCAGTGCTGAAATATCCCGGCTTA	924	835
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TTGTGTAAGACAGGTGTGAAATCCCCGGGCTTA	443	1097
CTTCGGGCTGGGCTGTGAAGGCTCATCGCAAGG	8	5
TTAGATAAGTCAGTGGTGTGAAAGCCCATCGCTCA	0	0
CTTCGTAAGACAGAGGTGAAATCCCCGGGCTCA	618	956
CTCTTTAAGTCAGACGTGAAAGCCCTAGGCTTA	655	778
CTTTTCAAGTCAGAGGTGAAATCCCCAGGCTCA	16	11
AACAGCTCATTGTAAAAGATGAGACGGAGGCGG	0	0
TTTGTGCGCTCTGCAGTGAAATCCGGGGCTCA	0	0
CCTTGTAAGTCTTGTGTGAAAGCCCTCGGCTTA	603	407
CTTTGTAAGACAGGTGTGAAATCCCCGGGCTTA	411	1024
CGCCATAAGACAGCTGTGAAATCCCCGGGCTTA	404	950
TTTGTTAAGTCTGCTGTGAAATCCCCGGGCTCA	475	1349
CTTGGTAAGTCAGGGGTGAAAGCTTCCCGCTCA	478	683
CTTCTTAAGCCAGACGTGAAATCCCCGAGCTTA	0	0
CTTGGCAAGTGAGGCGTGAAAGTCCTGGGCTCA	487	781
TCTATCAAGTCAGGCGTGAAATCCCGGGCTCA	0	3
TTTCTGTGAGATTGGAATTGTTTGGCCTGCGGG	1193	449
TGATTTAAGTCAGTGGTGTGAAATACGGCAGCTTA	3	4
CTTTTCAAGTCAGACGTGAAAGCCCTGGGCTTA	642	628
CTTGATAAGTCAGATGTGAAAGCCCTCGGCTCA	35	69
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ACTTGTAAGTCAGTGGTGTGAAATCTTTGGGCTTA	487	466
CTCTTCAAGTCAGGCGTGAAAGCCCTGAGCTCA	183	476
TTTGTCAAGTCTGATGTTAAAGATCGGGGCTCA	265	593
TTGCGTAAGACAGATGTGAAATCCCCGGGCTCA	263	202
TTCTGTAAGATTGGTGTGAAATCTCCCGGCTTA	443	356
GTTTGTAAGTCAGTGGTGTGAAAGCCGGCAGCTTA	4	8
GTTCTGATTGTTGCGGCCTCGCGCTTTATAGCC	0	16
CTTTTTACGTCTGCTGTGAAATATCCCGGCTTA	0	0
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CATTGTAAGTGTCTGGTGTGAAATCCCACGGCTCA	9	9
GACCTCAAGTCGGTTGTGAAATCCCTCAGCTCA	0	0
CGATGTGTGTGAGGCGTGAAAGCCCGGGGCTTA	0	0
TCTTGTAAGTCAGTGGTGTGAAATACGGCAGCTTA	0	0

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4	CCAAGTGTGTGAGGCGTGAAAGCCCCGGGGCTTA	392	364
5	TTTAGTAAGTCAGTGGTGAAATCCGGCAGCTTA	0	0
6	CTTTGTAAGTCAGTGGTGAAAGCTCGGAGCTCA	343	391
7	CTTCGGGCTGAGCTGTGAAGGCTCACCGCAAGG	321	341
8	CCGAGCGGGTCGTGGGTGAAATCCCCCAGCTTA	189	558
9	CCGATCAAGTCAGGCGTGAAATCCCGGGCTCA	12	12
10	GCTCGCAAGCGTCCTGTGAAATACCTCAGCTCA	148	153
11	AACATCTCAGTCAATCGATTGAGACGGAGGCGG	0	0
12	CTCGATTAGTCTCTTGTGAAAGCCTTGGGCTTA	94	664
13	TTTGCTAAGTCTGGTGTGAAATCTCCTGGCTTA	294	236
14	CTTTTTAAGTCGGATGTGAAATCCCCGGGCTCA	210	437
15	CTTGACAAGTCGGATGTGAAATCCCTCGGCTCA	2	0
16	CATCGTAAGTGTCTGGTGAAATCCCACGGCTCA	289	458
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18	GCGCTTAAGTCAGCGGTGAAATGCGGGGGCTCA	0	0
19	ACTATTAAGTCAGTGGTGAAAGCCCACAGCTCA	19	4
20	CTTGGCAAGTCGGGTGTGAAAGCCCCGGGCTCA	0	0
21	TTGGATAAGTCAGTTGTGAAATTCCTCGCTTA	0	0
22	ACCTTCAAGCGTTCTGTGAAATCCCCCGGCTCA	264	392
23	CTTGATAAGTCAGAGGTGAAAGCCCCGCAGCTTA	0	0
24	ATGGGTCAGTCAGCCGTGAAAGCCCCGGGCTCA	10	17
25	TCTCGGGTGACAGGCCGACGGTCCACCTCGCGGT	387	165
26	GTTTGCAAGCGTTTTGTGAAAGCCCCCGGCTCA	234	378
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29	AACATCTTGCTCTTTGAGTGAGACGGAGGCGGA	0	0
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31	GCTATTAAGTCAGTGGTGAAATCTCCGAGCTTA	288	218
32	TTGTTTAAGTCTGTCGTGAAAGCCCTGGGCTCA	77	56
33	CTAGATAAGTCAGTGGTGAAAGCTGGTCGCTTA	0	0
34	GTTGGTAAGTCAGTGGTGAAATCCCCGAGCTTA	281	177
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38	TTTTTGTTTGATTGCTTTGAAAGGTTACTGTT	214	308
39	TCGGGTAAGTCTGATGTGAAAGCTCGGAGCTCA	227	217
40	TTAATCAAGTCAGACGTGAAAGCCTTGGGCTTA	0	0
41	AACAGCTCACACATTGATGTGAGACGGAGGCGG	0	0
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AGCGCTAAGTCGGGCGTGAAATCCCCAGGCTCA	77	247
TATAGTAAGTTAGAAGTGAAAGCCTTGGGCTCA	0	0
ACCTGTAGGCGCGTTGTGAAAGCCCCCGGCTCA	0	3
CCTTATAAGTCAGTGGTGAAATCTCTGGGCTTA	255	133
TGGATTAAGTCGGGTGTGAAATCTCCGGGCTCA	4	0
GTAAGTAAGTCAGCGGTGAAATCTCCGAGCTTA	171	322
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TCCTGCAAGTCGGATGTGAAATCCCACGGCTCA	159	291
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CGCATTAAAGTCTGACGTGAAATCTCCCGGCTTA	152	235
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GAGAGAAAGTCAGATGTGAAATCCCCGGGGCTCA	0	0
TTCACTAAGTCTGATGTGAAATCCCCCGGCTCA	6	0

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4	TTGGGTAAGATTGACGTGAAACCTTCTGGCTTA	0	0
5	CTCTTTAAGTCGGATGTGAAATCCCCGGGCTCA	113	153
6	CTTGTCGCGTCTGCTGTGAAAACCCGGAGCTCA	0	0
7	CCCGATTAGTTGGAGGTGAAATCCCCGGAGCTCA	0	0
8	TCTCGTAAGTCGACTGTGAAAGCCCTTGGCTCA	81	209
9	CTTGACAAGTCAGATGTGAAAGCCCTCGGCTCA	100	154
10	TCTTGTGCGTCGGAGGTGAAATCCCCGGGCTTA	61	244
11	TTTCTTAAGCCAGATGTGAAATCCCCGGGCTTA	0	0
12	TTTTGTAAGACAGGCGTGAAATCCCCGGGCTCA	114	129
13	TCAAATAAGTCAACTGTTAAATCTTGAGGCTCA	0	0
14	TTAGACAAGTGAGGCGTGAAAGCCCTGGGCTCA	66	216
15	TTTCTGGCGTGGTGCGTCTGGTCGCGCGGGGCG	123	109
16	GCTCTTAAGTGTCGCGTGAAAGCCCACGGCTTA	121	166
17	TATTGTAAGTCAGATGTGAAAGCCCCGGGCTTA	173	150
18	TGACTCAAGTCAGAGGTGAAAGCCTGGAGCTCA	2	7
19	CTATTCAAGTCAGAGGTGAAAGCCTGGAGCTCA	0	0
20	CATCGTAAGTCATGGTTGAAATCCGGCGGCTCA	2	0
21	ACATTTAAGTCAGAGGTGAAAGCCCAGGGCTCA	20	72
22	ATTGGCAAGTCAGAAGTGAAATCTTACGGCTCA	0	3
23	TTTAATAAGTCAGTGGTGAAAGCCCATCGCTTA	0	0
24	TGGGGAATGAAAGGAGGAAGGAGAAGGGGAACC	182	90
25	CTTTTTAAGTCAGACGTGAAAGCCCTAGGCTTA	117	119
26	ATCAGAAAAGTCAGAGGTGAAATCCCAGGGCTCA	74	110
27	CCCACCAAGTGTCTTGTGAAATACCTTAGCTCA	0	0
28	TTCGGTCAGTCAGCCGTGAAAGCCCTGGGCTTA	0	0
29	TTAGGTAAGTCAGATGTGAAAGCCCCGGGCTCA	0	0
30	TCTAATAAGTGAGGGGTGAAATCCTGCGACTCA	75	157
31	CTTCGATAGTCAGGCGTGAAAGGCCTGGGCTCA	2	11
32	ATGATTAAGTTAGGAGTGAAATCCCCGGGCTCA	0	0
33	CTTGTCACGTCGGATGTGAAAACCTCGGGGCTCA	82	132
34	CGATTCAAGTCAGATGTGAAATGCCTGAGCTCA	38	74
35	ACTGGAAAGTCAGGGGTGAAATCCCCGGGGCTCA	0	0
36	ACTTGCAAGTCGATGGTGAAATCTTACGGCTCA	92	163
37	TTGGCTAAGTTTGGTGTGAAATCTCCCGGCTCA	135	79
38	TTTTGTAAGTTGGACGTTAAATCTCCAGGCTCA	0	0
39	TTACGTAAGTCTGATGTGAAAGCCCCGGGCTCA	0	0
40	CCGTTTAAGTTAGGTGTGAAAGTCCTGGGCTCA	0	0
41	TTTCGTAAGTTTGGTGTGAAATCTCCCGGCTTA	64	163
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AATTTTGGTCATGTTTTACACACATTTTGTG	0	2
CGCGGTAAGTTGGGTGTGAAATCTCCCGGCTCA	72	90
TTCGGTAAGTTGGGCGTGAAATCTCCCGGCTCA	35	98
CATGGCAAGTCGGGAGTGAAAGCCCGGGGCTCA	42	127
ATGGTTAAGTCGGGTGTGAAATCCTGGGGCTCA	0	0
TTGGATAAGTCTGGCGTGAAATCATTGCGCTTA	0	0
TTTCGGGTATTTGTTGCCGGTTGGTCTTCGCGA	17	27
TATATTCAAACATATATATAATTTTAACAGGTG	0	3
CTATTTAAGTCAGTGGTGAAATACGGCAGCTTA	112	110
TTAGTCACGTCGGATGTGAAAACCCGGAGCTTA	84	104
TCGTGCAAGACAGATGTGAAATCCCCGGGCTCA	74	103
GTGTATAAGTCAGTGGTGAAATCCCCGAGCTTA	0	0
CTTGCCAAGTCTGGTGTGAAAGCCACGGCTCA	47	132
CTTTGTAAGACAGTGGTGAAATCCCCGGGCTCA	0	0
TCTCGGGGTGCCGTTGTGGTTCTCTGTTTTCTT	7	12
CGTGGCAAGTCAGATGTGAAAGCCCGGGGCTCA	83	69
ATCGTTAAGTCAGAGGTGAAAGCTCACAGCTCA	0	0
TCTTGCAGGTCGGATGTGAAATCCCTCGGCTCA	33	131
TTTTGTTAGTTTGGTGTGAAATCTCCCGGCTTA	77	74
GCAGGTAAGTCAGCGGTGAAATCTCCGAGCTTA	83	92
CGGGGTAAGTCAGATGTGAAATCCCCGGGGCTCA	0	0
ATCGGTAAGTGTTCTGTGAAAGCCCCCGGCTCA	64	110
GCCGCTAAGTGTCGTGTGAAATCCCAGGGCTCA	83	101
TCTGCTAAGTCGCGTGTGAAATGTCCCGGCTCA	76	126
GTTTTTAAGTCAGGGGTGAAATCCTGGAGCTCA	56	165
CGCCATAAGACAGATGTGAAATCCCCGGGCTTA	48	64
CCATCTAAGTCAGATGTGAAATCCCTTGGCTCA	0	0
CTCGGAAAGTCGGATGTGAAAGCCCTGGGCTCA	48	128
TTTGTTAAGTTGGGGGTTTAATCTCTGGGCTCA	31	74
CTTGCCAAGCGTCCTGTGAAATCCCGCGGCTCA	71	101
TTCTGTAAGTCAGATGTGAAATCCCCGGGCTTA	57	105
TTTGTCGCGTCGGGAGTGAAAACACACAGCTTA	53	141
TTTCGGCGTGCGCTCGGGCTGGTCGGCCGTCAA	104	27
CTGTTCAAGTCTGACGTGAAATCGCTCGGCTTA	47	93
TTCGGTAAGTTGGGCGTGAAATCTCCTGGCTTA	0	0
TATTGTAAGTCGGATGTGAAAGCCCCGGGCTTA	91	91
CGCGCCAAGTCAGATGTGAAAGCCCCGGGCTTA	58	114
TTTTGTAAGACAGTGGTGAAATCCCCGGGCTCAA	0	0

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TCTTGTAAGTCGAATGTGAAAGCCCCTGGCTCA	51	68
CTTGGCAAGTCTGATGTGAAAGCCCATGGCTCA	0	0
ACTTTTAAGTCGGAGGTGAAAGCCCAGGGCTCA	65	51
CTTCGGACTTGGAGGAACGGTCTGCCTTACGGT	18	298
TCTAAAAATTTTGAATGGAGAAAAGTTTAAAGC	32	47
CTTGCTAAGACTGACGTGAAAGCTCCTGGCTTA	46	94
GCTAGTAAGTCAGTGGTGAAATCTTCGAGCTTA	0	0
CTTGTTAAGATTGACGTGAAAAGCTGCTGGCTTA	66	92
CGGCGCAAGTGTGAGTGAAATCCCACTGCTCA	44	110
TCATGCAAGACAGATGTGAAATCCCCGAGCTCA	58	120
CTTATTAAGCAGGGTGTGAAAGCCCCCGGCTCA	65	85
CTGGGTAAAGCGTGTGGTGAAAGCCCCGGGGCTCA	60	51
TTAGATACGTCTGATGTGAAAGTCCTGGGCTTA	0	0
ATAGTTTAGTCAGAGGTGAAAGCCCAGGGCTCA	32	151
TTCTGAAAGTCAGATGTGAAATCCCTGGGCTTA	32	52
AATTTTTGGTCATGTCTGTACACACATGTTGTG	0	2
CACGGATAGTTGGGTGTGAAAGCCCCGGAGCTTA	40	32
CTTGGCAAGTCGGATGTGAAATCCCACGGCTCA	30	99
TTGTCTAAGACTGACGTGAAAGCTCCTGGCTTA	16	46
CCTTGTAAGTCTTGGGTGAAATCCCTCAGCTCA	38	118
CTAAGAGTGGGTGTGTAGTAATTAGTTTTATCA	0	0
CGATTTTAGTCAGGCGTGAAAGCCCTGGGCTCA	0	0
GCCCGCAAGCACTTTGTGAAATCCCTCGGCTCA	0	0
ACTGTCAAGTCAGAGGTGAAATCCCAAGGCTCA	21	107
CTTTGCAAGTCAGAGGTGAAATCCCCAGGCTCA	0	0
CGTTACAAGTCACTTGTGAAATCTCCGGGCTTA	68	61
GCATTTAAGTCAGTGGTGAAATCTCCGAGCTCA	45	63
TTTGGTAAGCCCTCTGTGAAAGCTTCGGGCTCA	62	100
TTTCTCTTAAGATCAACCAAATTGATAGTAAAA	3	9
CTTTGTAAGTCAGATGTGAAATCCCCGGGCTTA	65	83
ACCTGTAAGTGTCGTGTGAAAGCCCACCGCTCA	77	62
TTAAATAAGTCAGTTGTGAAATTCTCCGGCTTA	7	9
TTTGCTAAGTTTGGTGTGAAATCTCCGGGCTTA	79	66
TGGGGAATGAGTGGAGGAAGGAGAAGGGGAACC	100	45
TCATGTAAGACAGATGTGAAATCCCCGGGCTTA	0	0
TTGAGAAAGTCTGACGTGAAATTTCTTGGCTTA	10	26
CTTTGCCAGTCAGGGGTGAAATCCCACAGCTTA	3	162
CTACTCAAGTCAGAGGTGAAAGCCCCGGGGCTCA	12	35

CTCTTCAAGTCAGGCGTGAAAGCCCCGGGCTCA	67	67
CTTGTTAAGTCAGGGGTGAAATCCCGGAGCTCA	2	9
ACCAGAAAGTCAGAGGTGAAATCCCAGGGGCTCA	0	0
TGGCTCAAGTTTGGTGTGAAATCTCCCGGCTCA	60	81
CCTTGCAAGTCAGAGGTGAAAGTCCTGGGCTCA	0	0
TTTTTCAAGTCAGGCGTGAAAGCCCCGAGGCTTA	0	0
TATCAGGTTTGCGGTGAGGGCAGTGTTTAGTTG	0	0
CCTGATAAGTCGGGGGTGAAACGCTGCGGCTCA	52	61
TTGGGTAAGTTTGGTGTGAAATCTCCCGGCTTA	0	0
GCAGGTAAGTCAGTGGTGAAATCTCCGAGCTTA	49	68
CTTGGTAAGCGTGCGGTGAAAGCTCGAGGCTCA	52	71
GCTGGTAAGTCAGTGGTGAAATCCCCGAGCTTA	0	0
TTTCTTAAGTCGGATGTGCAATCCCCGGGCTCA	52	86
CCCCGTAAGTCAGTGGTGAAATATCTCAGCTTA	0	0
ACATTTAAGTCAGGGGTGAAATCCCGAGGCTCA	4	10
ACACTTAAGTCAGGGGTGAAATCCCAGGGGCTCA	0	0
TTTTTTAAGTCAGATGTGTAATCCCCGAGCTCA	55	66
GCATTTAAGTCAGTGGTGAAATCTCCGAGCTTA	44	74
ACTTCTAAGTGTCGCGTGAAAGCCCACGGCTTA	32	60
TTTGATAAGTCAGTTGTGAAATTCGCCGGCTTA	58	39
TCCTGTAAGATTGGTGTGAAATCTCCCGGCTTA	49	60
GATGATAAGTCAGCGGTCAAATCCGACAGCCTA	65	50
TTTGCTAAGACAGGTGTGAAATCCCCGGGCTTA	70	28
ACTTTTAAGTGTCGCGTGAAAGCCCACGGCTTA	62	64
TCTTGCGCGTCGGAGGTGAAATCCCCGGGCTTA	29	87
TTATCTAAGTCAGGTGTGAAATCTCTCGGCTCA	63	28
CTGAGGGCGCCCAAGTAGACGGTCAAGTCCCAT	0	5
CTTGACAAGTCAGGAGTGAAATCCCAGGGCTTA	0	0
TTTTGTAAGTCAGAAAGTGAAATCCTAGGGCTTA	0	0
TCCTGTGCGTCGGAGGTGAAATCCCCGGGCTTA	45	75
TTTGTCGCGTCTGCTGTGAAAATCCGGGGCTCA	35	69
TTGTTTAAGTCTGATGTGAAAGCCCTGGGCTCA	50	85
CTGAGCAAGTGCGATGTGAAAGCCCCCGGCCTA	30	82
CGTGGTAAGTCAGCTGTGAAATCTCCGAGCTTA	59	39
TTTGATCAGTTAGGTGTGAAATTCCTGGGCTTA	5	2
ACTATTAAGTCAGGGGTGAAAGCCCCGAGCTCA	0	0
CTTGGATAGTCGGGTGTGAAAGCCCAGGGCTCA	5	2
GTTCGTAAGTGCTTGTGAAATCCCCCGGCTCA	61	70

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CCTGGTAAGTCGGGGGTGAAACGCTGCGGCTCA	42	63
TTTATTATTTTAAAGGTAAAATCCGAGGATTA	44	55
TTGGCTAAGTCAGATGTGAAAGCCCCGGGCTCA	0	0
AATGAACTTTTTTTTTTCGATTCTGTTTTTTTT	41	42
CTTTTTGCGTCAGAGGTGAAATCCACGGGCTTA	0	43
TCCTCCAAGCGTCTTGTGAAATCCACGGCTCA	52	52
TCGGGTAAAGTCTGACGTGAAATCTTCAAGCTCA	51	57
TTTTTAAGACAGGCGTGAAATCCCCGGGCTTAA	33	19
ATTGGTAAGTCAGAGGTGAAAGCCCGTAGCTTA	0	0
GCTTTTAAGTCAGTGGTGAAATCTCCGGGCTCA	22	65
ATTGTTAAGTTAGGGGTGAAATCCCAGGGCTCA	40	19
CTGGGTAAAGCGTGTGGTGAAAGTCCGGGGCTCA	21	17
TATCCGGCGTCTCTGACGTCTGCCTGACTCGGC	58	62
CTGAGGGCCGCTCAAGGTTTTCAAGCAAGTCCC	0	0
TCTGTTAAGTCAGTGGTGAAATACGGCAGCTCA	38	57
TTTGCTAAGTCTTGTGTGAAAGCCCTGGGCTCA	42	69
TCCGGTCAGTCAGCCGTGAAAGCCCCGGGCTCA	0	0
ACTATTAAGTCAGGGGTGAAATCCCGGGGCTCA	12	35
TTTTTCAAGTCAGGGGTGAAAGCCCGGAGCTCA	0	0
CCGTGTGTGTGAGGTGTGAAATCCCGGAGCTTA	29	26
TCTTGTAAGACAGTGGTGAAATCCCCGGGCTCA	0	0
TCCTACAAGCCAGAGGTGAAATCCCGGAGCTTA	0	34
TTTAATAAGTCAGTGGTGAAAGCCTATCGCTTA	74	65
CTTGGCAAGTCGGGCATGAAATCTCCTGGCTTA	20	64
ACTGGAAAGTCAGAGGTGAAATCCCAGGGCTCA	0	0
ATCGTTAAGTCGGGGGTGAAATCCTGGAGCTCA	11	23
TGTTATAAGTCTGATGTGAAACCTTCTGGCTTA	15	42
CCCGATAAGTCCCGCGTGAAATCCCCCGGCTCA	29	74
TTTGTTAAGTTTGGTGTTAAAGATTGGGGCTCA	22	72
GTTGGTAAGTCAGTGGTGAAATCTCCGGGCTTA	68	39
TCCTATAAGTCGGATGTGAAAGCCCCGGGCTCA	70	34
TTTACTAAGTCAAACGTGAAAGCCCCGGGCTTA	0	2
TCTGCCAAGCTCGATGTGAAATCCCCGGGCTTA	32	56
ACATTTAAGTCAGACGTGAAATCCCCGGGCTTA	0	0
TTTTGTAAGTCAGTGGTGAAATGTCTCGGCTTA	7	55
ACCAGAAAGTCAGAGGTGAAAGCCCCGGGGCTCA	32	33
TTTTGTAAGTCAGTGGTGAAATCCGGCAGCTCA	0	0
ACTTTTAAGTCGGGGGTGAAATCCCGGGGCTCA	65	28



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4	TGGAGTAAGTCAGTTGTGAAATTCCTCGCTTA	21	16
5	CTACTTAAGTCAGTGGTCAAATACGGCAGCTTA	44	48
6	ATTGTTAAGTGAGGGGTGAAATCCCAGGGCTCA	0	5
7	TTTGTTAAGTTGGTGGTTTAATCTCTGGGCTCA	2	0
8	GTTGCTAAGTCAGGGGTGAAATCCTGGAGCTCA	27	49
9	TTTCTGGTGTGGTACGCCGAGCCCGCCCTTAGG	33	25
10	TTTGTGCGCTCTGCCGTGAAAATCCGGGACTCA	6	7
11	TTTGATAAGACAGGCGTGAAATCCCCGGGCTTA	41	40
12	TTAGATAAGTCAGTCGTGAAATCGCTGGGCTTA	29	38
13	TTAGTCACGTCGGATGTGAAAACCCGGGGCTTA	53	45
14	TTCTTAGAGACAGTAGGAACTAGAATTTGATAG	10	165
15	CGGACTAAGTCGGGTGTGAAATCTCCGGGCTCA	27	66
16	TGCCATAAGTCAGGTGTGAAAGATTCCGGCTCA	0	2
17	CCCTGCGCGTCGAGCGTGAAAGGCCTGGGCTCA	7	15
18	TTTCGCAAGTCAGATGTGAAAGCCCCGGGCTTA	32	37
19	TTCGGTAAGTTGGGCGTGAAATCTCTTGGCTTA	12	0
20	TTTGTGCGCTCTGCTGTGAAATCCCGAGGCTCA	0	27
21	ATTGATAAGTTATTGTTTAAATTCATGGGCTTA	63	33
22	TTCATCAAGTGTTCTGTGAAATCCCTCGGCTCA	31	50
23	CATGGTGTGTCGGGCGTGAAACTCCGGAGCTTA	41	40
24	ATCTTTAAGTCAGTGGTCAAAGCCTGCAGCTTA	25	27
25	CTCTGCAGGTCGGATGTGAAATCCCTCGGCTCA	2	4
26	TCTCGTAAGTTCGGTGTGAAATCTCCCGGCTCA	33	46
27	TCGCTTAAGTAATGCGTTAAAGCCTTGGGCTCA	43	38
28	ATCTGTAAGTCAGTGGTCAAATCTCGCAGCTTA	16	122
29	TGGGTAAGTCAGATGTGAAATCCCCGGGCTCAA	16	2
30	CTTGGCAAGTCAGATGTGAAAGCCCTCGGCTTA	38	55
31	ATTTGTAAGACAGTGGTCAAATCCCCGGGCTCA	0	0
32	TCATTTAAGTCGGGTGTGAAATCCCCGGGCTCA	33	55
33	CTAGGTAAGTCAGGGGTCAAAGCTTCCCGCTCA	32	40
34	TCTGGTAAGTCGGATGTGAAAGCCCCGGGCTTA	24	51
35	TTGGGTGTGTCAGATGTGAAATCCCGAGGCTTA	25	28
36	TTTTACAAATCCTGTTGGAATAGCTTCCGTTGG	0	0
37	GCTCGTAAGTGTTCTGTGAAAGCCCACGGCTCA	24	51
38	TTTAATAAGTCAGTGGTCAAAGCCCGCAGCTCA	40	52
39	ACCCGAAGGTGCATCGTGAAATCCCTTGGCTCA	0	0
40	TCTGTGCGCTCGGAAGTGAAAACCTCGGGGCTCA	15	50
41	CCTGATAAGCCTGGCGTGAAAGTCACCGGCTCA	0	0
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4	TTTTGTAAGTCGGTTGTGAAATCCCTGGGCTCA	0	0
5	TTGTAAGACAGTGGTCAAATCCCCGGGCTCAAC	0	0
6	CATCGTAAGTGTCGGGTGAAATCCCACGGCTCA	29	47
7	TTGGTAAGTCAGATGTGAAATCCCCGGGCTCAA	11	5
8	GTTGGTAAGTCAGTGGTCAAATCTCCGAGCTTA	40	28
9	AGAGGTCAGTCGGCCGTGAAAGCCCCGGGCTCA	0	0
10	TCTGGTAGGTGAGGTGTGAAATCCCCGGGCTCA	12	18
11	TGTTGTAAGTCAGTGGTCAAATCCGGCAGCTTA	0	0
12	GTTTGTAAGTAGAGGGTGAAATCCCAGGGCTCA	0	0
13	TTTTGTAAGACAGAGGTGAAATCCCCGGGCTCA	46	18
14	TTTCGTAAGTCTGGCGTGAAATTTCTCGGCTTA	41	32
15	TTGTATAAGTCAGTGGTCAAAGGCCGTAGCTTA	0	0
16	ACTTTTAAGTCGGGTGTGAAATCCCCGGGGCTCA	0	43
17	CCTTATAAGTCAGTGGTCAAATCTTTGGGCTTA	52	17
18	AATGATAAGTCAGTGGTCAAATCCTGCAGCTTA	23	49
19	ATGGGTCAGTCAGCCGTGAAAGCCCCGGGCTTA	0	0
20	TTGCGTGTGTCTGGTGTGAAATCTCCTGGCTCA	13	27
21	TGTTGTAAGTCAGATGTGAAATCCCCGGGCTTA	13	7
22	TTGGGTAAGTCAGATGTGAAATCCCGGGCTCAA	14	0
23	ACTGGAAAGTTGGGGGTGAAATCCCCGGGGCTCA	18	21
24	ATAGGTAAGTCAGAGGTCAAAGCCTGGAGCTTA	0	0
25	TTAGATAAGTCAGTTGTGAAATCCCCGGGCTTA	24	23
26	TTAGATAAGTCAGTTGTGAAATCCTCGGCTTA	30	27
27	ACCACTCAGTCAGGCGTGAAAGCCCCGGGCTCA	18	42
28	CGGATCAAAGTGAGGCGTGAAAGGCCTGGGCTCA	14	62
29	TTCGGAAAGAAAGATGTGAAATCCCAGAGCTTA	2	0
30	TCCCTTAAGTTTGTCTGTGAAATCTCCCGGCTCA	26	40
31	ACTTGTAAGTCAGTGGTCAAATCTGTGGGCTTA	13	52
32	CTCTTCAAGTCAGACGTGAAAGCCCCGGGCTCA	33	27
33	TTTTGTAAGCCAGATGTGAAATCCCCGGGCTCA	37	17
34	TTATTTAAGTCCGTTGTGAAAGCCCTGGGCTCA	17	87
35	TCTAAAACTTCGAATGGAGAAAAGTTTAAAGC	0	0
36	TCTGTTAAGTGAGAAGTGAAATCTCCAGCGCTC	7	53
37	TTGGGTAAGTCTAATGTGAAATCTCCGAGCTCA	27	32
38	CCTGTTAAGTCAGGGGTGAAATCCTGGAGCTCA	0	0
39	TTTGTTACAATTGGCAGGACATTTGCAATTTA	47	25
40	TTTTGTAAGACAGGCGTGAAATCCCCGGGCTTA	0	0
41	TGATGTAAGACAGAGGTGAAATCCCCGGGCTCA	16	28
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CGTCGCAAGTCAGGCGTGAAATCCCCGGGCTTA	17	38
TTTTTTAAGTTGTATTTTAAAGACTAGAGCTCA	7	0
GCTCGCAAGCGTCTTGTGAAATCCCATGGCTCA	0	5
CCATGTAAGTCGGATGTGAAAGCCCTCAGCTCA	17	35
CGCTACAAGTCAGGGGTGAAATCCCAGAGCTTA	11	30
TTCGTTAAGTCTGATGTGAAAGCCCCGGGCTCA	3	23
AATGATAAGTCAGTGGTGAAAGCCTGCAGCTTA	22	10
AATTCTAAGTCAGTGGTGAAAGCCTCCCGCTTA	22	13
TTTCTTAAGTTTGACGTGAAAGCTCTCGGCTTA	0	0
TCTTGTAAGACAGATGTGAAATCCCCGGGCTCA	3	0
AATGAACTTTTTTTTTTTCGATTCTTGTTTTGGC	20	22
TGTCGTAAGTGTCTGGTGAAATCCCACGGCTCA	0	0
CCTTTTAAGTCTTAATCAAAGAAGCTAAGCCTA	35	7
CGCGACAAGTGAGGTGTGAAAGCTCCTGGCTCA	18	24
GTTTGTAAGTCAGTGGTGAAAGCCGGTCGCTTA	20	41
TTTCGGAAGTGGGAATGATTGGTCGGGCCTTGA	45	2
TTTTGTAAGACAGTGGTGAAATCCCCGGGCTCG	0	0
CTCAGAAAGTTGGGTGTGAAATCCCCCGGCCTA	4	0
TTGGGTAAAGTCTGTGGTGAAATTTTCGAGGCTCA	25	11
TTTTATAAGACAGAGGTGAAATCCCCGGGCTCA	0	0
CTCGGTAAAGCGTGTGGTGAAAGCCCCGGGGCTCA	6	12
TTATACAAGTCTGGTGTGCAAGACCAAGGCTTA	0	0
TGGTTTAAGTCTGCTGTGAAAGCCCTGGGCTCA	0	0
TGATCCATGTCAGAGGTGAAAGCCTGGGGCTCA	0	0
GCCGGTGCGTCGGCGCCTGAAAGCCCCCGGCTC	4	0
TCGCACAAGACAGATGTGAAATCCCCGGGCTTA	30	22
ATCGTTAAGTCAGAGGTGAAATCCCAGGGCTCA	0	0
GTTGTTGAGTTGGAGGATGAAATGTCTGGTAGT	0	0
TTTTGTAAGACAGATGTGAAATCCCCGGGCTCA	2	0
TTGAAAGCTGTCAAGAATAGTCAAAATATCCTT	0	0
TTTTGTACGTTTGATGTGAAAGTCCTGGGCTTA	0	0
CTTCGCAAGTCGGGCATGAAATCTCCTCGCCTA	14	23
CTTTTTAAGTCAAATGTGAAATCCTAGGGCTCA	0	0
TCCAATAAGTCAGCCGTGAAATCGCTGGGCTTA	0	0
TTCGCTAAGTCTGATGTGAAATCTCCCGGCTTA	22	0
TTTTGTAAGACAGTGGTGAAATCCCCGGGCTCAA	0	0
TTATCTAAGTCTGGTGTGAAATCTGTCTGGCTTA	0	0
TTTTTTATTTTAAAAAAGAAATGCTGAGACTCC	20	16

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4	TTCGTTGCGTCGTGCGTGAAAGACCCTGGCTCA	16	30
5	ATTTGTAAGTCAGTGGTGAAAGCCGGCAGCTTA	20	2
6	TTTTGTAAGTCAGATGTGAAATCCCCGGGCTCA	31	25
7	ACGCGTAGGCGCTTTGTGAAATCCCTCGGCTCA	16	28
8	AACGGTAAGTCAGTGGTGAAATCCTGTTGCTTA	23	26
9	TTTCGGAATATGCAGGAGGCGGTCCACAGAAAT	29	12
10	AGCGACACGTCGGTCGTTGAAAGCCCCCGGCTC	27	21
11	CTGCTTAAGTCTGACGTGAAAGCTCCTGGCTTA	0	0
12	TTATACAAGTCAGGAGTGAAATCCCAGGGCTCA	0	0
13	TCTTGCAAGACAGATGTGAAATCCCCGGGCTTA	19	23
14	CTTTGTAAGTCAGTGGTGAAATGTCGCAGCTTA	6	27
15	TTTTGTAAGACAGTGGTGAAATCCCTGGGCTCA	0	0
16	ATTGTTAAGTCAGTGGTGAAATCAACGGGCTCA	0	0
17	TTTTTTTAAGACAGGCGTGAAATCCCCGGGCTT	12	14
18	ATCGTTAAGTCAGTGGTGAAAGCCCACAGCTCA	19	41
19	CCTTCTAAGTCGGACGTGAAAGCCCCAGGCTTA	7	6
20	CTTAACAAGTCGGGCATGAAATCTCCTGGCCTA	14	24
21	CTGGGCAAGTCCAAGGTGAAATCCCTCGGCTCA	8	41
22	GCAGGTAAGTCAGTGGTGAAATCTCCGGGCTTA	28	24
23	CGAATCAAGTCAGGTGTGAAAGGCCTGAGCTCA	0	0
24	ATTGTTAAGTCAGAGGTGAAATCCCGGAGCTCA	0	0
25	ATTAATAAGTCAGTGGTGAAAGCCTGCAGCTTA	18	45
26	CCTGTTAAGTCAGGGGTGAAAGACGGTGGCTCA	0	0
27	TTTTGTAAGACAGTGGTGAAATCCCCGGGCTCAA	0	0
28	TCATGCAAGACAGATGTGAAATCCCCGGGCTCA	10	43
29	CTCGGCGAGTCGGGCATGAAATCTCCTGGCCTA	8	34
30	CTGAGGGCCGCCAAGCGCACAAGCAAGTCCCGC	0	0
31	CTTAGTAAGTCAGCGGTAAAAGGCGACAGCTTA	37	10
32	TCTGTTAAGTGTGAAGTGAAATCTCCAGCGCTC	10	34
33	CTTGTCGCGTCTGCTGTGAAAACCCGGGGCTCA	3	10
34	TTTGATAAGTCAGGTGTGAAATCCCACAGCTTA	0	0
35	ACTGATAAGTCAGGTGTGAAATCCCTGGGCTCA	2	64
36	TTTTGTAAGACAGTGGTGAAATCCCGGGCTCA	0	0
37	TTTAATAAGTCAGTGGTGAAAGCTGGTTGCTCA	38	7
38	CGCAGAAAGTTGGGTGTGAAATCCCTCGGCTCA	4	2
39	CTTTGCAAGTTAGAGGTGAAAGCCTGGGGCTCA	43	25
40	CTTTTTAAGTCAGGTGTGAAATCCTAGGGCTTA	10	32
41	CGAGGTAAGTCAGATGTGAAAGCCCCGGGGCTCA	0	0
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CCTCCTAAGTCATACGTGAAATCCCACGGCTCA	13	14
CCGTTTAAGTTAGATGTGAAAGTCCTGGGCTCA	5	12
AACGGCACGTCGGTCGCTGAAAGCCCCCGGCTC	10	20
CTTTGTAAGTTGGATGTGAAAACCTCTGGGCTTA	11	19
CCATGCAAGTGAGGCGTGAAAGGCCTGGGCTCA	14	36
CTCGTTAAGACAGATGTGAAATCCCCGGGCTTA	11	4
CTTGTTAAGTCAGGGGTGAAATCCTGGAGCTCA	0	0
CATCGCAAGTGTGGGGTGAAATCCCACGGCTTA	0	0
CTTGATAAGTAGGGGGTGAAATCTCATGGCTCA	19	21
CCTATTAAGTGAATGGTGAAATCTCCAGCGCTC	0	0
TTCCGTGCGTCAGAGGTGAAATCCCCGGGCTTA	14	19
TCTAATAAGTCAGTGGTGAAATCTGGTCGCTCA	36	16
TTCTCTAAGTTTGGTGTGAAATCTCCCGGCTCA	20	25
CCTAGCAGGTCAGGTGTGAAATCCCACAGCTCA	8	30
CCTTATAAGTCAGTTGTGAAATATCCTCGCTTA	12	4
TCTTATAAGTCTGTTGTGAAATCCCCGAGCTTA	0	0
TTTAGTCAGTCTGATGTGAAATCCCCGGGCTCA	0	0
CTTTGTAAGTCAGAGGTGAAAGCCTGGAGCTCA	19	16
TTTTGTAAGACAGTGGTGGAATCCCCGGGCTCA	0	0
TGAGTTAAGTCTGATGTGAAAGCCCCGGGCTCA	0	0
TTTAGTGGGTTATCAGGTGATTGGTCGGATAG	0	0
CCATCTAAGTCGGGTGTGAAATCTCCGGGCTCA	0	0
ATGATTAAGTTAGAAGTGAAATCCCCGGGCTCA	0	0
TCTAATAAGTTTTTTATAAAAGCTTATGGCTTA	10	25
TCTTGTAAGACAGTCGTGAAAGCCCCGGGCTTA	0	0
CGATCTTAGTCAGGCGTGAAAGCCCCGGGCTTA	0	0
ATAGTTAAGTCTAAAGTGGAAGCCCCGGGCTCA	6	0
TGCGGTACGGTTCGGGTGAAATCCCTCGGCTCA	0	0
TCTCCTAAGTCTGGTGTGAAATCCCTCGGCTCA	21	10
GGCGTTAAGTCAGTGGTGAAAGCCTACAGCTCA	0	0
ACCCGTAAGTGTTCTGTGAAATCCCCGGGCTCA	0	0
CTGGGTAAAGTCAGATGTGAAATCCCCGGGCTCA	3	0
CCCCGCGCGTCGAGCGTGAAAGGCCTGGGCTCA	9	11
CCCGTCAAGTCCCGTGTGAAAGCCCCGGGCTCA	16	22
TTTTGTAAGTCTGTCGTGAAATCCCCGGGCTTA	6	46
TTGCTTAAGTCTGTCGTGAAAGCCCTGGGCTCA	0	0
TGATTCAAGTTGGATGTGTAATCCCCGGGCTCA	0	3
CTTTGTAAGTCGGATGTGAAAGCCCCGGGCTTA	0	0

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ACCAGCAGGTCGGTCGTGAAAGCCCCGGGGCTCA	2	0
CGGATCAAGTGGGGCGTGAAAGGCCTGGGCTCA	14	19
GTTATTAAGTCAGTGGTGAAATCCTGTCGCTTA	0	4
CCTACTAAGTCATACGTGAAATCCCACGGCTCA	0	0
CTTGGCAAGTCAGAAGTGAAATCCCAGGGCTTA	0	0
ACAGGTCAGTTTAAAGTGGAATCCCAGGGCTCA	0	0
TATTGAGAGTCGCGGGTGAAATCCCAGGGCTTA	0	0
TTGGGTAAGCCCTCCGTGAAATCTCCGGGCCTA	14	9
ATTATTAAGTCAGATGTGAAACTCTGGGCTCA	0	0
ATATGTAAGTTAGATGTGAAATCCCCGAGCTTA	0	0
CTTTGCAAGTCAGGTGTGAAAGCCTAGGGCTTA	16	10
CTTTGTAAGTTTGGTGTGAAATCTCCCGGCTTA	17	21
CTAAACAGGTGAGGTGTGAAAGCCCTCGGCTCA	12	13
CTTTTCAAGTCAGACGTGAAAGCCCCGGGCTCA	24	21
CTCGCCAAGTCAGATGTGAAAGCCCCGGGCTTA	11	28
TTTGGTAAGTCGGTGGTTTAACTATGGGCTCA	0	0
ATTTGTAAGTCAGTGGTGAAATCCTGCAGCTTA	15	18
CTTGGTAAGTCTGGTGTGAAACTTGGGGCTTA	3	6
TTTAGTAAGTCAGTGGTGAAAGCCCGCAGCTCA	17	13
TTTGTCGCGTCTGCTGTGAAAATCCGAGACTCA	0	0
CTCGTTAAGTCGGATGTGAAAGCCCCGGGCTCA	12	15
CCGGGCAAGTCTGGTGTGAAATCGTCACCGCTC	0	0
GCTGTTGAGTTGGAGGATGAAATGTCTGGTAGT	0	0
TTGCGTAAGTGTGAGTGAAATCCTGCCGCTCA	6	5
CGAACCAAGTCTGGTGTGAAATCCCACGGCTCA	0	0
TCTGCTAAGCGTGCGGTGAAAGCCCCGGGGCTCA	0	0
TTGAACAAGTCTGCTGTTAAAGCGTGGAGCTAA	0	0
CTTATCAAGTCAGGCGTGAAATCCCAGGGCTCA	0	0
TTATTTAAGCCAGTCGTGAAATCCCCGGGCTTA	3	3
TTTTGTAAGACAGTGGTGAAATCCCCGGGCTTA	0	0
CGCTGTAAGTCTGACGTGAAATCTCCTGGCTTA	11	19
ACTTTCAAGTCAGGGGTGAAATCCCAGGGCTCA	9	7
ATCGGTAAGTGCCTTGTGAAAGCCCCTCGCTCA	0	0
ACCATTAAGTCAGGGGTGAAAGCCTGGAGCTCA	0	0
CCAAATAAGTAGGGTGTGAAAGCCTCCGGCTTA	3	15
CTTTCTACGTCTGCTGTGAAATATCCCAGGCTTA	0	4
TTTGTTAAGTCGGGTGTGAAATCCCTGGGCTCA	18	6
ACAAATAAGTCAGGTGTGAAATACCAAAGCTCA	18	11



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5	CACGACAAGCGAGGTGTGAAAGCTTCTGGCTCA	4	12
6	ATTATTTTCGGCGTCAGGCTGGCTGGAAAATTTA	19	16
7	TTTGATAAGTCAGTTGTGAAATACCCCGGCTTA	5	7
8	TGTTGTAAGTCAGTCGTGAAATCCCCGGCTCA	8	41
9	TTTAATAAGTCAGTGGTGAATCTGGTCGCTCA	2	0
10	CCCTTCAAGTCAGTCGTGAAATCGCTGGGCTCA	11	20
11	ATCTGCAGGCGCGTTGTGAAAGCCCCCGGCTCA	0	0
12	CGAGGTAAGTCAGTTGTGAAATCCCCGGCTTA	7	10
13	TCTGCTAAGCGTGCGGTGAAAGCCTGGGGCTCA	22	14
14	CTGGGTAAGTGTGGCGTGAAAGTCCTGGGCTCA	9	14
15	TTTGGTAAGTTGGGCGTGAAAGCTCCCGGCTCA	7	2
16	CTCTGTAAGTCGGACATGAAAGCTCCTGGCTTA	12	21
17	TTATGTAAGACAGAGGTGAAATCCCCGGGCTCA	22	20
18	ATTTGTCAGTCAGGGGTGAAATCCCGGAGCTCA	0	0
19	ACCTGCAAGTCGGTGGTGAAGCCCCGGGGCTCA	0	2
20	TTTCGTAAGACAGTGGTGAATCCCCGGGCTCA	0	0
21	TAAAGTAAGTCAGTGGTGAATCCCTTCGCTCA	12	12
22	TTCGTTAAGTCTGTCTGTGAAATCCCCGGGCTCA	8	20
23	CGTGACAAGTCACTTGTGAAATCTCCGGGCTTA	23	13
24	GCTGCCAAGTCTGTGGTGAATCCTCCAGCTTA	11	25
25	ACAGTTTAGTCAGAGGTGAAAGCCCAGGGCTCA	0	27
26	TCTCGTTTGTCTGAGGTGAAATCCCCGAGCTTA	18	8
27	CCGGTCAAGTCGGATGTGAAAGCCCTGGGCTCA	7	24
28	CTTCGTAAGTTGGACGTAAATCTTTCGGCCTA	8	15
29	CTGAGTAAGTTGAGGTTGAAATCCGGCGGCTCA	0	0
30	AATGCTAAGTCAGTGGTGAATCTCCCGGCTTA	3	6
31	CGTCGTAAGTCGGATGTGAAAGCCCTCGGCTCA	0	0
32	TCTCGTAAGTCTACTGTGAAATCCCCGGGCTTA	0	0
33	CCTTATAAGTCAGTGGTGAATCTTTCGCTTA	10	7
34	CTACTTAAGTTGGGTGTGAAATCCCCGGGCTTA	7	18
35	TTATGCAAGACAGAGGTGAAATCCCCGGGCTCA	9	28
36	TAAGATAAGTCAGATGTGAAATCCCGGAGCTTA	0	10
37	ACTTATAAGTCAGTGGTGAATCCTGTCGCTTA	0	30
38	TTTGTTAAGTCAGGTGTGAAATCCCCCGGCTCA	7	15
39	TTTCGGAGCATTACGATGCTGACCGCTGAAAC	5	0
40	CGACTCAAGTCAGAGGTGAAAGCCCCGGGGCTCA	8	26
41	AGCGTTAAGTCAGTGGTGAATCCTGCAGCTCA	0	3
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5	ATTTGTCAGTCAGGGGTGAAATCCCGGGGCTCA	0	0
6	TCAGGTCAGTCGGATGTGAAATCCCGGGGCTCA	0	0
7	GTTCTGGCTGTATTGGGCCTTGCACCTTGATGC	0	25
8	CGCATCAAGTCGGGCGTGAAAGCCCCGGGCTCA	0	0
9	ACATTTAAGTCAGGGGTGAAATCCCAGAGCTCA	4	7
10	CTGTGTCAGTCAGGCGTGAAATTCCTGGGCTTA	6	9
11	CCTGTTAAGACTGACGTGAAAGCTCCTGGCTTA	5	7
12	TTTTTTAAGTCAGATGTGAAAGCCCCGGGCTCA	0	0
13	ATTGGTAAGTTGGATGTTTAAGCGTTAGGCTCA	0	2
14	TTTGCTAAGATTGACGTGAAAACCTTTGGCTTA	18	11
15	TTGACTAAGTCGGATGTGAAAGCTCCTGGCTTA	10	15
16	GACGGCACGTCCGGTGACTGAAAGCCCCCGGCTC	10	10
17	TGTTGTAAGTCACTTGTGAAATCTCTGAGCTTA	12	11
18	ATCTGTAGGCGCGTTGTGAAAGCCCTCGGCTCA	0	0
19	ATTTACAAGTCAGGAGTGAAATCCCAGGGCTTA	0	0
20	GGTGGCACGTCCGGATGCTGAAAGCCCCCGGCTC	3	2
21	TTTGTCGCGTCGGATGTGAAAACCAATGGCTT	16	14
22	TTTCGATAGTCAGGCGTGAAATCCCCAGGCTCA	2	14
23	TGAGAAAAGTCGGGTGTGAAATCCCTCGGCCCA	5	10
24	CTGAACAAGTTGGATGTGAAAGCCCTGGGCTCA	0	0
25	TTTGTAAGACAGATGTGAAATCCCGGGGCTTAA	7	0
26	TTTAATAAGTCAGTGGTGAAAGGCCGTCGCTTA	0	0
27	ACTGGAAAGTTGGGGGTGAAATCCCAGGGGCTCA	29	5
28	ATGGGTAAGTACCTTGTGAAATCCCACGGCTCA	0	0
29	CCACTTAAGTCGGGTGTGAAAGCCCGGGGCTCA	10	12
30	CATGTCAAGTCAGACGTGAAAGACCGGGGCTCA	0	0
31	TCCGCCAAGTGCTTTGTGAAATCCCACGGCTCA	8	13
32	TTGAGTAAGTCCGCGGTGAAATTTTCGAGGCTTA	0	0
33	TTGTGCAAGACAGATGTGAAATCCCGGGGCTTA	7	23
34	TTTTGTAAGTTGGGCGTGAAAACCTCCGGGCTTA	12	11
35	CTCTCAAGTCAGCCGTGAAATCTCCGGGCTTA	11	12
36	TGATCCATGTCAGAGGTGAAATCCCGGAGCTCA	0	0
37	CGGTGTAAGCATGGCGTGAAAGCCCCTGGCTTA	7	8
38	ACTTGTGCGTCAGAGGTGAAATCCACGGGCTTA	0	0
39	ATATATAAGTTAGATGTGAAATCCCGAGCTTA	22	0
40	TTCGGTAAGTCTGTCATGAAATCTCCCGGCTTA	0	22
41	TAGCGTTAGTCGGCCGTGAAAGCCCTGGGCTTA	10	12
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CTTGCCAAGCGTCCTGTGAAATCCCACGGGCTCA	16	11
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TTGTGCAAGACAGATGTGAAATCCCCGGGCTCA	12	5
CACGACAAGTGAGGTGTGAAAGCTCCTGGGCTCA	6	8
TGAATTAAGTCGGGTGTGAAATCTCCGGGCTCA	0	0
ACTTCTAAGTCGGGGGTGAAATCCCAGGGGCTCA	16	15
TTATTCAAGTCAGGGGTGAAATCCTGAGGCTCA	0	0
ATCTTTAAGTCAGGGGTGAAATCCCAGGGGCTCA	0	0
GTCGTTAAGTGCTTTGTGAAAGCCCCCTGGGCTCA	6	9
CGGCGTAAGTCAGAGGTGAAATCCCATCGGCTC	16	10
ACTCTTAAGTCGGGGGTGAAAGCCCAGGGGCTCA	4	2
ACAGTTTAGTCAGAGGTGAAAGCCCCGGGGCTCA	10	7
CGACATAAGTCAGAGGTGAAATCCCATCGGCTC	4	17
ACCCGAAGGTGCATCGTGAAATCCCCCGGCTCA	0	0
TTCGTTGCGTCGTGCGTGAAAGACCCCGGCTCA	0	3
TTTGTTGCGTCGGAAGTGAAACTCAGAGCTTA	9	11
CTTAGTAAGTCAGATGTGAAATCCCTGGGCTCA	11	10
CCTATTAAGTGTTGGTGTGAAATCTCCAGGGCTC	0	0
ACTTGCAGGCACCTTGTGAAAGCCCTCGGCTCA	0	0
CTTGCTAAGTCCTGTGTGAAAGCCCCGGGCTCA	5	12
TCTGAATAGTCCAAGTTGAAATCCCGGAGCTCA	0	0
GTTGTTGAGTTGGAGGATGAAATGTCTGGCAGT	0	0
TTTTGTAAGACAGTGTGAAATCCCCGGGCTCAA	0	0
ATGATTAAGTTACTGGTGAAAGCGCCGGGCTAA	0	0
CTGTGGGCGTCGTAGATGATCAGGTTCCGTCC	0	0
TTTATCAGGTTGGATGTGAAAGACCCGGGCTTA	8	2
ATTGTTAAGTCGAGGGGTGAAATCCCAGGGCTCA	0	0
CCGGGTGTGTTAGATGTGAAATCCCGAGGCTCA	0	0
AAAGCTAAGTCAGTGGTGAAAGCCCGCAGCTCA	0	0
ATGGGTAAGTCAGATGTGAAATCCCCGGGCTCA	4	0
GCATGTAAGTCAGATGTGAAATTCCGGAGCTCA	15	7
TTCCACGCGTCGGAGGTGAAATCCCCGGGCTTA	12	9
CTTGACAAGTCAGAGGTGAAAGCCTGGAGCTCA	8	6
CCTGATTAGTTGGAGGTGAAATCCCGGAGCTCA	0	0
GAAAGTCAGTCAGATGTGAAAGCCCAGGGCTCA	0	0
TTTCGTAAGTCTGTCGTGAAATCCCCGGGCTTA	0	0
CGCGGAAAGTTGGGTGTGAAAGCCCTCGGCTCA	0	0
TTGGACAAGTGAGGCGTGAAAGCCCTGGGCTCA	7	11

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4	CTCGGCAAGTCTGGTGTGAAAACGCTACCGCTT	0	0
5	TTGGGTAAAGTCAGATGTGAAATCCCCGGGCTTA	2	0
6	ATTGGTAAGTCAGAGGTGAAATCCCACAGCTTA	0	0
7	TTTTGTAGACAGTGGTGTGAAATCCCCGGGCTCAA	0	0
8	TTTTAGTAGGATTTTTAGAGATAGGTCGGTTAG	0	0
9	TTTTGTAAAGACGGATGTGAAATCCCCGGGCTTA	11	17
10	TTATACAAGTCAGGGGTGAAATCCCAGAGCTTA	14	8
11	CTTGTCGCGTCTGCTGTGAAAATCCGGGGCTCA	4	13
12	GTTTCGTAAGTCTTAGAGTAAATCTCACGGCTCA	0	0
13	TTTTAGTAAGATTATTAGAAATAGGTCGGTTAG	0	0
14	CTAGATAAGTCGGATGTGAAAGCCCCGGGCTTA	9	8
15	TAGCGTTAGTTGGCCGTGAAAGCCCTGGGCTTA	9	9
16	CTCTATAAGACAGATGTGAAATCCCCGGGCTTA	6	16
17	CTTTTTAAGTCAGATGTGAAATCCCCGGGCTTA	0	0
18	TTCGGTAAGTCAGATGTGAAAACCTCCAGGCTCA	0	2
19	CTTGTTAAGTAGGGTGTGAAATCCCCCGGCCCA	2	8
20	AAATCTAAGTCAGTGGTGTGAAATCCTGCAGCTTA	2	11
21	ATCATTAAGTCAGGTGTGAAAACCTCCGGGCTCA	5	12
22	TTTTAGTAAGATTATTAGAAATAGGTCGGGTTA	0	0
23	TTTTGTAAAGACAGTGGTGTGAAATCTCCGGGCTCA	0	0
24	CCAGATCAGTCGGGTGTGAAAGCCCCGGGGCTCA	0	5
25	TTTTAGTGAGTTATTTAGATGATTGGTCGGATT	0	0
26	CAGCCTAAGTCTGGCGTGAAATATCCCGGCTTA	0	0
27	CCCGCAAAGTGCTTTGTGAAATCCCGGAGCTCA	7	9
28	CTTGTCGAAGTCGGGCGTGAAAGCTCCGGGCTTA	11	2
29	CTTGGTAAGTTGGGCGTGAAATCTCCGGGCTTA	0	5
30	TGTCGTAAGTTTGGTGTGAAATCTCCCGGCTTA	0	0
31	TTTTAAGACAGGCGTGAAATCCCCGGGCTTAAC	7	3
32	ACTCTTAAGTCGGAGGTGAAAGCCCAGGGCTCA	0	0
33	GTTTTTAAGTCAGATGTGAAATCTCGGAGCTCA	14	0
34	TGCGGTAAGTTGGGCGTGAAATCTCCCGGCTCA	2	2
35	CTTCGGGCCTGGCGGGATGGTCTGCCTTACGGT	2	28
36	TTTAGACAGTCAGATGTGAAATCCTGGAGCTTA	0	0
37	AAAGAAGAGGGCAGATATTTTTGCAAGAGAATA	3	3
38	CCTGTTAAGTGTGAAGTGTGAAATCTCCAGGGCTC	6	10
39	TTTCTTAAGTCAGAGGTGAAAGGCTACGGCTCA	7	9
40	ATAAAAAAGAGAAAAGAGAGAGAGAAAAACAATG	8	2
41	CTAGGTAAGCGTGTGGTGTGAAAGCTCGGGGCTCA	10	11
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TTTGCTAAGTTCGGTGTGAAATCTCCTGGCTTA	9	14
GCAAGCAAGTCGAAGGTGAAATCCCACGGCTCA	4	12
ATCGGAAAGTGTTTTGTGAAATCCCTCGGCTCA	0	0
CGCTCTAAGTTTGGTGTGAAATCTCCCGGCTTA	0	0
TTTCCGGCAGCATTGCCTGTCTGCAAGAGTATT	15	7
TTGGGTAAAGTCAGATGTGAAATCCCCGGGCTCAA	5	0
TTTTGTAAGACAGTGGTGTGAAATCCTCGGGCTCA	0	0
CTTGGTAAGTCAGATGTGAAAGCCCTCGGCTCA	10	0
CTCCGTAGGTGAGGTGTGAAATCCCTCGGCTCA	8	4
CCAAGCAAGTCTGTTGTGAAATCCCGGGGCTCA	0	0
CTTGAAAAGTTGGATGTGAAAGCTCCTGGCTTA	3	14
TTCGTCAAGTCTGATGTGAAAGCCCCGGGCTCA	2	13
TTTTCTAAGTCACGTGTGAAATCTTCCGGCTCA	4	10
CTCTATAAGTCAGATGTGAAAGCCCTGGGCTTA	0	0
CCCGACAAGTCTGGTGTGAAAACGCTACGGCTC	0	0
GCTTTTGCCTCGAGGGTTAAAGACCAAAGCTTA	0	0
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CTATTCAAGTCAGAGGTGAAATCCCTGGGCTCA	10	6
CGGTCTAAGTCGGGTGTGAAATCTCCGGGCTCA	0	0
TCTTGTTTGTCTGTGGTGTGAAAGCCTTGGGCTTA	0	18
TCTTGTAAGACAGAGGTGAAATCCCGGGGCTTA	3	3
TTGTCATAGTCAGGTGTGAAAGCCTTGAGCTCA	3	2
TCTTTTAAGTTGGGTGTGAAATCCCGGGGCTTA	0	0
TTATGTAAGTCAGATGTGAAATCCCGGGGCTTA	7	4
CAATCTAAGTCAGAGGTGAAATACTATCGGCTC	4	8
GGTGGTAAGTCAGTGGTGTGAAATCCTGCGGCTCA	0	0
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TATCAGTGGGGGTTCAATCTATTTATATAAAAA	0	15
TTTTTCGTGTGTTAGCAACTAAAAATCAAACCG	0	0
GCTGTTGAGTTGGAGGATGAAATGTCTGGCAGT	0	0
CTTCGTAAGTCGGATGTGAAATCCCGGGGCTTA	6	6
TTTACTGTATTTTAGTAAAAGTCTCCGGCTTA	0	0
TTCGTTAAGTCCGATGTGAAAGCCCTGGGCTCA	6	11
CCGCTTAAGTCGGGTGTGAAAGCCCCGGGGCTCA	5	21
TTCGCTAAGTCTGATGTGAAATCTCCTGGCTTA	7	3
TCTGCTAAGCGTGCGGTGAAAGCCCAGGGCTCA	0	0
GAAATTAAGTCAGTGGTGTGAAAGCTTACAGCTTA	3	9
TCGTGTAGTCAGATGTCAAATCCTTCGACTCA	0	0

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4	TAAGGAAAGTCAGATGTGAAATCCCCGGGGCTCA	9	4
5	TTGGGTAAAGTCAGATGTGAATCCCCGGGGCTCAA	0	0
6	TCGGGTAAAGTCAGATGTGAAATCCCCGGGGCTCA	3	0
7	GTCGTAAAGTCAGGGGTGAAATCCCCGGAGCTCA	2	11
8	GCTCTGGCGCCGGCCGCGCGGCCGCCCTTCGGG	0	0
9	TTTTGTAAAGACAGGTGTGAAATCCCCGGGGCTTA	3	4
10	ATTCTGGTTGTATTGGGCCTATGCACTTGTTGT	4	7
11	GCTTGTAAGTCAGAGGTGAAAGCCCCGGAGCTTA	0	0
12	AGTGGTAAGTACCTTGTGAAATCCCCGGTCTCA	2	6
13	TTCCATAAGTCAGTGGTGAATACGGCAGCTTA	0	0
14	CTTGTTAAGCAGGGTGTGAAATCCCTCGGCTCA	3	2
15	CTTTCTAAGTCAGGGGTGAAATCCTGGAGCTCA	0	0
16	CTCTCAAGTCAGGCGTGAAAGCCCCGGGGCTTA	9	7
17	ATGTGTCAGTCAGGGGTGAAATCCCCGGAGCTCA	6	10
18	TTGGTTAAGACTGACGTGAAAGCTCCTGGCTTA	0	0
19	GTTGATAAGTCAGTGGTGAAGCTCCGAGCTTA	12	4
20	TTTACCAAGTCTGGTGTGAAATCTCTCGGCTTA	3	4
21	TTTTAGTGGGTTTTAAGATGATTGGTCGGATAG	0	0
22	CTTCGTAAGTTCGGTGTGAAATCTCCCGGCTCA	7	9
23	GCTCGCAAGCGTCTTGTGAAAGCCCCCGGCTCA	10	6
24	AAGTGTAAGTCAGGTGTGAAATACCAAAGCTCA	8	8
25	TTGTGTAAGACAGATGTGAAATCCCCGGGGCTCA	10	4
26	TGGGGTAAGTTCAAGGTGAAAGCTTCGGGGCTCA	2	2
27	TTTGTAATAATTTAAATAAAATTTAAATTTAA	6	9
28	TTGTATAAGTTAGTTGTGAAATACCTGTGCTTA	0	0
29	TTCGGTAAGTTGGGCGTGAAATCTCCTGGCTCA	8	9
30	TCCTACAAGCCAGAGGTGAAATCCCCGGAGCTCA	0	5
31	TTTGTCGCGTCTGCTGTGAAAACCCGAGGCTCA	2	5
32	CCCATCAAGTCTGCGGTTAAAGACCGGAGCTCA	0	0
33	ATTCTGGCTGTATTGGGCCTCTGCACTCGATGC	0	18
34	CTTGGTAAGCGTGTGGTGAAGTCCGGGGGCTCA	8	5
35	TTCAGCAAGTTGGATGTGAAATCCCCGGGGCTCA	0	23
36	CTTGTCACGTCGGGTGTGAAAACCGGGGCTTA	7	18
37	TTCGTTAAGTCAGATGTGAAAGCCCCGGGGCTCA	0	0
38	CTCGGCAGGTCACTGGTGAATCCCACGGCTCA	0	0
39	CCTTGTAAGTCAGGTGTGAAAGCCCTCGGCTCA	0	0
40	ACCTGTAGGCGCGTTGTGAAAGCCCTCGGCTCA	0	0
41	TTGTGTAAGTTGGATGTGAAATTTCCAAGCCTA	4	5
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TTTAGTAAGTCGATTGTGAAAGCCCCAGGCTTA	0	0
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ATTGATAAGTCAGATGTGAAATCTCGGGGCTTA	0	0
ATCGTCAAGTGCCTTGTGAAACCTCCCGGCTCA	3	9
GTAAGTAAGTCAGATGTGAAATTTTGAAGCTCA	9	2
TTTTTAAGACAGTGGTGAAATCCCCGGGCTCAA	0	0
TCGCACAAGTCAGGTGTGAAATCCCCGGGCTCA	0	5
CCTTTTAAGTCGGATGTGAAATCCCCGGGCTCA	3	5
ACAGGTGCGTCAGAGGTGAAATCTCCCGGCTTA	0	21
TTTCTTAAGTTCGTGCGTGAAATCGCCCGGCTTA	0	0
CATGGTATGTGCGGGCGTGAAACTCCGGAGCTTA	6	3
TATCCGGCGTCTCTGACGTCTGCCTGATACGAC	3	24
CTTTTTGCGTCAGAGGTGAAATCCACAGGCTCA	0	0
GTCGTTAAGTTGGGGGTGAAATCCCGAGGCTCA	0	0
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CACTGTAAGTGTGCGAGTGAAATCCCACGGCTTA	0	0
TTGTGGATTGTGATTCCGAGGTTCAAGTCCTTCG	0	0
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TTCGGTAAGTTGGTTATGAAAGCTCCTGGCTTA	0	0
TCCATCAAGTTGGGTGTGAAAGCCCTCGGCTTA	9	6
CGATTTTAGTCAGGCGTGAAAGCCCTGGGCTTA	0	0
CCGATTAAGTCGGGTGTGAAATCTCCGGGCTCA	0	0
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CCAGGTAAGTTTGATGTGAAAGCTCGGAGCTCA	4	8
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CTTGGCAAGTCAGATGTGAAAGCCCTCGGCTCA	5	2
GTGGGCACGTGCGACCCTGAAAGCCCCGGGCTC	4	0
TTTTGTAAGACAGTGGAGAAATCCCCGGGCTCA	0	0
TGATATGAGTGTGATGTGAAAGCCCTGGGCTTA	2	0
TTGGGTAAGTCAGATGTGAAATTCCTGGGCTCA	4	0
GTCGGTAAGTCAGTGGTCAAATCCTATAGCTTA	13	6
TTGCGTAAGTTAGGCGTGAAAGACTTCGGCTAA	0	0
GCTGGAAAGTTGGGGGTGAAATCCCGAGGCTCA	0	9
CTTGGCAAGTCGGGTGTGAAATCCCCGGGCTCA	6	9
TTTTGTAAGACAGTGGAAATCCCCGGGCTCAAC	0	0

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4	TTGAATAAGTTATCTGTGAAATCCCCGGGCTCA	6	3
5	AATGAACTTTTTTTTCGATTCTGTTTTTTTTT	5	6
6	TCTGTTGCGTCGGAAGTGAAACTCAGGGCTTA	2	6
7	AACAGCTCAGTCTTCAAAGGATTGAGACGGAG	0	0
8	TCTTATAAGTCAGTGGTGAAATCTCCGGGCTTA	0	2
9	CCTGGCAAGTTTGAGGTGAAATCTCCCGGCTCA	6	5
10	ATTGTTAAGTCGGGTGTGAAATCCCGGGGCTCA	0	10
11	ATTATTAAGTCGGGGGTGAAATCCCGAGGCTCA	0	0
12	TCGGGTAAGTCTGCTGTGAAAGCTCCGGGCCTA	6	4
13	CATGGAAAGTTGGACGTGAAACTCCTGGCTTA	0	11
14	GTCGTTAAGTCGGGGGTGAAAGCCCAGAGCTCA	0	10
15	CTCGAAAAGCGTTCGGTGAAATCCCCGGGCTCAA	0	2
16	CTTTGTAAGTCAGGTGTGAAAGCCTGGGCTCAA	0	0
17	TTTCGGACAAGGCATTCTGGTCTACTTTTAGG	9	4
18	CCTGTTAAGTAGGGTGTGAAATCCCCCGGCCCA	5	4
19	TGTGTGGTGTGGTGCCTCTGGTCGCCTGCGAGC	3	8
20	ACTATTAAGTCAGGTGTGAAACTATGGGCTCA	5	3
21	TTCCCTAAGTTTGGTGTGAAATCTCCCGGCTCA	8	0
22	CTGATCAAGTCTGGCGTGAAAGCCCCCGGCTCA	0	4
23	ATGGGCGCATCGATCGCTGAAATCCCCCGGCTC	2	2
24	TTGGTTAAGTCAGATGTGAAATCCCCGGGCTCA	2	0
25	CTTTGTAAGTCAGGTGTGAAAGCCCCGGGCTCA	0	0
26	ATTGTTGAGTTGGAGGATGAAATGTCTGGCAGT	0	0
27	TTTTGTAAGACAGTGGTGAAATCCCCAGGCTCA	0	0
28	AATGAACTTTTTTTTTCGATTCTTGTGTTGGGC	6	3
29	TTGGGTAAGTCAGATGTGAAATCCCTGGGCTCA	4	0
30	TGGGGCACGTGGGGTGTGAAAGCGGCCCGCTTA	3	4
31	CCATGTAAGTCAGGTGTGAAAGCCCCGGGCTCA	0	0
32	ACTTTTAAGTCAGGGGTGAAATCCCGGGGCTCA	0	0
33	CGCTGCAAGTCAGGCGTGAAATCCTGGGCTTA	0	0
34	TTGGGTAAGTCAGATGTGAAATCTCCGGGCTCA	0	0
35	CTCTTTAAGTCAGATGTGAAATCCCGAGCTTA	0	0
36	GAACGTAAGTCAGATGTTAAATCTCGGGGCTCA	0	0
37	TTTGATAAGTCTGTTGTGAAAGCTCCCGGCTTA	3	8
38	AATGAACTTTTTTTTTCGATTCTTGTGTTGGCA	4	3
39	CTTTCTAAGTCAGAGGTGAAATCCCGGGGCTCA	4	5
40	CGTCCCAAGTTAGGCGTGAAAGCCCCGGGCTCA	0	0
41	CCCGTTAAGACAGGTGTGAAATCCTGGGCTCA	0	3
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CTGTGGAGTTTGATCCAGAGATCCCGTCCTTTT	0	0
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TGCGTTAAGTCTGACGTGAAATCTCCTGGCTTA	6	4
TGATACAAGTCGGGTGTGAAATTCCGGGGCCTA	3	3
TCAGACAAGTGAGGCGTGAAAGCCCTGGGCTCA	3	9
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GACGTCAAGCGGGGTGTGAAAGCTCCTGGCTTA	3	9
CTATGCAAGTTAGATGTGAAAGCCCCGGGCTCA	0	0
ATTATTAAGTCGGATGTGAAACTATGGGCTCA	0	8
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GTCTGTAAGTGTCTCGTGAAATCCCCGGGCTCA	2	5
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TCCAAAAGTCTACTGTGAAATCCCTGGGCTTA	0	0
TTACGTATGTCTGGGGTGAAATCCCTGAGCTTA	0	0

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5	CTTAGCAAGTTGGATGTGAAATCCCTCGGCTTA	2	10
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8	TTTTTTAAGTCAGAGGTGAAAGCCCCGGGGCTCA	6	7
9	CTTGGCAAGTTTCGAGTGAAATCTCCCGGCTCA	3	7
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11	TTAGATAAGTCAGTGGTGAAATCCGGCAGCTTA	0	0
12	ATGGGCAAGCGAGGTGTGAAAGCTCCCGGCTCA	6	6
13	TATGCAAGACAGATGTGAAATCCCGGGGCTCAA	0	5
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15	CCTCTCAAGCGTCCTGTGAAAGCCTCCCGCTCA	3	6
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18	CTTGGCAAGTGAGGCGTGAAAGGCCTGGGCTCA	0	7
19	TTCTTCAAGTCAGTCGTGAAATCTCCGGGCTTA	9	2
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23	CCTATTAAGTCAGGGGTGAAATACGGTGGCTCA	2	11
24	ATCAGCAAGTCAGGTGTGAAATCTCGGAGCTTA	0	9
25			
26	CGATGTAAGTCAGATGTGAAAGCCCTGGGCTTA	0	0
27			
28	CATGACAAGTCAGGGGTGAAATCCTTCGGCCCA	6	4
29	CTTTCTAAGTCGGATGTGAAATCCCTCGGCTTA	2	0
30	ACCGGAAAGTCAGAGGTGAAATCCCAGGGCTCA	0	0
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33	TTTGCCAAGTCTGATGTGAAATCCCTGGACTCA	0	0
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35	GTTTGTAAGTCAGATGTGAAATCCGAAGCTCA	0	0
36	CATGAAAAGCAGGGTGTGAAAGCCCTCGGCTCA	3	7
37	CTCATTAAGTAGGGTGTGAAAGCCCCCGGCTCA	0	9
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50	ATTAGTAAGTTGGGAGTGAAAGCCCCGGGGCTTA	13	0
51	GTAAGCAAGTCAGATGTGAAATTCCGGAGCTCA	0	0
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53	TTTGTGGTGCCGCCTGCAGTCCAATTAGCTTTG	0	0
54	CGCGTTAAGTCTGACGTGAAATCTCCCGGCTTA	2	6
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56	TTTGTCACGTGCGAAAGTGAAAACCTCGGGCCTTA	0	12
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CTTTGTAAGTCGGGTGTGAAAGCCCAGGGCTCA	0	0
CACGGTAAGTGGGGTGACAGCGGACGGCTTA	0	6
CAGTGTAAGTCCGGGTGTGAAATCTCGGGGCTCA	8	5
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CTCTTCAAGTCAGACGTGAAATCCTCGGGCTTA	7	5
TTTCGGGGCGGCGGAGGGCTGCGGCCGGCGCGC	0	4
ACCGTTAAGTCGGAGGTGAAATCCTGGGGCTCA	0	0
CGTGCTAAGTTAGTTGTTAAATCTCTCGGCCTA	2	12
ACCGGCAAGCGTCTTGTGAAATCCCACGGCTCA	2	2
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GCTGGTAAGTCAGTGGTGAAATCTCCGAGCTTA	2	0
CTGCGTAAGTCGGATGTGAAAGCCCCGGGCTTA	0	0
TTAATTAAGTTTATTGTTAAATTCAATGAGCTT	0	0
TTTGTAAGTCAGATGTGAAATCCCCGGGCTTAA	0	2
TTTGTTAAGTCTGATGTGAAAGCCCCGGGCTCA	0	7
TAATGTAAGACAGTTGTGAAATCCCCGGGCTCA	0	7
CCCGTTAAGTCAGTTGTGAAAGCCCCGGGCTCA	0	6

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6	TTTCTTAAGTTGGATGTGAAATCCCCGGGCTTA	0	0
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8	AACAACCTCATTCAAGTCAATTGATTGAGACGAAG	0	0
9	TCTTGTTAGTCAGGTGTGAAAGCCCTCAGCTCA	3	6
10	AACAACCTCATTCAATGAGTGAGACGGAGA	0	0
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12	TTTAATAAGTTTTTTGTAAAATCTTATGGCTCA	0	7
13	TTTTGTAAGACAGTGGCGAAATCCCCGGGCTCA	0	0
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15	CTTTTTAAGTCAGTGGTGAATTTCTACCGCTTA	0	0
16	TAAGGTAAGTTTGGTGTGAAAGCTTCGAGCTTA	4	7
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18	CTTAGCAAGTCAGATGTGAAAGCCCCGGGGCTTA	2	0
19	ATTTGTTAGTCAGGGGTGAAATCCCCGGGGCTCA	4	4
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23	ATCGCTAAGTCGGGGGTGAAAGCCCCGAGGCTCA	5	2
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25	CCTTGTAAGCCTGGCGTGAAAGTCACCGGCTTA	0	0
26	TTTGTGCGCTCTGCTGTGAAATCCCGAGGCTTA	2	3
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28	CCGAGCGGGTCGCGGGTGAAATCCTCCAGCTTA	2	0
29	TCGATTAAGTCAGTGGTGAATACTTCAGCTCA	0	2
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31	GTCTTTAAGTCAGGGGTGAAATCCTGGAGCTCA	0	9
32	CTTTTTAAGTCGGATGTGAAATCCCTGAGCTTA	3	3
33	CTTCGGGCTGGACTGTGAAGGCTCACCGCAAGG	7	4
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35	TTGCGTAAGTTCGGCGTGAAATTTTTCGGCTTA	0	0
36	ACTTCTAAGTGTCGTGTGAAAGCCCATGGCTTA	0	0
37			
38	CAAGGTAAGTTCGATGTGAAATCTCCGGGCTCA	5	3
39	CTTTGCAAGACAGATGTGAAATCCCCGGGCTTA	7	2
40	CTTGGTAAGTCAGGTGTGAAAGCCCAGGGCTCA	0	0
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42	ATTTTTTTATTTTTTTGAATATTTTAAATTAGT	0	6
43	TTTCGCAAGTCAGATGTGAAAGCCCCGGGCTCA	0	0
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45	ATGTGTAAGTGCTTGTGAAAGCCCCGGGCTCA	0	0
46	AACAGCTCAGTCGCAAGATTGAGACGGAGGCGG	0	0
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48	TAAGTGAAGTCAGATGTGAAATCCCCGGGGCTCA	5	2
49	TTGGGTAAGTCAGATGTGAAATCCCCAGGCTCA	0	2
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51	TCTGTTAAGTGTGAAGTGAATCTCCAGGGCTC	3	4
52	TTTGTACGTCGGAAGTGAAACTCAGGGCTTA	4	2
53	ATAAAAAAGAGAAAGAGAGAGAGAAAAACAATT	3	3
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55	CTTTTCAAGCCAGGGGTGAAATCCCAGAGCTCA	0	0
56	TCAGACTAAGTCAGATGTAAAATCCCAGGGCTT	2	0
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AGATATTAGTCAGATGTGAAATCCCGGGGCTCA	0	3
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TTTTGTAAGTCTGACGTGAAATCCCGGGGCTTA	0	12
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TTGAGTCAGTCAGTCGTGAAAGCCCTGGGCTTA	0	0
GAAAATAAGTCAGTGGTGAAATCCTGCAGCTTA	0	0
CCGAGCGGGTCGCGGGTGAAATCCCCAGCTTA	3	2
ACTTGTAAGTCAGTGGTGAAATCTCTTCGCTTA	10	0
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CTTTGTAAGACAGATGTGAAATCCCGGGGCTTA	0	0
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GTGTTCAAGTGGTGTATGAAATCGCTCGGCTCA	0	5
TTTCGGGTATTTGTTGCTAGCTGGTCTCATTGG	2	2
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CGTGGTAAGTCAGATGTGAAAGCCCGGGGCTCA	3	5
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ACTGTTTAGTCAGAGGTGAAAGCCCAGGGCTCA	8	2
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AACAACCTATTCAAGTCAATTGATTGAGACGGGG	0	0
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ACTGTCAAGTCAGGGGTGAAATCCCGAGGCTCA	0	3
TTTTGTAAGTTTGGTGTGAAATCTCCCGGCTTA	6	0
TTGGGTAAGTCAGATGTGAAATCCTCGGGCTCA	5	0
CTTTGTAAGTCAGGTGTGAAGGCCTGGGGCTCA	0	0
GCGATTAAGTCAGGGGTGAAATCCCGGAGCTCA	2	2

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4	TTTTTTAAGACAGGCGTGAAATCCCGGGCTTAA	0	0
5	TCCGTTGCGTCGGAAGTGAAAACCTCAGGGCTTA	0	6
6	TTTAGTGAGTTTATTTAAGAGATAGGTCGGAT	0	0
7	TCTGTTAAGTGAAAAGTGAAATCTCCATCGCTC	0	0
8	TTGGGTAAGTCAGATGAGAAATCCCCGGGCTCA	3	0
9	TTGGGTAAGTCGGATGTGAAATCCCCGGGCTTA	0	0
10	GTTTGTAAGACAGTGGTGAAATCCCCGGGCTCA	0	0
11	ACTAATAAGTCAGTGGTGAAAGCCTGCAGCTTA	4	2
12	CTTTGTAAGTTAGAGGTGAAAGCCTGGAGCTCA	2	6
13	TCTTCTAAGTCGGATGTGAAAGCTCCTGGCTTA	4	3
14	TAATGTTAGTCATTTGTAAAAGCCCCGGGCTCA	0	0
15	TTCGTTAAGTCTGGCGTGAAAGCCTCCGGCTCA	0	0
16	ATCGTTAAGTCGGGGGTGAAATCCCGGGGCTCA	2	2
17	TTTGTTAAGTCTGCTGTGAAAGCCCTGGGCTCA	0	2
18	CTTTATAAGTCAGCTGTGAAATGTCTGGGCTTA	0	8
19	TTTGGCCAGTCAGCCGTGAAAGCCCTGGGCTTA	0	0
20	CCTGATAAGTCAGAGGTGAAAGCCTGCAGCTTA	0	0
21	TTTGTAAGACTGTCGTGAAATCCCGGGGCTTAA	0	7
22	CTATGCAAGTCAGAGGTGAAATCCCAGGGCTTA	0	0
23	TTCTATAAGTCAGATGTGAAAGCCTCGGGCTCA	0	5
24	TCTAGTAAGTCAGTCGTGAAATCGCTGGGCTTA	2	2
25	CCTGTTAAGTAGGGTGTGAAAGCCCCGGGCTCA	2	2
26	CCTGTTAAGTGTGAAGTGAAATCTCCAGAGCTC	4	2
27	CGCATTAAGTCTGACGTGAAATCTCTCGGCTTA	2	0
28	TTATTTAAGTCGGGTGTGAAAGCCCCGGGCTCA	2	5
29	TTCGGTAAGTCGGGTGTGAAAACCTTTGGGCTCA	0	0
30	ATTGAAAAGTTGGAGGTGAAATCCCAGGGCTCA	8	0
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32	CCTTGTAAGCCTGGCGTGAAAGTCACCGGCTCA	0	0
33	CTGAGGGTTACCAAGGAGAGGTTTCAGTCCCAC	0	0
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37	CCTGCTAAGACTGACGTGAAAGCTCCTGGCTTA	0	2
38	TCTTGGCGTAAAAGATTAAAACTTTTAATTTT	4	0
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41	CCATGCAAGTCAGATGTGAAATCCCGGGGCTCA	0	2
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6	ACGGGTAAGTGGGTGTGAAAGCGCTCGGCTAA	0	2
7	TTGGGTAGTCAGATGTGAAATCCCGGGGCTCAA	3	0
8	GAGTGCAAGTCAGATGTGAAATCCCGGGGCTCA	2	2
9	TTGGGTAAAGTCAGATGTGAAATCCCGGGGTTCA	0	0
10	TCTTATAAGTCAGTGGTGAATCTCCTCGCTTA	4	3
11	TTAGTAAGACAGTGGTGAATCCCGGGGCTCA	0	0
12	CCTTGTAAGTGTCTGATGAAATCCCACGGCTTA	0	0
13	ACTGAAAAGTTGGAGGTGAAATCCCAGGGGCTCA	3	0
14	CGCTGTAGTCGGGTGTGAAATCCCTCGGCTCA	2	3
15	CTTGTAAGTCAGGTGTGAAAGCCTGGGGGCTCAA	0	0
16	CCCCATAAGTCCCGTGTGAAATCCCCCGGCTCA	2	0
17	CTTGGTAAGTCTGGTGTGAAAACCTGGGGGCTCA	4	5
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20	AAGGGTAAGTACCTTGTGAAATCCCACGGCTCA	0	3
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22	TTTTGTAGTCGTCTTTTAAATCTCCCGGCCTA	0	0
23	TTTGTTAAGTTGGTGGTTTAATCTTCGGGCTCA	2	6
24	TTTAATAAGTTCTTTATAAAAGCTTATGGCTTA	0	3
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26	TTTAGAGAGTGTTAACATCGAAATCCCAAAACG	0	0
27	CCGGCTAAGTCAGTTGTAAAATTCCTGCGCTCA	2	2
28	TTTTGTAAGACAGTGGTAAAATCCCGGGGCTCA	0	0
29	CTATGCAAGACAGATGTGAAATCCCGGGGCTCA	2	3
30	GACTGTAAGTCAGGTGTGAAAACCTACGAGCTCA	0	0
31	AACATCCCTGATTGCAAAATCAGAGACGGAGGC	0	0
32	CGCGATAAGTCAGTTGTGAAATCCCGGGCTTA	0	4
33	ACTTGTAAGTCAGAGGTGAAACTCCGAAGCTTA	0	2
34	CGGTATAAGTCAGCGGTGAAATCCTTCGGCCCA	0	2
35	GAAGGTAAGTCAGATGTGAAATTCCGAAGCTCA	0	0
36	CTTGTCGCGTCTGCCGTGAAAACCCGAGGCTCA	3	2
37	TCTTGCAAGACAGGTGTGAAATCCCGGGGCTTA	4	3
38	ATCAATAAGTCTGCTGTGAAAGTCGAAGGCTCA	0	0
39	TTTTGTAAGACAGTGGTGAATCCCGGACTCA	0	0
40	CCTTTCAAGCGTCCTGTGAAAGCCTCCCGCTCA	2	0
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6	CGCATTAAGTCTGACGTGAAATCTCCTGGCTTA	0	4
7	CTTGGCGAGTGAGGCGTGAAAGGCCTGGGCTCA	3	5
8	TTTTGTAAGACAGTGGTCAAATCCCCGGGTTC	0	0
9	GCGCGTAAGTGCTTTGTGAAAGCCCTGGGCTCA	0	8
10	ATCTGTAAGTGTCGTGTGAAAGCCCACTGCTCA	3	0
11	TATAATAAGTTGAAAGTGAAAGCCCGGGGCTCA	0	0
12	TTTTTTAAGACAGTGGTCAAATCCCCGGGCTCA	0	0
13	TGATTTAAGTGAGTTGTGAAATACCCGTGCTCA	3	0
14	GATAATAAGTCAGTGGTCAAAGCTCACAGCTTA	0	3
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18	TGTTATAAGTGTGTTGTGAAATCCCTGGGCTTA	0	3
19	CCAAGCAGGTCGGGTGTGAAATCCCTCGGCTCA	0	0
20	AATAATAAGTCAGTGGTCAAAGCCTACAGCTTA	0	8
21	CTTTGTAAGTCAGGTCAAAGCCTGGGGCTCAAC	0	0
22	ATAAGAAAGGGAGAGAGAGAGAGAAAAATAATT	4	2
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26	CTTTTTAAGACAGGCGTGAAATCCCCGGGCTTA	2	0
27	CGATGTAAGACAGATGTGAAATCCCCGGGCTCA	0	0
28	GACGGAAAGTCAGAGGTGAAATCCCGGGGCTCA	0	0
29	GGCGTTAAGTCAGTGGTCAAATCCTGCAGCTCA	0	0
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35	TTTGTGGTGGCCTCGATGGTCCATTCATTTTGT	0	0
36	TCTTGGCGTAAAAAATTAAAACTTTTAAAAAA	3	0
37	TAGGGTAAGTCAGATGTGAAATCCCCGGGCTCA	0	0
38	CAAGATAAGTCAATCATTAATCTCCTGGCTTA	0	0
39	TCGTTTAAGTCCGTTGTGAAAGCCCTGGGCTCA	0	5
40	AACAACACACATTGATGTGAGACGGAGGCAG	0	0
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5	GTCAGCAAGTCAGATGTGAAATCCGGAAGTCA	0	0
6	TCTGTCGCGTCGGAAGTGAAACTCGGGGCTTA	2	2
7	TTTAGAGTTTATTCAGTAGAGTCCGCTTGAAA	3	2
8	TTTGTTAAGTTGGAGGTTTAATCTCTGGGCTCA	0	0
9	CTACGTAAGTGTCTGTGAAATCTCATGGCTCA	0	2
10	ACCAGAAAGTTGGGGGTGAAATCCCGGGGCTCA	3	0
11	TTCTTCGTGTGTTAGCACCTAAAAACCAGAACG	0	0
12	TTTGGTTAGTTGGATGTGAAATCTCCTGGCTCA	0	0
13	CCTGACAAGTCTGATGTGAAAGACCTGGCTTAA	0	0
14	TTTTGGGGCGGGTGGGGCTGTGTCTGCCGTATG	4	3
15	TCCTATTTGTCTGAGGTGAAATCCCAGGGCTTA	0	0
16	CTCATTAAGTGTGTGGTGAATCTCTGTGCTCA	4	2
17	TTTTGTAAGACAGTGGTGAATCCCCGGGTCAT	0	0
18	GTCGTTAAGTCGGGGGTGAAATCCCAGAGCTCA	0	0
19	TTGCCTAAGCCAGGCGTGAAATCCCCGGGCTTA	0	3
20	CTATATGAGTTGGGTGTGAAATCCCCGGGGCTTA	0	0
21	TTGGGTAAAGTCAGATGTGAAATCCCCGGGCTCG	3	0
22	CTTTGTAAGTCGGGTGTGAAAGCCTGGGGCTCA	0	0
23	CCGTGCGAGTGAGGCGTGAAAGCCCCGGGCTCA	0	6
24	CTATTTAAGTCAGTGGTGAATCCTTCAGCTTA	5	0
25	TGATGTAAGACAGATGTGAATCCCCGGGCTCAA	2	2
26	TACCATAAGTCAGATGTGAAAGCCCTAGGCTTA	5	0
27	TTTTGGGGCGGGCGGGGCTGTGTCTGCCGTACG	0	5
28	TTTTTTAAGACAGGCGTGAAATCCCCGGGCTCA	4	0
29	CCTTGGGCCTGGCTGGCCGGTCCCCCTCACCGG	0	6
30	TTCGTTAAGTTGGATGTGAAAGCCCCGGGCTCA	0	7
31	TTTGTCGCGTCTGCCGTGAAATTCCTGGCTTA	0	7
32	CTTGTCGCGTCGACCGTGAAACCTGGGGCTCA	0	0
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34	TTCTTATAAATATTAGGAACTAGAATTTGATAG	0	9
35	TTGTTTAAGTGAGGTGTTAAAGCCCTGGGCTCA	0	0
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37	ATACTTAAGTTAGGGGTGAAATCCCGAGGCTCA	0	0
38	CTCGAAAAGCGTTCGGTGAAATCCCCGGGCTCA	0	0
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9	CTTTATA	2	3
10	CTGGGCA	2	0
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13	CCTCGTA	2	0
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18	TTCGCTA	0	0
19	AACAAC	0	0
20	TTCTGTA	0	0
21	TTTCGTA	0	4
22	GCGTGTA	0	0
23	TCCTGTA	0	0
24	CTTGCCA	4	0
25	TTCGTTA	0	0
26	CAAGGCA	0	0
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28	CGTCGTA	0	3
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30	CCTTGCG	0	0
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34	TCTGTTA	0	3
35	GGATTTA	0	0
36	CTTGGCC	0	0
37	TCTATTG	0	2
38	CGTTTCG	3	0
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40	TTGGGA	2	0
41	GTTGATA	0	0
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41	CTGGGTAAGTTCGATGTGAAAGCTCCGGGCCCA	2	0
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53	GAATGTAAGTCAGACGTGGAATCCCGGAGCTCA	0	0
54			
55	TCCATCAAGTGCTTTGTGAAATCCCACGGCTCA	0	0
56	TTTTGTAAGACAGATGTGGAATCCCGGGGCTTA	0	0
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4	TTTGGCCAGTCAGCCGTGAAAGCCCCGGGCTTA	0	0
5	AACAATTCACACATTGATGTGAGACGGAGGCGG	0	0
6	CTCGAAAAGTGTTCCGTGAAATCCCCGGGCTCA	0	0
7	TTGGGTAAGTCATGTGAAATCCCCGGGCTCAAC	0	0
8	TTGTCCAAGTCGGGTGTGAAAGCCTTGAGCTCA	0	0
9	AACAATTCATTGAGTCAATTGACTGAGACGGAG	0	0
10	AACAGCTCATTGTAAAGATGAGACGGAGGCGGA	0	0
11	TCTTGTAAGTCAGATGTGAAATCCCCGGGCTTA	0	0
12	TTAAAAAAGTTAGATGTGAAATCCCTGGGCGTA	0	0
13	CTTAATAAGTCAGGTGTGAAATCCTGGGGCTCA	0	0
14	CCTCGCAAGCGTCCTGTGAAATACCTCAGCTCA	0	0
15	ACCAACTCACACATTGATGTGAGACGGAGGCGG	0	0
16	CCCCATAAGTCAGTCGTAATCGCTGGGCTCAAC	0	0
17	ACATTTGAGTCAGGGGTGAAATCCCGAGGCTCA	0	0
18	GAATGTAAGTCAGACGTGAAATTCCGGAGCTCA	0	0
19	AACAATCATTAAAGATGAGACGGAGGCGGATT	0	0
20	TTTTTTAAGACAGGCGTGAAATCCCCGGGCTAA	0	0
21	TGACTCAAGTCAGCGGTGAAAGCCTGGAGCTCA	0	0
22	TTTGATTAGTCGTTTGTTAAAAGTCCCGGCTTA	0	0
23	CCGTTTAAGTTAGGTGCGAAAGTCCTGGGCTCA	0	0
24	TCTAACAAGTCAGGCGTGAAATCCCGGGCTCA	0	0
25	AACAATCATTGTAAAGATGAGACGGAGGCGGA	0	0
26	CCAATAAGTCAGAAGTGAAAGCCCCGGGCTCAA	0	0
27	ACAATCATTCAATGAGTGAGACGGAGGC	0	0
28	CTTTGTAAGTCAGGTGTGAAATCCCAGGGCTTA	0	0
29	AACAATCATTCAATCAAAAAGATGAGACGGAG	0	0
30	AACAGCTTACACATTGATGTGAGACGGAGGCGG	0	0
31	AGGCATAAGTCAGATGTGAAATCCCGGGGCTCA	0	0
32	CTTGGCAAGTCTGATGTGAAAGCCCATGGCTTA	0	0
33	GAATGTAAGTCAGACGTGAAATCCCGGAGCACA	0	0
34	TCAGACTAAGTCGAATGTAAAATATCAAGGCTT	0	0
35	CCTGACAAGTCTGATGTGAAAGACCGGGCTTAA	0	0
36	GAAGGCAAGTCTGGCGTGAAATCTCTCGGCTCA	0	0
37	TTTGAAAAGTTTCGTGTGAAAGGTCAGGGCTCA	0	0
38	TTGGGTAAGTCAGATGTGAAATCCCCGGTCTCA	0	0
39	CTTTGTAAGTCAGATGTGAAAGCCTGGGGCTCA	0	0
40	TTGGGTAAGTCAGTTGTGAAATCCCCGGGCTCA	0	0
41	TTAGGTAAGTCAGATGTGAAATCCCCGGGCTCA	0	0
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3	TTTAAGACAGGCGTGAAATCCCCGGGCTTAACC	0	0
4	CCTCGGGTGCAGGCCGACGGTCCACCTCGCGGT	0	0
5	TATAGCAAGTCAGTGGTGAAATCTTGCAGCTCA	0	0
6	TTTAGCAAGTCTGGTGTGAAAGCCTCCGTTTCA	0	0
7	TTTCTGTGAGATTGAGTTGTTTGGCCTGCGGG	0	0
8	ACCTTTAAGTCGGAGGTGAAAGCCCAGGGCTCA	0	0
9	TCTATAAGTCAGATGTGAAATCCCCGGGCTTAA	0	0
10	TCTAGCAAGTCTGATGTGAAATCCCCTGCAAAA	0	0
11	TCTGGTGTGTCAGGTGTGAAATCCCCCGGCTTA	0	0
12	GACGGCACGTCTGTCGTTGAAATCCCTCGGCTT	0	0
13	CTTTGTAAGTCAGGTGTGAAGCCTGGGGCTCAA	0	0
14	AATGAACTTTTTTTTTCGATTCTTGTTTGGGCA	0	0
15	TTGGCTAAGTTTGGTGTGAAATCTCCCGGCTTA	0	0
16	TCTCAGGCTAGTGGCCGGTGGTCCGCTCGATAC	0	0
17	AACGGTAAGTACCTTGTGAAATCCCCGGACTCA	0	0
18	ACTTTCAAGTCGGAGGTGAAAGCCCAGGGCTCA	0	0
19	TCGGGTAAGTCTGACGTGAAATCTTCATGCTCA	0	0
20	TTGGGTAAGTCAGATGTGAAATCCGGGCTCAAC	0	0
21	GTTAATAAGTCAGTGGTGAAAGCCGGTTGCTCA	0	0
22	ACTTATAAGTCAGTGGTGAAATCTCTGGGCTTA	0	0
23	CTTCGTAAGTCAGGTGTGAAAGCCTGGGGCTCA	0	0
24	CTTGCCAAGTGCTTTGTGAAATCCCACGACTCA	0	0
25	TTTTTTAAGACAGGCGTGAAATCCCCGGACTTA	0	0
26	TCTTTCAAGCGTCCCGTGAAAGCCTCCGGCTCA	0	0
27	TTTAGTAAGTTCTTTATGAAATCTTACAGCTCA	0	0
28	CTTGCCAAGTGCTCTGTGAAATCCCACGGCTCA	0	0
29	CTTCATAAGTCGGATGTGAAATTCCTCGGCTTA	0	0
30	TGATGTAAGACACATGTGAAATCCCCGGGCTCA	0	0
31	TTTCGGGGTGAGGCGAGCCCGGTCCGCCGCGAG	0	0
32	CTTCGCAGGTCAGGGGTGAAAGCCCGCGGCTCA	0	0
33	TTTGATAAGTCAGATGTGAAATCCCGGGCTCAA	0	0
34	TTTGGTAAGTTAGATGTGAAATCCCGGGCTCA	0	0
35	TTTTTTAAGACGGGCGTGAAATCCCGGGCTTA	0	0
36	CGGCTCAAGTCAGGTGTGAAATCCCCCGGCTCA	0	0
37	TCTGATAAGTCAGTGGTGAAATCTGGTCGCTCA	0	0
38	ATGTGTAAGACAGGTGTGAAATCCCCGGGCTTA	0	0
39	TTGGCTAAGCTTGGTGTGAAATCTCCCGGCTCA	0	0
40	TTAAGTAAGACAGATGTGAAATCCCCGGGCTCA	0	0
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4	CAAGGTGTGTTTCTGGTGAAATCCCGGGGCTTA	0	0
5	ATTAGTAAGTCAGTGGTGAAAACCCATCGCTTA	0	0
6	TAGGGTAAGTACAATGTGAAAGCTTCGGGCTCA	0	0
7	TCTCGTTTGTCTGAGGTGAAATCCCTGGGCTTA	0	0
8	CTCTTTAAGTCAGACGTGACAGCCCTAGGCTTA	0	0
9	TTTTTAATTATTTATTTTTGTTAGTTGGAGATT	0	0
10	TTGACTAACTCGGATGTGAAAGCTCCTGGCTTA	0	0
11	TTGTGTAGACAGGTGTGAAATCCCCGGGCTTAA	0	0
12	TTTTGCAAGTCAGAGGTGAAAGCCTGGAGCTCA	0	0
13	CTATCCAAGTCAGAGGTGAAATGCCGGGGCTCA	0	0
14	TTTTTTAAGACAGGCGTGAAATCTCCGGGCTTA	0	0
15	CTATGTAAGTCAGGTGTGAAAGCCTGGGGCTCA	0	0
16	TGGGGTAAGTTCAAGGTGAAAGCTTCGGGCTAA	0	0
17	CCCGGTAAAGTCCGGCGTGAAATCCCAGAGCTCA	0	0
18	CTCTGTAAGTCAACGGTGAAATCCCTCGGCTCA	0	0
19	CGATACAAGTCAGGGGTGAAATCCCCGGGGCTCA	0	0
20	ATAAGAAAGGGAGAGAGAGAGAGAAAAATAATTGT	0	0
21	TTTTTTAAGACAGGCGTGAAATCCTCGGGCTTA	0	0
22	CGAAGAAAGTAGGGTGTGAAATGCCTTGGCTCA	0	0
23	CTTTGTAAGTCAGAGGTGAAAGCCTGGGGCTCA	0	0
24	ATTGATAAGTCAGGTGTGAAATCTTCGGGCTCA	0	0
25	CTTTTTAAGTCGGATGTGAAATCCTCGGGCTTA	0	0
26	ACTTTAAGTCGGAGGTGAAAGCCCAGGGCTCAA	0	0
27	TTTGGTAAGTCAGATGTGAAATCCCCGGGGCTCA	0	0
28	TTTTTTAAGGCAGGCGTGAAATCCCCGGGCTTA	0	0
29	TCGGAAAGAAAGATGTGAAATCCCAGAGCTTAA	0	0
30	TCTGGTAAGTCGGATGAAAGCCCCGGGCTTAAC	0	0
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32	TTGTGCAAGTCGTGTGTGAAAGTCCCCGGGCTCA	0	0
33	ACCAGCAAGTGCCTTGTGAAAGCCCCCGACTCA	0	0
34	TTGTGTAAGTTTGGTGTGAAAGCTCCGGGCTTA	0	0
35	CTTTTTAAGTTGGATGTGAAATCCCCGGGCTCA	0	0
36	TCCTTCAAGCGTCCTGTGAAAGCCTCCGGCTCA	0	0
37	CTTGCCAAGTGCTTGTGAAATCCCACGGCTCAA	0	0
38	ATCTTTAAGTCAGAGGTGAAATCCCAAGGCTCA	0	0
39	TCGTCCAAGTCGAATGTGAAAGCCCCCGGCTCA	0	0
40	CTTAATAAGTCAGGTGTGAAATCACGGGGCTCA	0	0
41	GCTATTAAGTCAGTGGTGAAATCTCCGGGCTCA	0	0
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4	TCAGACCAAGTCGAATGTGAAATCCAAGGCTT	0	0
5	CTGAGTAAGTCGGATGTCAAATCCCCAGGCTCA	0	0
6	TCTTTCAAGCGTCCTGTGAAAGCCTCCGACTCA	0	0
7			
8	CTTGCCAAGTGCTTTGTAAAATCCCACGGCTCA	0	0
9	CTTTTTAAGTCGGATGTGAAATCCCCGGACTTA	0	0
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11	CTTGGTAAGTCGGATGTGAAAGCCCCGGGCTCA	0	0
12	TCGTGCAAGACAGATGTGAAATCCCCGGGCTTAA	0	0
13	TTTGGTAAGTCGGATGTGAAATCCCCGGGCTCA	0	0
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15	TCTCGGGGTGAGGCGAGCCCGGTCCGCCGCGAG	0	0
16	TCATTCTAGTCAGGCGTGAAAGCCTCGAGCTCA	0	0
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18	CGCGCCAAGTCAGATGTGAAAGCCCCGGGCTTAA	0	0
19	CGGACTAAGTCGGTTGTGAAATCTCCGGGCTCA	0	0
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21	CTTTGTGAGTCAGGCGTGAAATTCCTGGGCTTA	0	0
22	TTCGCCAAGTTCGGTGTGAAATCTCCCGGCTTA	0	0
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24	CTTGGCAAGTGCGGCGTGAAAGTCCTGGGCTCA	0	0
25	CCTTGTAAGTCCTTGTGTGAAAGCCCTCGGCCTA	0	0
26	TTCGTTAAGTCTGGTGTGAAAGCCCTGGGCTCA	0	0
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28	TGATATAAGACAGATGTGAAATCCCCGGGCTCA	0	0
29	CCGAGCGGGTTCGTGGGTGAAATCCCCAGTTTA	0	0
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31	TTCGTTAAGTCTGACGTGAAAGCCCTGGGCTCA	0	0
32	CTTTGCAAGTCAGGTGTGAAAGCCTGGGGCTCA	0	0
33	TTTTATAAGTTTGATGTGAAAGCCCTGGACTCA	0	0
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35	TCGTGTGCGTCAGAGGTGAAATCCCCGGGCTTA	0	0
36	CCTTTTAAGTCGGATGTGAAATCCCCGGGCTTA	0	0
37	TTTGGTAAGATAGGTGTGAAATTTTTGGGTTTA	0	0
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39	AACATCTCACATATTGATGTGAGACGGAGGCGG	0	0
40	TTGAGTAAGTCAGATGTGAAATCCCCGGGCTCA	0	0
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42	TGATGAAAGACAGATGTGAAATCCCCGGGCTCA	1	0
43	AACAACACACATTGATGTGAGACGGAGGCCG	0	0
44	TTCGGTAAGTCAGATGTGAAATCCCCGGGCTCA	0	0
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46	CCTGACAAGTCCGATGTGAAAGACCTGGGCTTA	0	0
47	CCTGACAAGTCTGATGTGAAAGAACTGGGCTTA	0	0
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49	TTGGGTAAAGTCAGAAGTGAAATCCCCGGGCTCA	0	0
50	CTGGCCAAGTGCTTTGTGAAATCCCACGGCTCA	0	0
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52	CCTGACAAGTCTGATGTGAAAAACCTGGGCTTA	0	0
53	CCTGACAAGTCTGATGTGAAAGACCTGGGCTAA	0	0
54			
55	CCTAACAAGTCTGATGTGAAAGACCTGGGCTTA	0	0
56	TGATGTAAGACAGATGTGAAATCCCCGGACTCA	0	1
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4	TGATGTAAGGCAGATGTGAAATCCCCGGGCTCA	0	1
5	TGATGTAAGACTGATGTGAAATCCCCGGGCTCA	0	0
6	CTTTGTAAATCAGGTGTGAAAGCCTGGGGCTCA	0	0
7	CTTTGTAAGTCAGGTGTGAAAGCCTGGGGCTCT	0	0
8	CTCGAAAAGCGTTCCGTGTAATCCCCCGGCTCA	0	0
9	CCTGACAAGTCTGATGTGAAAGGCCTGGGCTTA	0	0
10	CCTGACTAGTCTGATGTGAAAGACCTGGGCTTA	0	0
11	CCTGACAAGTCTAATGTGAAAGACCTGGGCTTA	0	0
12	CTCGAAAAGCGTTCAGTGAAATCCCCCGGCTCA	0	0
13	CCTGACAAGTCTGATGTGAAAGACCTGGGCCTA	0	0
14	CTCAAAAAGCGTTCCGTGAAATCCCCCGGCTCA	0	0
15	AACAACCTCACACATTGATGTGAGACGGAGGCGT	0	0
16	CCTGACAAGTCTGATGTGAAAGACCTCGGCTTA	0	0
17	CTCGAAAAGCGTTTCGTGAAATCCCCCGGCTCA	0	0
18	TTGGCTAAGTCAGATGTGAAATCCCCGGGCTCA	0	0
19	CTCTGTAAGTCAGGTGTGAAAGCCTGGGGCTCA	0	0
20	TGATGTAAGACAGATGTGAAATCCCCGGGCACA	0	0
21	TGATGTAAGACAGATGTGAAATCCCCGGGCTCG	0	0
22	CTTTGTAAAGTCAGGTGTGAAAGCCTGGTGCTCA	0	0
23	CTTTGTAGGTCAGGTGTGAAAGCCTGGGGCTCA	0	0
24	CTTTGTAAGTCAGGTGTGAAAGCCTGGGGCTGA	0	0
25	CTTGCCAAGTGCTTTGTGAAATCCCACGGCTCG	0	0
26	CTTTGAAAGTCAGGTGTGAAAGCCTGGGGCTCA	0	0
27	TGATGTAGGACAGATGTGAAATCCCCGGGCTCA	0	0
28	TTGGGTAAGTCAGATGTGAAAACCCCGGGCTCA	0	0
29	TGATGTAAGACAGATGTGAAATCCCGGGGCTCA	0	0
30	CTTTGTAAAGTCAGGTGTGAAAGCCTGGCGCTCA	0	0
31	CTTTGTAAAGTCAGGTGAGAAAGCCTGGGGCTCA	0	0
32	CTTTGTAAAGTAAGGTGTGAAAGCCTGGGGCTCA	0	0
33		72516	77602
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Flocs Control 3	Flocs Treated 1	Flocs Treated 2	Flocs Treated 3
0	0	0	0
4239	25486	19194	21336
5190	21586	22848	29131
2	5	3	0
5077	5942	4249	4840
2554	6123	4364	5020
354	258	229	192
4126	3287	2075	3787
882	869	839	944
0	0	0	0
0	0	2	3
6	0	2	0
208	92	130	130
1459	1491	1161	1086
0	2	2	2
3546	1848	976	1736
2	0	0	0
10	22	33	29
0	0	0	0
0	0	2	0
406	233	294	783
1193	954	758	737
174	163	129	204
1387	1087	1154	646
681	563	368	479
1460	942	679	929
752	358	504	545
192	111	142	144
1766	433	545	121
927	980	472	1207
437	410	278	352
0	0	0	0
0	2	0	0
890	1262	1312	498
180	86	103	111
0	0	0	0
536	1163	972	855

862	654	505	564
777	483	505	537
690	485	346	639
3	2	0	0
663	793	743	587
0	0	2	4
0	0	0	0
683	406	443	659
805	611	443	483
17	12	5	8
0	0	0	0
0	0	0	0
524	865	400	872
525	563	621	349
607	444	503	280
822	150	221	157
748	544	448	507
0	0	0	0
737	346	410	420
0	0	0	0
539	281	119	312
2	2	0	3
437	399	314	447
76	38	25	29
529	34	252	6
583	417	243	449
136	110	161	148
391	293	330	252
268	797	516	576
385	291	260	329
2	2	3	3
2	3	14	0
0	0	0	0
134	71	780	13
8	9	3	11
0	0	0	0
0	0	0	0
0	0	0	0

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2				
3				
4	348	246	183	229
5	4	0	0	0
6	302	241	153	184
7				
8	431	314	303	307
9	310	359	400	197
10				
11	16	11	10	12
12	148	93	84	95
13	0	0	0	0
14				
15	318	284	483	75
16	264	217	191	248
17				
18	458	262	233	245
19	0	0	0	0
20				
21	280	358	269	202
22	16	7	7	12
23	0	0	0	0
24				
25	6	4	0	10
26	0	0	0	0
27	0	0	0	0
28				
29	261	294	270	179
30	0	0	0	0
31				
32	14	8	8	10
33	367	261	109	342
34	312	227	259	174
35				
36	286	189	175	177
37	363	237	186	203
38				
39	0	0	0	0
40	265	141	213	212
41				
42	267	247	182	243
43	286	436	309	280
44	0	0	0	0
45				
46	227	172	161	248
47	291	13	25	0
48				
49	0	0	0	0
50	44	28	28	17
51				
52	271	165	194	132
53	261	195	215	184
54	0	0	0	0
55				
56	0	0	0	0
57				
58				
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139	105	118	99
0	0	0	0
3	0	0	0
269	226	83	218
2	20	9	8
250	148	148	100
0	0	0	0
224	118	142	188
227	151	133	161
202	159	90	217
0	0	0	0
216	159	159	98
323	236	130	129
277	11	153	2
230	122	158	154
179	140	76	161
116	95	81	122
0	401	515	282
235	173	152	123
128	66	88	95
203	185	123	129
217	157	113	124
194	151	149	101
10	3	11	2
209	99	129	91
171	86	113	56
252	299	47	81
0	0	0	0
20	24	79	4
84	71	56	73
188	118	96	116
0	0	0	0
27	12	19	11
157	103	136	146
155	121	116	125
167	62	105	51
0	0	0	0
4	138	60	70

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2				
3				
4	0	0	3	0
5	186	103	118	125
6	0	311	86	396
7	0	0	0	0
8	0	0	0	0
9	157	115	131	62
10	182	137	110	85
11	141	111	136	52
12	0	0	0	0
13	0	0	0	0
14	101	91	52	104
15	0	0	0	0
16	0	0	0	0
17	155	92	116	66
18	159	141	86	107
19	142	114	77	81
20	129	52	52	131
21	7	3	3	0
22	0	0	0	0
23	0	0	0	0
24	0	0	0	0
25	58	36	15	10
26	0	0	0	0
27	0	49	48	416
28	125	50	50	144
29	119	121	73	106
30	147	110	150	35
31	0	0	0	0
32	0	0	0	0
33	0	0	0	0
34	0	0	0	0
35	138	96	88	48
36	2	8	6	0
37	0	0	0	0
38	0	0	0	0
39	0	0	0	0
40	116	94	93	64
41	54	31	55	31
42	0	0	0	0
43	0	0	0	0
44	87	81	82	63
45	122	74	61	92
46	0	0	0	0
47	0	0	0	0
48	0	0	0	0
49	0	0	0	0
50	110	72	71	58
51				
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0	2	0	2
107	106	90	91
82	68	105	51
122	80	102	66
0	0	0	0
0	0	0	0
48	24	11	31
0	0	0	0
104	76	42	59
130	66	70	56
83	89	86	88
0	0	0	0
97	72	95	69
0	0	0	0
12	10	6	4
80	73	55	73
0	0	0	0
85	103	125	31
132	75	61	70
86	75	76	82
0	0	0	0
116	82	56	55
102	73	63	54
75	74	68	61
82	35	41	35
50	41	49	35
0	0	0	0
82	61	99	53
75	34	87	45
105	70	54	61
99	61	58	55
103	47	76	35
62	64	20	103
91	37	50	50
0	0	0	0
100	51	48	70
102	41	73	53
0	0	0	0

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2				
3				
4	98	34	52	52
5	0	0	0	0
6	111	86	35	61
7	42	4	34	3
8				
9	34	20	30	19
10	90	48	48	56
11	0	0	0	0
12	93	45	47	48
13	87	42	44	33
14	76	47	63	48
15	67	61	64	54
16	55	108	35	42
17	0	0	0	0
18				
19	145	18	26	14
20	40	19	34	36
21	3	3	0	5
22	30	25	13	30
23	67	54	90	39
24	21	15	26	7
25	76	45	65	47
26	0	0	0	0
27	0	0	0	0
28	0	0	0	0
29	0	0	0	0
30	79	70	92	16
31	0	0	0	0
32	94	62	40	52
33	64	45	39	36
34	56	46	54	53
35	12	2	0	2
36	85	46	38	44
37	69	49	43	67
38	3	5	8	4
39	68	62	36	52
40	71	28	22	94
41	0	0	0	0
42	18	12	14	13
43	56	41	83	10
44	17	3	9	6
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65	52	43	28
7	9	4	3
0	0	0	0
66	43	55	38
0	0	0	0
0	0	0	0
0	0	0	0
84	49	32	45
4	0	6	3
68	51	41	44
53	76	33	44
0	0	0	0
52	44	45	37
0	0	0	0
30	4	4	2
0	0	0	0
71	45	42	32
57	42	60	38
43	36	20	24
39	60	46	78
61	52	33	43
51	51	38	54
21	42	25	42
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2447	4485	2872	1778
2927	1773	1742	2207
1175	594	642	693
1726	3065	1982	1282
47	31	81	21
1543	2696	1829	1272
2625	2024	1164	1926
1097	1584	1768	730
2362	1685	619	1490
909	803	780	582
196	199	169	295
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Granules Treated 2	Granules Treated 3	tag	use	taxon_level
0	0	TTTTGTAAGA	long	g
13794	11628	TTGGGTAAGT	long	g
293	253	CTTTGTAAGT	long	g
8347	4740	CCTGACAAGTCTGATGTGAAAGACCTGGGC		
1255	1754	TGATGTAAGA	long	g
1122	1088	TTTTTTAAGA	long	g
3715	3906	CTCGAAAAGCGTTCCGTGAAATCCCCGGGC		
2	5	CTTGCCAAGTGCTTTGTGAAATCCCACGGCT		
1571	2002	TTTTGTAAGA	long	g
2864	2725	AACATCTCACACATTGATGTGAGACGGAGG		
2733	2761	AACAACTCACACATTGATGTGAGACGGAGG		
2679	2763	AACAACTCATTCAAGTCAATTGATTGAGACGC		
1642	1718	TTTGGTCAGT	long	g
653	710	TTTGGTAAGT	long	g
1818	1871	AACAACTCATTCAATGAGTGAGACGG		
16	113	TTCGTAAAGT	tag	f
1642	1722	AACAACTCATTGTAAAAGATGAGACGGAGC		
1351	1252	TCAGACTAAG	long	o
1142	1779	GAATGTAAGTCAGACGTGAAATCCCGGAGC		
1225	643	CCCTGTAAGT	long	f
670	853	TGCTGTAAGTCAGATGTGAAATCCCCGGGC		
108	142	TTTGATAAGT	tag	g
671	959	TTTGGTAAGT	long	g
18	13	TCTTTCAAGCGTCCTGTGAAAGCCTCCGGCT		
461	526	TTTTGTAAGT	tag	f
20	9	TTTGGTAAGA	long	g
392	419	TTTGGTAAGC	long	g
496	874	TTTCGGGCTGAGCTGTGAAGGCTCACCGCA		
0	0	TTATGCAAGA	long	f
5	4	TTATGTAAGA	tag	f
375	577	CTTGGCAAGTCAGATGTGAAAGCCCATGGC		
0	0	TTTGTAAGACAGTGGTGAAATCCCCGGGCT		
753	507	TAATATAAGTTGGGCGTGAAACCTCTGAGC		
0	0	TTTGTGCGCT	tag	g
480	554	TTCGGTCAGT	long	g
745	810	TATGATAAGTCAGGTGTGAAATCCCCGGGGC		
3	5	TCGTGCAAGA	tag	f

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4 15 8 TTTGCCAAGT tag o  
5 16 20 TTTTCCAAGT tag g  
6 42 57 CCCTGTAAGT long f  
7  
8 597 122 TCTTATAAGTCAGTGGTGAAATCTCGCAGCT  
9 0 0 TTGTGTAAGA long f  
10 477 679 CTTCGGGCTGGGCTGTGAAGGCTCATCGCA  
11 358 919 TTAGATAAGT long g  
12 29 23 CTTCGTAAGACAGAGGTGAAATCCCCGGGC  
13 0 0 CTCTTTAAGTCAGACGTGAAAGCCCTAGGC  
14 703 731 CTTTTCAAGTCAGAGGTGAAATCCCCAGGC  
15 518 587 AACAGCTCATTGTAAAAGATGAGACGGAGC  
16 333 591 TTTGTGCGCT long g  
17 0 0 CTTGTAAAGTCTTGTGTGAAAGCCCTCGGCT  
18 0 0 CTTTGTAAAGA long o  
19 29 57 CGCCATAAGA long g  
20 0 2 TTTGTTAAGT long f  
21 0 0 CTTGGTAAGTCAGGGGTGAAAGCTTCCCGC  
22 701 589 CTTCTTAAGCCAGACGTGAAATCCCCGAGCT  
23 0 0 CTTGGCAAGT tag g  
24 341 420 TCTATCAAGT long f  
25 0 0 TTTCTGTGAGATTCTGAATTGTTTGGCCTGCG  
26 413 226 TGATTTAAGTCAGTGGTGAAATACGGCAGC  
27 3 3 CTTTTCAAGTCAGACGTGAAAGCCCTGGGC  
28 430 396 CTTGATAAGTCAGATGTGAAAGCCCTCGGC  
29 0 0 TTTTGTAAAGA long g  
30 9 7 ACTTGTAAGT long f  
31 168 199 CTCTTCAAGT tag o  
32 52 97 TTTGTCAAGT long o  
33 11 15 TTGCGTAAGA tag c  
34 61 83 TTCTGTAAGATTGGTGTGAAATCTCCCGGCT  
35 355 350 GTTTGTAAAGTCAGTGGTGAAAGCCGGCAGC  
36 380 527 GTTCTGATTGTTTCGGGCCTCGCGCTTTATAG  
37 324 192 CTTTTTACGTCTGCTGTGAAATATCCCGGCT  
38 21 53 CTTAATAAGT tag c  
39 314 371 CATTGTAAGT tag c  
40 276 430 GACCTCAAGTCGGTTGTGAAATCCCTCAGCT  
41 279 370 CGATGTGTGTGAGGCGTGAAAGCCCGGGG  
42 167 12 TCTTGTAAGTCAGTGGTGAAATACGGCAGC  
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5	342	246 TTTAGTAAGT tag	f
6	33	67 CTTTGTAAGT long	f
7	0	0 CTTCGGGCTGAGCTGTGAAGGCTCACCGCA	
8	0	0 CCGAGCGGG long	g
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10	175	271 CCGATCAAGT long	f
11	164	110 GCTCGCAAGCGTCCTGTGAAATACCTCAGC	
12	281	332 AACATCTCAGTCAATCGATTGAGACGGAGG	
13	0	0 CTCGATTAGTCTCTTGTAAGCCTTGGGCT	
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15	63	62 TTTGCTAAGT long	o
16	2	0 CTTTTTAAGT long	f
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18	237	210 CTTGACAAGTCGGATGTGAAATCCCTCGGC	
19	0	0 CATCGTAAGTGTCTGGTGAAATCCCACGGC	
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21	252	172 TTTCTGAAAATAATCTTGATGATTGATTAACT	
22	258	274 GCGCTTAAGT long	g
23	276	164 ACTATTAAGTCAGTGGTGAAAGCCCACAGC	
24	232	312 CTTGGCAAGT long	g
25	251	241 TTGGATAAGTCAGTTGTGAAATTTCTCGCT	
26	0	0 ACCTTCAAGCGTTCTGTGAAATCCCCCGGT	
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28	185	321 CTTGATAAGT long	f
29	185	254 ATGGGTCAGT long	g
30	0	0 TCTCGGGTGC tag	p
31	0	0 GTTTGCAAGCGTTTTGTGAAAGCCCCCGGC	
32	0	0 ATTTTCAAGT tag	f
33	0	0 CTGATTAAGTCTGACGTGAAATCTCCTGGCT	
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35	197	251 AACATCTTGCTCTTTGAGTGAGACGGAGGC	
36	0	0 CTTCATAAGT long	g
37	5	3 GCTATTAAGT long	f
38	7	0 TTGTTTAAGT long	g
39	193	102 CTAGATAAGTCAGTGGTGAAAGCTGGTCGC	
40	21	22 GTTGGTAAGT tag	f
41	0	0 ATCTGTAAGT long	g
42			
43	230	205 TTTTATAAGTCAGATGTGAAAGCCTTGGGCT	
44	139	168 CTTCGATAGTCAGGCGTGAAATCCCCAGGC	
45	0	0 TTTTGTGTTGATTGCTTTGGAAAGGTTACTG	
46	0	0 TCGGGTAAGT tag	c
47	148	180 TTAATCAAGTCAGACGTGAAAGCCTTGGGC	
48	165	200 AACAGCTCACACATTGATGTGAGACGGAGC	
49			
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58 55 AGCGCTAAGTCGGGCGTGAAATCCCCAGGC  
174 254 TATAGTAAGTTAGAAGTGAAAGCCTTGGGC  
139 134 ACCTGTAGGCGCGTTGTGAAAGCCCCCGGC  
0 0 CTTATAAGTlong f  
153 190 TGGATTAAGTCGGGTGTGAAATCTCCGGGC  
0 0 GTAAGTAAGTlong g  
139 290 CCCATAAGTCAGTCGTGAAATCGCTGGGC  
0 0 TCCTGCAAGTCGGATGTGAAATCCACGGC  
0 0 TGCTCTAAGTlong o  
0 0 CTTTTCAAGTCAGGGGTGAAATCCACGGC  
129 199 CCCTGCAAGTCAGAGGTGAAAGTCCTGGGC  
0 0 TCCGCTAAGTlong c  
6 11 GCTGGTAAGTCCGTGGTGAAATCCCCGAGC  
0 0 TTTGGTAAGAlong g  
0 0 CGCATTAAAGTlong f  
34 22 TTCTATAAGTlong g  
71 35 CACTGTAAGTlong c  
0 0 ACTGATAAGTlong g  
0 0 CTTTTTAAGTtag p  
58 30 GCAGTTAAGTlong g  
0 0 TTCCGTGCGTlong o  
0 0 TCGTGTGCGTCGGAGGTGAAATCCCCGGGC  
0 4 ACTGGAAAGTlong g  
123 89 TCCATTAAGTlong f  
0 0 TTTGTCACGTlong f  
8 12 ATCTTTAAGTtag o  
0 0 CATGGCAAGTlong o  
114 143 CCAACTAAGTCAGAAGTGAAAGCCCCGGGC  
76 157 TCTTTTAAGTGAGTGGTGAAATCCCGAGGC  
39 51 TTTCGTAAGA long f  
0 0 TCACCGAAGCTTTTCGCAGACTACCACGTCC  
47 129 TTTGTTAAGTlong f  
113 80 TTGGTTAAGTCTGACGTGAAAGCTCCTGGC  
0 0 TCTTGCAAGA long g  
5 3 CTTTGCAAGA long f  
0 0 CCAAGCAGGTCGGATGTGAAATCCCTCGGC  
121 161 GAGAGAAAGTCAGATGTGAAATCCCGGGC  
89 84 TCACTAAGTCTGATGTGAAATCCCCGGCT

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4	102	94	TTGGGTAAGATTGACGTGAAACCTTCTGGC
5	0	0	CTCTTTAAGT(tag g
6	28	33	CTTGTCGCGT long g
7	79	118	CCCGATTAGTTGGAGGTGAAATCCCGGAGC
8	0	0	TCTCGTAAGTCGACTGTGAAAGCCCTTGGC
9	0	0	CTTGACAAGTCAGATGTGAAAGCCCTCGGC
10	0	0	TCTTGTGCGTCGGAGGTGAAATCCCCGGGC
11			
12	91	147	TTTCTTAAGC(long f
13	12	24	TTTTGTAAGA tag c
14	74	35	TCAAATAAGT tag c
15	0	0	TTAGACAAGT long g
16	0	0	TTTCTGGCGTGGTGCGTCTGGTCGCGCGGG
17	0	0	GCTCTTAAGTGTCGCGTGAAAGCCCCACGGC
18	0	0	TATTGTAAGTCAGATGTGAAAGCCCCGGGC
19			
20	102	35	TGACTCAAGT long f
21	63	95	CTATTCAAGT(long f
22	97	77	CATCGTAAGTCATGGTTGAAATCCGGCGGC
23	39	48	ACATTTAAGT tag g
24	77	98	ATTGGCAAGTCAGAAGTGAAATCTTACGGC
25	48	6	TTTAATAAGT(long g
26	0	0	TGGGGAATGAAAGGAGGAAGGAGAAGGG
27	0	0	CTTTTTAAGT(tag o
28	0	0	ATCAGAAAGT(long f
29	63	125	CCCACCAAGTGTCTTGTGAAATACCTTAGCT
30	90	91	TTCGGTCAGTCAGCCGTGAAAGCCCTGGGC
31	116	150	TTAGGTAAGT tag c
32	0	0	TCTAATAAGTGAGGGGTGAAATCCTGCGAC
33	75	75	CTTCGATAGTCAGGCGTGAAAGGCCTGGGC
34	65	102	ATGATTAAGT long f
35	0	5	CTTGTCACGT(long c
36	30	30	CGATTCAAGT long g
37	46	125	ACTGGAAAGT(long g
38	0	0	ACTTGCAAGTCGATGGTGAAATCTTACGGC
39	0	0	TTGGCTAAGT tag f
40	77	75	TTTTGTAAGT tag p
41	152	52	TTACGTAAGT long g
42	66	55	CCGTTTAAGT long g
43	0	0	TTTCGTAAGT tag o
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88 40 AATTTTGGTCATGTTTTCACACACATTTTGT  
0 0 CGCGGTAAGTlong f  
12 20 TTCGGTAAGTlong f  
0 3 CATGGCAAGTlong f  
47 139 ATGGTTAAGTCGGGTGTGAAATCCTGGGGC  
83 85 TTGGATAAGTlong f  
55 62 TTTCGGGTATTTGTTGCCGGTTGGTCTTCGC  
79 101 TATATTCAAACATATATATAATTTTAACAGG  
3 0 CTATTTAAGTlong f  
0 0 TTAGTCACGTlong o  
0 0 TCGTGCAAGTlong f  
92 49 GTGTATAAGTCAGTGGTGAAATCCCCGAGC  
0 0 CTTGCCAAGTCTGGTGTGAAAGCCCCACGGC  
0 0 CTTTGTAAGA long g  
51 65 TCTCGGGGTGCCGTTGTGGTTCTCTGTTTTCT  
4 5 CGTGGCAAGTtag k  
58 57 ATCGTTAAGTCAGAGGTGAAAGCTCACAGC  
0 0 TCTTGCAGGT tag p  
0 0 TTTTGTTAGTTTGGTGTGAAATCTCCCGGCT  
0 0 GCAGGTAAGTlong g  
66 76 CGGGGTAAGTlong f  
0 0 ATCGGTAAGTGTCTGTGAAAGCCCCCGGC  
0 0 GCCGCTAAGTGTCGTGTGAAATCCCAGGGC  
0 0 TCTGCTAAGT long c  
8 2 GTTTTAAAGTlong g  
18 36 CGCCATAAGTlong f  
56 26 CCATCTAAGTCAGATGTGAAATCCCTTGGCT  
0 0 CTCGGAAAGTlong g  
24 21 TTTGTAAAGT long g  
0 0 CTTGCCAAGCGTCCTGTGAAATCCCGCGGC  
5 6 TTCTGTAAGTlong g  
0 0 TTTGTCGCGTlong g  
12 12 TTTCGGCGTGCGCTCGGGCTGGTCGGCCGT  
8 15 CTGTTCAAGTCTGACGTGAAATCGCTCGGCT  
68 98 TTCGGTAAGTlong f  
0 0 TATTGTAAGTCGGATGTGAAAGCCCCGGGC  
0 0 CGCGCCAAGTCAGATGTGAAAGCCCCGGGC  
0 0 TTTTGTAAGACAGTGGTGTGAAATCCCGGGCT

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	13	15	TCTTGTAAGTtag c
	39	117	CTTGGCAAGTCTGATGTGAAAGCCCATGGC
	0	5	ACTTTTAAGTlong g
	0	0	CTTCGGACTTlong g
	25	47	TCTAAAAATTTCTGAATGGAGAAAAGTTTAA/
	4	3	CTTGCTAAGACTGACGTGAAAGCTCCTGGC
	61	31	GCTAGTAAGTlong g
	5	0	CTTGTTAAGATTGACGTGAAAAGTCTGGC
	9	10	CGGCGCAAGTGTCTGAGTGAAATCCCACTGC
	0	0	TCATGCAAGAlong f
	3	0	CTTATTAAGClong g
	6	3	CTGGGTAAGCGTGTGGTGAAAGCCCGGGG
	64	49	TTAGATACGTCTGATGTGAAAGTCTGGGC
	0	0	ATAGTTTAGTtag f
	28	38	TTCTGAAAGTCAGATGTGAAATCCCTGGGC
	56	22	AATTTTTGGTCATGTCTGTACACACATGTTG
	30	28	CACGGATAGTTGGGTGTGAAAGCCCGGAG
	2	5	CTTGGCAAGTCGGATGTGAAATCCACGGC
	34	36	TTGTCTAAGACTGACGTGAAAGCTCCTGGC
	0	0	CCTTGTAAGTlong f
	30	16	CTAAGAGTGtag g
	41	57	CGATTTTAGTlong f
	34	72	GCCCGCAAGCACTTTGTGAAATCCCTCGGC
	0	0	ACTGTCAAGTCAGAGGTGAAATCCCAAGGC
	83	72	CTTTGCAAGTCAGAGGTGAAATCCCCAGGC
	0	0	CGTTACAAGTtag o
	7	3	GCATTTAAGTlong f
	0	0	TTTGGTAAGCCCTCTGTGAAAGCTTCGGGC
	69	39	TTTCTCTTAAGATCAACCAAATTGATAGTAA
	0	3	CTTTGTAAGTlong g
	0	0	ACCTGTAAGTtag g
	39	68	TTAAATAAGTCAGTTGTGAAATTCTCCGGCT
	0	0	TTTGCTAAGTTTGGTGTGAAATCTCCCGGCT
	0	0	TGGGGAATGAGTGGAGGAAGGAGAAGGG
	42	25	TCATGTAAGACAGATGTGAAATCCCCGGGC
	27	31	TTGAGAAAGTCTGACGTGAAATTTCTTGGC
	0	0	CTTTGCCAGTCAGGGGTGAAATCCACAGC
	23	15	CTACTCAAGTtag g

6 5 CTCTTCAAGTtag k  
38 50 CTTGTAAAGTlong o  
39 70 ACCAGAAAGtag f  
0 0 TGGCTCAAGTTTGGTGTGAAATCTCCCGGC  
42 51 CCTTGCAAGTCAGAGGTGAAAGTCCTGGGC  
57 17 TTTTCAAGTCAGGCGTGAAAGCCCGAGGC  
34 54 TATCAGGTTTGCGGTGAGGGCAGTGTTTAG  
0 0 CCTGATAAGTCGGGGGTGAAACGCTGCGG  
24 29 TTGGGTAAAGTlong f  
0 0 GCAGGTAAAGtag g  
0 0 CTTGGTAAGCtag f  
34 40 GCTGGTAAGtag f  
0 0 TTTCTTAAGTCGGATGTGCAATCCCCGGGC  
40 28 CCGGTAAAGTlong f  
34 21 ACATTTAAGTtag c  
29 7 AACTTAAGTlong g  
0 0 TTTTTAAAGTlong g  
0 0 GCATTTAAGTCAGTGGTGAAATCTCCGAGC  
17 7 ACTTCTAAGTGTCGCGTGAAAGCCACGGC  
0 0 TTTGATAAGTCAGTTGTGAAATTCGCCGGC  
0 0 TCCTGTAAGA long o  
0 0 GATGATAAGtag p  
10 13 TTTGCTAAGA long g  
0 0 ACTTTTAAGTGTCGCGTGAAAGCCACGGC  
0 0 TCTTGCGCGTCGGAGGTGAAATCCCCGGGC  
0 0 TTATCTAAGTlong g  
48 40 CTGAGGGCGlong g  
42 37 CTTGACAAGTtag o  
44 69 TTTTGTAAGTlong f  
0 0 TCCTGTGCGTCGGAGGTGAAATCCCCGGGC  
0 0 TTTGTGCGGTtag f  
0 0 TTGTTTAAGTlong g  
0 0 CTGAGCAAGTGCGATGTGAAAGCCCCGGC  
0 0 CGTGGTAAGTlong o  
22 45 TTTGATCAGTlong g  
56 21 ACTATTAAGTCAGGGGTGAAAGCCCGCAGC  
41 31 CTTGGATAGTCGGGTGTGAAAGCCCAGGGC  
0 0 GTTCGTAAGTGTCTTGTGAAATCCCCGGC



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2			
3			
4	0	0	CCTGGTAAGT tag f
5	4	6	TTTATTATTTTAAAGGTAAAATCCGAGGAT
6	35	62	TTGGCTAAGT long g
7	0	7	AATGAACTTTTTTTTTTCGATTCTGTTTTTTT
8	20	26	CTTTTTGCGT tag f
9	0	0	TCCTCCAAGCGTCTTGTAATCCCACGGCT
10	0	0	TCGGGTAAGT long c
11	11	9	TTTTTAAGAC long g
12	32	20	ATTGGTAAGTCAGAGGTGAAAGCCCGTAGC
13	0	0	GCTTTTAAGT long f
14	14	7	ATTGTAAAGT tag g
15	25	13	CTGGGTAAGC tag f
16	0	0	TATCCGGCGTCTCTGACGTCTGCCTGACTCG
17	33	40	CTGAGGGCCGCTCAAGGTTTCAAGCAAGT
18	0	0	TCTGTAAAGT long f
19	0	0	TTTGCTAAGTCTTGTTGTGAAAGCCCTGGGC
20	37	28	TCCGGTCAGTCAGCCGTGAAAGCCCCGGGC
21	13	15	ACTATTAAGT long f
22	20	14	TTTTTCAAGT tag f
23	10	20	CCGTGTGTGTGAGGTGTGAAATCCCGGAGC
24	0	0	TCTTGTAAGACAGTGGTGAAATCCCCGGGC
25	22	45	TCCTACAAGCCAGAGGTGAAATCCCGGAGC
26	0	0	TTTAATAAGT long g
27	0	0	CTTGGCAAGTCGGGCATGAAATCTCCTGGC
28	17	31	ACTGGAAAGT long g
29	6	19	ATCGTTAAGT long g
30	9	10	TGTTATAAGTCTGATGTGAAACCTTCTGGCT
31	0	0	CCCGATAAGTCCCGCGTGAAATCCCCGGGC
32	0	0	TTTGTTAAGT long o
33	0	0	GTTGGTAAGT tag f
34	0	0	TCCTATAAGTCGGATGTGAAAGCCCCGGGC
35	26	40	TTTACTAAGTCAAACGTGAAAGCCCCGGGC
36	5	0	TCTGCCAAGCTCGATGTGAAATCCCCGGGC
37	34	42	ACATTTAAGTCAGACGTGAAATCCCCGGGC
38	14	8	TTTTGTAAGTCAGTGGTGAAATGTCTCGGC
39	0	0	ACCAGAAAGT long g
40	37	28	TTTTGTAAGT long f
41	0	0	ACTTTTAAGT tag c
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13 21 TGGAGTAAGTCAGTTGTGAAATCCCTCGCT  
0 0 CTACTTAAGTCAGTGGTGAAATACGGCAGC  
13 23 ATTGTTAAGT long g  
38 39 TTTGTTAAGT long g  
0 6 GTTGCTAAGT long g  
0 0 TTTCTGGTGTGGTACGCCGAGCCCGCCCTTA  
21 30 TTTGTCGCGTCTGCCGTGAAAATCCGGGAC  
0 2 TTTGATAAGA long f  
0 0 TTAGATAAGTCAGTCGTGAAATCGCTGGGC  
0 0 TTAGTCACGTCGGATGTGAAAACCCGGGGC  
0 0 TTCTTAGAGACAGTAGGAACTAGAATTTGA  
0 0 CGGACTAAGTCGGGTGTGAAATCTCCGGGC  
25 33 TGCCATAAGTCAGGTGTGAAAGATTCCGGC  
20 15 CCCTGCGCGTCGAGCGTGAAAGGCCTGGGC  
0 0 TTTCGCAAGT tag f  
26 31 TTCGGTAAGT long f  
0 0 TTTGTCGCGT tag f  
0 0 ATTGATAAGTTATTGTTTAAATTCATGGGCT  
0 0 TTCATCAAGTGTTCTGTGAAATCCCTCGGCT  
0 0 CATGGTGTGTCGGGCGTGAAACTCCGGAGC  
2 12 ATCTTTAAGT tag p  
16 20 CTCTGCAGGTCGGATGTGAAATCCCTCGGC  
0 0 TCTCGTAAGTTCGGTGTGAAATCTCCCGGCT  
0 0 TCGCTTAAGTAATGCGTTAAAGCCTTGGGC  
0 0 ATCTGTAAGT long g  
20 17 TGGGTAAGTCAGATGTGAAATCCCCGGGCT  
0 0 CTTGGCAAGT long o  
0 0 ATTTGTAAGACAGTGGTGAAATCCCCGGGC  
0 0 TCATTTAAGTCGGGTGTGAAATCCCCGGGC  
0 0 CTAGGTAAGTCAGGGGTGAAAGCTTCCCGC  
0 0 TCTGGTAAGT tag g  
10 6 TTGGGTGTGT long g  
0 0 TTTTACAAATCCTGTTGGAATAGCTTCCGTT  
0 0 GCTCGTAAGTGTTCTGTGAAAGCCCACGGC  
0 0 TTTAATAAGT long g  
23 18 ACCCGAAGGTGCATCGTGAAATCCCTTGGC  
0 0 TCTGTCGCGT long g  
26 39 CCTGATAAGCCTGGCGTGAAAGTCACCGGC

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4	32	34	TTTTGTAAGTCGGTTGTGAAATCCCTGGGCT
5	0	0	TTGTAAGACAGTGGTGAAATCCCCGGGCTC
6	2	3	CATCGTAAGT tag c
7	30	11	TTGGTAAGTC tag g
8	0	0	GTTGGTAAGT long f
9	33	22	AGAGGTCAGTCGGCCGTGAAAGCCCCGGGCT
10	17	16	TCTGGTAGGT long g
11	24	15	TGTTGTAAGT long f
12	26	27	GTTTGTAAAGT long g
13	0	0	TTTTGTAAGA tag f
14	0	0	TTTCGTAAGT long f
15	16	23	TTGTATAAGT long f
16	7	6	ACTTTTAAGTCGGGTGTGAAATCCCCGGGGCT
17	0	0	CCTTATAAGTCAGTGGTGAAATCTTTGGGCT
18	0	0	AATGATAAGT tag o
19	21	25	ATGGGTCAGT long g
20	9	10	TTGCGTGTGTCTGGTGTGAAATCTCCTGGCT
21	8	25	TGTTGTAAGTCAGATGTGAAATCCCCGGGGCT
22	22	20	TTGGGTAAGTCAGATGTGAAATCCCCGGGCT
23	0	0	ACTGGAAAGT tag f
24	21	25	ATAGGTAAGTCAGAGGTGAAAGCCTGGAGCT
25	2	0	TTAGATAAGT long f
26	0	0	TTAGATAAGT long f
27	0	0	ACCACTCAGTCAGGCGTGAAAGCCCCGGGGCT
28	0	0	CGGATCAAGT tag g
29	0	0	TTCGGAAAGT long f
30	0	0	TCCCTTAAGTTTGTCTGAAATCTCCCGGCT
31	0	0	ACTTGTAAGTCAGTGGTGAAATCTGTGGGGCT
32	3	0	CTCTTCAAGTCAGACGTGAAAGCCCCGGGGCT
33	5	7	TTTTGTAAGCT tag f
34	0	0	TTATTTAAGT long g
35	26	26	TCTAAAACTTCGAATGGAGAAAAGTTTAACT
36	0	0	TCTGTTAAGT tag p
37	0	0	TTGGGTAAGT tag c
38	13	22	CCTGTTAAGT long g
39	0	0	TTTGTTACAA long f
40	27	29	TTTTGTAAGA long g
41	8	11	TGATGTAAGT long f
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0 CGTCGCAAGT long f  
39 TTTTTTAAGTTGTATTTTAAAGACTAGAGCT  
19 GCTCGCAAGCGTCTTGTGAAATCCCATGGC  
0 CCATGTAAGTCGGATGTGAAAGCCCTCAGC  
0 CGCTACAAGTCAGGGGTGAAATCCCAGAGC  
13 TTCGTTAAGT tag p  
10 AATGATAAGT long f  
0 AATTCTAAGTCAGTGGTGAAAGCCTCCCGC  
18 TTTCTTAAGTTTGACGTGAAAGCTCTCGGCT  
8 TCTTGTAAGA long f  
5 AATGAACTTTTTTTTTTCGATTCTGTTTTGG  
19 TGTCGTAAGT long c  
2 CCTTTTAAGTCTTAATCAAAGAAGCTAAGCC  
0 CGCGACAAGTGAGGTGTGAAAGCTCCTGGC  
0 GTTTGTAAGT tag f  
0 TTTCGGAAGTGGGAATGATTGGTCGGGCCT  
0 TTTTGTAAGACAGTGGTGAAATCCCCGGGC  
24 CTCAGAAAGTTGGGTGTGAAATCCCCGGC  
0 TTGGGTAAGTCTGTGGTGAAATTTTCGAGGC  
11 TTTTATAAGA long g  
3 CTCGGTAAGC long f  
24 TTATACAAGTCTGGTGTGCAAGACCAAGGC  
0 TGGTTTAAGT long g  
16 TGATCCATGTCAGAGGTGAAAGCCTGGGGC  
21 GCCGGTGCCTCGGCGCCTGAAAGCCCCGGC  
0 TCGCACAAGACAGATGTGAAATCCCCGGGC  
2 ATCGTTAAGT long g  
21 GTTGTTGAGTTGGAGGATGAAATGTCTGGT  
18 TTTTGTAAGA long f  
34 TTGAAAGCTGTCAAGAATAGTCAAAATATC  
9 TTTTGTACGTTTGATGTGAAAGTCCTGGGCT  
3 CTTCGCAAGTCGGGCATGAAATCTCCTCGC  
21 CTTTTTAAGTCAAATGTGAAATCCTAGGGCT  
38 TCCAATAAGTCAGCCGTGAAATCGCTGGGC  
0 TTCGCTAAGTCTGATGTGAAATCTCCCGGCT  
0 TTTTGTAAGACAGTGGTGAATCCCCGGGCT  
22 TTATCTAAGTCTGGTGTGAAATCTGTCGGCT  
4 TTTTTTATTTTAAAAAAGAAATGCTGAGACT

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4	4	0 TTCGTTGCGTCGTGCGTGAAAGACCCTGGC
5	6	13 ATTTGTAAGT long f
6	0	0 TTTTGTAAAGTtag c
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8	0	0 ACGCGTAGGCGCTTTGTGAAATCCCTCGGC
9	0	0 AACGGTAAGTCAGTGGTGAAATCCTGTTGC
10	0	0 TTTCGGAATATGCAGGAGGCGGTCCACAGA
11	0	3 AGCGACACGTCGGTCGTTGAAAGCCCCGG
12		
13	14	17 CTGCTTAAGT long f
14	17	18 TTATACAAGTCAGGAGTGAAATCCCAGGGC
15	0	0 TCTTGCAAGA long f
16	0	0 CTTTGTAAAGTlong f
17		
18	0	0 TTTTGTAAAGACAGTGGTGAAATCCCTGGGC
19		
20	12	6 ATTGTTAAGTCAGTGGTGAAATCAACGGGC
21	4	0 TTTTTTTAAGACAGGCGTGAAATCCCCGGG
22		
23	0	0 ATCGTTAAGTCAGTGGTGAAAGCCCACAGC
24		
25	0	7 CCTTCTAAGTlong o
26	0	0 CTTAACAAGTCGGGCATGAAATCTCCTGGC
27	0	0 CTGGGCAAGlong f
28	0	0 GCAGGTAAGtag f
29		
30	12	19 CGAATCAAGT long g
31	12	19 ATTGTTAAGT long f
32	0	0 ATTAATAAGT tag o
33	9	0 CCTGTTAAGT long f
34		
35	0	0 TTTTGTAAAGACAGTGGTGAAATCCCCGGCT
36	0	0 TCATGCAAGA long f
37	0	0 CTCGGCGAGTCGGGCATGAAATCTCCTGGC
38		
39	14	7 CTGAGGGCClong g
40	0	0 CTTAGTAAGTCAGCGGTAAAAGGCGACAGC
41	0	0 TCTGTTAAGTGTGAAGTGAAATCTCCAGCG
42		
43	2	7 CTTGTCGCGT long g
44	11	10 TTTGATAAGTCAGGTGTGAAATCCCACAGC
45	0	0 ACTGATAAGTCAGGTGTGAAATCCCTGGGC
46	0	0 TTTTGTAAAGACAGTGGTGAAATTCCTGGGC
47		
48	5	0 TTTAATAAGTlong g
49	9	16 CGCAGAAAGlong f
50	0	0 CTTTGCAAGT long g
51	0	0 CTTTTTAAGTCAGGTGTGAAATCCTAGGGC
52		
53	15	11 CGAGGTAAGtag k
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3 4 CCTCCTAAGTCATACGTGAAATCCCACGGCT  
10 8 CCGTTTAAAGTTAGATGTGAAAGTCCTGGGC  
7 4 AACGGCACGTCGGTCGCTGAAAGCCCCCGC  
0 0 CTTTGTAAGTTGGATGTGAAAACCTCTGGGC  
0 0 CCATGCAAGT long g  
0 0 CTCGTTAAGACAGATGTGAAATCCCCGGGC  
18 14 CTTGTTAAGT tag f  
18 20 CATCGCAAGT tag c  
0 2 CTTGATAAGTAGGGGGTGAAATCTCATGGC  
14 15 CCTATTAAGT tag p  
0 0 TTCCGTGCGT tag o  
0 0 TCTAATAAGTCAGTGGTGAAATCTGGTCGC  
0 0 TTCTCTAAGT tag o  
0 0 CCTAGCAGGT tag g  
7 10 CCTTATAAGTCAGTTGTGAAATATCCTCGCT  
0 36 TCTTATAAGTCTGTTGTGAAATCCCCGAGCT  
15 12 TTTAGTCAGTCTGATGTGAAATCCCCGGGC  
0 0 CTTTGTAAGT long g  
0 0 TTTTGTAAGACAGTGGTGGAATCCCCGGGC  
12 19 TGAGTTAAGT tag g  
14 24 TTTTAGTGGGTTATCAGGTGATTGGTCGGA  
17 20 CCATCTAAGTCGGGTGTGAAATCTCCGGGC  
13 9 ATGATTAAGT tag f  
0 0 TCTAATAAGTTTTTTTATAAAAGCTTATGGCT  
14 14 TCTTGTAAGA long f  
9 13 CGATCTTAGTCAGGCGTGAAAGCCCCGGGC  
8 6 ATAGTTAAGTCTAAAGTGGAAGCCCCGGGC  
10 18 TGCGGTACGGTTCGGGTGAAATCCCTCGGC  
0 3 TCTCCTAAGTCTGGTGTGAAATCCCTCGGC  
12 14 GGCGTTAAGTCAGTGGTGAAAGCCTACAGC  
9 9 ACCCGTAAGTGTTCTGTGAAATCCCCGGGC  
14 8 CTGGGTAAGTCAGATGTGAAATCCCCGGGC  
0 6 CCCC GC GCGTCGAGCGTGAAAGGCCTGGGC  
0 0 CCCGTCAAGT long o  
0 0 TTTTGTAAGT long g  
13 22 TTGCTTAAGTCTGTCGTGAAAGCCCTGGGC  
11 15 TGATTCAAGTTGGATGTGTAATCCCCGGGC  
14 15 CTTTGTAAGT long f

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3			
4		0	0 ACCAGCAGGTCGGTCGTGAAAGCCCCGGGGC
5		0	0 CGGATCAAGTlong g
6			
7	12	17	GTTATTAAGT long f
8		5	18 CCTACTAAGTCATACGTGAAATCCCACGGCT
9		14	12 CTTGGCAAGT long o
10		14	8 ACAGGTCAGTlong p
11		8	29 TATTGAGAGT tag f
12		0	0 TTGGGTAAGCtag g
13		7	27 ATTATTAAGTtag f
14			
15		14	15 ATATGTAAGTTAGATGTGAAATCCCCGAGC
16		0	0 CTTTGCAAGTCAGGTGTGAAAGCCTAGGGC
17		0	0 CTTTGTAAGTTTGGTGTGAAATCTCCCGGCT
18		8	7 CTAAACAGGTlong g
19		0	0 CTTTTCAAGTCAGACGTGAAAGCCCCGGGC
20		0	0 CTCGCCAAGT long f
21		9	16 TTTGGTAAGTCGGTGGTTTAACCTATGGGC
22		0	0 ATTTGTAAGT tag p
23		11	13 CTTGGTAAGTCTGGTGTGAAAACCTGGGGC
24		0	0 TTTAGTAAGTCAGTGGTGAAAGCCCGCAGC
25		15	14 TTTGTCGCGTCTGCTGTGAAAATCCGAGAC
26		0	0 CTCGTTAAGTCGGATGTGAAAGCCCCGGGC
27		6	4 CCGGGCAAGTCTGGTGTGAAATCGTCACCG
28		5	8 GCTGTTGAGTTGGAGGATGAAATGTCTGGT
29		9	6 TTGCGTAAGTGTCGAGTGAAATCCTGCCGC
30		7	10 CGAACCAAGTCTGGTGTGAAATCCCACGGC
31		7	8 TCTGCTAAGC tag g
32		8	4 TTGAACAAGTCTGCTGTTAAAGCGTGGAGC
33		8	11 CTTATCAAGTtag f
34		8	15 TTATTTAAGClong f
35		0	0 TTTTGTAAGACAGTGGTGAAATCCCCGGGC
36		0	0 CGCTGTAAGTCTGACGTGAAATCTCCTGGCT
37		0	5 ACTTTCAAGTlong g
38		11	9 ATCGGTAAGTGCCTTGTGAAAGCCCCTCGC
39		4	11 ACCATTAAGT long f
40		3	7 CCAAATAAGT long g
41		14	4 CTTTCTACGTCTGCTGTGAAATATCCCGGCT
42		0	0 TTTGTTAAGTtag p
43		0	0 ACAAATAAGTCAGGTGTGAAATACCAAAGC
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0 ATCGATAAGTGTCTGTGAAAGCCCACTGC  
2 CACGACAAGT long f  
0 ATTATTTTCGGCGTCAGGCTGGCTGGAAAAT  
0 TTTGATAAGT tag f  
0 TGTTGTAAGTCAGTCGTGAAATCCCCGGCT  
8 TTTAATAAGT tag g  
0 CCCTTCAAGTCAGTCGTGAAATCGCTGGGC  
11 8 ATCTGCAGGCGCGTTGTGAAAGCCCCCGGC  
0 CGAGGTAAGT long f  
0 TCTGCTAAGC long g  
0 CTGGGTAAGTGTGGCGTGAAAGTCCTGGGC  
0 2 TTTGGTAAGT long f  
0 CTCTGTAAGTCGGACATGAAAGCTCCTGGC  
0 TTATGTAAGA tag f  
8 12 ATTTGTCAGT long g  
0 ACCTGCAAGTCGGTGGTGAAAGCCCCGGGG  
0 TTTCGTAAGA long g  
2 3 TAAAGTAAGTCAGTGGTGAAATCCCTTCGC  
0 TTCGTAAAGT long g  
0 CGTGACAAGT long f  
0 GCTGCCAAGTCTGTGGTGAAATCCTCCAGC  
0 ACAGTTTAGT long g  
0 TCTCGTTTGTCTGAGGTGAAATCCCCGAGCT  
0 CCGGTCAAGTCGGATGTGAAAGCCCTGGGC  
0 CTTCGTAAGTTGGACGTTAAATCTTTCGGCC  
8 11 CTGAGTAAGTTGAGGTTGAAATCCGGCGGC  
0 AATGCTAAGTCAGTGGTGAAATCTCCCGGC  
5 18 CGTCGTAAGTCGGATGTGAAAGCCCTCGGC  
7 10 TCTCGTAAGTCTACTGTGAAATCCCCGGGCT  
3 3 CTTATAAGTCAGTGGTGAAATCTTTCGCT  
0 CTACTTAAGTTGGGTGTGAAATCCCCGGGC  
0 TTATGCAAGA long f  
4 6 TAAGATAAGTCAGATGTGAAATCCCCGGAGC  
0 ACTTATAAGT tag g  
0 TTTGTAAAGT long g  
3 7 TTTCGGAGCA long g  
0 CGACTCAAGT long o  
6 14 AGCGTTAAGT long f



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4	9	14 CCTTTTAAGTTTTAAAGTAAATGCTCGAGCT
5	10	7 ATTTGTCAGTtag g
6	2	13 TCAGGTCAGTCGGATGTGAAATCCCCGGGC
7	0	0 GTTCTGGCTG long f
8	9	4 CGCATCAAGT long g
9	0	0 ACATTTAAGT long g
10	0	0 CTGTGTCAGTCAGGCGTGAAATTCCTGGGC
11	7	3 CCTGTTAAGACTGACGTGAAAGCTCCTGGC
12	17	6 TTTTTTAAGTlong g
13	4	9 ATTGGTAAGTTGGATGTTTAAGCGTTAGGC
14	0	0 TTTGCTAAGATTGACGTGAAAACCTTTGGCT
15	0	0 TTGACTAAGT long c
16	0	4 GACGGCACGTCCGGTGACTGAAAGCCCCCGC
17	0	0 TGTTGTAAGT tag o
18	11	2 ATCTGTAGGC long g
19	7	2 ATTTACAAGT long c
20	8	6 GGTGGCACGTCCGGATGCTGAAAGCCCCCGC
21	0	0 TTTGTCGCGT long o
22	9	4 TTTCGATAGT long f
23	2	2 TGAGAAAAGTCGGGTGTGAAATCCCTCGGC
24	10	8 CTGAACAAGTTGGATGTGAAAGCCCTGGGC
25	5	2 TTTGTAAGACAGATGTGAAATCCCCGGGCT
26	10	6 TTTAATAAGTlong f
27	0	0 ACTGGAAAGtag f
28	9	6 ATGGGTAAGtag o
29	0	0 CCACTTAAGTCGGGTGTGAAAGCCCGGGGC
30	4	17 CATGTCAAGTCAGACGTGAAAGACCGGGGC
31	0	0 TCCGCCAAGTGCTTTGTGAAATCCCACGGCT
32	9	0 TTGAGTAAGTCCGCGGTGAAATTTTCGAGGC
33	0	0 TTGTGCAAGlong o
34	0	0 TTTTGTAAGTTGGGCGTGAAAACCTCCGGGC
35	0	0 CTCTTCAAGTCAGCCGTGAAATCTCCGGGCT
36	6	5 TGATCCATGT long c
37	3	2 CGGTGTAAGCATGGCGTGAAAGCCCCTGGC
38	3	16 ACTTGTGCGT long f
39	0	0 ATATATAAGTTAGATGTGAAATCCCCGAGCT
40	0	0 TTCGGTAAGTCTGTCATGAAATCTCCCGGCT
41	0	0 TAGCGTTAGT long g
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0 CTTGCCAAGCGTCCTGTGAAATCCCACGGCT  
5 ATCGTTAAGTCGGGGGTGAAAGCCCCGAGG(  
0 TTGTGCAAGA long c  
6 CACGACAAGTGAGGTGTGAAAGCTCCTGGC  
5 TGAATTAAGTCGGGTGTGAAATCTCCGGGC  
0 ACTTCTAAGTCGGGGGTGAAATCCCAGGGC  
4 TTATTCAAGTCAGGGGTGAAATCCTGAGGC  
8 ATCTTTAAGT tag o  
2 GTCGTTAAGTGCTTTGTGAAAGCCCCCTGGCT  
0 CGGCGTAAGTCAGAGGTGAAATCCCATCGC  
3 ACTCTTAAGT long g  
0 ACAGTTTAGT tag g  
0 CGACATAAGTCAGAGGTGAAATCCCATCGG  
9 ACCCGAAGGTGCATCGTGAAATCCCCCGGC  
5 TTCGTTGCGT tag c  
0 TTTGTTGCGT long g  
0 CTTAGTAAGTCAGATGTGAAATCCCTGGGC  
17 CCTATTAAGTGTGGTGTGAAATCTCCAGGG(  
7 ACTTGCAGGCACCTTGTGAAAGCCCTCGGC  
0 CTTGCTAAGTCCTGTGTGAAAGCCCCGGGC  
5 TCTGAATAGTCCAAGTTGAAATCCCCGAGC  
9 GTTGTTGAGTTGGAGGATGAAATGTCTGGC  
0 TTTTGTAAGA tag g  
6 ATGATTAAGTTACTGGTGAAAGCGCCGGGC  
5 CTGTGGGCCGTCGTAGATGATCAGGTTCCG  
5 TTTATCAGGTTGGATGTGAAAGACCCGGGC  
0 ATTGTTAAGT long c  
9 CCGGGTGTGTTAGATGTGAAATCCCAGAGC  
7 AAAGCTAAGTCAGTGGTGAAAGCCCCGAGC  
4 ATGGGTAAGTCAGATGTGAAATCCCCGGGC  
0 GCATGTAAGTCAGATGTGAAATTCCGGAGC  
0 TTCCACGCGTCGGAGGTGAAATCCCCGGGC  
0 CTTGACAAGTCAGAGGTGAAAGCCTGGAGC  
5 CCTGATTAGTTGGAGGTGAAATCCCCGAGC  
7 GAAAGTCAGTCAGATGTGAAAGCCCAGGG(  
14 TTTCGTAAGT long f  
4 CGCGGAAAG tag f  
0 TTGGACAAGTGAGGCGTGAAAGCCCTGGG(  
For Peer Review

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3		
4	5	6 CTCGGCAAGTCTGGTGTGAAAACGCTACCG
5	5	5 TTGGGTAAGTtag o
6	8	9 ATTGGTAAGTCAGAGGTGAAATCCCACAGC
7	0	0 TTTTGTAGACtag g
8	5	7 TTTTAGTAGGATTTTTAGAGATAGGTCGGT
9	0	0 TTTTGTAAAGAlong g
10	0	0 TTATACAAGTCAGGGGTGAAATCCCAGAGC
11	0	0 CTTGTGCGCTCTGCTGTGAAAATCCGGGGC
12	0	6 GTTCGTAAGTCTTAGAGTAAATCTCACGGCT
13	6	5 TTTTAGTAAGATTATTAGAAATAGGTCGGT
14	0	0 CTAGATAAGTCGGATGTGAAAGCCCCGGGC
15	0	0 TAGCGTTAGTTGGCCGTGAAAGCCCTGGGC
16	0	0 CTCTATAAGAlong g
17	7	16 CTTTTTAAGTtag g
18	7	6 TTCGGTAAGTtag o
19	0	5 CTTGTTAAGTtag g
20	0	0 AAATCTAAGTCAGTGGTGAAATCCTGCAGC
21	0	0 ATCATTAAGTCAGGTGTGAAAACCTTCGGGC
22	4	9 TTTTAGTAAGATTATTAGAAATAGGTCGGG
23	0	0 TTTTGTAAAGACAGTGGTGAAATCTCCGGGC
24	4	4 CCAGATCAGTtag g
25	5	8 TTTTAGTGAGTTATTTAGATGATTGGTCGGA
26	6	5 CAGCCTAAGTCTGGCGTGAAATATCCCGGC
27	0	0 CCCGCAAAGTGCTTTGTGAAATCCCGGAGC
28	0	0 CTTGTCAAGTCGGGCGTGAAAGCTCCGGGC
29	4	0 CTTGGTAAGTTGGGCGTGAAATCTCCGGGC
30	4	5 TGTCGTAAGTlong f
31	0	2 TTTTAAGACAGGCGTGAAATCCCCGGGCTT
32	3	3 ACTCTTAAGTlong g
33	0	0 GTTTTTAAGTCAGATGTGAAATCTCGGAGCT
34	0	0 TGCGGTAAGTtag f
35	0	0 CTTCGGGCCTtag o
36	4	10 TTTAGACAGTCAGATGTGAAATCCTGGAGC
37	7	2 AAAGAAGAGGGCAGATATTTTTGCAAGAG
38	0	0 CCTGTTAAGTtag k
39	0	0 TTTCTTAAGTlong g
40	0	3 ATAAAAAAGAGAAAGAGAGAGAGAAAAAC
41	0	0 CTAGGTAAGCGTGTGGTGAAAGCTCGGGC
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0 TTTGCTAAGTTCGGTGTGAAATCTCCTGGCT  
0 GCAAGCAAGTCGAAGGTGAAATCCCACGGC  
5 ATCGGAAAGTGTTTTGTGAAATCCCTCGGC  
3 CGCTCTAAGT tag o  
0 TTTCCGGCAGCATTGCCTGTCTGCAAGAGTA  
5 TTGGGTAAGTCAGATGTGAAATCCCCGGCT  
0 TTTTGTAAGACAGTGGTGAATCCTCGGGC  
5 CTTGGTAAGTCAGATGTGAAAGCCCTCGGC  
0 CTCCGTAGGT tag g  
7 CCAAGCAAGTCTGTTGTGAAATCCCCGGGGC  
0 CTTGAAAAGTTGGATGTGAAAGCTCCTGGC  
0 TTCGTCAAGT tag o  
0 TTTTCTAAGT tag g  
4 CTCTATAAGTCAGATGTGAAAGCCCTGGGC  
4 CCCGACAAGT tag p  
0 GCTTTTGCCTCGAGGGTTAAAGACCAAAGC  
0 TTTTGTAAGATAGTGGTGAATCCCCGGGC  
0 CTATTCAAGTCAGAGGTGAATCCTCGGGC  
8 CGGTCTAAGT long c  
0 TCTTGTTTGTCTGTGGTGAAGCCTTGGGCT  
4 TCTTGTAAGA long f  
0 TTGTCATAGT tag g  
5 TCTTTTAAGTTGGGTGTGAAATCCCCGGGC  
0 TTATGTAAGT tag c  
0 CAATCTAAGTCAGAGGTGAAATACTATCGG  
4 GGTGGTAAGTCAGTGGTGAATCCTGCGGC  
6 TTCATTAAGTCTGATGTGAAAGCCCTGGGC  
0 TATCAGTGGGGTTCAATCTATTTATATAAA  
14 TTTTCGTGTGTTAGCAACTAAAAATCAAAC  
5 GCTGTTGAGTTGGAGGATGAAATGTCTGGC  
0 CTTCGTAAGTCGGATGTGAAATCCCCGGGC  
5 TTTACTGTATTTTGTAGTAAAGTCTCCGGCT  
2 TTCGTTAAGT tag f  
0 CCGCTTAAGTCGGGTGTGAAAGCCCCGGGC  
0 TTCGCTAAGTCTGATGTGAAATCTCCTGGCT  
4 TCTGCTAAGCGTGCAGGTGAAAGCCCAGGGC  
0 GAAATTAAGT tag f  
6 TCGTGTTAGTCAGATGTCAAATCCTTCGACT

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4	0	2 TAAGGAAAGTCAGATGTGAAATCCCCGGGGC
5	8	3 TTGGGTAAGTCAGATGTGAATCCCCGGGCT
6	2	6 TCGGGTAAGTCAGATGTGAAATCCCCGGGC
7	0	0 GTCGTAAAGT long o
8	0	
9	7	18 GCTCTGGCGCCGCGCCGCGCGCCGCCCTTC
10	4	6 TTTTGTAAGA tag c
11	0	0 ATTCTGGTTGTATTGGGCCTATGCACTTGTT
12	8	4 GCTTGTAAGT long f
13	4	0 AGTGGTAAGTACCTTGTGAAATCCCCGGTC
14	7	2 TTCCATAAGT long f
15	4	4 CTTGTAAAGC long g
16	4	3 CTTTCTAAGT tag o
17	0	0 CTCTCAAGT tag f
18	0	0 ATGTGTCAGT long g
19	5	3 TTGGTTAAGACTGACGTGAAAGCTCCTGGC
20	0	0 GTTGATAAGT long f
21	0	0 TTTACCAAGTCTGGTGTGAAATCTCTCGGCT
22	12	8 TTTTAGTGGGTTTTAAGATGATTGGTCGGA
23	0	0 CTTCGTAAGTTCGGTGTGAAATCTCCCGGCT
24	0	0 GCTCGCAAGCGTCTTGTGAAAGCCCCCGGC
25	0	0 AAGTGTAAGTCAGGTGTGAAATACCAAAGC
26	0	0 TTGTGTAAGA long f
27	0	0 TGGGGTAAGTTCAAGGTGAAAGCTTCGGGC
28	0	0 TTTGTAAAATTTAAAATAAAATTTAAATTT
29	5	8 TTGTATAAGT long f
30	0	0 TTCGGTAAGT long f
31	0	0 TCCTACAAGC long f
32	2	0 TTTGTCGCGT long f
33	5	5 CCCATCAAGTCTGCGGTTAAAGACCGGAGC
34	0	0 ATTCTGGCTGTATTGGGCCTCTGCACTCGAT
35	0	0 CTTGGTAAGC long f
36	0	0 TTCAGCAAGT long o
37	0	0 CTTGTCACGTCGGGTGTGAAAACTCGGGGC
38	7	2 TTCGTAAAGT tag p
39	4	5 CTCGGCAGGTCACTGGTGAATCCCACGGC
40	3	3 CTTGTAAGT long g
41	4	9 ACCTGTAGGCGCGTTGTGAAAGCCCTCGGC
42	0	0 TTGTGTAAGTTGGATGTGAAATTTCCAAGC
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3 4 TTTAGTAAGTCGATTGTGAAAGCCCCAGGC`  
4 0 CTTAGAATTATTACAAGTTATTTTACTTGATT  
3 12 ATTGATAAGTCAGATGTGAAATCTCGGGGC  
0 0 ATCGTCAAGTGCCTTGTGAAACCTCCCGGC  
0 0 GTAAGTAAGTCAGATGTGAAATTTTGAAGC  
0 0 TTTTAAAGACAGTGGTGAAATCCCCGGGCTC  
0 3 TCGCACAAGTlong g  
0 0 CCTTTTAAAGTtag f  
0 0 ACAGGTGCGTlong f  
6 6 TTTCTTAAGTlong k  
0 0 CATGGTATGTCGGGCGTGAAACTCCGGAGC  
0 0 TATCCGGCGTCTCTGACGTCTGCCTGATACC  
0 0 CTTTTTGCGTlong f  
4 2 GTCGTTAAGTlong g  
0 0 ATAAAACATGGTTTTCTATTTTTTTTTATTT/  
5 11 CACTGTAAGTGTCGAGTGAAATCCACGGC  
5 0 TTGTGGATTGTGATTCCGAGGTTTCAGTCCTT  
0 0 ATTGTTAAGTlong f  
0 12 TTCGGTAAGTTGGTTATGAAAGCTCCTGGCT  
0 0 TCCATCAAGTTGGGTGTGAAAGCCCTCGGC  
7 2 CGATTTTAGTCAGGCGTGAAAGCCCTGGGC  
0 0 CCGATTAAGTCGGGTGTGAAATCTCCGGGC  
7 3 ATTGGAAAGTtag f  
0 0 CCAGGTAAGTTTGATGTGAAAGCTCGGAGC  
4 8 CTTGGTAAGCtag f  
6 17 GCTCTGGCGCCGGCCGCGCGGCCGCTTCG  
0 0 TATTGTAAGACAGTGGTGAAATCCCCGGGC  
0 0 TTTGTCGCGTtag g  
0 0 CTTGGCAAGTtag o  
5 4 GTGGGCACGTCGGACCCTGAAAGCCCCCGC  
0 0 TTTTGTAAGACAGTGGAGAAATCCCCGGGC  
6 5 TGATATGAGTGTGATGTGAAAGCCCTGGGC  
2 0 TTGGGTAAGTCAGATGTGAAATTTCCGGGC  
0 0 GTCGGTAAGTCAGTGGTCAAATCCTATAGC`  
4 5 TTGCGTAAGTtag f  
2 2 GCTGGAAAGTlong g  
0 0 CTTGGCAAGTCGGGTGTGAAATCCCCGGGC  
0 0 TTTTGTAAGACAGTGGAAATCCCCGGGCTC/

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4	0	0 TTGAATAAGTTATCTGTGAAATCCCCGGGCT
5	2	0 AATGAACTTTTTTTTTTCGATTCTGTTTTTTTT
6	4	0 TCTGTTGCGTlong g
7		
8	2	2 AACAGCTCAGTCTTTCAAAGGATTGAGACG
9	0	2 TCTTATAAGTCAGTGGTGAAATCTCCGGGCT
10	0	0 CCTGGCAAGTTTGAGGTGAAATCTCCGGGC
11	0	0 ATTGTTAAGTCGGGTGTGAAATCCCCGGGGC
12	3	5 ATTATTAAGTCGGGGGTGAAATCCCAGAGGC
13	0	0 TCGGGTAAGTCTGCTGTGAAAGCTCCGGGC
14	0	0 CATGGAAAGTTGGACGTGAAAACCTCCTGGC
15	0	0 GTCGTTAAGTlong f
16		
17	2	4 CTCGAAAAGCGTTCCGTGAAATCCCCGGGCT
18	0	0 CTTTGTAAGTCAGGTGTGAAAGCCTGGGGCT
19	0	0 TTTCGGACAAGGCATTCTGGTCTACCTTTTA
20	0	0 CCTGTTAAGTlong g
21	0	0 TGTGTGGTGTlong c
22		
23	0	0 ACTATTAAGTCAGGTGTGAAAACCTATGGGC
24	0	0 TTCCCTAAGTtag o
25	2	0 CTGATCAAGTCTGGCGTGAAAGCCCCCGGC
26	0	5 ATGGGCGCAlong g
27	0	2 TTGGTTAAGTtag f
28	0	11 CTTTGTAAGTCAGGTGTGAAAGCCCCGGGC
29	0	5 ATTGTTGAGTTGGAGGATGAAATGTCTGGC
30	0	0 TTTTGTAAGACAGTGGTGAAATCCCCAGGC
31	0	0 AATGAACTTTTTTTTTTCGATTCTTGTTTGGG
32	0	0 TTGGGTAAGTCAGATGTGAAATCCCTGGGC
33	0	0 TGGGGCACGlong g
34	0	10 CCATGTAAGTtag g
35	0	0 ACTTTTAAGTtag f
36	3	3 CGCTGCAAGTlong g
37	5	2 TTGGGTAAGTCAGATGTGAAATCTCCGGGC
38	2	8 CTCTTTAAGTCAGATGTGAAATCCCCGAGCT
39	2	8 GAACGTAAGTCAGATGTTAAATCTCGGGGC
40	0	0 TTTGATAAGTtag c
41	2	0 AATGAACTTTTTTTTTTCGATTCTTGTTTGGC
42	3	2 CTTTCTAAGTCAGAGGTGAAATCCCCGGGGC
43	4	4 CGTCCCAAGTTAGGCGTGAAAGCCCCGGGC
44	3	4 CCCGTTAAGAlong f
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0 CGCGGAAAG` tag f  
0 GCTTGTGCGTCGAGGGTTAAAGACCTCAGC  
2 TTGTATTAGT`long g  
2 GATGATAAGTCAGTGGTGAAAGCTCGTTGC  
0 ATATTTAAGT`long o  
0 TTCAAAAAGTCTGGTGTTAAATCCCGCAGCT  
0 CCGCTCGCGTGAGGCGTGAAAGCCCCGGG  
5 CCAAGTGTGTTAGATGTGAAATCCCGAGGC  
3 CTGTGGAGTTTGATCCAGAGATCCCGTCCTT  
0 TTTGTTAAGT`tag f  
0 TGCGTTAAGTCTGACGTGAAATCTCCTGGCT  
0 TGATACAAGTCGGGTGTGAAATTCGGGGC  
0 TCAGACAAGTGAGGCGTGAAAGCCCTGGG  
2 GAAGGAAAGTCAGATGTGAAATGCCGGGG  
0 GACGTCAAGCGGGGTGTGAAAGCTCCTGG  
3 CTATGCAAGTTAGATGTGAAAGCCCCGGG  
0 ATTATTAAGTCGGATGTGAAAACCTATGGGC  
0 ATAAAACATGGTTCTCTATTTTTTTTATTTTA  
0 ACATTTAAGT`tag c  
2 CCTGTTAAGT`long o  
0 TGATGTAAGACAGATGTGAAATCCCGGGCT  
0 TAGGGTAAGTTCAATGTGAAAGCTTCGGGC  
0 GTGGATAAGTCAGGGGTGAAAGCCCACGG  
0 TCTCGTTTGTCCGGGGTGAAATCCTTGAGCT  
5 CTGGGCAAGTCTGGTGTTGAAAACGCTATCG  
0 TCTTGTAAGTCGGGTGTGAAAGCCCTCAGC  
0 CTTCTAAGT`long o  
0 TATATTAAGT`long p  
2 CTTGGTAAGT`tag k  
0 CCGTTTAAGT`long g  
0 GCTGTCAAGT`tag g  
0 GTCTGTAAGTGTCTCGTGAAATCCCCGGCT  
0 TCTTGTAAGTCGAGTGTGAAAGCCCCTGGC  
0 TTTTGAAGACAGTGGTGAAATCCCCGGGCT  
2 AGTGGAGAAAGGTTCCATAACAACAGTGAT  
0 TTTGTTAAGT`long g  
3 TCCCAAAAGTCTACTGTGAAATCCCTGGGCT  
0 TTACGTATGTCTGGGGTGAAATCCCTGAGC



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3		
4	0	0 TCTTGTAAGTCGGATGTGAAAGCCCCGGGC
5	0	0 CTTAGCAAGTTGGATGTGAAATCCCTCGGC
6	3	4 TTTTAGTGAGTTATTTAGATGATTGGTCGGA
7	0	0 TTTTTTAAGTtag g
8	0	0 CTTGGCAAGTTTCGAGTGAAATCTCCCGGC
9	4	4 TTAGATAAGTlong g
10	0	0 ATGGGCAAGCGAGGTGTGAAAGCTCCCGG
11	0	0 TATGCAAGACAGATGTGAAATCCCGGGCT
12	0	0 CCTCTCAAGCGTCCTGTGAAAGCCTCCCGCT
13	0	0 TTTTGTAAGA long g
14	0	0 CTTGGCAAGTGAGGCGTGAAAGGCCTGGG
15	0	0 TTCTTCAAGTCAGTCGTGAAATCTCCGGGCT
16	0	0 ATAAAACATGGTTTTCTATTTTTTTTATTTA
17	0	0 CACATTAAGTCAGTTGTGAAATACGGCAGC
18	0	0 CCTATTAAGTtag g
19	0	0 ATCAGCAAGTCAGGTGTGAAATCTCGGAGC
20	3	4 CGATGTAAGTCAGATGTGAAAGCCCTGGGC
21	0	3 CATGACAAGTCAGGGGTGAAATCCTTCGGC
22	2	3 CTTTCTAAGTCGGATGTGAAATCCCTCGGCT
23	0	2 ACCGGAAAGlong g
24	0	0 TTTGGTAAGTTGGGCGTGAAATCTCCCGGC
25	0	12 TTGCCAAGTCTGATGTGAAATCCCTGGACT
26	0	8 GTTTGTAAGTtag g
27	0	0 CATGAAAAGCAGGGGTGTGAAAGCCCTCGG
28	0	0 CTCATTAAGTlong g
29	0	0 CTTGTTAAGTtag p
30	3	0 CCCGTCAAGCtag g
31	2	6 TTATGAAAGTGGAACTTTTCAGCGACGGGC
32	0	0 TTTTTTAAGTTGTTTTTAAAGACTAGAGCT
33	0	0 TTGTGTAAGCCCTCCGTGAAAGCTTCGGGC
34	0	0 CTTTGTAAGA tag g
35	3	8 TTTGTTAAGTtag o
36	3	6 TTGGGTAAGTCAGATGTGGAATCCCGGGC
37	0	0 ATTAGTAAGTlong g
38	5	2 GTAAGCAAGlong g
39	2	3 TTTGTGGTGCCGCCTGCAGTCCAATTAGCTT
40	0	0 CGCGTTAAGTCTGACGTGAAATCTCCCGGC
41	0	0 TTTGTCACGTtag f
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2 0 TCGTATAAGTCGAATGTGAAAGCCCCCGGC  
6 4 TTCGAAAAGTTTCTAGCGAAATCTGTCAGCT  
0 0 TCTCATTTGT(long f  
4 3 TGGACTAAGTCGGGTGTGAAATCTCCGGGC  
0 0 ATATGTAAGTCAGTGGTGAAATCCCTGGGC  
0 0 GCTGATAAGT(long f  
0 3 CTTTGTAAGT(tag c  
0 0 CACGGTAAGTGGGGTGTGACAGCGGACGG  
0 0 CAGTGTAAGTCCGGTGTGAAATCTCGGGGC  
4 5 TCGTATTAGTCTCCTTTCAAAGCTCCCGGCC  
2 0 TCGCGTAAGTAAGTGGTGAAATCCCTGAGC  
0 0 CTGGGCACG(tag g  
0 4 TTTTAGTGAGATTTAGAAATAGGTCGGGT  
4 6 CCCGAAAAGTTTTAGCGAAATCTGTCAGCT  
0 0 CTCTTCAAGTCAGACGTGAAATCCTCGGGCT  
0 5 TTTCGGGGCGGCGGAGGGCTGCGGCCGGC  
2 0 ACCGTTAAGT(long f  
0 0 CGTGCTAAGTTAGTTGTTAAATCTCTCGGCC  
2 0 ACCGGCAAGCGTCTTGTGAAATCCACGGC  
0 0 TTTGGTAAGT tag g  
3 4 TTTCGTAAGTTAGGCGTGAAAGACTTCGGC  
0 0 CTAGATAAGTTATTCTTCAAAGACTACGGCT  
3 2 TTCAGTAAGT tag g  
0 0 TCCCGTAAGTCGAATGTGAAAGCCCTCGGC  
6 0 CTGTGGGCT(long g  
0 0 TCTAGTGTGTCTGGTGTGAAAGCCCTGGCT  
7 0 CTTCTGTTCA(long g  
3 4 TTTCTTAAGC(long f  
0 0 CTTGTAAGT tag o  
0 0 CAAGGTAAGTTCGATGTGAAATCTCCGGGC  
0 2 CTTTGTGCGTCAGATGTGAAAGTCCTGGGC  
0 0 GCTGGTAAG(tag g  
5 2 CTGCGTAAGT(long c  
2 3 TTAATTAAGTTTATTGTTAAATTCAATGAGC  
0 2 TTTGTAAGTCAGATGTGAAATCCCCGGGCT  
0 0 TTTGTTAAGT(tag p  
0 0 TAATGTAAG(long g  
0 0 CCCGTTAAGTCAGTTGTGAAAGCCCCCGGC

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3			
4	0	0 TCTGTCAAGT long	f
5	0	0 TCTCGGGTAC tag	p
6	5	0 TTTCTTAAGT long	g
7			
8	4	4 AACAACTCATTCAAGTCAATTGATTGAGACG/	
9	0	0 TCTTGTTAGTCAGGTGTGAAAGCCCCTCAGCT	
10			
11	0	0 AACAACTCATTCAATGAGTGAGACGG/	
12	0	0 TTTAATAAGTTTTTTGTAAAATCTTATGGCTC	
13	0	0 TTTTGTAAGACAGTGGCGAAATCCCCGGGC	
14			
15	4	2 CTTTTTAAGTCAGTGGTGAAATTCTACCGCT	
16	0	0 TAAGGTAAGTTTGGTGTGAAAGCTTCGAGC	
17			
18	0	0 CTTAGCAAGTCAGATGTGAAAGCCCCGGGGC	
19	0	0 ATTTGTTAGT long	g
20			
21	0	0 CGATGTAAGTCAGAGGTGAAATCCCATCGG	
22	0	0 TAGCGTCAGT tag	g
23	0	0 ATCGCTAAGT tag	o
24			
25	2	7 CCTTGTAAGCCTGGCGTGAAAGTCACCGGC	
26	0	0 TTTGTCGCGT long	g
27			
28	0	0 CCGAGCGGG long	g
29	2	0 TCGATTAAGTCAGTGGTGAAATACTTCAGCT	
30	0	0 GTCTTTAAGT long	g
31			
32	2	2 CTTTTTAAGT long	g
33	0	0 CTTGCGGCTG long	g
34			
35	0	5 TTGCGTAAGTTCGGCGTGAAATTTTCGGCT	
36	3	2 ACTTCTAAGT tag	g
37			
38	0	0 CAAGGTAAGTTCGATGTGAAATCTCCGGGC	
39	0	0 CTTTGCAAGA long	g
40	2	0 CTTGGTAAGT tag	g
41			
42	0	0 ATTTTTTTATTTTTTTGAATATTTTAATTAGT	
43	0	0 TTTCGCAAGT tag	c
44			
45	4	2 ATGTGTAAGTGTCTTGTGAAAGCCCCGGGC	
46	0	2 AACAGCTCAGTCGCAAGATTGAGACGGAGC	
47	0	0 TAAGTGAAGTCAGATGTGAAATCCCCGGGC	
48			
49	0	4 TTGGGTAAGTCAGATGTGAAATCCCCAGGC	
50	0	0 TCTGTTAAGT long	p
51			
52	0	0 TTTGTCACGT long	g
53	0	0 ATAAAAAAGAGAAAGAGAGAGAGAAAAAC	
54	5	0 CTTTTCAAGCCAGGGGTGAAATCCCAGAGC	
55			
56	0	0 TCAGACTAAGTCAGATGTAAAATCCCAGGG	
57			
58			
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0 TATGGTAAGTTGGATGTGAAAGCTCCCGGC  
0 TTGGATAAGTGGGGCGTGAAATATCCCGGC  
2 AGATATTAGTCAGATGTGAAATCCCGGGGC  
4 TTTTAGTGAGTTTATTTAGGTAGTTGGTCGG  
0 TTTTGTAAGT long g  
0 TTTTGTAGGACAGTGGTGAAATCCCGGGGC  
2 TTGAGTCAGT long g  
0 GAAAATAAG tag c  
0 CCGAGCGGGTCGCGGGTGAAATCCCCCAGC  
0 ACTTGTAAGTCAGTGGTGAAATCTCTTCGT  
0 TTGACTGGGGATCTTTGTTTACTTTGAATAA  
4 TCTGGTAAGTTGGGAGTGAAAGCCCGGGGC  
0 TTATTTAAGT tag f  
0 ACATTTAAGTGAGTTGTGAAATACCCGTGCT  
0 TCTTTTAAGT long g  
0 CTTTGTAAGA long f  
0 CTTGTCGCGT long g  
0 TTAGTCACGTCGGATGTGAAAACCTCGGAGC  
0 GTGTTCAAGTGGTGTATGAAATCGCTCGGC  
0 TTTCGGGTATTTGTTGCTAGCTGGTCTCATT  
0 ATAAAACATGGTCTTCTATTTTTTTTTTATTT  
3 GACGGCACG tag f  
0 CGTGGTAAG tag f  
3 CTTAGAATTATTACAAGTTTGGTTTAATTGA  
4 TGACGGAAGTCATGTGTGAAAGCTCCCAGG  
0 ATCAGTCAGT tag g  
0 CTCTGTGCGT tag f  
5 CTTAATAAGTTACGGCTGAAATCCGGCGGC  
0 ACTGTTTAGT long g  
2 TTTTTTAAGT long f  
4 AACAACTCATTCAAGTCAATTGATTGAGACGC  
0 TCAGATAAGT long p  
0 TTTTATAAGACAGTGGTGAAATCCCGGGGC  
0 ACTGTCAAGTCAGGGGTGAAATCCCGAGGC  
0 TTTTGTAAGT tag o  
3 TTGGGTAAGTCAGATGTGAAATCCTCGGGC  
0 CTTTGTAAGTCAGGTGTGAAGGCCTGGGGC  
0 GCGATTAAGTCAGGGGTGAAATCCCGGAGC

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4	0	0 TTTTTTAAGACAGGCGTGAAATCCCCGGGCT
5	0	0 TCCGTTGCGT long f
6	0	3 TTTTAGTGAGTTTATTTAAGAGATAGGTCGC
7	0	0 TCTGTTAAGTGAAAAGTGAAATCTCCATCGC
8	0	0 TCTGTTAAGTGAAAAGTGAAATCTCCATCGC
9	3	2 TTGGGTAAGTCAGATGAGAAATCCCCGGGC
10	5	2 TTGGGTAAGTCGGATGTGAAATCCCCGGGC
11	0	0 GTTTGTAAGACAGTGGTGAAATCCCCGGGC
12	0	0 ACTAATAAGT long f
13	0	0 CTTTGTAAGT tag g
14	0	0 TCTTCTAAGTCGGATGTGAAAGCTCCTGGCT
15	0	3 TAATGTTAGTCATTTGTAAAAGCCCCGGCT
16	0	3 TTCGTTAAGTCTGGCGTGAAAGCCTCCGGC
17	0	0 ATCGTTAAGT long g
18	2	0 TTTGTTAAGT long g
19	0	0 CTTTATAAGT tag f
20	3	2 TTTGGCCAGTCAGCCGTGAAAGCCCTGGGC
21	0	5 CCTGATAAGTCAGAGGTGAAAGCCTGCAGC
22	0	0 TTTGTAAGACTGTCGTGAAATCCCCGGGCT
23	0	3 CTATGCAAGTCAGAGGTGAAATCCCAGGGC
24	0	0 TTCTATAAGTCAGATGTGAAAGCCTCGGGC
25	0	4 TCTAGTAAGTCAGTCGTGAAATCGCTGGGC
26	2	0 CCTGTTAAGT long g
27	0	0 CCTGTTAAGT tag p
28	0	0 CGCATTAAGTCTGACGTGAAATCTCTCGGCT
29	0	0 TTATTTAAGT long o
30	3	0 TTCGGTAAGT long g
31	0	0 ATTGAAAAGT tag f
32	0	2 ACAGGTCAGTCTAAAGTGGAAGCCCCGGGC
33	0	4 CCTTGTAAGCCTGGCGTGAAAGTCACCGGC
34	0	0 CTGAGGGTT long g
35	0	0 TTTCGCAAGTCAGGCGTGAAAGCCCCGGGC
36	3	2 CTGTGCAAGTCTGAGGTGAAATTCCGAGGC
37	0	0 TTTTGTAAGACAGTAGTGAAATCCCCGGGC
38	3	0 CCTGCTAAGACTGACGTGAAAGCTCCTGGC
39	0	0 TCTTGCGGTAAAAGATTAAAAACTTTTAATT
40	0	0 CTTTGTAAGTCAGGTGTGAAAGCCTGGGGT
41	2	2 ATTGCTAAGT tag g
42	4	0 CCATGCAAGTCAGATGTGAAATCCCCGGGC
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0 CCTGATCAGT long g  
0 TTGTGCAAGTCGGGTGTGAAATCCGGAGC  
0 ACGGGTAAGTGGGTGTGAAAGCGCTCGG  
2 TTGGGTAGTCAGATGTGAAATCCCCGGGCT  
0 GAGTGCAAGTCAGATGTGAAATCCCCGGGG  
0 TTGGGTAAAGTCAGATGTGAAATCCCCGGGT  
0 TCTTATAAGTCAGTGGTGAAATCTCCTCGCT  
0 TTTAGTAAGACAGTGGTGAAATCCCCGGGC  
0 CCTTGTAAGTGTCTGATGAAATCCCACGGCT  
0 ACTGAAAAGT long g  
2 CGCTGTTAGT tag g  
0 CTTGTAAGTCAGGTGTGAAAGCCTGGGGCT  
0 CCCATAAGTCCCGTGTGAAATCCCCGGCT  
0 CTTGGTAAGT long o  
0 CGGCGCAAGCGTCGTGTGAAATCCCATCGC  
0 TGGGGAATGAGTGGAGGAAGGAAAAGGG  
0 AAGGGTAAG long o  
0 TTTTGTAAGACAGTGGTGAAATCCCCGGGC  
3 0 TTTTGTTAGTCGTCTTTTAAATCTCCCGGCT  
0 TTTGTTAAGTTGGTGGTTAATCTTCGGGCT  
0 TTTAATAAGTTCTTTATAAAAGCTTATGGCT  
0 TTTCGGAAGC tag g  
2 TTTAGAGAGTGTTAACATCGAAATCCCCAA  
0 CCGGCTAAGTCAGTTGTAAATTCCTGCGCT  
0 TTTTGTAAGACAGTGGTAAATCCCCGGGC  
0 CTATGCAAGA long o  
3 4 GACTGTAAGTCAGGTGTGAAACTACGAGC  
0 AACATCCCTGATTGCAAAATCAGAGACGGA  
0 CGCGATAAGT tag f  
2 ACTTGTAAGT tag f  
0 CGGTATAAGTCAGCGGTGAAATCCTTCGGC  
5 0 GAAGGTAAGTCAGATGTGAAATCCGAAGC  
0 CTTGTCGCGT tag g  
0 TCTTGCAAGA long f  
0 5 ATCAATAAGTCTGCTGTGAAAGTCGAAGGC  
0 TTTTGTAAGACAGTGGTGAAATCCCCGGAC  
0 CCTTCAAGCGTCCTGTGAAAGCCTCCCGCT  
2 2 GTCTGTAAGTGCCTTGTGAAATCCCCGGGC

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3		
4	5	0 TTGGGTAAGCCAGATGTGAAATCCCCGGGC
5	0	0 ATTATTAAGTlong f
6	0	0 CGCATTAAAGTCTGACGTGAAATCTCCTGGCT
7	0	0 CTTGGCGAGTGAGGCGTGAAAGGCCTGGG
8	0	0 TTTTGTAAGACAGTGGTGAAATCCCCGGGT
9	0	0 GCGCGTAAGTGCTTTGTGAAAGCCCTGGGC
10	0	0 GCGCGTAAGTGCTTTGTGAAAGCCCTGGGC
11	2	2 ATCTGTAAGTGTCGTGTGAAAGCCCACTGC
12	0	3 TATAATAAGTTGAAAGTGAAAGCCCGGGGC
13	0	0 TTTTTTAAGACAGTGGTGAAATCCCCGGGCT
14	0	0 TGATTTAAGTGAGTTGTGAAATACCCGTGCT
15	0	0 GATAATAAGTCAGTGGTGAAAGCTCACAGC
16	3	0 CTATTTAAGTCAGTTGTGAAAGCCTGGGGC
17	0	2 TGAGGTAAGTCAGGTGTGAAATCCCGGAGC
18	0	2 CGCAGAAAGTTGGGTGTGAAAGCCCTCGGC
19	0	0 TGTTATAAGTGTGTTGTGAAATCCCTGGGCT
20	0	0 CCAAGCAGGTCGGGTGTGAAATCCCTCGGC
21	0	0 AATAATAAGTtag f
22	0	0 CTTTGTAAGTCAGGTGAAAGCCTGGGGCTC
23	0	0 ATAAGAAAGGGAGAGAGAGAGAGAAAAAT
24	0	0 CCTTGTGTGTGAAGTGTGAAAGCCCGGGGC
25	0	0 TTGATTAAGTTATCTGTGAAATCCCCGGGCT
26	0	0 TTTTGTAAGACAGTGATGAAATCCCCGGGCT
27	2	0 CTTTTTAAGACAGGCGTGAAATCCCCGGGC
28	4	2 CGATGTAAGACAGATGTGAAATCCCCGGGC
29	3	0 GACGGAAAGTCAGAGGTGAAATCCCGGGG
30	5	0 GCGGTTAAGtag f
31	0	0 CTGGGCGCGTGGGGTGTGAAAGCCGGCGG
32	3	0 TCTGATAAGTCTGGCGTGAAATTGACCGGC
33	0	0 TTGGTTAAGTTTGGTGTGAAATCTCCCGGCT
34	0	0 CTTGTCAAGTCTGACGTGAAATCTCCCGGCT
35	0	0 TTGGGTAAGTCAGATGCGAAATCCCCGGGC
36	0	0 TTTGTGGTGGCCTCGATGGTCCATTCATTTT
37	0	0 TCTTGGCGTAAAAAATTA AAAA ACTTTTAAAA
38	0	0 TAGGGTAAGTCAGATGTGAAATCCCCGGGC
39	0	0 CAAGATAAGTCAATCATTAAATCTCCTGGCT
40	0	0 TCGTTTAAGTtag g
41	0	0 AACAACTCACACATTGATGTGAGACGGAGG
42	2	2 ATGGGTGTGTCAGATGTGAAATCCCCAGGC
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0 2 TATTACAAGTCTATAATTAAATCTCTGAAGC  
3 0 GTCAGCAAGTCAGATGTGAAATTCCGGAAC  
0 0 TCTGTCGCGT tag f  
0 0 TTTTAGAGTTTATTAGTAGAGTCCGCTTGA  
0 0 TTTGTTAAGTTGGAGGTTTAATCTCTGGGCT  
0 0 CTACGTAAGTGTCTGTGAAATCTCATGGCT  
0 0 ACCAGAAAGtag f  
0 6 TTCTTCGTGTGTTAGCACCTAAAAACCAGAA  
0 0 TTTGGTTAGTTGGATGTGAAATCTCCTGGCT  
5 0 CCTGACAAGTCTGATGTGAAAGACCTGGCT  
0 0 TTTTGGGGCGGGTGGGGCTGTGTCTGCCGT  
0 0 TCCTATTTGTCTGAGGTGAAATCCCAGGGCT  
0 0 CTCATTAAGTGTGTGGTGAATCTCTGTGCT  
0 0 TTTTGTAAGACAGTGGTGAATCCCCGGGT  
0 2 GTCGTTAAGT long f  
0 0 TTGCCTAAGC tag f  
2 0 CTATATGAGTTGGGTGTGAAATCCCCGGGGC  
0 2 TTGGGTAAGTCAGATGTGAAATCCCCGGGC  
0 0 CTTTGTAAGTCGGGTGTGAAAGCCTGGGGC  
0 0 CCGTGCGAGTGAGGCGTGAAAGCCCCGGG  
0 0 CTATTTAAGTCAGTGGTGAATCCTTCAGCT  
0 0 TGATGTAAGACAGATGTGAATCCCCGGGCT  
0 0 TACCATAAGT tag g  
0 0 TTTTGGGGCGGGCGGGGCTGTGTCTGCCGT  
0 0 TTTTTTAAGAtag f  
0 0 CCTTGGGCCT long f  
0 0 TTCGTTAAGT long g  
0 0 TTTGTCGCGT long g  
0 0 CTTGTCGCGT long g  
0 0 GCCGATGCGTCCGTGGCTGAAATCCCCCGG  
0 0 TTCTTATAAATATTAGGAACTAGAATTTGAT  
2 0 TTGTTTAAGTGAGGTGTTAAAGCCCTGGGC  
0 0 CTTGGAAAGTCGGATGTGAAAGCCCCGGGG  
0 3 ATACTTAAGT tag g  
2 2 CTCGAAAAGCGTTCCGTGAAATCCCCGGC  
0 0 ATTTTTTTATTTTTTTTGAATAAAATTATTT  
0 0 TTTGTCGCGTtag f  
0 0 CGATGTAAGTGTAGGGTGAATCCCACGGC



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4	3	3 AACAACTCATTCAAGTCAATTGATTGAGACGC
5	2	0 CTAGATACGTTTGATGTGAAATCCCTGGGC
6	0	0 CTATTCAAGTtag f
7	0	0 TTTCGTATGTlong o
8	0	0 TCTCGTGCGT long o
9	0	0 CTTTATAAGTCAGTGGTGAAAGCCCGGAGC
10	0	0 CTGGGCAAGTCGGATGTGAAATACCTCGGC
11	0	3 CCTGACAAGTCTGATGTGAAGGACCTGGGC
12	0	0 TGCTATAAGTCTGATGTGAAACCTTCTGGCT
13	3	0 CCTCGTAAGTGCTTTGTGAAAGCCCCGGGC
14	0	0 TTTAAAAAGTATTCTGTCAAAGATTAGGGCT
15	0	0 TCTTGTAAGT long f
16	5	3 AACATCTTGCTCTTTGAGTGAGACGGAGGC
17	0	2 CCTTTCAAGTCAGTCGTGAAATCGCTGGGC
18	2	0 TTCGCTAAGTCTGGCGTGAAATATTTCTGGCT
19	3	0 AACAACTCACACATTGATGTGAGACGGAGG
20	0	0 TTCTGTAAGC tag f
21	2	0 TTTCGTAAGA long g
22	0	0 GCGTGTAAGTGTCTTGTGAAAGCCCCGGGC
23	0	0 TCCTGTAAGCCTGACGTGAAAGGCTATGGC
24	0	0 CTTGCCAAGTGCCTTGTGAAATCCCACGGCT
25	3	0 TTCGTTAAGT long g
26	0	0 CAAGGCAAGTCTCGCGTAAAAGCTCCCGGC
27	0	0 CATTGTAAGTCGGGGGTGAAAGCCTGGAGC
28	0	0 CGTCGTAAGT tag f
29	0	0 ATATGCAAGACAGATGTGAAATCCCCGGGC
30	0	0 CCTTGCGCGTCTCGCGTTAAATTCCATTGCT
31	0	0 AACAGCTCAGTCGTAAAAGATTGAGACGGA
32	2	0 ATTGTTAAGC tag g
33	0	0 GTTCGTAAGTGCTATGTGAAAGCCCTCGGC
34	0	0 TCTGTTAAGCATGAAGTGAAATCCCCAGGG
35	0	2 GGATTTAAGTCAGATGTGAAATCCCGAGGC
36	2	0 CTTGGCCAGT long g
37	0	0 TCTATTGCGTCGAAAGTGAAAACCTCAGGGC
38	0	0 CGTTCGGGTTCCGCGGGACGGGGCCGCC
39	0	0 AGTTAATAAAAGTTTTACTAAATAGAGTGA
40	0	0 TTGGGAAGTCAGATGTGAAATCCCCGGGCT
41	0	2 GTTGATAAGT tag g
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3 0 TTTTGAAAGTCAATTGTTAAATCCCAGGGCT  
0 3 TTGGCTAAGT tag f  
0 0 TTTTTGTAAGACAGTGGTGAAATCCCCGGG  
0 4 TCTTGTCCGT long g  
0 0 GGCGATAAG long f  
0 0 TTGGGAAAGTCAGATGTGAAATCCCCGGGC  
0 0 TCTTGTATGTGAATGTGAAAGCCCCTGGCT  
0 0 TTGGGTAAGTCAGATGTGAAATCCCCGGGC  
0 0 ATGATTAAGT long g  
0 2 GCTCTGGCGCCGGCCGTGCGGCCGCCCTTC  
0 0 CTTAGCAAGTCAGAGGTGAAATGCCGGGGC  
2 0 TTGGGTAAGACAGATGTGAAATCCCCGGGC  
0 0 GACGGTAAGTCAGACGTGAAATCCCCGAGGC  
0 0 AGAGGAAAGTCGGTCGTGAAAGCCCCGGGG  
0 0 TTTAACAAGTCAGAAGTGAAAGCCCCTGGGC  
0 0 TTTTGTCAGT long g  
0 0 TCTGTCACGT tag f  
0 0 TCTGGTAAGTGGGGTGTGAAAGCCCCTCGGC  
0 0 ATTGTTAAGT tag c  
0 0 TTTGATAAGT long c  
3 0 AACAACTCATTCAAGTCAATTGATTGAGACAG  
6 0 CTTGACAAGTCTGATGTGAAAGACCTGGGC  
0 0 CTTACCAAGT tag p  
0 3 CCTGTCAAGTCTGATGTGAAAGACCTGGGC  
0 0 ATAGTTAAGTCAGAGGTGAAATCCCCGGGGC  
2 0 TTCGGTAAGTCGGGTGTGAAAACCTTAGGC  
3 0 TTGTGCAAGTCAGATGTGAAAGCCCCTGGGC  
0 0 TTTGTCGCGT tag f  
0 0 ATGGGCGCATCGATTGCTGAAAGCCCCCGG  
0 0 GCTGCAAAGTCCGGGGTGAAATCCTCCAGC  
0 0 CGGCACAAG long g  
3 2 CACTGTAAGTGTGGGGTGAAAGCCCACGGC  
2 0 TTGGGTAAGTCAGATGTAAAATCCCCGGGC  
0 0 ATTGTTAAGT long g  
0 2 GATGTAAGACAGATGTGAAATCCCCGGGCT  
0 0 CTTCGTAAGT tag f  
0 0 TTTTAGTAGGATTTTAGAGATAGGTCGGTTA  
0 0 TTGATAAGTCAGATGTGAAATCCCCGGGCT

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3		
4	0	3 AGGCGGGGCGCTGGGCGAGGTGGTAGGAC
5	0	0 TTTCTGCTTGTTAGAGTCAAGTCCTCGCGGA
6	0	0 TCTTTTAAGACAGGCGTGAAATCCCCGGGC
7	0	0 CCCGACAAGTCTGATGTGAAAGACCTGGGC
8	0	0 TCCGCCAAGCGTTTTGTGAAATCCCACGGCT
9	2	0 ATAGGTCAGTCAGGTGTGAAATTCCGGTAC
10	0	0 ATTATTAAGTtag g
11	0	0 TTAACAAGTlong g
12	0	0 TTTGTCGCGT long g
13	0	0 TTATTCAAGTtag c
14	0	0 TAGAGTCAGTCAGTCGTGAAAGGCCTGGGC
15	0	0 GCTATCAAGTtag g
16	0	0 CTTTGTAAGTCAGGTGTGAAAGCCCCGGGGC
17	3	0 TTGGGTAAGTtag g
18	0	0 GTTCCTAAGTtag f
19	0	0 ACTTTTAAGTtag g
20	0	0 CTTTGTGAGTCAGGTGTGAAAGCCTGGGGC
21	0	0 CGCAGTAAGTtag f
22	0	0 ATTGTTAAGT long f
23	4	0 ACTTTTAAGTtag o
24	0	0 CCAATTAAGTtag c
25	0	0 CCTTGTAAGTCAGGTGTGAAAGCCTGGGGC
26	0	0 AGATAAAAGTCAGATGTGAAATCCCCGGGGC
27	0	0 TTGGGTAAGTCAGATGTGAGATCCCCGGGC
28	3	0 AACATCTCACACATTGATGTGAGACGGAGG
29	0	1 TTGGGTAAGTCTGATGTGAAATCCCCGGGC
30	1	0 CTTTGTAAGT long g
31	0	0 TTTGTCACGTlong g
32	0	0 CTGAGAGCTGTACTTAGATAGCGATTCTACC
33	4	0 ATCCGTAAGTGTCTTGTAAGTCCCCGGGGC
34	0	0 TTGGGTAAGTCAGATGTGAAATCCCCGGGT
35	0	0 TCCCGTAAGTCGTGTGTGAAATCCCTCTGCT
36	0	0 ACTAACAAGT long g
37	0	0 CTTGCCAAGTGCTTTGTGAAATCCACGGCTC
38	0	0 ATCGGTGCATCGATTGCTGAAAGCCCCCGG
39	0	2 TTGTGCAAGtag f
40	0	0 CTTGCTAAGTGCTTTGTGAAATCCCACGGCT
41	0	0 GTTCTGGCTGtag g
42	3	
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0 2 ATATTTAAGT tag g  
2 0 TTTTCTAAGTCTTCTGTGAAATCTACGGGCT  
0 0 CTTTGTAAGTTAGGTGTGAAAGCCTGGGGC  
0 0 TTTTTTAAGACAGGCGTGAAATCCCCGGGCT  
0 0 CTTTGTAAGTCAGGTGTGGAAGCCTGGGGC  
0 0 TTTTCTAAGACAGTGGTGAAATCCCCGGGCT  
0 0 AATTGTAAGT tag p  
0 0 TTTGTACAGTCAGATGTGAAATTCCCCGGGCT  
0 2 TTTCTGGTCTCGAGACGCGGTCAGCCCCAA  
0 2 CAATATAAGTCAGGGGTGAAAGCCTACGGC  
0 0 TTTTTTAAGACAGGCGTGAAATTCCCCGGGCT  
0 4 AACAACTCATTGTAAAAGATGAGACGGAGA  
0 2 CGTGCCAAGTCGGGTGTGAAAGCCTCGAGC  
0 0 ATAGGCAAGTCCGGCGTGAAAGCCCTAGGC  
0 0 TTTTGTAAGACAGTGGTGAAAGTCCCCGGGC  
4 0 CACGGACAGTGGGGTGTGAAATCCCTCGGC  
0 0 TTGAATAAGTCAGTCGTGAAATTTCTTGGCT  
2 0 TTGGGTAAGTTAGATGTGAAATCCCCGGGC  
2 0 ATCGGAAAGTGTTCTGTGAAATCCCTCGGC  
0 2 TCAAGCAAGTCTGTTGTGAAATCCCCGGGGC  
0 0 CCTGACAAGTCTGAAGTGAAAGACCTGGGC  
0 0 GGTAAG tag f  
0 0 CTTTGTAAGT tag g  
0 0 CTTGGTAAGTCAGGTGTGAAAGCCTGGGGC  
3 0 CCTGACAAGTCTGATGTAAAAGACCTGGGC  
3 0 TCATGTAAGTCTGTTGTGAAATCCCCGGGCT  
0 0 TGATGTAAGACAGATGTGGAATCCCCGGGC  
0 0 TCAGATGCGTCAGATGTGAAAGTCTGGGC  
0 0 TTCAGCAAGTCTGATGTGAAAGCCTCCGTC  
0 0 TTGTTTAAGT long g  
0 0 TCACGCAGGTCGGATGTGAAAGCCCCGGGC  
0 0 TGCCGCAAGTCAGGGGTGAAATCCCCGAGC  
0 0 TTTGTCGCGT long g  
0 2 AGTGGAAAGTTAGATGTGAAAGCCCCGGGC  
0 3 CTTTTTAAGT long g  
0 0 TTATTTAAGTTAGATGTGAAATACCCGGGCT  
0 0 TTTGCTAAGT long g  
0 0 TTGGCCAAGT tag f

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3			
4	0	0	TGATGTAAGA tag f
5	0	0	CTTGCCAAGT long g
6	0	0	CTCGAAAAGCGTTCCGTGAAATCCCCTGGC
7	0	0	CTTGCCAAGTGCTTTGTGAAATCTCACGGCT
8	0	0	TTAGTTAAGT long g
9	0	0	TTTTAGTGGGTTTTAAGATGATTGGTCGGA
10	2	0	ATCAATTAGT tag f
11	0	0	CTCTGTAAGTCAACGGTGAAATCCCTCGGC
12	0	2	TCTGTCGCGT long g
13	0	0	CTTTGTAAGTCAGGTGTGAAAGCTTGGGGC
14	0	0	CTTTGTAAGTCAGGTGTGAAAGCCCGGGGC
15	0	0	TTGTTTAAGT tag k
16	0	0	TGATCCATGTCAGAGGTGAAAGCCTGGAGC
17	0	0	ATTTGTAAGACAGATGTGAAATCCCCGGGC
18	2	0	TTTGATAAGT long f
19	0	2	TTGGGTAAGTCGGATGTGAAATCCCCGGGC
20	0	0	TTATGTAAGACAGATGTGAAATCCCCGGGCT
21	0	0	CTTGTCGCGT long g
22	0	3	TTAGTTAAGTCGATTGTAAAATTCGAGGCT
23	0	3	AACATCTCATACATTGATGTGAGACGGAGG
24	0	3	GTTCTGATTGTTTCGGGCCTCGCGCTTATAGC
25	0	3	TTTTGTAAGT tag f
26	0	0	ACGTATAAGTCAGATGTGAAAGTCCTGGGC
27	0	0	ACGAGAAAG tag g
28	0	0	ATAAGAAGTAAAATAAAAGAAAGAATAAC
29	0	0	TGGAGCAAGTCTGACGTGAAATTTCTTGGC
30	0	0	TTATGCAAGA tag f
31	0	2	TTTGTCGCGT long o
32	0	0	GCTGTCAAGTCAGGGGTGAAATCCCCGGGC
33	0	0	TACCGTAAGTCAGATGTGAAAGCCCCAGGC
34	0	0	CTTAGTAAGTTGGGAGTGAAAGCCTTTGGC
35	0	0	CCTTGTAAGTCGGGTGTGAAATCCCTCAGCT
36	0	0	ACTCGATCAGTGAGCTATTACGCTTTCTTA
37	0	0	CCTGGTCAGTCGGGTGTGAAAGCCCCGGGC
38	0	0	TTCGTTATGTCGGATGTGAAAGCCCTCGGCT
39	0	0	TTTTGTAAGACAGTGGTGAAATCCCCGAGC
40	0	0	GCAGGCAAGTCCGGGGTGAAATCCCACGGC
41	0	0	CAACATAAGTCAGAGGTGAAATCCTATCGG
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0 TTTTGTAAGA tag f  
0 TTTTGTAAGACAGTGGTGAAATCCACGGGC  
0 TTTTGTAAGACAGTGGTTAAATCCCCGGGC  
0 CTTGGCAAGTCAGATGTGAAAGCCATGGCT  
0 GCAGGTAAG tag f  
0 CCAGATAAGT long g  
0 ACTCTTAAGT tag o  
0 ATAGGCAAGCGAGGTGTGAAAGCTCCCCGGC  
0 AACAGCTCAATCTTATGGGTTGAGACGGAG  
0 CTTGCAAGTCTGGTGTGAAAACGCTACCGC  
0 CTTTTCAAGTCAGGGGTGAAATCCTGGGGC  
0 TTATATTAGTCGTATGTTAAAGACTCGGGCT  
0 TCGTCCAAGTCGGGGGTGAAATCCTCTCGC  
0 TGATGTAAGACAGATGTGAAATCCCCGGCT  
1 0 TTGGGTAAGTCAGATATGAAATCCCCGGGC  
0 0 TTTGATAAGTTACGGTTGAAATCCGGCGGC  
0 0 CTTAATAAGTCAGCCGTGAAATGTTTGGGC  
0 0 ACGCAAACCGACACTGGTGCGCGAGATGAC  
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0 0 CTTTTTAAGT tag c  
0 0 AGGCGGGGCGGTGGATCCGGGTGGTAGGA  
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0 0 AGTTATAAGTTATATGTTAAAGGCTACGGC  
0 2 ATGGGTAAG tag g  
0 0 GCTGCCAAG tag g  
0 0 ATTAATAAGTCAGATGTGAAATACCAAAGC  
0 0 CGCGGTAAG tag o  
0 0 TTTTGTAAGA tag g  
0 0 TCTGTCGCGT long g  
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9	0	0 CTTGGTAAGT tag f
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19	0	0 AACAACTCATTGTAAAAGATGAAACGGAGC
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24	0	0 TGTAAGACAGTGGTGAAATCCCCGGGCTCA
25	0	2 CTTTGCAAGTCAGAGGTGAAATGCCAGGGC
26	0	2 CCCGGTAAGTCAGTGGTGAAAGATTGCCGC
27	0	4 CTTTTCAAGTCAGAGGTGAAATCCCCAGGC
28	2	0 AACAACTCATTTATTCAATGAGTGAGACGG
29	2	0 ACCAACTCATTCAGTCAATTGATTGAGACGC
30	0	0 CCTTGTAAGT long o
31	2	2 TTAGATAAGTCAGATGTGAAAGACCTGGGC
32	0	0 AATGAACTTTTTTTTTTCCAAAGACCTTGAA
33	0	0 CCTGGTAAGTCAGGGGTGAAAGCTTCCCGC
34	0	0 TTCGGTAAGTCAGATGTGAAATCCCTGGTC
35	0	0 TTTGTCGCGT long g
36	0	0 CTCGAAAGGCGTTCCGTGAAATCCCCCGGC
37	0	0 TGATGTAAG tag g
38	0	0 GAATGTAAGTCAGACGTGAAATCCCAGAGC
39	0	0 TTTGATAAGT tag f
40	0	0 ATTGAAAAGTTGGGGGTGAAATCCCAGGGC
41	0	0 TTCGTTAAGT long o
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0 CTTTGTAAGTCAGGGGTGAAAGCCTGGGGC  
0 TTTGTAAGAC tag o  
0 CCATTTAAGT tag g  
0 TTTTGTAAGCCAGACGTGAAATCCCGGGC  
0 CTTGGTATGT long f  
0 ACCGTTAAGT tag f  
0 CCATGTAAGTTAGAAGTGAAAGCCTGGGGC  
0 ATAGTTAAGT long f  
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2 0 TGATGTAAGTCAGATGTGAAATCCCGGGC  
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0 0 CGCTGTTAGT tag g  
0 0 CGCTGAAAGT tag f  
0 0 ATCGGCGCGT tag g  
0 0 CTTGTCGCGTCGAATGTGAAAACCCGGGGC  
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0 0 CCGTTCAAGTGAGGCGTGAAAGGCCTGGGC  
0 0 CTTTTAAGTCGGATGTGAAATCCCGGGCT  
0 0 TCCGTTGCGT long f  
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0 0 TTTGGTGCGTTTTGTTGCAAATACTCAAACA  
0 0 TTTGGTAAGTCAGATGTGAAAGCCCCGGCT  
0 0 CCGAGCGG tag g  
0 0 CTTGGGCCT tag p  
0 0 CCATTCAAGTTAGGAGTGAAATCCTGAAGC  
0 0 CTCGTTAGGTGAGGTGTGAAATCCCACGGC  
0 0 CTTTGTAAGT long g  
0 0 GATCGTAAGT long p  
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12	0	0 CTTGCCAAGTGCTTTGTGAAATCCCACGGCC
13	0	0 TTGGGTAAGTCAGATGAAATCCCCGGGCTC
14	0	0 ACTTATAAGT long g
15	2	0 GTTTAGGATT tag o
16	2	0 TTTTAGTGAGATTTTAGAAATAGGTCGGTT
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21	0	0 AACAACTCACATTGATGTGAGACGGAGGCC
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24	0	2 AACATCTCACACTTGATGTGAGACGGAGGC
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31	0	0 TCTTTCAAGACTGCTGTGAAATCCCTGGGCT
32	0	0 TTCGATAAGT long o
33	0	0 TGCAGAAAG tag f
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37	0	0 CCGTGTGTGT tag g
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39	0	0 TTTGATAAGT tag p
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0 TTTTGTAAGACAGTGGTGAGATCCCCGGGC  
1 TTGGGTAAAGTCAGATGTGAAGTCCCCGGGC  
0 TCTTGTAAGTTGGGCGTGAAAGCCCCGGGC  
0 ATAAGAAAGGGAGAGAGAGAGAGAAAAAC  
0 TTCGTTAAGT(long g  
0 TATGATAAGTTTGACGTGAAATCCCATCGCT  
0 TTTGTTAAGT(long o  
0 CGCGGAAAG tag f  
0 ATTTTAAAGT(long g  
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0 TTCGTTAAGT long o  
0 TTCTGTAAGA long g  
0 TTTGTTAAGTCTGCTGTGAAATCCCCGGGCTC  
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0 TTTTGTAAGACAGTGGTGAAATCCCCGGGC  
0 CTCTTAAAGT(long f  
0 TTGGATAAGT tag p  
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7		
8	0	0 TTTGGTAAGTCAGATGTGGAAGCCCCGGGC
9	0	0 TTTGATAAGT long g
10		
11	0	0 TTCTGTAAGT long f
12	0	0 CAATCCAAGT long g
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0 0 ATATTTAAGTtag g  
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0	2 TCTCGGAACAGGGAATAACTGGTCTGCCGG
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8	0	2 CCCTGTAAGTCAGTGGTGAAATATCTTAGCT
9	0	2 CTCGAAAAGCGTTCCGTGAAATCCACCGGC
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16	0	2 TCAGACTAGTCGAATGTAAATACCAAGGC
17	0	2 TTTGTTAAGTCAGATGTGAAAGCCCTGGGT
18	0	2 GTTTAGGATTTCTTTCTATGGTCGGCTGTG
19	0	2 CCGATCAGGTCAGGCGTGAAATCCCGGGC
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21	0	2 CTTGATAAGTCAGATGTGAAAGCCCTGGGC
22	0	2 CGATGTGTGTGAGACGTGAAAGCCCGGGC
23	0	2 TTGTTCAAGT long g
24	0	2 GAATGTAAGTCAGACGTGAAATCCGAGCTC
25	0	0 TGATGTAAGACAGATGTGAAATCCTCGGGC
26	0	0 CTCGATTAGCCTCTTGTAAGCCCTGGGCT
27	0	0 CTTTGCAAGT long f
28	0	0 CTTAACAAGTCGAGAGTGAAATCCCAGGGC
29	0	0 GCGGTCACGTCCGGGGTGAAATCCCGTGGC
30	0	0 ATTTGTAAGT long g
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0 TTCGCTAAGA long o  
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21	0	0 CGATGTAAGTlong f
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35	0	0 GCAAATAAGTCAGTGGTGAAAGCCTGTTGC
36	0	0 CTCGATAAGCGTTCCGTGAAATCCCCGGCT
37	0	0 TTTGGTAAGTCAGATGTGAAAGCCCAGGGC
38	0	0 AACATCTCACACATTGATGTGAGATGGAGG
39	0	0 GAATGTAAGTCAGACGTGGAATCCCGGAGC
40	0	0 TCCATCAAGTGCTTTGTGAAATCCCACGGCT
41	0	0 TTTTGTAAGACAGATGTGGAATCCCCGGGC
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0 TTTGGCCAGTCAGCCGTGAAAGCCCCGGGC  
0 AACAAATTCACACATTGATGTGAGACGGAGG  
0 CTCGAAAAGTGTTCCGTGAAATCCCCGGGC  
0 TTGGGTAAGTCATGTGAAATCCCCGGGCTC  
0 TTGTCCAAGT long g  
0 AACAACTCATTCAAGTCAATTGACTGAGACGC  
0 AACAGCTCATTGTAAAGATGAGACGGAGGC  
0 TCTTGTAAGT tag g  
0 TTAAAAAAGTTAGATGTGAAATCCCTGGGC  
0 CTTAATAAGTCAGGTGTGAAATCCTGGGGC  
0 CCTCGCAAGCGTCCTGTGAAATACCTCAGCT  
0 ACCAACTCACACATTGATGTGAGACGGAGG  
0 CCCCATAAAGTCAGTCGTAATCGCTGGGCTC  
0 ACATTTGAGTCAGGGGTGAAATCCCAGGGC  
0 GAATGTAAGTCAGACGTGAAATCCGGAGC  
0 AACAACTCATTAAAGATGAGACGGAGGCGC  
0 TTTTTTAAGACAGGCGTGAAATCCCCGGGC  
0 TGACTCAAGTCAGCGGTGAAAGCCTGGAGC  
0 TTTGATTAGTCGTTTGTTAAAAGTCCCGGCT  
0 CCGTTTAAGTTAGGTGCGAAAGTCCTGGGC  
0 TCTAACAAGTCAGGCGTGAAATCCCAGGGC  
0 AACAACTCATTGTAAAGATGAGACGGAGGC  
0 CCAACTAAGTCAGAAGTGAAAGCCCCGGCT  
0 ACAACTCATTCAATGAGTGAGACGGAGC  
0 CTTTGTAAGTCAGGTGTGAAATCCCAGGGC  
0 AACAACTCATTCAATCAAAAAGATGAGACGC  
0 AACAGCTTACACATTGATGTGAGACGGAGG  
0 AGGCATAAGTCAGATGTGAAATCCCAGGGC  
0 CTTGGCAAGTCTGATGTGAAAGCCCATGGC  
0 GAATGTAAGTCAGACGTGAAATCCCGGAGC  
0 TCAGACTAAGTCGAATGTAAAATATCAAGG  
0 CCTGACAAGTCTGATGTGAAAGACCGGGCT  
0 GAAGGCAAGTCTGGCGTGAAATCTCTCGGC  
0 TTTGAAAAGTTTCGTGTGAAAGGTCAGGGC  
0 TTGGGTAAGTCAGATGTGAAATCCCCGGTC  
0 CTTTGTAAGTCAGATGTGAAAGCCTGGGGC  
0 TTGGGTAAGTCAGTTGTGAAATCCCCGGGC  
0 TTAGGTAAGT tag o

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4	0	0 TTTAAGACAGGCGTGAAATCCCCGGGCTTA
5	0	0 CCTCGGGTGCAGGCCGACGGTCCACCTCGC
6	0	0 TATAGCAAGTCAGTGGTGAAATCTTGCAGC
7	0	0 TTTAGCAAGTCTGGTGTGAAAGCCTCCGTTT
8	0	0 TTTCTGTGAGATTGAGATTGTTTGGCCTGCG
9	0	0 ACCTTTAAGTCGGAGGTGAAAGCCCAGGGC
10	0	0 TCTATAAGTCAGATGTGAAATCCCCGGGCTT
11	0	0 TCTAGCAAGTCTGATGTGAAATCCCCTGCA
12	0	0 TCTGGTGTGTCAGGTGTGAAATCCCCGGGC
13	0	0 GACGGCACGTCTGTCGTTGAAATCCCTCGG
14	0	0 CTTTGTAAGTCAGGTGTGAAGCCTGGGGCT
15	0	0 AATGAACTTTTTTTTTTCGATTCTTGTTTGGG
16	0	0 TTGGCTAAGT long f
17	0	0 TCTCAGGCTAGTGGCCGGTGGTCCGCTCGA
18	0	0 AACGGTAAGTACCTTGTGAAATCCCCGGAC
19	0	0 ACTTTCAAGTCGGAGGTGAAAGCCCAGGGC
20	0	0 TCGGGTAAGTCTGACGTGAAATCTTCATGCT
21	0	0 TTGGGTAAGTCAGATGTGAAATCCGGGCTC
22	0	0 GTTAATAAGTCAGTGGTGAAAGCCGGTTGC
23	0	0 ACTTATAAGTCAGTGGTGAAATCTCTGGGC
24	0	0 CTTCGTAAGTCAGGTGTGAAAGCCTGGGGC
25	0	0 CTTGCCAAGTGCTTTGTGAAATCCCACGACT
26	0	0 TTTTTTAAGACAGGCGTGAAATCCCCGGACT
27	0	0 TCTTTCAAGCGTCCCGTGAAAGCCTCCGGCT
28	0	0 TTTAGTAAGTTCTTTATGAAATCTTACAGCT
29	0	0 CTTGCCAAGTGCTCTGTGAAATCCCACGGCT
30	0	0 CTTCATAAGTCGGATGTGAAATTCTCGGCT
31	0	0 TGATGTAAGACACATGTGAAATCCCCGGGC
32	0	0 TTTCGGGGTGAGGCGAGCCCGGTCCGCCGC
33	0	0 CTTCGCAGGTCAGGGGTGAAAGCCCAGCGC
34	0	0 TTTGATAAGTCAGATGTGAAATCCCCGGGCT
35	0	0 TTTGGTAAGTTAGATGTGAAATCCCCGGGC
36	0	0 TTTTTTAAGACGGGCGTGAAATCCCCGGGC
37	0	0 CGGCTCAAGT long g
38	0	0 TCTGATAAGTCAGTGGTGAAATCTGGTCGC
39	0	0 ATGTGTAAGACAGGTGTGAAATCCCCGGGC
40	0	0 TTGGCTAAGCTTGGTGTGAAATCTCCCGGCT
41	0	0 TTAAGTAAGACAGATGTGAAATCCCCGGGC
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0 CAAGGTGTGTTTCTGGTGAAATCCGGGGC  
0 ATTAGTAAGTCAGTGGTGAAAACCCATCGC  
0 TAGGGTAAGTACAATGTGAAAGCTTCGGGC  
0 TCTCGTTTGTCTGAGGTGAAATCCCTGGGCT  
0 CTCTTTAAGTCAGACGTGACAGCCCTAGGCT  
0 TTTTAAATTATTTATTTTGTAGTTGGAGAT  
0 TTGACTAACTCGGATGTGAAAGCTCCTGGC  
0 TTGTGTAGACAGGTGTGAAATCCCCGGGCT  
0 TTTTGCAAGTCAGAGGTGAAAGCCTGGAGC  
0 CTATCCAAGTCAGAGGTGAAATGCCGGGGC  
0 TTTTTTAAGACAGGCGTGAAATCTCCGGGCT  
0 CTATGTAAGT tag g  
0 TGGGGTAAGTTCAAGGTGAAAGCTTCGGGC  
0 CCCGGTAAGTCCGGCGTGAAATCCCAGAGC  
0 CTCTGTAAGTCAACGGTGAAATCCCTCGGCT  
0 CGATACAAGTCAGGGGTGAAATCCCCGGGGC  
0 ATAAGAAAGGGAGAGAGAGAGAAAAATAA  
0 TTTTTTAAGACAGGCGTGAAATCCTCGGGCT  
0 CGAAGAAAGTAGGGTGTGAAATGCCTTGGC  
0 CTTTGTAAGTCAGAGGTGAAAGCCTGGGGC  
0 ATTGATAAGTCAGGTGTGAAATCTTCGGGC  
0 CTTTTTAAGTCGGATGTGAAATCCTCGGGCT  
0 ACTTTAAGTCGGAGGTGAAAGCCCAGGGCT  
0 TTTGGTAAGTCAGATGTGAAATCCCCGGGGC  
0 TTTTTTAAGGCAGGCGTGAAATCCCCGGGC  
0 TCGGAAAGAAAGATGTGAAATCCCAGAGCT  
0 TCTGGTAAGTCGGATGAAAGCCCCGGGCTT  
0 TTTGTCGCGTCTGCTGTGAAAACTCGGGGT  
0 TTGTGCAAGT long p  
0 ACCAGCAAGTGCCTTGTGAAAGCCCCGAC  
0 TTGTGTAAGTTTGGTGTGAAAGCTCCGGGC  
0 CTTTTTAAGTTGGATGTGAAATCCCCGGGCT  
0 TCCTTCAAGCGTCCTGTGAAAGCCTCCGGCT  
0 CTTGCCAAGTGCTTGTGAAATCCCACGGCTC  
0 ATCTTTAAGT long g  
0 TCGTCCAAGT long c  
0 CTTAATAAGTCAGGTGTGAAATCACGGGGC  
0 GCTATTAAGT long f

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4	0	0 TCAGACCAAGTCGAATGTGAAATTCCAAGG
5	0	0 CTGAGTAAGTlong g
6	0	0 TCTTTCAAGCGTCCTGTGAAAGCCTCCGACT
7	0	0 CTTGCCAAGTGCTTTGTAAAATCCCACGGCT
8	0	0 CTTTTTAAGTCGGATGTGAAATCCCCGGACT
9	0	0 CTTGGTAAGT tag g
10	0	0 TCGTGCAAGACAGATGTGAAATCCCCGGGCT
11	0	0 TTTGGTAAGT tag g
12	0	0 TCTCGGGGTGAGGCGAGCCCGGTCCGCCGC
13	0	0 TCATTCTAGTCAGGCGTGAAAGCCTCGAGC
14	0	0 CGCGCCAAGTCAGATGTGAAAGCCCGGGCT
15	0	0 CGGACTAAGTCGGTTGTGAAATCTCCGGGC
16	0	0 CTTTGTGAGTCAGGCGTGAAATTCCTGGGC
17	0	0 TTCGCCAAGT long o
18	0	0 CTTGGCAAGT tag g
19	0	0 CCTTGTAAGTCTTGTGTGAAAGCCCTCGGCC
20	0	0 TTCGTTAAGTCTGGTGTGAAAGCCCTGGGC
21	0	0 TGATATAAGA tag c
22	0	0 CCGAGCGGGTCGTGGGTGAAATCCCCCAGT
23	0	0 TTCGTTAAGTCTGACGTGAAAGCCCTGGGC
24	0	0 CTTTGCAAGTCAGGTGTGAAAGCCTGGGGC
25	0	0 TTTTATAAGTTTGATGTGAAAGCCCTGGACT
26	0	0 TCGTGTGCGT tag o
27	0	0 CCTTTTAAGTCGGATGTGAAATCCCCGGGCT
28	0	0 TTTGGTAAGATAGGTGTGAAATTTTTGGGT
29	0	0 AACATCTCACATATTGATGTGAGACGGAGG
30	0	0 TTGAGTAAGTCAGATGTGAAATCCCCGGGC
31	0	0 TGATGAAAGACAGATGTGAAATCCCCGGGC
32	1	0 AACAACTCACACATTGATGTGAGACGGAGG
33	1	0 TTCGGTAAGTCAGATGTGAAATCCCCGGGC
34	1	0 CCTGACAAGTCCGATGTGAAAGACCTGGGC
35	1	0 CCTGACAAGTCTGATGTGAAAGAACTGGGC
36	1	0 TTGGGTAAGTCAGAAGTGAAATCCCCGGGC
37	0	0 CTGGCCAAGTGCTTTGTGAAATCCCACGGC
38	0	0 CCTGACAAGTCTGATGTGAAAAACCTGGGC
39	0	0 CCTGACAAGTCTGATGTGAAAGACCTGGGC
40	0	0 CCTAACAAGTCTGATGTGAAAGACCTGGGC
41	0	0 TGATGTAAGACAGATGTGAAATCCCCGGAC
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0 TGATGTAAGGCAGATGTGAAATCCCCGGGC  
0 TGATGTAAGACTGATGTGAAATCCCCGGGC  
0 CTTTGTAAATCAGGTGTGAAAGCCTGGGGC  
0 CTTTGTAAAGTCAGGTGTGAAAGCCTGGGGC  
0 CTCGAAAAGCGTTCCGTGTAATCCCCGGGC  
0 CCTGACAAGTCTGATGTGAAAGGCCTGGGGC  
0 CCTGACTAGTCTGATGTGAAAGACCTGGGGC  
0 CCTGACAAGTCTAATGTGAAAGACCTGGGGC  
0 CTCGAAAAGCGTTCAGTGAAATCCCCGGGC  
0 CCTGACAAGTCTGATGTGAAAGACCTGGGGC  
0 CTCAAAAAGCGTTCCGTGAAATCCCCGGGC  
0 AACAACTCACACATTGATGTGAGACGGAGG  
0 CCTGACAAGTCTGATGTGAAAGACCTCGGGC  
0 CTCGAAAAGCGTTTCGTGAAATCCCCGGGC  
0 TTGGCTAAGTCAGATGTGAAATCCCCGGGC  
0 CTCTGTAAGTCAGGTGTGAAAGCCTGGGGC  
0 TGATGTAAGACAGATGTGAAATCCCCGGGC  
0 TGATGTAAGACAGATGTGAAATCCCCGGGC  
0 CTTTGTAAAGTCAGGTGTGAAAGCCTGGTGC  
0 CTTTGTAGGTCAGGTGTGAAAGCCTGGGGC  
0 CTTTGTAAAGTCAGGTGTGAAAGCCTGGGGC  
0 CTTGCCAAGTGCTTTGTGAAATCCCACGGCT  
0 CTTTGAAAGTCAGGTGTGAAAGCCTGGGGC  
0 TGATGTAGGACAGATGTGAAATCCCCGGGC  
0 TTGGGTAAGTCAGATGTGAAAACCCCGGGC  
0 TGATGTAAGACAGATGTGAAATCCCCGGGC  
0 CTTTGTAAAGTCAGGTGTGAAAGCCTGGCGC  
0 CTTTGTAAAGTCAGGTGAGAAAGCCTGGGGC  
0 CTTTGTAAAGTAAGGTGTGAAAGCCTGGGGC

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4		taxon_data	long	long_total	long_this	support	confidence
5		g	TGGGCGTAA/	6	6	942	0.97664544
6		g	TGGGCGTAA/	12	12	19	1
7		g	TGGGCGTAA/	12	12	2	1
8		TTA	TGGGCGTAA/	10	10		
9		g	TGGGCGTAA/	12	12	75	0.94666667
10		g	TGGGCGTAA/	12	12	42	0.90476191
11		TCA	TGGGCTTAAA	12	12		
12		CA	TGGGCTTAAA	11	11		
13		g	TGGGCGTAA/	12	12	396	0.8989899
14		CGG	TGCAGTTAAA	6	6		
15		CGG	TGCAGTTAAA	8	8		
16		GAG	TGCAGTTAAA	8	7		
17		g	TGGGCGTAA/	10	10	34	1
18		g	TGGGCGTAA/	12	12	93	0.98924731
19		AGG	TGCAGTTAAA	9	9		
20		g				1173	0.99829497
21		CGG	TGCAGTTAAA	6	6		
22		o	TGGGCGTAA/	11	11	2	1
23		TCA	TGGGCGTAA/	6	6		
24		f	TGGGTTTAAA	7	7	8	1
25		TTA	TGGGCGTAA/	12	12		
26		g				7	0.85714286
27		g	TGGGCGTAA/	12	12	11	1
28		CA	TGGGCTTAAA	12	12		
29		g				193	0.97409326
30		g	TGGGCGTAA/	12	12	6	0.83333333
31		g	TGGGCGTAA/	12	12	95	1
32		AGG	TGCAGTTAAA	12	12		
33		g	TGGGCGTAA/	6	6	503	0.99403579
34		g				3415	0.86061493
35		TTA	TGGGCGTAA/	12	12		
36		CAA	TGGGCGTAA/	6	6		
37		TTA	TGGGCGTAA/	7	7		
38		g	TGGGCGTAA/	7	7	23	0.82608696
39		g	TGGGCGTAA/	12	12	24	0.95833333
40		TCA	TGGGCATAA/	6	6		
41		g				16	0.9375
42							
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o	TGGGCGTAA/	12	12	15	1
g	TGGGCGTAA/	11	11	8	1
g	TGGGTTTAAA	12	12	17	1
TA	TGGGTTTAAA	8	8		
g	TGGGCGTAA/	7	7	341	0.98533724
AGG	TGCAGTTAAA	10	10		
g	TGGGTTTAAA	6	6	3	1
TCA	TGGGCGTAA/	12	12		
TA	TGGGCGTAA/	6	6		
TCA					
CGG	TGCAGTTAAA	6	6		
g	TGGGCGTAA/	6	6	13	1
TA	TGGGCGTAA/	7	7		
o	TGGGCGTAA/	6	6	10	0.8
g	TGGGCGTAA/	12	12	10	0.8
g	TGGGCGTAA/	10	10	27	1
TCA	TGGGTTTAAA	7	7		
TA	TGGGCGTAA/	6	6		
g				14	1
f	TGGGCGTAA/	7	7	3	1
GG	TGCAGTTAAA	6	6		
TTA	TGGGTTTAAA	10	10		
TA	TGGGCGTAA/	11	11		
TCA	TGGGCGTAA/	12	12		
g	TGGGCGTAA/	6	6	23	0.95652174
f	TGGGTTTAAA	12	12	6	1
o	TGGGCGTAA/	12	12	2	1
o	TGGGCGTAA/	12	12	2	1
f	TGGGCGTAA/	12	12	3	1
TA	TGGGCGTAA/	12	12		
TTA	TGGGTTTAAA	11	11		
CC	TGCAGTTAAA	10	10		
TA	TGGGCGTAA/	6	6		
c	TGGGCATAA/	12	12	7	1
c	TGGGCTTAAA	12	12	3	1
TCA	TGGGCATAA/	6	6		
CTTA	TGGGCGTAA/	6	6		
TTA	TGGGTTTAAA	6	6		

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4	g	TGGGCGTAA/	12	12	8	1
5	f	TGGGTTTAAA	7	7	2	1
6	f	TGGGTTTAAA	12	12	8	1
7						
8	AGG	TGCAGTTAAA	6	6		
9	g	TGGGCTTAAA	6	6	3	1
10	f	TGGGCGTAA/	12	12	2	1
11						
12	ICA	TGGGCTTAAA	12	12		
13	CGG	TGCAGTTAAA	6	6		
14	TA	TAGGCGTAA/	6	6		
15						
16	o	TGGGCGTAA/	12	12	11	1
17	f	TGGGCGTAA/	7	7	7	1
18						
19	TCA	TGGGCGTAA/	7	7		
20						
21	TCA	TGGGCTTAAA	6	6		
22	CG	TGCGGTTAAA	12	12		
23	g	TGGGTTTAAA	6	6	6	0.83333333
24						
25	TCA					
26	g	TGGGCGTAA/	6	6	2	1
27	TA	TGGGTTTAAA	6	6		
28						
29	CA	TGGGCTTAAA	6	6		
30	f	TGGGTTTAAA	6	6	5	1
31						
32	g	TGGGCGTAA/	12	12	28	0.96428571
33	p	TGCAGTTAAA	6	6	3	1
34	ICA	TGGGCTTAAA	6	6		
35						
36	f	TGGGTGTAA/	6	6	3	1
37	TA	TGGGCGTAA/	6	6		
38						
39	GGA	TGCAGTTAAA	6	6		
40	g	TGGGCGTAA/	7	7	3	1
41	f	TGGGTTTAAA	12	12	2	1
42						
43	g	TGGGCGTAA/	8	8	172	1
44	TTA	TGGGTTTAAA	6	6		
45						
46	g				168	1
47	g	TGGGTTTAAA	6	6	559	1
48	TA	TGGGCGTAA/	6	6		
49						
50	TCA					
51	TT	TGGGCGTAA/	6	6		
52						
53	c	TGGGCGTAA/	6	6	4	1
54	TTA	TGGGCGTAA/	6	6		
55						
56	iCGG	TGCAGTTAAA	6	6		
57						
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4	.TCA	TGGGCGTAA/	12	12			
5	.TCA	TGGGCGTAA/	6	6			
6	.TCA	TGGGCTTAAA	8	8			
7	f	TGGGTTTAAA	6	6	6		1
8							
9	.TCA						
10	g	TGGGTTTAAA	6	6	2		1
11	TCA	TGGGTTTAAA	6	6			
12	TCA	TGGGCGTAA/	6	6			
13	o	TGGGCGTAA/	6	6	6		1
14	TCA	TGGGCGTAA/	6	6			
15	.TCA	TGGGCGTAA/	6	6			
16	c	TGGGCATAA/	6	6	2		1
17							
18	.TTA	TGGGTTTAAA	12	12			
19	g	TGGGCGTAA/	6	6	399		1
20	f	TGGGCGTAA/	6	6	2		1
21	g	TGGGCGTAA/	12	12	3		1
22	c	TGGGCTTAAA	12	12	4		1
23	g	TGGGTTTAAA	4	4	97		1
24	c	TGGGCGTAA/	6	6	2		1
25	g	TGGGTTTAAA	10	10	39	0.92307692	
26	o	TGGGCGTAA/	6	6	2		1
27	.TTA						
28	g	TGGGCGTAA/	7	7	9		1
29	f	TGGGTTTAAA	11	11	2		1
30	g	TGGGCGTAA/	6	6	51		1
31	g				284	0.99647887	
32	o	TGGGCGTAA/	6	6	7		1
33	.TCA	TGGGCGTAA/	6	6			
34	TCA	TGGGCGTAA/	12	12			
35	g	TGGGCGTAA/	12	12	81	0.97530864	
36	.TT	TTCGGTTATA	6	6			
37	g	TGGGCGTAA/	6	6	38		1
38	TA	TGGGCGTAA/	12	12			
39	g	TGGGCGTAA/	6	6	36	0.86111111	
40	g	TGGGCGTAA/	12	12	180		1
41	.TCA	TGGGCGTAA/	6	6			
42	CTCA	TGGGCGTAA/	6	6			
43	.CA	TGGGCATAA/	11	11			
44							
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3						
4	TTA	TGGGCGTAA/	7	7		
5	g	TGGGCGTAA/	6	6	3	1
6	g	TGGGCGTAA/	7	7	15	0.93333333
7						
8	.TCA	TGGGCGTAA/	6	6		
9	ICA	TGGGCGTAA/	8	8		
10	TCA	TGGGCGTAA/	6	6		
11	TTA	TGGGCGTAA/	6	6		
12						
13	f	TGGGCGTAA/	6	6	4	1
14						
15	g				873	0.99427262
16	c				185	1
17						
18	g	TGGGCGTAA/	6	6	6	1
19	GCG	TGCAGTTAAA	6	6		
20	TTA	TGGGCTTAAA	6	6		
21	TTA	TGGGCGTAA/	6	6		
22						
23	g	TGGGCGTAA/	11	11	43	0.95348837
24	f	TGGGCGTAA/	6	6	48	0.95833333
25						
26	TCA	TGGGCTTAAA	7	7		
27	g	TGGGCGTAA/	12	12	14	1
28	TCA	TGGGTGTAA/	7	7		
29	g	TGGGTTTAAA	6	6	6	1
30						
31	GAACC					
32						
33	o	TGGGCGTAA/	6	6	4	1
34	g	TGGGCGTAA/	7	7	109	0.98165138
35						
36	CA	TGGGCTTAAA	6	6		
37	TTA	TGGGCGTAA/	6	6		
38						
39	o	TGGGCGTAA/	6	6	5	0.8
40	.TCA	TGGGTGTAA/	6	6		
41	.TCA	TGGGCGTAA/	11	10		
42						
43	f	TGGGCGTAA/	6	6	6	1
44	f	TGGGCGTAA/	9	9	4	1
45	g	TGGGCTTAAA	12	12	39	1
46	g	TGGGCGTAA/	6	6	78	1
47						
48	TCA	TGGGTGTAA/	6	6		
49						
50	f				15	1
51	p	TGGGCGTAA/	6	6	2	1
52						
53	g	TGGGCGTAA/	6	6	15	0.93333333
54	g	TGGGCGTAA/	6	6	10	0.9
55	o	TGGGCGTAA/	6	6	3	1
56						
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4	G	TGCAGTTAAA	9	9		
5	f	TGGGCGTAA/	6	6	5	1
6	f	TGGGCGTAA/	12	12	19	1
7	f	TGGGCGTAA/	7	7	2	1
8						
9	.TCA	TGGGCGTAA/	6	6		
10	f	TGGGCGTAA/	6	6	3	1
11	GA	TGTGTTTAAA	12	12		
12	TG	TGGGCGTAA/	7	7		
13	f	TGGGTTTAAA	7	7	5	1
14	o	TGGGCGTAA/	6	6	5	1
15	g	TGGGCGTAA/	6	6	15	1
16						
17	TTA					
18	TCA	TGGGCGTAA/	6	6		
19	g	TGGGCGTAA/	6	6	2	1
20	TT	TGCAGTTAAA	11	11		
21	g	TGGGCGTAA/	12	12	4	1
22	.TCA	TGGGTGTAA/	6	6		
23	o	TGGGCGTAA/	6	6	2	1
24	TA	TGGGCGTAA/	6	6		
25	g	TGGGTTTAAA	6	6	10	1
26	f	TGGGCGTAA/	6	6	9	1
27	TCA	TGGGCTTAAA	6	6		
28	.TCA	TGGGCTTAAA	7	7		
29	c	TGGGCATAA/	6	6	3	1
30	g	TGGGCGTAA/	12	12	399	0.99749373
31	g	TGGGCGTAA/	12	12	4	1
32	.CA	TGGGCGTAA/	6	6		
33	g	TGGGCGTAA/	6	6	4	1
34	g	TGGGCGTAA/	12	12	5	1
35	.TCA	TGGGCTTAAA	7	7		
36	g	TGGGCGTAA/	10	10	3	1
37	g	TGGGCGTAA/	6	6	3	1
38	CAA	TGCAGTTAAA	12	12		
39	.TA	TGGGCGTAA/	12	12		
40	f	TGGGCGTAA/	6	6	38	1
41	.TTA	TGGGCGTAA/	6	6		
42	.TTA	TGGGCGTAA/	6	6		
43	CAA	TGGGCGTAA/	6	6		
44						
45						
46						
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51						
52						
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54						
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56						
57						
58						
59						
60						

1						
2						
3						
4	c	TGGGCGTAA/	12	12	2	1
5	TCA	TGGGCGTAA/	6	6		
6	g	TGGGCGTAA/	10	10	44	1
7	g	TGCAGTTAAA	6	6	21	1
8	g	TGCAGTTAAA	6	6		
9	AGC	TGGGCGTAA/	12	12		
10	TTA	TGGGCGTAA/	12	12		
11	g	TGGGTTTAAA	6	6	3	1
12	TTA	TGGGCGTAA/	11	11		
13	TTA	TGGGCGTAA/	11	11		
14	TCA	TGGGCTTAAA	11	11		
15	TCA	TGGGCTTAAA	11	11		
16	g	TGGGCGTAA/	6	6	5	0.8
17	g	TGGGCTTAAA	9	9	5	1
18	g	TGGGCTTAAA	9	9		
19	CTCA	TGGGCGTAA/	12	12		
20	TTA	TGGGCGTAA/	6	6		
21	TTA	TGGGCGTAA/	6	6		
22	g				262	0.98854962
23	TTA	TGGGCGTAA/	12	12		
24	TG	TGCAGTTAAA	8	8		
25	TG	TGCAGTTAAA	8	8		
26	CTTA					
27	TCA					
28	TCA					
29	TTA	TGGGCGTAA/	12	12		
30	f	TGGGCGTAA/	6	6	3	1
31	f	TGGGCGTAA/	6	6		
32	g				10	1
33	f	TGGGCGTAA/	6	6	8	1
34	f	TGGGCGTAA/	6	6		
35	TCA	TGGGCTTAAA	6	6		
36	TCA	TGGGCGTAA/	6	6		
37	TCA	TGGGCGTAA/	6	6		
38	TCA	TGGGCGTAA/	6	6		
39	o	TGGGCGTAA/	6	6	2	1
40	f	TGGGTTTAAA	11	11	3	1
41	f	TGGGTTTAAA	11	11		
42	TCA	TGGGCGTAA/	6	6		
43	AA					
44	g	TGGGCGTAA/	7	7	47	0.95744681
45	g	TGGGCTTAAA	6	6	2	1
46	g	TGGGCTTAAA	6	6		
47	TA	TGGGTTTAAA	12	12		
48	TA	TGGGCGTAA/	6	6		
49	TA	TGGGCGTAA/	6	6		
50	GAACC	TGCAGTTAAA	6	6		
51	TTA	TGGGCGTAA/	6	6		
52	TTA	TGGGCGTAA/	6	6		
53	TTA	TGGGCGTAA/	12	12		
54	TTA	TGGGCGTAA/	6	6		
55	g					
56	g				82	0.91463415
57						
58						
59						
60						

o	TGGGCGTAA/	11	11	5	1
f	TGGGCGTAA/	12	12	4	1
g	TGGGCGTAA/	6	6	10	1
ΓCA	TGGGCGTAA/	6	6		
.TCA	TGGGCGTAA/	6	6		
TTA	TGGGCGTAA/	6	6		
TTG	TGCAGTTAAA	6	6		
CTCA	TGGGCGTAA/	8	8		
f	TGGGCGTAA/	9	9	2	1
g				56	0.83928571
f	TGGGCGTAA/	6	6	2	1
g	TGGGTTTAAA	6	6	5	1
CA	TGGGCGTAA/	6	6		
f	TGGGTTTAAA	6	6	4	1
o				52	1
g	TGGGCGTAA/	6	6	3	1
g	TGGGCGTAA/	6	6	31	0.96774194
TTA	TGGGTTTAAA	6	6		
TTA	TGGGCTTAAA	12	12		
ΓTA	TGGGTTTAAA	8	8		
o	TGGGCGTAA/	9	9	2	1
p	TGGGTGTAA/	6	6	3	1
g	TGGGCGTAA/	12	12	40	0.875
TTA	TGGGCTTAAA	6	6		
.TTA	TGGGCGTAA/	6	6		
g	TGGGCTTAAA	6	6	6	1
g	TGCTGTAAA	10	10	2	1
o	TGGGCGTAA/	6	6	2	1
f	TGGGTGTAA/	6	6	11	1
.TTA					
g				997	0.99799398
g	TGGGCGTAA/	6	6	16	1
CTA	TGGGCTTAAA	6	6		
o	TGGGCGTAA/	6	6	10	1
g	TGGGCGTAA/	9	9	3	1
.TCA	TGGGTTTAAA	6	6		
CTCA	TGGGCGTAA/	12	12		
CA	TGGGCTTAAA	6	6		



1						
2						
3						
4	f	TGGGCGTAA/	7	7	3	1
5	TA	TGGGCGTAA/	12	12		
6	g	TGGGCGTAA/	6	6	2	1
7		TGCAGTTAAA	9	9		
8						
9	f	TGGGTATAAA	8	8	9	1
10						
11	CA					
12	c	TGGGCGTAA/	6	6	13	1
13	g	TGGGCGTAA/	11	11	3	1
14						
15	TTA	TGGGTGTAA/	6	6		
16	f	TGGGTTTAAA	6	6	7	1
17						
18	g				416	0.84855769
19	f	TGGGCGTAA/	12	12	12	1
20						
21	GC	TGCAGTTAAA	6	6		
22	CCC	TGCTGTTAAA	6	6		
23	f	TGGGTTTAAA	6	6	12	1
24						
25	CA	TGGGCGTAA/	6	6		
26	CA	TGGGCGTAA/	6	6		
27						
28	g	TGGGCGTAA/	12	12	504	0.80555556
29	f	TGGGCGTAA/	6	6	8	1
30						
31	TTA					
32	TCA	TGGGCGTAA/	6	6		
33	TTA	TGGGCGTAA/	10	10		
34						
35	g	TGGGTTTAAA	6	6	16	1
36	TTA	TGGGCGTAA/	6	6		
37						
38	g	TGGGCGTAA/	8	8	83	0.80722892
39	g	TGGGCGTAA/	12	12	107	0.99065421
40	TA	TGGGCGTAA/	12	12		
41						
42	TCA	TGGGCGTAA/	6	6		
43	o	TGGGCGTAA/	6	6	9	1
44						
45	g	TGGGTTTAAA	6	6	18	1
46	TCA	TGGGCGTAA/	6	6		
47	TTA	TGGGCGTAA/	8	8		
48						
49	TTA	TGGGCGTAA/	11	11		
50	TTA	TGGGCGTAA/	6	6		
51						
52	TTA	TGGGTTTAAA	12	12		
53						
54	g	TGGGCGTAA/	6	6	19	0.94736842
55	f	TGGGTTTAAA	6	6	4	1
56	g	TGGGCGTAA/	6	6	4	1
57						
58						
59						
60						

1						
2						
3						
4	TTA	TGGGTTTAAA	12	12		
5	TTA	TGGGTTTAAA	6	6		
6	g	TGGGCGTAA/	10	10	778	0.93958869
7	g	TGGGCGTAA/	7	6	5	1
8	g	TGGGCGTAA/	10	10	3	1
9	AGG	TGCAGTTAAA	6	6		
10						
11	TCA					
12	f	TGGGCGTAA/	7	7	3	1
13	TTA	TGGGTTTAAA	6	6		
14	TTA	TGGGCGTAA/	6	6		
15	TAG	TAGGTGTAAA	4	4		
16	TCA	TGGGCGTAA/	7	6		
17						
18	TCA					
19	TCA					
20	TCA					
21	TCA	TGGGCGTAA/	11	11		
22	f	TGGGCGTAA/	6	6	5	1
23	f	TGGGCGTAA/	10	10	5	1
24						
25	g				2117	0.99196977
26	TA	TGGGCGTAA/	6	6		
27	CA	TGGGCTTAAA	7	7		
28	TTA	TGGGCGTAA/	6	6		
29	f				26	1
30	TCA	TGGGCGTAA/	10	10		
31	TCA	TGGGCGTAA/	6	6		
32	TCA	TGGGCGTAA/	6	6		
33	g	TGGGTTTAAA	4	4	2	1
34	CAA					
35	o	TGGGCGTAA/	6	6	7	1
36	TCA	TGGGCGTAA/	6	6		
37	TCA	TGGGCGTAA/	6	6		
38	TCA					
39	g	TGGGCGTAA/	6	6	6	1
40	g	TGGGCGTAA/	11	11	7	1
41	GG	CGCGGTCAA/	6	6		
42	TCA	TGGGCTTAAA	6	6		
43	g	TGGGTTTAAA	6	6	18	1
44	TCA	TGGGCTTAAA	6	6		
45	g	TGGGCGTAA/	6	6	4	1
46	TCA	TGGGCGTAA/	6	6		
47						
48						
49						
50						
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56						
57						
58						
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1						
2						
3						
4	CA	TGGGCGTAA/	6	6		
5	AAC	TGGGCGTAA/	4	4		
6	c				3	1
7						
8	g	TGGGCGTAA/	11	11	2	1
9	f	TGGGTTTAAA	10	10	65	1
10						
11	CTCA	TGGGCGTAA/	6	6		
12	g	TGGGCTTAAA	12	12	8	1
13	f	TGGGTTTAAA	6	6	7	1
14						
15	g	TGGGCGTAA/	6	6	6	1
16	g				7493	0.99959963
17						
18	f	TGGGCGTAA/	8	8	4	1
19	f	TGGGTTTAAA	6	6	12	1
20						
21	TCA	TGGGCGTAA/	10	10		
22	TA	TGGGTTTAAA	6	6		
23						
24	f	TGGGTTTAAA	6	6	4	1
25	g	TGGGCGTAA/	6	6	3	1
26	CA	TGGGCGTAA/	12	12		
27						
28	TTA	TGGGCGTAA/	12	12		
29	CAA	TGGGCGTAA/	11	11		
30						
31	g				622	0.99678457
32	CTTA	TGGGTTTAAA	6	6		
33	f	TGGGTTTAAA	7	7	3	1
34	f	TGGGTTTAAA	7	7	2	1
35						
36	CTCA	TGGGCGTAA/	6	6		
37	g	TGGGCGTAA/	6	6	3	1
38	g	TGGGCGTAA/	5	5	1450	0.99862069
39						
40	CA	TGGGCGTAA/	6	6		
41						
42	TTA	TGGGTTTAAA	6	6		
43	TCA	TGGGCGTAA/	9	9		
44						
45	f				65	0.83076923
46	g	TGGGCGTAA/	4	4	706	0.99858357
47						
48	AGC	TGGGCGTAA/	6	6		
49	p	TGGGCGTAA/	6	6	4	1
50	c	TGGGCGTAA/	6	6	2	1
51						
52	g	TGGGCGTAA/	6	6	2	1
53	f	TGGGCGTAA/	6	6	2	1
54						
55	g	TGGGCGTAA/	6	6	301	0.86046512
56	g	TGGGCGTAA/	12	12	135	1
57						
58						
59						
60						

f	TGGGCGTAA/	6	6	3	1
CA	TGGGCGTAA/	10	10		
TCA	TGGGCTTAAA	9	9		
TCA	TGGGCGTAA/	6	6		
CTTA	TGGGCGTAA/	6	6		
o				78	0.98717949
f	TGGGTTTAAA	12	12	3	1
ITA	TGGGTTTAAA	6	6		
TA	TGGGCGTAA/	6	6		
g	TGGGCGTAA/	7	6	3	1
C	TGCAGTTAAA	8	8		
c	TGGGCTTAAA	6	6	2	1
TA	TGGGCGTAA/	12	12		
CTCA	TGGGCGTAA/	8	8		
f	TGGGTTTAAA	6	6	3	1
TGA	TGCAGTTAAA	4	4		
TCG	TGGGCGTAA/	5	5		
CTA	TGGGCTTAAA	9	9		
TCA	TGGGCGTAA/	6	6		
g	TGGGCGTAA/	6	6	8	0.875
f	TGGGCGTAA/	12	12	3	1
TTA	TGGGCGTAA/	6	6		
g	TGGGCGTAA/	3	3	49	0.97959184
CTCA	TGGGCGTAA/	6	6		
CTC	TGGGCTTAAA	9	9		
CTTA	TGGGCGTAA/	5	5		
g	TGGGCGTAA/	5	5	393	1
AGT	TGCAGTTAAA	6	6		
g	TGGGCGTAA/	8	8	87	1
CTT	TGCTGTTAAA	5	5		
TA	TGGGCGTAA/	6	6		
CTA					
CA	TGGGCGTAA/	6	6		
TTA	TGGGTTTAAA	6	6		
TA	TGGGCGTAA/	5	5		
CAA	TGGGCGTAA/	6	6		
TA	TGGGCGTAA/	6	6		
CC	TGGGCGTAA/	9	9		

1						
2						
3						
4	TCA					
5	f	TGGGTTTAAA	11	11	2	1
6	g	TGGGCGTAA/	6	6	225	0.90666667
7						
8	TCA	TGGGCTTAAA	6	6		
9	TTA	TGGGTTTAAA	6	6		
10	AAAT	TGCAGTTAAA	6	6		
11	iCTC	TGGGCTTAAA	8	8		
12						
13	f	TGGGCGTAA/	7	7	4	1
14						
15	TCA	TGGGCGTAA/	6	6		
16	g	TGGGCGTAA/	6	6	22	1
17	f	TGGGTTTAAA	6	6	2	1
18						
19	TCA	TGGGCGTAA/	6	6		
20	TCA	TGGGTTTAAA	6	6		
21	CTT	TGGGCGTAA/	10	10		
22						
23	TCA	TGGGTTTAAA	6	6		
24						
25	o	TGGGCGTAA/	11	11	18	0.94444444
26	CTA	TGGGCGTAA/	6	6		
27	f	TGGGCGTAA/	6	6	4	1
28						
29	g				135	1
30	g	TGGGCTTAAA	6	6	6	1
31	f	TGGGCGTAA/	6	6	78	0.96153846
32						
33	f	TGGGTTTAAA	6	6	5	1
34	g	TGGGTTTAAA	5	5	25	1
35						
36	CAA	TGGGCGTAA/	5	5		
37	g	TGGGCGTAA/	6	6	21	0.95238095
38						
39	CTA	TGGGCGTAA/	6	6		
40	g	TGCTGTTAAA	6	6	7	1
41	CTTA	TGGGTTTAAA	6	6		
42	CTC	TGGGCGTAA/	6	6		
43						
44	g	TGGGCGTAA/	9	9	20	0.95
45						
46	TA	TGGGCGTAA/	6	6		
47	TCA	TGGGCGTAA/	6	6		
48						
49	TCA	TGGGCGTAA/	6	6		
50	g	TGGGTTTAAA	11	11	7	1
51	f	TGGGCTTAAA	9	9	2	1
52						
53	g	TGGGCGTAA/	4	4	2	1
54	TA	TGGGCGTAA/	6	6		
55						
56	f	TGGGCGTAA/	6	6	3	1
57						
58						
59						
60						

1						
2						
3						
4	CA	TGGGCGTAA/	10	10		
5	TCA	TGGGCGTAA/	11	11		
6	CTC	TGGGCTTAAA	11	11		
7	TA	TGGGCGTAA/	6	6		
8	TA	TGGGCGTAA/	6	6	4	1
9	g	TGGGCGTAA/	6	6		
10	TTA	TGGGCGTAA/	5	5		
11	g	TGGGCGTAA/	6	6	12	0.91666667
12	c	TGGGCTTGAA	6	6	5	1
13	CTCA	TGGGCGTAA/	7	7		
14	p	TGGGCGTAA/	6	6	2	1
15	o	TGGGCGTAA/	6	6	2	1
16	CA	TGGGTTTAAA	6	6		
17	f	TGGGCGTAA/	6	6	22	0.95454546
18	g	TGGGCTTAAA	5	5	10	1
19	TA	TGGGTTTAAA	12	12		
20	TA	TGGGCGTAA/	4	4		
21	CA	TGGGCGTAA/	6	6		
22	g	TGGGCGTAA/	6	6	464	0.98491379
23	TCA	TGGGCGTAA/	6	6		
24	g	TGGGCGTAA/	6	6	4	1
25	TAG	TGCAGTTAAA	6	5		
26	TCA	TGGGCGTAA/	9	9		
27	f	TGGGCGTAA/	6	6	4	1
28	TA	TGGGCGTAA/	6	6		
29	f	TGGGCGTAA/	6	6	14	0.92857143
30	TTA	TGGGCGTAA/	6	6		
31	CTCA	TGGGCGTAA/	11	11		
32	TCA	TGGGCTTAAA	6	6		
33	CA	TGGGCATAAA	7	7		
34	CTCA	TGGGTTTAAA	6	6		
35	CA	TGGGCTTAAA	6	6		
36	CTCA	TGGGCGTAA/	10	10		
37	CTCA	TGGGCGTAA/	11	11		
38	o	TGGGCGTAA/	6	6	7	1
39	g	TGGGCGTAA/	4	4	30	0.93333333
40	CA	TGGGCGTAA/	6	6		
41	CA	TGGGCGTAA/	7	7		
42	f	TGGGCGTAA/	6	6	19	1
43						
44						
45						
46						
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1						
2						
3						
4	CTCA	TGGGCGTAA/	5	5		
5	g	TGGGCGTAA/	5	5	4	1
6	f	TGGGTTTAAA	8	8	4	1
7						
8	CA	TGGGCGTAA/	6	6		
9	o	TGGGCGTAA/	6	6	2	1
10	p	TGGGCGTAA/	6	6	12	1
11	f				14	1
12						
13	g				131	1
14	f	TGGGCGTAA/	6	6	3	1
15						
16	TA	TGGGCGTAA/	6	6		
17	.TA	TGGGCGTAA/	6	6		
18	TA	TGGGCGTAA/	6	6		
19						
20	g	TGGGCTTAAA	11	11	16	1
21	TCA	TGGGCGTAA/	6	6		
22	f	TGGGCGTAA/	6	6	2	1
23	CA	TGGGCGTAA/	6	6		
24	c	TGGGTTTAAA	6	6	4	1
25	TTA	TGGGCGTAA/	8	8		
26	TCA	TGGGTTTAAA	6	6		
27	CA	TGGGCGTAA/	6	6		
28	.TCA	TGGGCGTAA/	6	6		
29	CTC	TGGGCGTAA/	5	5		
30	AGT					
31	TCA					
32	TCA	TGGGCGTAA/	6	6		
33	g	TGGGCGTAA/	6	6	4	1
34	TAA					
35	f				68	0.95588235
36	f	TGGGCGTAA/	11	11	2	1
37	TTA	TGGGCGTAA/	6	6		
38	TA	TGGGCGTAA/	6	6		
39	g	TGGGCGTAA/	10	10	42	0.95238095
40	CA	TGGGCTTAAA	5	5		
41	f	TGGGCGTAA/	6	6	41	0.97560976
42	g	TGGGCTTAAA	12	12	3	1
43	TA					
44	c	TGGGCGTAA/	6	6	2	1
45	.TCA	TGGGCGTAA/	6	6		
46						
47						
48						
49						
50						
51						
52						
53						
54						
55						
56						
57						
58						
59						
60						

TCA	TGGGCTTAAA	9	9		
f	TGGGCGTAA/	11	11	2	1
TTA	TGCAGTTAAA	6	6		
f	TGGGTTTAAA	6	6	2	1
TC					
g				112	1
TC	TGGGTTTAAA	8	8		
TC	TGGGCTTAAA	6	6		
f	TGGGTTTAAA	7	7	3	1
g	TGGGCGTAA/	8	8	6	1
CTCA	TGGGCGTAA/	6	6		
f	TGGGCGTAA/	10	10	6	1
TTA	TGGGCGTAA/	6	6		
g				592	0.98817568
g	TGGGCGTAA/	6	6	2	1
CTCA	TGGGCGTAA/	4	4		
g	TGGGCGTAA/	6	6	5	1
TC	TGGGTTTAAA	11	11		
g	TGGGCGTAA/	6	6	41	1
f	TGGGCGTAA/	6	6	2	1
TTA	TGGGCTTAAA	6	6		
g	TGGGCGTAA/	4	4	40	0.925
TA	TGGGCGTAA/	6	6		
CTCA	TGGGCGTAA/	6	6		
TA	TGGGCGTAA/	5	5		
CTCA	TGGGCTTAAA	6	6		
TTA	TAGGTTTAAA	6	6		
TC	TGGGCGTAA/	6	6		
TA	TGGGCGTAA/	6	6		
TA	TGGGTTTAAA	12	12		
TTA	TGGGCGTAA/	4	4		
g	TGGGCGTAA/	6	6	303	0.99009901
TTA					
g				49	1
g	TGGGCTTAAA	6	6	2	1
g	TGCAGTTAAA	9	9	8	1
g	TGGGCGTAA/	6	6	31	1
f	TGGGTTTAAA	7	7	2	1



1						
2						
3						
4	CA	TGGGCGTTAA	8	8		
5	g				17	0.94117647
6	.TCA	TGGGCGTAA/	5	5		
7	f	TGCAGTTAAA	4	4	4	1
8						
9	g	TGGGCGTAA/	6	6	7	1
10	g	TGGGCGTAA/	8	8	142	1
11	TTA	TGGGCGTAA/	6	6		
12	TTA	TGGGCGTAA/	11	11		
13						
14	g	TGGGCGTAA/	6	6	145	0.9862069
15	TCA	TGGGCGTAA/	8	8		
16	TA	TGGGCGTAA/	6	6		
17						
18	c	TGGGCGTAA/	7	7	12	0.91666667
19	gCTC	TGGGCTTAAA	9	9		
20						
21	o	TGGGCGTAA/	6	6	2	1
22						
23	g	TGGGCTTAAA	6	6	2	1
24						
25	o	TGGGCTTAAA	6	6	2	1
26	gCTC	TGGGCTTAAA	11	11		
27						
28	o	TGGGCGTAA/	6	6	5	0.8
29	f	TGGGCGTAA/	10	10	3	1
30						
31	.CCA	TGGGCATAAA	11	11		
32	.TCA	TGGGCGTAA/	6	6		
33	TAA	TGGGCGTAA/	9	9		
34	f	TGGGTTTAAA	6	6	8	1
35						
36	g	TGGGCGTAA/	6	6	337	1
37	o	TGGGCTTAAA	6	6	3	1
38						
39	.TCA	TGGGCGTAA/	5	5		
40	.TCA	TGGGCGTAA/	6	6		
41						
42	.TCA	TGGGCTTAAA	6	6		
43	TTA	TGGGCGTAA/	5	5		
44	g	TGGGCGTAA/	5	5	255	0.99607843
45	TTA	TGGGCGTAA/	6	6		
46						
47	.TCA	TGGGCGTAA/	5	5		
48						
49	o	TGGGCGTAA/	6	6	2	1
50	.TTA	TGGGCGTAA/	10	10		
51	f	TGGGTGTAA/	6	6	7	1
52						
53	.TCA	TGGGCGTAA/	4	4		
54	TA	TAGGCGTAA/	4	4		
55						
56	g	TGGGCGTAA/	6	6	2	1
57						
58						
59						
60						

1						
2						
3						
4	ΓCA					
5	CTCA	TGGGCGTAA/	6	6		
6	f	TGGGCGTAA/	6	6	128	1
7						
8	CTCA	TGGGCGTAA/	11	11		
9	TCA	TGGGCGTAA/	6	6		
10						
11	CTCA	TGGGCGTAA/	6	6		
12	TCA	TGGGCGTAA/	6	6		
13						
14	g				63	0.98412698
15	ΓCA	TGGGCTTAAA	10	10		
16	ICTC	TGGGCTTAAA	7	7		
17						
18	g	TGGGCGTAA/	11	9	57	1
19	g	TGGGCGTAA/	6	6	6	1
20						
21	ICTC					
22	TCA	TGGGCTTAAA	6	6		
23	c	TGGGCGTAA/	9	8	3	1
24						
25	g	TGGGCGTAA/	5	5	2	1
26	TCA	TGGGCGTAA/	5	5		
27	CTC	TGGGCGTAA/	6	6		
28						
29	TCA	TGGGCTTAAA	6	6		
30	TCA	TGGGCGTAA/	6	6		
31						
32	TCA	TGGGCGTAA/	6	6		
33	AGT					
34						
35	g	TGGGCGTAA/	5	5	2	1
36	CTAA	TGGGCGTAA/	6	6		
37	TCC	TGCTGTAAA	6	6		
38						
39	TTA	TGGGCGTAA/	11	11		
40	g	TGGGCGTAA/	5	5	3	1
41	CTCA	TGGGCGTAA/	6	6		
42						
43	CTCA	TGGGTTTAAA	6	6		
44	CTCA	TGGGCGTAA/	10	10		
45	CTCA	TGGGCGTAA/	5	5		
46	CTTA	TGGGCGTAA/	6	6		
47						
48	CTCA	TGGGCGTAA/	6	6		
49	CTCA	TGGGCGTAA/	6	6		
50	CTCA	TGGGCGTAA/	6	6		
51	CTCA	TGGGCGTAA/	6	6		
52						
53	g	TGGGCGTAA/	4	4	55	1
54	f	TGGGCTTAAA	9	9	23	1
55						
56	CTCA					
57						
58						
59						
60						

1						
2						
3						
4	CTT	TGGGCGTAA/	6	6		
5	o				3	1
6	.TTA	TGGGTTTAAA	6	6		
7	g	TGGGCGTAA/	3	3	5	1
8	AG	TGCAGTTAAA	6	6		
9	g	TGGGCGTAA/	6	6	97	1
10	.TTA	TGGGCGTAA/	6	6		
11	TCA	TGGGCGTAA/	6	6		
12	TCA	TGGGCGTAA/	5	5		
13	AG	TGCAGTTAAA	6	6		
14	.TTA	TGGGCGTAA/	5	5		
15	.TTA	TGGGCGTAA/	6	6		
16	g	TGGGCGTAA/	6	6	17	0.88235294
17	g				3	1
18	o	TGGGCGTAA/	7	7	2	1
19	g	TGGGCTTACA	10	10	8	1
20	TTA	TGGGTTTAAA	5	5		
21	TCA	TGGGCGTAA/	6	6		
22	TTA	TGCAGTTAAA	6	6		
23	TCA	TGGGCGTAA/	5	5		
24	g	TGGGCGTAA/	10	10	3	1
25	.TT	TGCAGTTAAA	5	5		
26	TTA	TGGGCGTAA/	5	5		
27	TCA	TGGGCTTAAA	6	6		
28	.TTA	TGGGCGTAA/	6	6		
29	TTA	TGGGCGTAA/	7	7		
30	f	TGGGCGTAA/	6	6	26	1
31	AAC	TGGGCGTAA/	7	7		
32	g	TGGGCGTAA/	6	6	14	1
33	TCA	TGGGCGTAA/	4	4		
34	f	TGGGCGTAA/	6	6	2	1
35	g				17	0.94117647
36	TTA	TGGGCGTAA/	4	4		
37	.ATA	TGCAGTTAAA	8	8		
38	p	TGGGCGTAA/	6	6	4	1
39	g	TGGGCGTAA/	6	6	1106	0.99457505
40	.AATG	TGCAGTTAAA	7	7		
41	CTCA	TGGGCGTAA/	5	5		
42						
43						
44						
45						
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54						
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56						
57						
58						
59						
60						

TA	TGGGCGTAA/	5	5		
CTCA					
ΓCA					
o				10	1
ATT	TGCAGTTAAA	5	5		
CAA	TGGGCGTAA/	8	8		
TCA	TGGGCGTAA/	5	5		
TCA	TGGGCGTAA/	8	8		
g				7	1
TCA	TGGGTGTAA/	5	5		
TTA	TGGGCGTAA/	6	6		
o	TGGGCGTAA/	7	6	10	1
g				7	1
TTA	TGGGCGTAA/	5	5		
p	TGGGCGTAA/	6	6	2	1
TTA	TGGGTATAAA	4	4		
TCA	TGGGCGTAA/	4	4		
TCA	TGGGCGTAA/	6	6		
c	TGGGCGTAA/	5	5	2	1
TA	TGGGCGTAA/	3	3		
f	TGGGCGTAA/	8	8	2	1
g				59	1
ΓTA	TGGGCGTAA/	5	5		
f				26	0.96153846
CTC	TGGGCTTAAA	6	6		
CTCA	TGGGTTTAAA	5	5		
ΓCA	TGGGCGTAA/	4	4		
AA	TGGGCGTAA/	4	4		
CG	TGGGCGTAA/	4	4		
AGT	TGCAGTTAAA	6	6		
TTA	TGGGCGTAA/	6	6		
ΓA	TGGGCGTAA/	5	5		
g				233	0.99570816
CTCA	TGGGCGTAA/	6	6		
TA	TGGGCGTAA/	6	6		
CTCA	TGGGCGTAA/	6	6		
f	TGGGTTTAAA	6	6	2	1
CA	TGGGCGTAA/	6	6		

1						
2						
3						
4	CTCA					
5	CAA	TGGGCGTAA/	6	6		
6	.TCA	TGGGCGTAA/	11	11		
7	f	TGGGCGTAA/	6	6	102	1
8	GGG	TGCAGTTAAA	4	4		
9	g				170	0.99411765
10	GT	TGCAGTTAAA	5	5		
11	f	TGGGTGTAA/	6	6	2	1
12	TCA	TGGGCTTAAA	8	8		
13	f	TGGGTTTAAA	5	5	4	1
14	g	TGGGCTTACA	8	8	35	1
15	f				71	0.98591549
16	f	TGGGCGTAA/	6	6	17	1
17	g	TGGGCGTAA/	6	6	20	1
18	TTA	TGGGCGTAA/	5	5		
19	f	TGGGTTTAAA	5	5	2	1
20	TA	TGGGCGTAA/	6	6		
21	TAG	TGCAGTTAAA	6	6		
22	CA	TGGGCGTAA/	5	5		
23	TCA	TGGGCTTAAA	6	6		
24	.TCA					
25	g	TGGGCGTAA/	6	6	11	0.90909091
26	CTCA	TGGGCGTAA/	4	4		
27	AA	TGGGCGTAA/	5	5		
28	f	TGGGCGTAA/	4	4	2	1
29	f	TGGGTGTAA/	6	6	3	1
30	f	TGGGCGTAA/	4	4	2	1
31	g	TGGGCGTAA/	9	9	674	0.92581602
32	TCA	TGGGCGTAA/	6	6		
33	GC	TGCAGTTAAA	3	3		
34	f	TGGGCGTAA/	6	6	28	1
35	g	TGGGCGTAA/	2	2	5220	1
36	.TTA	TGGGCGTAA/	4	4		
37	g	TGGGCGTAA/	7	7	68	1
38	TCA	TGGGCATAA/	6	6		
39	g	TGGGCTTAAA	6	6	8	1
40	TCA	TGGGCTTAAA	5	5		
41	CTA	TGGGCGTAA/	6	6		
42						
43						
44						
45						
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48						
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TTA	TGGGCGTAA/	6	6		
TG					
TTA	TGGGCGTAA/	4	4		
TCA	TGGGCTTAAA	6	6		
TCA	TGGGTGTAA/	4	4		
CAA	TGGGCGTAA/	5	5		
g	TGGGCTTAAA	6	6	4	1
f				12	0.91666667
f	TGGGTGTAA/	4	4	2	1
p	TGGGCGTAA/	5	5	2	1
TTA	TGGGCGTAA/	6	6		
iAC	TGCAGTTAAA	3	3		
f	TGGGTATAAA	4	4	2	1
g	TGGGCGTAA/	4	4	22	1
A	TGCAGTTAAA	6	6		
TTA	TGGGCTTAAA	4	4		
CG	TGCTGTTAAA	5	5		
f	TGGGCGTAA/	6	6	57	0.96491228
TTA	TGGGCGTAA/	3	3		
TTA	TGGGCGTAA/	6	6		
TTA	TGGGCGTAA/	6	6		
TCA					
g				804	0.99502488
TCA	TGGGCGTAA/	6	6		
f	TGGGCGTAA/	5	5	6	1
GGC	TGCAGTTAAA	4	4		
TCA	TGGGCGTAA/	5	5		
g				72	1
o	TGGGCGTAA/	6	6	11	1
CTC	TGGGCTTAAA	8	8		
TCA	TGGGCGTAA/	4	4		
TTA					
TCA					
TTA	TGGGTGTAA/	5	5		
f				3	1
g	TGGGCGTAA/	6	6	15	1
TCA	TGGGCGTAA/	5	5		
AAC	TGGGCGTAA/	2	2		

1						
2						
3						
4	TCA	TGGGCGTAA/	5	5		
5	T					
6	g	TGGGCGTAA/	7	7	4	1
7	GAG	TGCAGTTAAA	4	4		
8	TA	TGGGTTTAAA	7	6		
9	TCA	TGGGCGTAA/	4	4		
10	.TCA	TGGGCGTAA/	4	4		
11	.TCA	TGGGCGTAA/	5	5		
12	.CTA	TGGGCGTAA/	6	6		
13	.TTA	TGGGCGTAA/	4	4		
14	f	TGGGCGTAA/	5	5	7	1
15	CAA					
16	CAA	TGGGCGTAA/	3	3		
17	GG	TGCAGTTAAA	5	5		
18	g	TGGGCTTACA	6	6	5	1
19	c	TGCAGTTAAA	6	6	2	1
20	TCA	TGGGCGTAA/	5	5		
21	o	TGGGCGTAA/	4	4	3	1
22	TCA	TGGGCGTAA/	7	7		
23	g	TGGGCTTAAA	8	8	2	1
24	g	TGGGCGTAA/	8	8	13	0.92307692
25	TCA	TGGGCGTAA/	4	4		
26	AGT	TGCAGTTAAA	4	4		
27	TCA	TGGGCGTAA/	5	5		
28	iC	TGCAGTTAAA	4	4		
29	TCA	TGGGCGTAA/	7	7		
30	g	TGGGCGTAA/	7	7	2	1
31	g	TGGGCGTAA/	5	5	2	1
32	g				2037	0.84977909
33	g	TGGGCGTAA/	5	5	5	1
34	TCA	TGGGCGTAA/	7	7		
35	TA					
36	.TCA	TGGGCGTAA/	6	6		
37	o	TAGGCGTAA/	6	6	3	1
38	A	TGCAGTTAAA	7	7		
39	TCA					
40	.TCA	TGGGCGTAA/	5	5		
41	f	TGGGCGTAA/	7	7	9	1
42						
43						
44						
45						
46						
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49						
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51						
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56						
57						
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60						

f					91	1
TTA	TGGGTGTAA/	6	6			
g	TGGGCGTAA/	5	5	9		1
TTA	TGGGTTTAAA	8	8			
g	TGGGCGTAA/	4	4	621	0.99677939	
TTA	TGGGCGTAA/	4	4			
CTCA	TGGGCGTAA/	6	6			
TCA	TGGGCGTAA/	5	5			
TT	TGCTGTAAA	6	6			
g				706	0.82152975	
TTA	TGGGCGTAA/	5	5			
CTA	TGGGCGTAA/	6	6			
CTCA	TGGGCGTAA/	4	4			
CTCA	TGGGCGTAA/	5	5			
CTTA	TGGGCGTAA/	5	5			
TCA	TGGGCGTAA/	4	4			
TCA	TGGGCGTAA/	4	4			
A	TGCAGTTAAA	5	5			
o				2109	0.99952584	
o	TGGGCGTAA/	4	4	10		1
CAA	TGGGCGTAA/	7	7			
TCA	TGGGCGTAA/	4	4			
CTCA	TGGGCTTAAA	5	5			
TA	TGGGCGTAA/	4	4			
CTC	TGGGCGTAA/	5	5			
TCA	TGGGCGTAA/	2	2			
o	TGGGCGTAA/	4	4	6		1
p	TGGGCGTAA/	3	3	2		1
p				3		1
g	TGGGCGTAA/	6	6	5		1
g				37		1
TCA	TGGGCTTAAA	6	6			
TCA	TGGGCGTAA/	7	7			
CAA	TGGGCGTAA/	2	2			
TGC						
g	TGGGCGTAA/	4	4	1998	0.997998	
TTA	TGGGCGTAA/	5	5			
TTA						



1						
2						
3						
4	TTA					
5	TTA	TGGGCGTAA/	5	5		
6	TTA					
7						
8	g				150	0.97333333
9	TCA	TGGGCGTAA/	5	5		
10	g	TGGGTTTAAA	5	5	10	1
11	CTCA	TGGGCGTAA/	5	5		
12	CAA					
13	CA	TGGGCTTAAA	6	6		
14	g	TGGGCGTAA/	3	3	2	1
15	CTCA					
16	TA	TGGGCGTAA/	5	5		
17	A					
18	TTA					
19	g				194	0.99484536
20	TTA	TGGGCGTAA/	2	2		
21	TTA	TGGGCGTAA/	5	5		
22	CCA	TGGGCATAA/	6	6		
23	TA	TGGGCGTAA/	5	5		
24	g	TGGGCGTAA/	4	4	16	0.8125
25	TCA	TGGGCGTAA/	4	4		
26	CA					
27	g	TGGGCGTAA/	2	2	12	1
28	CTCA	TGGGCTTAAA	6	6		
29	g	TGGGCTTAAA	4	4	4	1
30	p	TGGGCGTAA/	6	6	6	1
31	g				2	1
32	TCA	TGGGCGTAA/	4	4		
33	CA	TGGGCGTAA/	5	5		
34	CTA	TGGGCGTAA/	4	4		
35	g				19	0.84210526
36	o				6	1
37	TTCA	TGGGCGTAA/	6	6		
38	g	TGGGCGTAA/	4	4	29	1
39	g	TGGGTGTAA/	4	4	2	1
40	TG	TGCAGTTAAA	5	5		
41	TTA	TGGGCGTAA/	6	6		
42	f	TGGGCGTAA/	5	5	2	1
43						
44						
45						
46						
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1							
2							
3							
4	TCA	TGGGCGTAA/	6	6			
5	TA	TGGGTTTAAA	4	4			
6	f	TGGGCGTAA/	3	3	4		1
7							
8	.TCA	TGGGCGTAA/	5	5			
9	TTA	TGGGTTTAAA	3	3			
10							
11	f	TGGGTTTAAA	5	5	8		1
12	o	TGGGCGTAA/	5	5	2		1
13	CTTA	TGGGCGTAA/	4	4			
14							
15	.TCA	TGGGCGTAA/	4	4			
16	TA	TGGGCGTAA/	4	4			
17	TTA	TGGGCGTAA/	3	3			
18							
19	g				3		1
20	TAG	TGCAGTTAAA	5	5			
21	TA	TGGGTTTAAA	5	5			
22	TA	TGGGCGTAA/	4	4			
23							
24	GCGC						
25							
26	f	TGGGCGTAA/	3	3	15	0.93333333	
27	.TA	TGGGCGTAA/	4	4			
28	TCA						
29							
30	g	TGGGCGTAA/	5	5	9	0.88888889	
31	TAA						
32							
33	TA	TGGGCGTAA/	4	4			
34							
35	g				18	0.94444444	
36	TCA	TGGGCGTAA/	4	4			
37	g	TGCTGTTAAA	3	3	2		1
38	CA	TGGGCGTAA/	5	5			
39							
40	g	TGCAGTTAAA	3	3	13		1
41	f	TGGGCGTAA/	4	4	38	0.94736842	
42							
43	o				2		1
44	TTA	TGGGCGTAA/	4	4			
45	TA	TGGGCGTAA/	3	3			
46							
47	g				5		0.8
48	c	TGGGCGTAA/	5	5	4		1
49	TT	TGGGCGTAA/	5	5			
50							
51	AA						
52							
53	g				195	0.9948718	
54	g	TGGGCGTAA/	3	3	163	0.90184049	
55	TCA	TGGGCATAA/	4	4			
56							
57							
58							
59							
60							

1						
2						
3						
4	g	TGGGCGTAA/	3	3	12787	0.94635176
5	p	TGCAGTTAAA	5	5	8	1
6	g	TGGGCGTAA/	3	3	17	1
7						
8	\AG					
9	ICA	TGGGCTTAAA	5	5		
10						
11	AGA					
12	CA	TGGGCGTAA/	5	5		
13	TCA	TGGGCGTAA/	2	2		
14						
15	TA	TGGGTTTAAA	5	5		
16	TTA	TGGGCGTAA/	4	4		
17	CTTA	TGGGCGTAA/	5	5		
18						
19	g	TGGGCGTAA/	5	5	93	0.89247312
20	ICTC	TGGGCTTAAA	5	5		
21						
22	g				5	1
23	o	TGGGCGTAA/	5	5	3	1
24						
25	TTA	TGGGCGTAA/	5	5		
26	g	TGGGCGTAA/	4	4	2	1
27	g	TGGGCTTAAA	5	5	13	1
28						
29	ICA	TGGGTTTAAA	4	4		
30	g	TGGGCGTAA/	3	3	2591	0.97452721
31	g	TGGGCGTAA/	6	6	1521	1
32	g	TGCAGTTAAA	4	4	2	1
33						
34	TA					
35						
36	g				4	1
37	TCA					
38						
39	g	TGGGCGTAA/	5	5	15	0.86666667
40	g	TGGGCGTAA/	5	5	2	1
41	-					
42						
43	f	TGGGCGTAA/	3	3	4	1
44	TCA	TGGGCTTAAA	5	5		
45						
46	CGG					
47	CTCA	TGGGCGTAA/	4	4		
48						
49	TCA	TGGGCGTAA/	6	6		
50	p	TGGGCGTAA/	5	5	6	1
51	g	TGGGCGTAA/	4	4	14	1
52						
53	AATT					
54	TCA	TGGGCGTAA/	5	5		
55	CTT	TGGGCGTAA/	4	4		
56						
57						
58						
59						
60						

TTA	TGGGTGTAA/	5	5		
CTAA					
CTCA	TGGGCGTAA/	5	5		
CTAT					
g	TGGGCGTAA/	3	3	50	0.98
TCA	TGGGCGTAA/	2	2		
g	TGGGCGTAA/	5	5	18	1
c				9	0.88888889
CTTA	TGGGCTTAAA	5	5		
CTA	TGGGTTTAAA	3	3		
AA					
CTTA	TGGGCGTAA/	5	5		
f	TGGGCGTAA/	3	3	3	1
CTCA					
g	TGGGCGTAA/	3	3	2	1
g	TGGGCGTAA/	7	7	15	1
g	TGGGCGTAA/	4	4	25	1
TTA	TGGGCGTAA/	5	5		
TCA	TGGGCGTAA/	5	5		
GG	TGTGTTTAAA	6	6		
A	TGCAGTTAAA	4	4		
f	TGGGCTTAAA	5	5	15	1
g				36	0.94444444
TT					
CTT	TGGGCGTAA/	4	4		
g				38	0.97368421
f	TGGGCGTAA/	3	3	4	1
TCA	TGGGCTTAAA	5	5		
g	TGGGCGTAA/	3	3	105	1
f	TGGGCGTAA/	4	4	2	1
GGG					
p	TGGGCGTAA/	5	5	6	1
TCA	TGGGCGTAA/	3	3		
CTCA	TGGGCGTAA/	3	3		
f				4	1
TCA	TGGGCGTAA/	5	5		
CTCA	TGGGCGTAA/	3	3		
CTCA	TGGGCGTAA/	6	6		

1							
2							
3							
4	ΓAA	TGGGCGTAA/	4	4			
5	f	TGGGCGTAA/	3	3	2		1
6	ΔAT	TGCAGTTAAA	5	5			
7							
8	ΔTC						
9	ΔTCA	TGGGCGTAA/	6	6			
10	ΔTTA	TGGGCGTAA/	4	4			
11	ΔTCA	TGGGCGTAA/	2	2			
12							
13	f	TGGGTTTAAA	5	5	7		1
14							
15	g				1577	0.99048827	
16	ΓTA						
17							
18	ΔCA	TGGGCGTAA/	4	4			
19	ΓCA						
20							
21	g	TGGGCGTAA/	5	5	12	0.83333333	
22	g	TGGGCGTAA/	5	5	49	0.93877551	
23	f	TGGGTTTAAA	3	3	3		1
24							
25	TTA	TGGGCGTAA/	4	4			
26	ΔTTA	TGGGTTTAAA	4	4			
27							
28	ΓAA	TGGGCGTAA/	3	3			
29	ΔTTA	TGGGCGTAA/	5	5			
30	TCA	TGGGCGTAA/	4	4			
31							
32	TTA	TGGGTTTAAA	4	4			
33	g	TGGGCTTACA	6	6	2		1
34	p				6		1
35							
36	ΓTA	TGGGCGTAA/	4	4			
37	o	TGGGCGTAA/	3	3	42	0.97619048	
38							
39	g	TGGGCGTAA/	4	4	2		1
40	g	TGGGCGTAA/	3	3	4		1
41							
42	ΔTCA	TGGGCGTAA/	4	4			
43	TCA	TGGGCGTAA/	3	3			
44							
45	g	TGCTGTTAAA	3	3	2		1
46	ΔTTA	TGGGCGTAA/	5	5			
47	ΔTCA	TGGGCGTAA/	6	6			
48							
49	TCA	TGGGCGTAA/	4	4			
50	TTA	TGGGCGTAA/	5	5			
51							
52	TT						
53	TCA	TGGGCGTAA/	3	3			
54							
55	g				36		1
56	ΔTCA						
57							
58							
59							
60							

1							
2							
3							
4	g	TGGGCGTAA/	4	4	2	1	
5	CTA	TGGGCGTAA/	3	3			
6	CTAA	TGGGCGTAA/	4	4			
7	CAA	TGGGCGTAA/	5	5			
8	CTCA	TGGGCGTAA/	5	5			
9	TCA						
10	TA	TGGGTTTAAA	5	5			
11	TCA	TGGGCGTAA/	2	2			
12	TA						
13	g	TGGGCGTAA/	4	4	10	0.8	
14	g	TGGGCTTAAA	4	4	9	1	
15	CAA	TGGGCGTAA/	3	3			
16	TCA	TGGGCGTAA/	4	4			
17	o	TGGGCGTAA/	4	4	3	1	
18	TCA	TGGGCTTAAA	5	5			
19	GAACC						
20	o	TGGGCTTAAA	6	6	4	1	
21	TAA						
22	A	TGGGCGTAA/	3	3			
23	CA						
24	TA						
25	g	TGCAGTTAAA	1	1	6	1	
26	ACG	TGGGCGTAA/	4	4			
27	TCA	TGGGCGTAA/	5	5			
28	TCA	TGGGCGTAA/	2	2			
29	g	TGGGCGTAA/	4	4	88	0.95454546	
30	CTCA	TGGGCGTAA/	3	3			
31	GGC						
32	f				3	1	
33	f				2	1	
34	CCA						
35	CTCA						
36	g				506	0.98814229	
37	g	TGGGCGTAA/	4	4	44	0.97727273	
38	TCA	TGGGCGTAA/	4	4			
39	TCA	TGGGCGTAA/	3	3			
40	CA	TGGGCTTAAA	4	4			
41	TCA	TGGGCTTAAA	4	4			
42							
43							
44							
45							
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57							
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60							

1						
2						
3						
4	.TCA					
5	f	TGGGTTTAAA	2	2	3	1
6	TA					
7						
8	CTCA	TGGGCGTAA/	3	3		
9	TCA	TGGGCGTAA/	2	2		
10						
11	.TCA					
12	TCA	TGGGCTTAAA	5	5		
13	.TCA	TGGGCGTAA/	4	4		
14						
15	TCA	TGGGCGTAA/	3	3		
16	TCA					
17	.TTA					
18						
19	TCA	TGGGCGTAA/	3	3		
20	.TCA	TGGGCGTAA/	4	4		
21	.TCA	TGGGCTTAAA	4	4		
22	TA	TGGGCGTAA/	2	2		
23	.TCA	TGGGCGTAA/	4	4		
24	f				7	0.85714286
25						
26	AAC	TGGGCGTAA/	2	2		
27	TAATT					
28	.TTA	TGGGCGTAA/	3	3		
29	CA					
30	TCA	TGGGCGTAA/	3	3		
31	TA	TGGGCGTAA/	4	4		
32	.TCA	TGGGCGTAA/	5	5		
33	CTCA					
34	f	TGGGTTTAAA	3	3	7	1
35	CTTA					
36	TTA	TGGGCGTAA/	3	3		
37	CA	TGGGCGTAA/	3	3		
38	TA					
39	.TCA	TGGGCGTAA/	7	7		
40	GT					
41	AA					
42	.TCA	TGGGCGTAA/	4	4		
43	TA	TGGGCGTAA/	2	2		
44	g				1713	0.9918272
45	iCAG					
46	.TCA	TGGGCGTAA/	3	3		
47						
48						
49						
50						
51						
52						
53						
54						
55						
56						
57						
58						
59						
60						

AT	TGGGCGTAA/	4	4		
.TCA	TGGGTGTAA/	4	4		
g				2	1
AA					
.CA	TGGGCGTAA/	3	3		
.CA					
g				528	0.99242424
.CG					
.CA	TGGGCGTAA/	3	3		
TAA	TGGGCGTAA/	3	3		
.ATG	TGCAGTTAAA	3	3		
.TA	TGGGCGTAA/	2	2		
.CA					
CAT	TGGGCGTAA/	2	2		
f	TGGGCGTAA/	3	3	24	0.91666667
f	TGGGCGTAA/	3	3	3	1
.TTA					
.TCG	TGGGCGTAA/	5	5		
.TCA	TGGGCGTAA/	4	4		
CTCA	TGGGCGTAA/	3	3		
TA	TGGGTTTAAA	2	2		
CAA	TGGGCGTAA/	4	4		
g				8	1
.ACG	TGCAGTTAAA	2	2		
g				36	0.88888889
g	TGTGGTTAAA	2	2	16	0.8125
g	TGGGCGTAA/	2	2	2957	0.99763274
g	TGGGCGTAA/	2	2	5	1
g	TGGGCGTAA/	1	1	136	1
CTC					
AG	TAGGTGTAA/	1	1		
TCA	TGGGCGTAA/	4	4		
CTTA	TGGGCGTAA/	4	4		
g	TGGGCGTAA/	3	3	2	1
TCA					
.					
g				70	1
.TTA	TGGGCATAAA/	4	4		



1						
2						
3						
4	5AA					
5	ITA	TGGGCGTAA/	3	3		
6	f	TGGGCGTAA/	2	2	4	1
7						
8	o	TGGGCGTAA/	4	4	10	1
9	o	TGGGCGTAA/	4	4	5	1
10						
11	TTA					
12	.TCA	TGGGCATAA/	3	3		
13	.TTA	TGGGCGTAA/	4	4		
14						
15	TA	TGGGCGTAA/	3	3		
16	ICA					
17	ITA	TGGGCGTAA/	2	2		
18						
19	f	TGGGCGTAA/	2	2	2	1
20						
21	GGG					
22	ICA	TGGGTTTAAA	3	3		
23						
24	TA					
25	iAGG					
26	f	TGGGCGTAA/	3	3	5	1
27						
28	g	TGGGCGTAA/	3	3	25	0.92
29	.TCA	TGGGCTTAAA	3	3		
30	TCA	TGGGCGTAA/	2	2		
31						
32	ICA					
33	g	TGGGCGTAA/	3	3	709	1
34	.TCA	TGGGCGTAA/	2	2		
35						
36	CTTA	TGGGCGTAA/	1	1		
37	f	TGGGCTTAAA	2	2	2	1
38						
39	.TCA	TGGGCGTAA/	2	2		
40	CA	TGGGCGTAA/	3	3		
41						
42	AGGC	TGCAGTTAAA	3	3		
43	g				308	0.98701299
44	TCA	TGGGCTTAAA	3	3		
45						
46	CTC					
47	.TCA	TGGGCGTAA/	3	3		
48						
49	g	TGGGCGTAA/	4	4	14	1
50	TCA	TGGGCGTAA/	3	3		
51	CGCG	TGCAGTTAAA	2	2		
52						
53	ATT					
54	.CAA	TGGGCGTAA/	3	3		
55						
56	g	TGGGTTTAAA	4	4	2	1
57						
58						
59						
60						

TA						
f				5		1
CTC	TGGGCGTAA/	1	1			
g	TGGGCGTAA/	2	2	57	0.94736842	
f	TGGGTTTAAA	2	2	4		1
CTCA	TGGGCGTAA/	4	4			
CTCA	TGGGCGTAA/	3	3			
CTCA						
g	TGGGCGTAA/	2	2	5		1
GGG	TGCAGTTAAA	3	3			
CTCA	TGGGCGTAA/	3	3			
CTCA	TGGGCGTAA/	7	6			
CTTA	TGGGCGTAA/	2	2			
CTCA	TGGGCGTAA/	2	2			
CTCA	TGGGCGTAA/	3	3			
g	TGGGCGTAA/	2	2	2		1
f				6		1
CTCA	TGGGCTTAAA	3	3			
o	TGGGCGTAA/	2	2	2		1
c	TGGGCGTAA/	2	2	7		1
GAG						
TTA						
c	TGGGCGTAA/	3	3	2		1
TTA	TGGGCGTAA/	3	3			
CTCA	TGGGCGTAA/	2	2			
TCA	TGGGCGTAA/	3	3			
CTCA	TGGGCGTAA/	3	3			
f	TGGGCGTAA/	2	2	4		1
CTC	TGGGCTTAAA	2	2			
CTCA	TGGGCTTAAA	2	2			
g	TGGGCTTAAA	2	2	7		1
CTCA	TGGGCTTAAA	3	3			
TCA	TGGGCGTAA/	3	3			
g	TGGGCGTAA/	1	1	22		1
CTCA						
f				3		1
AGG	TGCAGTTAAA	2	2			
CAA						

1						
2						
3						
4	5ACTG	TGCAGTTGAA	3	3		
5	.TG					
6	TTA					
7	.TTA	TGGGCGTAA/	3	3		
8	CA	TGGGCTTAAA	3	3		
9	TCA	TGGGCGTAA/	2	2		
10						
11	g				18	0.83333333
12	g	TGGGCGTAA/	2	2	116	0.95689655
13	g	TGGGCGTAA/	2	2	1536	1
14	f	TGGGCGTAA/	3	3	5	1
15						
16	TTA					
17	g	TGGGCTTAAA	2	2	4	1
18	.TTA	TGGGCGTAA/	2	2		
19	g				2	1
20	f	TGGGTGTAA/	3	3	2	1
21						
22	g				1377	0.99273784
23	.TCA	TGGGCGTAA/	4	4		
24	f				6	1
25	f	TGGGCGTAA/	2	2	10	0.8
26	f	TGGGCGTAA/	2	2	8	1
27	c	TGGGCGTAA/	2	2	2	1
28	.TCA	TGGGCGTAA/	3	3		
29	.TCA	TGGGCGTAA/	3	3		
30	.TCA	TGGGCGTAA/	3	3		
31	CAG					
32	TCA	TGGGCGTAA/	5	5		
33	g	TGGGCGTAA/	2	2	25	0.96
34	g	TGGGCGTAA/	2	2	6	1
35	.CC					
36	CA	TGGGCTTAAA	2	2		
37	TTA	TGGGCGTAA/	2	2		
38	CA	TGGGCGTAA/	2	2		
39	g	TGGGCGTAA/	2	2	83	1
40	.AA	TGGGCTTAAA	2	2		
41	CTC	TGGGCTTAAA	2	2		
42	g				125	0.84
43	.CA	TGGGCTTAAA	3	3		
44	g				9	0.88888889
45						
46						
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1							
2							
3							
4	g	TGGGCGTAA/	3	3	2	1	
5	TA	TGGGCGTAA/	2	2			
6	TCA	TGGGCGTAA/	3	3			
7	TA						
8	TA						
9	TA	TGGGCGTAA/	2	2			
10	TA						
11	c	TGGGTTTAAA	2	2	2	1	
12	TA	TGGGCGTAA/	2	2			
13	GGG	TGCAGTTAAA	3	3			
14	TTA						
15	TA						
16	CGG						
17	TA	TGGGCGTAA/	3	3			
18	TA	TGGGCGTAA/	2	2			
19	TCA	TGGGCGTAA/	2	2			
20	TTA	TGGGCTTAAA	2	2			
21	TA	TGGGTTTAAA	3	3			
22	TCA	TGGGCGTAA/	3	3			
23	TA						
24	TA	TGGGTGTAA/	3	3			
25	TTA	TGGGCGTAA/	3	3			
26	f				2	1	
27	g				552	0.91666667	
28	TA						
29	TA	TGGGCGTAA/	2	2			
30	TA	TGGGCGTAA/	3	3			
31	TTA	TGGGCGTAA/	2	2			
32	TA	TGGGCGTAA/	2	2			
33	g	TGGGCGTAA/	2	2	27	0.96296296	
34	TA	TGGGCGTAA/	2	2			
35	TTA	TGGGCGTAA/	2	2			
36	g	TGGGCGTAA/	3	3	8	0.875	
37	CTCA	TGGGCGTAA/	3	3			
38	g	TGGGCGTAA/	2	2	17	1	
39	TA	TGGGCGTAA/	3	3			
40	g	TGGGCGTAA/	3	3	7	1	
41	f				2	1	
42							
43							
44							
45							
46							
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49							
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57							
58							
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60							

1						
2						
3						
4	g	TGGGCGTAA/	2	2	5	1
5	g	TGGGCGTAA/	2	2	30	1
6	ICA	TGGGCTTAAA	2	2		
7						
8	ICA					
9	g	TGGGCGTAA/	2	2	56	1
10	ITA	TGCAGTTAAA	2	2		
11						
12	f				2	1
13	CCA	TGGGCGTAA/	2	2		
14						
15	g	TGGGCGTAA/	3	3	10	0.9
16	TCA	TGGGCGTAA/	3	3		
17						
18	.TCA	TGGGCGTAA/	3	3		
19	o	TGGGCGTAA/	2	2	9	1
20						
21	.TCA	TGGGCGTAA/	2	2		
22	TTA	TGGGCGTAA/	2	2		
23	f	TGGGTTTAAA	2	2	6	0.83333333
24						
25	.TCA					
26	CAA	TGGGCGTAA/	3	3		
27						
28	g	TGGGCGTAA/	2	2	57	0.92982456
29	ICA	TGGGCGTAA/	2	2		
30						
31	CGG					
32	.CG	TGCAGTTAAA	2	2		
33	f				16	1
34						
35	.TTA	TGGGCGTAA/	2	2		
36	g				19	0.89473684
37	ATTG	TGCAGTTAAA	2	2		
38						
39	ITA					
40	g				44	0.93181818
41						
42	g	TGGGCGTAA/	2	2	2	1
43	CTCA	TGGGCGTAA/	1	1		
44						
45	.TTA	TGGGCGTAA/	1	1		
46	TCA	TGGGCGTAA/	1	1		
47	ITA	TGGGCGTAA/	1	1		
48						
49	AA					
50	CTCA	TGGGCGTAA/	2	2		
51	ITA	TGGGCGTAA/	2	2		
52						
53	TCA	TGGGCGTAA/	2	2		
54						
55	CTCA					
56	CTC					
57						
58						
59						
60						

g					114	1
TCA	TGGGCGTAA/	1	1			
TCA	TGGGCGTAA/	1	1			
TAA	TGGGCGTAA/	2	2			
g	TGGGTTTAAA	1	1	21	1	
g	TGGGCTTAAA	1	1	13	1	
g				3	1	
CTCA	TGGGCGTAA/	1	1			
GCG						
CTT						
TTA	TGGGCGTAA/	2	2			
TA						
TCA						
CAA	TGGGCGTAA/	2	2			
TCA	TGGGCGTAA/	3	3			
TCA						
TTA	TGGGTTTAAA	2	2			
STAT	TGGGCGTAA/	1	1			
CAA	TGGGCGTAA/	1	1			
c				1765	0.99660057	
AACT						
TCA	TGGGCTTAAA	3	3			
TCA	TGGGCGTAA/	3	3			
TTA	TGGGCGTAA/	2	2			
TA	TGGGTTTAAA	2	2			
TAA	TGGGCGTAA/	2	2			
TCA	TGGGCGTAA/	2	2			
TCA						
CCA						
g	TGGGCTTAAA	2	2	3	1	
g	TGGGCTTAAA	2	2	2	1	
TCA						
f				202	0.99504951	
g	TGGGCGTAA/	2	2	2	1	
g	TGGGCGTAA/	2	2	9	1	
CTCA	TGGGCGTAA/	2	2			
CTTA						
TCA	TGGGCGTAA/	3	3			

1							
2							
3							
4	TCA	TGGGCTTAAA	2	2			
5	c	TGGGCATAAA	2	2	2		1
6	TCA	TGGGCGTAA	2	2			
7		TGGGCGTAA	1	1			
8	TTA						
9	TTA						
10	f	TGGGCGTAA	2	2	12		1
11	CTCA	TGGGCGTAA	2	2			
12	CTTA						
13	TTA	TGGGCGTAA	3	3			
14	TAA						
15	TTA						
16	TTA	TGGGTTTAAA	2	2			
17	gCAG						
18	TTA	TGGGCGTAA	3	3			
19	CA	TGGGCGTAA	2	2			
20	gCGG	TGCAGTTAAA	1	1			
21	CAA	TGGGCGTAA	1	1			
22	TCA	TGGGCGTAA	1	1			
23	CAG	TGGGCGTAA	1	1			
24	TCA	TGGGCGTAA	1	1			
25	ACC						
26	TTA	TGGGCGTAA	2	2			
27	TTA	TAGGTTTAAA	2	2			
28	TTA	TGGGCGTAA	1	1			
29	AGG						
30	gAG						
31	o	TGGGCGTAA	1	1	11	0.90909091	
32	TTA	TGGGCGTAA	2	2			
33	TT						
34	CTCA	TGGGTTTAAA	2	2			
35	TCA	TGGGCGTAA	1	1			
36	g	TGGGCGTAA	1	1	556	0.90827338	
37	TCA	TGGGCTTAAA	1	1			
38	g	TGGGCGTAA	2	2	3		1
39	CTCA	TGGGCGTAA	2	2			
40	f	TGGGCGTAA	2	2	2		1
41	CTCA	TGGGCGTAA	2	2			
42	o	TGGGCGTAA	2	2	12		1
43							
44							
45							
46							
47							
48							
49							
50							
51							
52							
53							
54							
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57							
58							
59							
60							

TTA	TGGGCGTAA/	2	2		
CA					
TA	TGGGCGTAA/	2	2		
TCA	TGGGCGTAA/	2	2		
CTCA	TGGGCGTAA/	2	2		
g				2	1
g				2	1
TCA	TGGGCGTAA/	2	2		
f	TGGGCGTAA/	2	2	66	0.98484849
f				113	0.9380531
TTA	TGGGCGTAA/	2	2		
f	TGGGCGTAA/	2	2	5	1
CG	TGCAGTTAAA	2	2		
TTA					
TCA	TGGGCGTAA/	2	2		
g				8	1
f	TGGGCTTAAA	1	1	3	1
g	TGGGCTTAAA	1	1	2	1
TCA					
o				77	1
TTA	TGGGTTTAAA	1	1		
CTCA	TGGGCGTAA/	1	1		
AA	TGGGCGTAA/	2	2		
f	TGGGCGTAA/	2	2	9	1
CA	TGGGCGTAA/	2	2		
CA	TGGGCGTAA/	1	1		
CAA	TGGGCGTAA/	1	1		
g				5	1
o				2718	0.99632082
TCA	TGGGCGTAA/	1	1		
CCA	TGGGCTTAAA	1	1		
g	TGGGCGTAA/	1	1	100	0.99
p	TGGGCGTAA/	1	1	5	1
TTA					
TCA	TGGGCGTAA/	1	1		
CTA	TGGGCTTACA	1	1		
TA	TGGGCGTAA/	1	1		
TCA	TGGGCTTAAA	2	2		



1						
2						
3						
4	T	TGCAGTTAAA	2	2		
5	.CGG					
6	TTA	TGGGCGTAA/	2	2		
7	TG					
8						
9	.TCA	TGGGCGTAA/	2	2		
10	ICA	TGGGCGTAA/	2	2		
11						
12	.TAA					
13	ATC	TGCAGTTAAA	2	2		
14	.CA	TGGGCTTAAA	2	2		
15	AAC	TGGGCGTAA/	2	2		
16						
17	g	TGGGCGTAA/	2	2	2	1
18						
19	o				2	1
20						
21	.AG					
22	CGG					
23	.TTA	TGGGCGTAA/	2	2		
24						
25	.CGG					
26	IAA					
27	.GAT					
28						
29	TTA	TGGGCGTAA/	3	3		
30	TAG	TGCAGTTAAA	2	2		
31						
32	GGA					
33	TCA					
34	TCA	TGGGCGTAA/	1	1		
35	.TCA	TGGGCGTAA/	2	2		
36	CCA	TGGGTTTAAA	2	2		
37						
38	.TTG					
39						
40	CTG	TGCAGTTAAA	2	2		
41	TA					
42						
43	o	TGGGCGTAA/	2	2	3	1
44	f	TGGGCTTAAA	2	2	4	1
45						
46	TCA	TGGGCGTAA/	2	2		
47	TTA	TGGGCTTAAA	2	2		
48						
49	.TCA					
50						
51	g				3	1
52	CTCA					
53	c				36	1
54	.AC					
55						
56	.CCA	TGGGCGTAA/	2	2		
57						
58						
59						
60						

1							
2							
3							
4	CAA						
5	TTA	TGGGCGTAA/	2	2			
6	o	TGGGCGTAA/	2	2	7		1
7							
8	TCA	TGGGCTTAAA	2	2			
9	TTA	TGGGCGTAA/	2	2			
10							
11	TCA	TGGGCGTAA/	1	1			
12	TTA	TGGGCGTAA/	3	3			
13							
14	TTA						
15	CAATT	TGCAGTTAAA	2	2			
16	g	TGGGCGTAA/	2	2	11	0.90909091	
17							
18	TA						
19	o	TGGGCGTAA/	2	2	17	0.88235294	
20	f	TGGGCTTAAA	2	2	7		1
21							
22	g	TGGGCGTAA/	2	2	641	0.97035881	
23	TTA	TGGGCGTAA/	2	2			
24							
25	TCA	TGGGCGTAA/	2	2			
26	AC	TGTGTTTAAA	2	2			
27							
28	TCA	TGGGCGTAA/	2	2			
29	TTA	TGGGCGTAA/	2	2			
30							
31	TCA	TGGGCGTAA/	2	2			
32	o	TGGGCGTAA/	2	2	6		1
33	g	TGGGCGTAA/	2	2	3		1
34	AA	TGGGCGTAA/	2	2			
35							
36	AC						
37							
38	g				258	0.81007752	
39	g	TGGGCGTAA/	1	1	2		1
40	TGA	TGGGCGTAA/	1	1			
41							
42	f	TGGGCGTAA/	1	1	13		1
43	g	TGGGCGTAA/	1	1	8		1
44	TTA	TGGGCGTAA/	1	1			
45							
46	TTA	TGGGCGTAA/	1	1			
47	CTCA	TGGGCGTAA/	1	1			
48							
49	TTA	TGGGCGTAA/	1	1			
50							
51	TTA						
52	g	TGGGTTTAAA	2	2	2		1
53	CGA						
54							
55	TA	TGGGCGTAA/	2	2			
56	TCA	TGGGCGTAA/	2	2			
57							
58							
59							
60							

1						
2						
3						
4	TTA	TGGGCGTAA/	2	2		
5	AGG	TGCAGTTAAA	2	2		
6	g	TGCAGTTAAA	1	1	158	0.98734177
7	.TCA	TGGGCGTAA/	1	1		
8						
9	g	TGGGTTTAAA	1	1	23	1
10	f	TGGGCGTAA/	1	1	2	1
11						
12	g	TGGGCTTAAA	1	1	10	1
13	CAA	TGGGCTTAAA	1	1		
14						
15	CGG	TGCAGTTAAA	1	1		
16	CA	TGGGCGTAA/	1	1		
17						
18	TTA					
19	CA	TGGGCGTAA/	1	1		
20	TTA	TGGGCGTAA/	1	1		
21						
22	iCGG					
23	iCGA	TGCAGTTAAA	1	1		
24	AA	TGGGCGTAA/	1	1		
25						
26	TTA	TGGGCGTAA/	1	1		
27	.TCA	TGGGCGTAA/	1	1		
28	TTA	TGGGCGTAA/	1	1		
29	.TCA	TGGGCGTAA/	1	1		
30						
31	AAACT					
32						
33	g	TGGGCGTAA/	1	1	3	1
34	TCA	TGGGCGTAA/	1	1		
35						
36	CTCA	TGGGCGTAA/	1	1		
37	CTCA	TGGGCGTAA/	1	1		
38						
39	TAA	TGCAGTTAAA	1	1		
40	TTA	TGGGCGTAA/	1	1		
41	.TCA	TGGGCGTAA/	1	1		
42	CAA	TGGGCGTAA/	1	1		
43	CTTA	TGGGCGTAA/	1	1		
44	CTCA	TGGGCGTAA/	1	1		
45						
46	g	TGGGCTTAAA	1	1	101	0.99009901
47	CAA	TGGGCGTAA/	2	2		
48						
49	AG	TGCAGTTAAA	1	1		
50	TTA	TGGGCGTAA/	1	1		
51						
52	CGG	TGCAGTTAAA	1	1		
53	TCA	TGGGCGTAA/	2	2		
54						
55	TTA					
56						
57						
58						
59						
60						

1							
2							
3							
4	.TCA	TGGGCTTAAA	2	2			
5	.TTA	TGGGCGTAA/	2	2			
6	TCA	TGGGCGTAA/	3	3			
7	TTA	TGGGCGTAA/	2	2			
8	ΓCA	TGGGCGTAA/	1	1			
9	g	TGGGCGTAA/	1	1	2		1
10	o	TGGGCGTAA/	1	1	36		1
11	.CT						
12	.TCA	TGGGCGTAA/	1	1			
13	o	TGGGCGTAA/	1	1	6		1
14	g	TGGGCGTAA/	1	1	4		1
15	g	TGGGCGTAA/	1	1	2		1
16	TA	TGGGCGTAA/	1	1			
17	TTA	TGGGCGTAA/	1	1			
18	TA	TGGGCGTAA/	1	1			
19	.TCA	TGGGCTTAAA	1	1			
20	.TCA	TGGGCGTAA/	1	1			
21	CG	TGCAGTTAAA	1	1			
22	g	TGGGCGTAA/	1	1	22	0.95454546	
23	GACCT	TGCAGTTGAA	1	1			
24	ΔAAG	TGCAGTTAAA	1	1			
25	g	TGGGCGTAA/	1	1	3709	0.99595578	
26	ΓCA	TGGGCTTAAA	2	2			
27	o	TGGGCGTAA/	1	1	22	0.81818182	
28	ΓCA	TGGGCGTAA/	1	1			
29	g	TGGGTTTAAA	1	1	10		0.9
30	TTA	TGGGTTTAAA	1	1			
31	CAA	TGGGCGTAA/	1	1			
32	ΓCA	TGGGCGTAA/	1	1			
33	TCA	TGGGTTTAAA	1	1			
34	ΓCA	TGGGCGTAA/	1	1			
35	f	TGGGCGTAA/	1	1	4		1
36	.TCA	TGGGCGTAA/	1	1			
37	.TTA	TGGGTTTAAA	1	1			
38	g	TGGGCGTAA/	1	1	6		1
39	CTTA	TGGGCTTAAA	1	1			
40	.TCA	TGGGCGTAA/	1	1			
41	ΔCTC	TGGGCTTAAA	1	1			
42							
43							
44							
45							
46							
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48							
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1						
2						
3						
4	TCA	TGGGCGTAA/	2	2		
5	TCA	TGGGCGTAA/	3	3		
6	f	TGGGCTTAAA	2	2	2	1
7	AAC	TGGGCGTAA/	2	2		
8	AATT	TGCAGTTAAA	2	2		
9	ICA					
10	TTA	TGGGCGTAA/	2	2		
11	TCA					
12	TTA	TGGGCGTAA/	3	3		
13	TTA					
14	TCA	TGGGCGTAA/	2	2		
15	TTA	TGGGCGTAA/	2	2		
16	TTA	TGGGCGTAA/	2	2		
17	TCA	TGGGCGTAA/	3	3		
18	TTA	TGGGCGTAA/	1	1		
19	TTA	TGGGTGTAA/	1	1		
20	TTA	TGGGCGTAA/	1	1		
21	TTA	TGGGCGTAA/	1	1		
22	TCA	TGGGCGTAA/	1	1		
23	TTA	TGGGCGTAA/	1	1		
24	TTA	TGGGCGTAA/	1	1		
25	TTA	TGGGCGTAA/	1	1		
26	TTA	TGGGCGTAA/	1	1		
27	TTA	TGGGCGTAA/	1	1		
28	TTA	TGGGCGTAA/	1	1		
29	TTA	TGGGCGTAA/	1	1		
30	TCA	TGGGCGTAA/	1	1		
31	TTA	TGGGTTTAAA	1	1		
32	TTA	TGGGCGTAA/	1	1		
33	g	TGGGCGTAA/	1	1	26	0.96153846
34	CTCA					
35	TCA	TGGGCGTAA/	1	1		
36	TTA	TGGGCGTAA/	1	1		
37	g	TGGGCGTAA/	1	1	5	1
38	CTC	TGGGCGTAA/	1	1		
39	TTA	TGGGCGTAA/	1	1		
40	g	TGGGCGTAA/	1	1	1271	1
41	GGC	TGCAGTTAAA	1	1		
42	ICA	TGGGCTTAAA	1	1		
43	TCA	TGGGCGTAA/	1	1		
44	TCA	TGGGCGTAA/	1	1		
45	TCT					
46	TCA					
47	g	TGGGCGTAA/	1	1	14	1
48	TCA	TGGGCGTAA/	2	2		
49						
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51						
52						
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1								
2								
3								
4	TCA	TGGGCGTAA/	2	2				
5	GGG							
6	.TTA	TGGGCGTAA/	1	1				
7	CTTA	TGGGCGTAA/	1	1				
8	TCA	TGGGCGTAA/	1	1				
9	TAG	TGCAGTTAAA	1	1				
10	.TTA	TGGGCGTAA/	1	1				
11	.TCG	TGGGCGTAA/	3	3				
12	.TCA	TGGGCGTAA/	2	2				
13	TCA	TGGGCGTAA/	2	2				
14	.TTA	TGGGCGTAA/	1	1				
15	TTA	TGGGCGTAA/	1	1				
16	AT	TGCAGTTAAA	1	1				
17	TTA	TGGGTTTAAA	1	1				
18	CAA	TGGGCGTAA/	1	1				
19	.TTA	TGGGCGTAA/	1	1				
20	TCA	TGGGCGTAA/	1	1				
21	TTA	TGGGCGTAA/	1	1				
22	TCA	TGGGCTTAAA	1	1				
23	TCA	TGGGCGTAA/	1	1				
24	o	TGGGCGTAA/	1	1	2		1	
25	TTA	TGGGCGTAA/	1	1				
26	TTA	TGGGCGTAA/	1	1				
27	TCA	TGGGCTTAAA	1	1				
28	TA	TGGGCGTAA/	1	1				
29	TCA	TGGGCGTAA/	1	1				
30	.CCA	TGGGCGTAA/	1	1				
31	CTCA	TGGGCGTAA/	1	1				
32	AAC	TGGGTTTAAA	1	1				
33	.CAA	TGGGCGTAA/	1	1				
34	TCA	TGGGCGTAA/	1	1				
35	TC	TGGGCGTAA/	1	1				
36	.TTA	TGGGCTTAAA	1	1				
37	TTA	TGGGCGTAA/	1	1				
38	.TTA	TGGGCGTAA/	1	1				
39	CTT	TGGGCGTAA/	1	1				
40	g	TGGGCGTAA/	1	1	41	0.90243902		
41	TTA	TGGGCGTAA/	1	1				
42								
43								
44								
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1						
2						
3						
4	TA	TGGGCGTAA/	1	1		
5	TCA					
6	TA					
7						
8	TCA	TGGGCGTAA/	1	1		
9	TTC	TGCAGTTAAA	1	1		
10						
11	TTA	TGGGCGTAA/	1	1		
12	TGA					
13	TCA	TGGGCGTAA/	1	1		
14						
15	g	TGGGCGTAA/	1	1	15	0.86666667
16	GAG	TGCAGTTAAA	1	1		
17						
18	g				2	1
19	TCA	TGGGCGTAA/	1	1		
20						
21	TCA	TGGGCGTAA/	1	1		
22	CAA	TGGGCGTAA/	1	1		
23	f	TGGGCGTAA/	1	1	2	1
24						
25	TCA	TGGGCGTAA/	1	1		
26	TTA	TGGGCGTAA/	1	1		
27	TTA	TGGGCGTAA/	1	1		
28						
29	GGA					
30	GAG	TGCAGTTAAA	1	1		
31						
32	CA	TGGGCTTAAA	1	1		
33	TCA	TGGGCTTAAA	1	1		
34						
35	TCA	TGGGCGTAA/	1	1		
36	TCA	TGGGCGTAA/	1	1		
37	TCA	TGGGCATAA/	1	1		
38						
39	CAA	TGGGCTTAAA	1	1		
40	TCA	TGGGCGTAA/	1	1		
41						
42	CC					
43	TCA	TGGGCGTAA/	1	1		
44	A	TGCAGTTAAA	1	1		
45						
46	g	TGGGCGTAA/	1	1	2	1
47	TTA	TGGGCGTAA/	1	1		
48						
49	GCGG					
50	CA	TGGGCGTAA/	1	1		
51	TCA	TGGGCGTAA/	1	1		
52						
53	GCGG	TGCAGTTAAA	1	1		
54	GAT					
55						
56	TCA	TGGGCGTAA/	1	1		
57						
58						
59						
60						

1				
2				
3				
4	C			
5	AG	TGCAGTTAAA	1	1
6	CA	TGGGCGTAA/	1	1
7				
8	TCA			
9	TCA	TGGGCGTAA/	1	1
10				
11	AGG			
12	TTA	TGGGCGTAA/	1	1
13	CAA	TGGGCGTAA/	1	1
14				
15	TA	TGGGCGTAA/	1	1
16	TCA	TGGGCGTAA/	1	1
17				
18	TCA			
19	ATTG	TGCAGTTAAA	1	1
20	TAA	TGGGTTTAAA	1	1
21				
22	TTA	TGGGCGTAA/	1	1
23	AG	TGCAGTTAAA	1	1
24				
25	AG			
26	TA	TGGGCGTAA/	1	1
27	TCA	TGGGTTTAAA	1	1
28				
29	CTCA	TGGGCGTAA/	1	1
30	TTA	TGGGCGTAA/	1	1
31				
32	TTA	TGGGCGTAA/	1	1
33	CTA	TGGGCGTAA/	1	1
34	TCA	TGGGCGTAA/	1	1
35				
36	TTA	TGGGTTTAAA	1	1
37	CTT	TGGGCGTAA/	1	1
38				
39	AG			
40	CCC			
41				
42	CAA			
43	AT	TGGGCGTAA/	1	1
44	TTA	TGGGCGTAA/	1	1
45				
46	TTG	TGGGCGTAA/	1	1
47	TA	TGGGCGTAA/	1	1
48				
49	CGG	TGCAGTTAAA	1	1
50	TCA	TGGGCGTAA/	1	1
51	TTA	TGGGCGTAA/	1	1
52				
53	TTG	TGCAGTTAAA	1	1
54				
55	AGG			
56	TCA	TGGGCGTAA/	1	1
57				
58				
59				
60				



1							
2							
3							
4	TAA	TGGGCGTAA/	1	1			
5	GAG						
6	CTCA	TGGGCGTAA/	1	1			
7	TCA	TGGGCGTAA/	1	1			
8	TA	TGGGTTTAAA	1	1			
9	TCA	TGGGCTTAAA	1	1			
10	CTTA						
11	CTA	TGGGCGTAA/	1	1			
12	TTA						
13	TTA	TGGGCGTAA/	1	1			
14	CA	TGGGCTTAAA	1	1			
15	TCA	TGGGTGTAA/	1	1			
16	TTA	TGGGCGTAA/	1	1			
17	TCA	TGGGCGTAA/	1	1			
18	AT	TGCAGTTAAA	1	1			
19	TCA	TGGGCGTAA/	1	1			
20	AGG	TGCAGTTAAA	1	1			
21	TCA						
22	CTTA	TGGGCGTAA/	1	1			
23	g	TGGGCGTAA/	1	1	4		1
24	AAC	TGGGCGTAA/	1	1			
25	TCA	TGGGCGTAA/	1	1			
26	TA	TAGGCGTAA/	1	1			
27	f	TGGGCGTAA/	1	1	8		1
28	TCA	TGGGCGTAA/	1	1			
29	CTCA	TGGGCTTAAA	1	1			
30	g	TGGGTGTAA/	1	1	2		1
31	TCA	TGGGCGTAA/	1	1			
32	TTA	TGGGCGTAA/	1	1			
33	TA	TGGGCGTAA/	1	1			
34	ATC						
35	AA	TGCAGTTAAA	1	1			
36	TCA	TGGGCTTAAA	1	1			
37	TCA	TGGGCGTAA/	1	1			
38	G	TACAGTTAAA	1	1			
39	TT	TGCAGTTAAA	1	1			
40	g	TGGGCGTAA/	1	1	7		1
41	TA	TGGGCGTAA/	1	1			
42							
43							
44							
45							
46							
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49							
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52							
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56							
57							
58							
59							
60							

TTA	TGGGCGTAA/	1	1		
CTCA					
CTCA	TGGGCGTAA/	1	1		
TTA	TGGGCTTAAA	1	1		
.TCA	TGGGCGTAA/	1	1		
g	TGGGCTTAAA	1	1	2	1
.TCA	TGGGTTTAAA	1	1		
ICA	TGGGCGTAA/	1	1		
CA	TGGGCGTAA/	1	1		
g	TGGGTCTAAA	1	1	151	1
GCA					
TA	TGGGCGTAA/	1	1		
TAG					
TCA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	5	1
g				122	0.81967213
TCA	TGGGCTTAAA	1	1		
CTTA	TGGGCGTAA/	1	1		
ICA	TGGGCTTAAA	1	1		
CA	TGGGCGTAA/	1	1		
ICA	TGGGCTTAAA	1	1		
g	TGGGCGTAA/	1	1	4	1
CTCA	TGGGCGTAA/	1	1		
AAA	TGTAGTTAAA	1	1		
f	TGGGCGTAA/	1	1	2	1
AGC	TGGGCGTAA/	1	1		
AG	TGCAGTTAAA	1	1		
TCA					
TTA					
f	TGGGCGTAA/	1	1	128	1
TA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	423	0.99763593
ICA	TGGGCGTAA/	1	1		
.TTG	TGCAGTTAAA	1	1		
TTA					
CTTA	TGGGCTTAAA	1	1		
ICGG	TGCAGTTAAA	1	1		
CAA	TGGGCGTAA/	1	1		

1						
2						
3						
4	CTCA	TGGGCGTAA/	1	1		
5	TTA	TGGGCGTAA/	1	1		
6	CTTA	TGGGCGTAA/	1	1		
7	AA	TGGGCGTAA/	1	1		
8						
9	g	TGGGCGTAA/	1	1	2	1
10	g	TGGGCGTAA/	1	1	20	1
11						
12	TTA	TGGGCGTAA/	1	1		
13	AAC	TGGGCGTAA/	1	1		
14						
15	TCA	TGGGCGTAA/	1	1		
16	GAG	TGCAGTTAAA	1	1		
17						
18	TCA	TGGGCGTAA/	1	1		
19	CAG					
20						
21	GCGG	TGCAGTTAAA	1	1		
22	CTCA	TGGGCATAAA/	1	1		
23						
24	TCA	TGGGCTTAAA	1	1		
25	TTA	TGGGCTTAAA	1	1		
26	TCA	TGGGCGTAA/	1	1		
27						
28	TCA	TGGGCTTAAA	1	1		
29	TCA	TGGGCGTAA/	1	1		
30						
31	TTA	TGGGCGTAA/	1	1		
32	CTCA	TGGGTTTAAA	1	1		
33	TCA	TGGGCGTAA/	1	1		
34	CTT	TGGGCGTAA/	1	1		
35						
36	TTA	TGGGCGTAA/	1	1		
37	GCG					
38						
39	g	TGGGCTTAAA	1	1	3	1
40	TCA	TGGGCGTAA/	1	1		
41						
42	TCA	TGGGCTTAAA	1	1		
43	TCG	TGGGCTTAAA	1	1		
44						
45	TTA	TGGGCGTAA/	1	1		
46	CTTA	TGGGCGTAA/	1	1		
47	TTA	TGGGCGTAA/	1	1		
48						
49	TTA	TGGGTTTAAA	1	1		
50	TTA	TGGGCGTAA/	2	2		
51	TCA	TGGGCTTAAA	1	1		
52						
53	TTA	TGGGCTTAAA	1	1		
54	g	TGGGCGTAA/	1	1	418	0.9784689
55						
56	TCA	TGGGCGTAA/	1	1		
57						
58						
59						
60						

TTA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	191	0.95811518
TCA					
TTA	TGGGCGTAA/	1	1		
CAA	TGGGCGTAA/	1	1		
AA	TGGGCGTAA/	1	1		
TCA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	420	0.99761905
TCA	TGGGCGTAA/	1	1		
CA	TGGGCTTAAA	1	1		
CG	TGGGCGTAA/	1	1		
CA	TGGGCGTAA/	1	1		
CAA					
CA	TGGGCGTAA/	1	1		
TTA	TGGGCTTAAA	1	1		
AA	TGGGCGTAA/	1	1		
g	TGCAGTTAAA	1	1	14	0.92857143
AA	TGGGCGTAA/	1	1		
TTA	TGGGCGTAA/	1	1		
TCA	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	2	1
o	TGGGCGTAA/	1	1	3	1
CA	TGGGCTTAAA	1	1		
TTA	TGGGCGTAA/	1	1		
TTA	TGGGTTTAAA	1	1		
g	TGGGCGTAA/	1	1	4	1
TTA	TGGGTTTAAA	1	1		
TCA	TGGGCGTAA/	1	1		
f	TGGGCGTAA/	1	1	62	1
TCA	TGGGCGTAA/	1	1		
CAA	TGGGCGTAA/	1	1		
CTCA	TGGGCGTAA/	1	1		
TCA	TGGGCATAAA/	1	1		
CA	TGGGCTTAAA	1	1		
f	TGGGCGTAA/	1	1	4	1
CA	TGGGCATAAA/	1	1		
TCA	TGGGCGTAA/	1	1		

1						
2						
3						
4	TCA	TGGGCGTAA/	1	1		
5	CTCA	TGGGCGTAA/	1	1		
6	ICTTA	TGGGCGTAA/	1	1		
7						
8	TCA	TGGGCTTAAA	1	1		
9	CTA	TGGGCGTAA/	1	1		
10						
11	ICA	TGGGCGTAA/	1	1		
12	TTA					
13	TTG	TGGGCGTAA/	1	1		
14	ITA	TGGGTTTAAA	1	1		
15						
16	GG	TGCAGTTAAA	1	1		
17						
18	TCA	TGGGCGTAA/	1	1		
19	g	TGGGCGTAA/	1	1	522	0.86015326
20	TA	TGGGCGTAA/	1	1		
21						
22	g	TGGGCTTACA	1	1	29	0.93103448
23	ITA	TGGGCGTAA/	1	1		
24						
25	o	TGGGCGTAA/	1	1	2	1
26	TA					
27	CTCA					
28						
29	GT	TGCAGTTAAA	1	1		
30	TA	TGGGCGTAA/	1	1		
31						
32	ITA					
33	CTCA	TGGGCGTAA/	1	1		
34	ICA	TGGGCTTAAA	1	1		
35						
36	AGG					
37	AC	TGGGCTTAAA	1	1		
38	AG	TGCAGTTAAA	1	1		
39	ITA	TGGGCGTAA/	1	1		
40	CTCA	TGGGCATAA/	1	1		
41	TTA	TGGGCGTAA/	1	1		
42						
43	c	TGCAGTTAAA	1	1	7	1
44	ICA	TGGGCGTAA/	1	1		
45						
46	f				2	1
47						
48	TTA	TGGGCGTAA/	1	1		
49	TAA	TGGGCGTAA/	1	1		
50						
51	AGA					
52						
53	f	TGGGCGTAA/	1	1	2	1
54	TTTA					
55						
56	GTG					
57						
58						
59						
60						

3	GAG	TGCAGTTAAA	1	1		
4	ATA	TGGGCGTAA/	1	1		
5	ATA	TGGGTTTAAA	1	1		
6	GGCA	TGGGCGTAA/	1	1		
7	CTC					
8	TCA					
9	TCA	TGGGCTTAAA	1	1		
10	ACAG					
11	GAT	TGGGCGTAA/	1	1		
12	CTTA	TGGGCGTAA/	1	1		
13	TCA	TGGGCGTAA/	1	1		
14	TCA					
15	ACGG	TGCAGTTAAA	1	1		
16	ACGG					
17	ACGG	TGCAGTTAAA	1	1		
18	o	TGGGCGTAA/	1	1	205	0.8
19	CC	TGCAGTTAAA	1	1		
20	TTA	TGGGCGTAA/	1	1		
21	TCA	TGGGCGTAA/	1	1		
22	TTA	TGGGCGTAA/	1	1		
23	.TTA	TGGGCGTAA/	1	1		
24	AAC	TGGGCGTAA/	1	1		
25	g	TGGGCGTAA/	1	1	6	0.83333333
26	AT	TGGGCGTAA/	1	1		
27	GT	TGCAGTTAAA	1	1		
28	g	TGGGCTTAAA	1	1	2	1
29	CAA					
30	ATA	TGGGCGTAA/	1	1		
31	.CTT	TGCAGTTAAA	1	1		
32	TTA	TGGGCGTAA/	1	1		
33	.TCA					
34	TA	TGGGCTTAAA	1	1		
35	g	TGGGCGTAA/	1	1	7456	0.88452253
36	o	TGGGCGTAA/	1	1	7	1
37	TA	TGGGCGTAA/	1	1		
38	.TCA	TGGGCATAA/	1	1		
39	TCG					
40	TCA	TGGGCGTAA/	1	1		

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4	ICTC	TGGGCTTAAA	1	1		
5	:TCA	TGGGCATAAA	1	1		
6	TTA	TGGGTGTAAA	1	1		
7	TTA	TGGGCGTAA/	1	1		
8	TTA	TGGGCGTAA/	1	1		
9	TTA	TGGGCGTAA/	1	1		
10	TCA	TGGGCGTAA/	1	1		
11	:TCA	TGGGCGTAA/	1	1		
12	:TCA	TGGGCGTAA/	1	1		
13	:CA	TGGGCGTAA/	1	1		
14	g	TGGGCGTAA/	1	1	76	1
15	:TTA	TGGGCGTAA/	1	1		
16	g	TGGGCGTAA/	1	1	5	1
17	TCA	TGGGCGTAA/	1	1		
18	TTA	TGGGTGTAAA	1	1		
19	:TCA	TGGGCGTAA/	1	1		
20	TCA	TGGGCTTAAA	1	1		
21	f	TGGGCTTAAA	1	1	4	1
22	g	TGGGCGTAA/	1	1	18182	0.82680673
23	:TCA	TGGGCGTAA/	1	1		
24	:CA	TGGGCGTAA/	1	1		
25	CAA	TGGGCGTAA/	1	1		
26	:TTA					
27	:TTA	TGGGCGTAA/	1	1		
28	TA	TGGGCGTAA/	1	1		
29	TTA	TGGGCGTAA/	1	1		
30	CA					
31	:TCA	TGGGCTTAAA	1	1		
32	:AA	TGGGCTTAAA	1	1		
33	:TCA	TGGGTGTAAA	1	1		
34	:TTA	TGGGCGTAA/	1	1		
35	:TCA					
36	TA	TGGGCGTAA/	1	1		
37	g	TGGGCGTAA/	1	1	1915	0.87780679
38	TTA	TGGGCGTAA/	1	1		
39	:TCA					
40	CA	TGGGCTTAAA	1	1		
41	CTCA	TGGGCTTAAA	1	1		
42	g	TGGGTTTAAA	1	1	81	1
43	TCA	TGGGCGTAA/	1	1		
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TTA	TGGGCGTAA/	1	1		
g	TGGGTTTAAA	1	1	3	1
TTA	TGGGCGTAA/	1	1		
CTCA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	2	1
AAC	TGGGCGTAA/	1	1		
AAAC	TGGGTTTAAA	1	1		
p				2	1
f	TGGGCGTAA/	1	1	4	1
CTCA	TGGGCTTAAA	1	1		
TA					
CA	TGGGCTTAAA	1	1		
c	TGGGCGTAA/	1	1	2	1
CTCA	TGGGCATAAA/	1	1		
CTCA					
TTA	TGGGCGTAA/	1	1		
CTA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	14	1
g	TGGGCGTAA/	1	1	274	0.97810219
TTA	TGGGCGTAA/	1	1		
g	TGGGCGTAA/	1	1	2	1
TTA	TGGGTTTAAA	1	1		
CTCA	TGGGCGTAA/	2	2		
CTTA	TGGGCGTAA/	2	2		
g	TGGGCGTAA/	2	2	10	1
CTCA	TGGGCGTAA/	2	2		
TTA					
g	TGGGCGTAA/	1	1	2	1
TTA	TGGGCGTAA/	1	1		
TTA	TGGGCGTAA/	1	1		
TAA	TGGGCGTAA/	1	1		
TA	TAGGCGTAA/	1	1		
TCA	TGGGCATAAA/	1	1		
TA	TGGGCGTAA/	1	1		
CTCA	TGGGCGTAA/	1	1		
TAA	TGGGCGTAA/	1	1		
f	TGGGCGTAA/	1	1	2	1
g	TGGGCGTAA/	1	1	13	1



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4	.TCA	TGGGCGTAA/	1	1		
5	CA	TGGGCTTAAA	1	1		
6	g	TGGGCGTAA/	1	1	2	1
7	AA	TGGGCGTAA/	1	1		
8	TCA	TGGGCGTAA/	1	1		
9	TCA	TGGGCGTAA/	1	1		
10	TCA	TGGGCGTAA/	1	1		
11	TCA	TGGGCGTAA/	1	1		
12	TA	TGGGCGTAA/	1	1		
13	CA	TGGGCTTAAA	1	1		
14	TA	TAGGCGTAA/	1	1		
15	CAA	TGGGCGTAA/	1	1		
16	CA	TGGGCGTAA/	1	1		
17	o	TGGGCGTAA/	1	1	7	1
18	g	TGCAGTTAAA	1	1		
19	g	TGGGCGTAA/	1	1	797	0.99749059
20	.TTA	TGGGCTTAAA	1	1		
21	o	TGGGCGTAA/	1	1	11	1
22	f	TGGGCGTAA/	1	1	2	1
23	TTA	TGGGCGTAA/	1	1		
24	TTAA	TGGGCGTAA/	1	1		
25	TCA	TGGGCATAA/	1	1		
26	CA	TGGGCTTAAA	1	1		
27	TTA	TGGGCTTAAA	1	1		
28	.TCA	TGGGCGTAA/	1	1		
29	g	TGGGCGTAA/	1	1	115	0.99130435
30	CAA	TGGGCGTAA/	1	1		
31	TCC	TGCTGTAAA	1	1		
32	f				12	1
33	.TCA	TGGGCGTAA/	1	1		
34	.TTA					
35	.TA	TGGGCGTAA/	1	1		
36	AAGA	TGCAGTTAAA	1	1		
37	TCA	TGGGCGTAA/	1	1		
38	g	TGGGCGTAA/	1	1	2	1
39	CA	TGGGCTTAAA	1	1		
40	AA	TGGGCTTAAA	1	1		
41	CTT	TGGGCGTAA/	1	1		
42	AA	TGGGCGTAA/	1	1		
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4	iCGG					
5	CAA	TGGGCGTAA/	1	1		
6	TCA	TGGGCGTAA/	1	1		
7	TTA	TGGGCGTAA/	1	1		
8	TAA	TGGGCGTAA/	1	1		
9	TTA	TGGGCGTAA/	1	1		
10	ATA	TGGGTTTAAA	1	1		
11	CTC	TTGGCTTAAA	1	1		
12	AG	TGCAGTTAAA	1	1		
13	iCGG	TGCAGTTAAA	1	1		
14	TTA	TGGGCGTAA/	1	1		
15	g				2	1
16	TCA	TGGGCGTAA/	1	1		
17	CTC	TGGGCGTAA/	1	1		
18	TCA	TGGGCGTAA/	1	1		
19	TTA	TAGGCGTAA/	1	1		
20	TCA	TGGGCGTAA/	1	1		
21	TCA	TGGGCGTAA/	1	1		
22	TG	TGGGCGTAA/	1	1		
23	AGG					
24	TGA	TGGGCGTAA/	1	1		
25	TCA	TGGGCGTAA/	1	1		
26	CAA	TGGGCGTAA/	1	1		
27	TT	TGGGCGTAA/	1	1		
28	g	TGGGCGTAA/	1	1	2	1
29	TCA	TGGGCTTAAA	1	1		
30	CGG	TGCAGTTAAA	1	1		
31	g	TGGGCGTAA/	1	1	2	1
32	GGG	TGGGTTTAAA	1	1		
33	TCA	TGGGCGTAA/	1	1		
34	TTA	TGGGCGTAA/	1	1		
35	TGA	TGCAGTTAAA	1	1		
36	TTA	TGGGCGTAA/	1	1		
37	AG	TGCAGTTAAA	1	1		
38	g	TGGGCGTAA/	1	1	2	1
39	f	TGGGTTTAAA	1	1	2	1
40	CGG	TGCAGTTAAA	1	1		
41	iCGG					
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4	.TCA	TGGGCGTAA/	1	1		
5	.TCA	TGGGCTTAAA	1	1		
6	g	TGGGCTTAAA	1	1	2	1
7	ΓCA	TGGGCTTAAA	1	1		
8	ΓTA	TGGGCGTAA/	1	1		
9	TTA	TGGGTTTAAA	1	1		
10	.TCA	TGGGCTTAAA	1	1		
11	TCA	TGGGCATAA/	1	1		
12	CTT	TGGGCGTAA/	1	1		
13	TAA	TGGGCGTAA/	1	1		
14	TTA	TGGGTTTAAA	1	1		
15	iCGG					
16	.TCA	TGGGCGTAA/	1	1		
17	g	TGGGCGTAA/	1	1	48	1
18	ΓTA	TGGGTTTAAA	1	1		
19	.TCA	TGGGTGTAA/	1	1		
20	A					
21	.AA	TGGGCGTAA/	1	1		
22	.TCA					
23	AAAC	TGGGCTTAAA	1	1		
24	.TCA	TGGGCGTAA/	1	1		
25	TTA	TGGGCGTAA/	1	1		
26	g	TGGGCGTAA/	1	1	13	1
27	TTA	TGGGCGTAA/	2	2		
28	CGG	TGCAGTTAAA	1	1		
29	CA					
30	iGAT	TGCAGTTAAA	1	1		
31	ΓCA	TGGGCTTAAA	1	1		
32	AGG	TGCAGTTAAA	1	1		
33	TCA	TGGGCGTAA/	1	1		
34	.TCA	TGGGCATAA/	1	1		
35	.TTA	TGGGTTTAAA	1	1		
36	ΓCA	TGGGCTTAAA	1	1		
37	.TCA	TGGGCGTAA/	1	1		
38	CGG					
39	.TCA	TGGGCGTAA/	1	1		
40	.CA	TGGGCTTAAA	1	1		
41	TTA	TGGGCGTAA/	1	1		
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4	.TTA	TGGGCGTAA/	1	1		
5	iCGG	TGCAGTTAAA	1	1		
6	TCA	TGGGCTTAAA	1	1		
7	AAC	TGGGCGTAA/	1	1		
8	g	TGGGCGTAA/	1	1	2	1
9	GAG					
10	CGGA	TGCAGTTAAA	1	1		
11	g	TGGGCGTAA/	1	1	15	1
12	GTA	TGGGCGTAA/	1	1		
13	TCA	TGGGCATAA/	1	1		
14	TCA	TGGGCTTAAA	1	1		
15	iCGG	TGCAGTTAAA	1	1		
16	AAC	TGGGTTTAAA	1	1		
17	.TCA	TGGGCGTAA/	1	1		
18	.TCA	TGGGCGTAA/	1	1		
19	GATT	TGCAGTTAAA	1	1		
20	TAA	TGGGCGTAA/	1	1		
21	.TCA	TGGGCGTAA/	1	1		
22	TA	TGGGCGTAA/	1	1		
23	TCA	TGGGCGTAA/	1	1		
24	TCA	TGGGCGTAA/	1	1		
25	CAA	TGGGCGTAA/	1	1		
26	GGC	TGCAGTTAAA	1	1		
27	TTA	TGGGCGTAA/	1	1		
28	GAG	TGCAGTTAAA	1	1		
29	iCGG	TGCAGTTAAA	1	1		
30	.TCA	TGGGCGTAA/	1	1		
31	TTA	TGGGCGTAA/	1	1		
32	.ACA	TGGGCGTAA/	1	1		
33	CTT	TGGGCGTAA/	1	1		
34	TAA	TGGGCGTAA/	1	1		
35	.TCA	TGGGCGTAA/	1	1		
36	TCA	TGGGCGTAA/	1	1		
37	TCA	TGGGCGTAA/	2	2		
38	TCA	TGGGCGTAA/	2	2		
39	TCA	TGGGCGTAA/	2	2		
40	o	TGGGCGTAA/	2	2	3	1
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4	ACC	TGGGCGTAA/	1	1		
5	GGT	TGCAGTTAAA	1	1		
6	TCA	TGGGTGTAA/	1	1		
7	CA	TGGGCGTAA/	1	1		
8	GG	TGCAGTTAAA	1	1		
9	CTCA	TGGGCGTAA/	1	1		
10	AA					
11	AAA	TGGGCGTAA/	1	1		
12	TTA	TGGGCGTAA/	1	1		
13	CTT	TGGGCTTAAA	1	1		
14	CAA	TGGGCGTAA/	1	1		
15	CA	TGCAGTTAAA	1	1		
16	f	TGGGCGTAA/	1	1	3	1
17	TAC	TGCAGTTAAA	1	1		
18	TCA	TGGGCTTAAA	1	1		
19	CTCA	TGGGCGTAA/	1	1		
20	CA	TGGGCGTAA/	1	1		
21	AAC	TGGGCGTAA/	1	1		
22	CTCA	TGGGTTTAAA	1	1		
23	TTA					
24	CTCA	TGGGCGTAA/	1	1		
25	CA	TGGGCGTAA/	1	1		
26	CA	TGGGCTTAAA	1	1		
27	CA	TGGGCGTAA/	1	1		
28	CA	TGGGCGTAA/	1	1		
29	CA	TGGGCGTAA/	1	1		
30	CA	TGGGCTTAAA	1	1		
31	CA	TGGGCGTAA/	1	1		
32	CA	TGGGCTTAAA	1	1		
33	CA	TGGGCGTAA/	1	1		
34	CA	TGGGCTTAAA	1	1		
35	CA	TGGGCGTAA/	1	1		
36	CA	TGGGCTTAAA	1	1		
37	CA	TGGGCGTAA/	1	1		
38	CA	TGGGCTTAAA	1	1		
39	CA	TGGGCGTAA/	1	1		
40	CA	TGGGCGTAA/	1	1		
41	CA	TGGGCGTAA/	1	1		
42	CA	TGGGCGTAA/	1	1		
43	CA	TGGGCTTAAA	1	1		
44	CA	TGGGCTTAAA	1	1		
45	CA					
46	CA					
47	CA	TGGGCGTAA/	1	1		
48	CA	TGGGCGTAA/	1	1		
49	CA	TGGGCTTAAA	1	1	4	1
50	CA	TGGGTTTAAA	1	1		
51	CA	TGGGCGTAA/	1	1		
52	CA					
53	CA	TGGGCGTAA/	1	1		
54	CA					
55	CA	TGGGCGTAA/	1	1		
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TTA	TGGGCGTAA/	1	1		
TTA	TGGGTTTAAA	1	1		
CTCA	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	1	1		
T	TGCAGTTAAA	1	1		
TA	TGGGCGTAA/	1	1		
TAA	TGGGCGTAA/	1	1		
CTCA	TGGGCGTAA/	1	1		
CTCA	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	2	2		
g				6	1
CTAA	TGGGCGTAA/	1	1		
CTCA	TGGGTGTAA/	1	1		
CA	TGGGCGTAA/	1	1		
CTCA	TGGGCGTAA/	1	1		
TTGT	TGCAGTTAAA	1	1		
TA	TGGGCGTAA/	1	1		
CTCA	TGGGCTTACA	1	1		
CTCA	TGGGCGTAA/	1	1		
TCA	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	1	1		
CAA	TGGGCGTAA/	1	1		
CCA	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	1	1		
TAA	TGGGCGTAA/	1	1		
AAC	TGGGCGTAA/	1	1		
TA	TGGGCGTAA/	1	1		
p	TGGGCGTAA/	1	1	3	1
TCA	TGGGCTTAAA	1	1		
TTA	TGGGCGTAA/	1	1		
CA	TGGGCGTAA/	1	1		
CA					
CAA					
g	TGGGCGTAA/	1	1	48	0.97916667
c	TGGGCGTAA/	1	1	2	1
CTCA	TGGGCATAA/	1	1		
f	TGGGTTTAAA	1	1	6	1

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4	CTT					
5	g	TGGGCGTAA/	1	1	4	1
6	CA	TGGGCTTAAA	1	1		
7	CA	TGGGCTTAAA	1	1		
8	TA	TGGGCGTAA/	1	1		
9						
10	g	TGGGCGTAA/	1	1	29	0.82758621
11	TAA	TGGGCGTAA/	1	1		
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13	g				5	0.8
14	CGAG	TGCAGTTAAA	1	1		
15	TCA	TGGGCGTAA/	1	1		
16	TTAA	TGGGCGTAA/	1	1		
17	TCA	TGGGCGTAA/	1	1		
18	TTA	TGGGCGTAA/	1	1		
19						
20	o	TGGGCGTAA/	1	1	3	1
21	g	TGGGCGTAA/	1	1	2	1
22	TA					
23	TCA	TGGGCGTAA/	1	1		
24	f	TGGGCGTAA/	1	1	3	1
25	TTA	TGGGCTTAAA	1	1		
26	TCA	TGGGCGTAA/	1	1		
27	CTCA	TGGGCGTAA/	1	1		
28	CA	TGGGCGTAA/	1	1		
29	o	TGGGCGTAA/	1	1	4	1
30	TTA	TGGGCGTAA/	1	1		
31	TTA	TGGGTGTAA/	1	1		
32	CGG					
33	TCA	TGGGCGTAA/	1	1		
34	CTCA	TGGGCGTAA/	1	1		
35	icCG					
36	TCA	TGGGCGTAA/	1	1		
37	CTTA	TGGGCGTAA/	1	1		
38	CTTA	TGGGCGTAA/	1	1		
39	CTCA	TGGGCGTAA/	1	1		
40	TCA	TGGGCTTAAA	1	1		
41	TTA	TGGGCGTAA/	1	1		
42	CTAA	TGGGCGTAA/	1	1		
43	CTCA	TGGGCGTAA/	1	1		
44	TCA	TGGGCTTAAA	1	1		
45	TTA	TGGGCGTAA/	1	1		
46	CTAA	TGGGCGTAA/	1	1		
47	CTCA	TGGGCGTAA/	1	1		
48	TCA	TGGGCTTAAA	1	1		
49	TTA	TGGGCGTAA/	1	1		
50	CTAA	TGGGCGTAA/	1	1		
51	TTA	TGGGCGTAA/	1	1		
52	CTCA	TGGGCGTAA/	1	1		
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4	.TCA	TGGGCGTAA/	1	1
5	TCA	TGGGCGTAA/	1	1
6	TCA	TGGGCGTAA/	1	1
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8	.TCT	TGGGCGTAA/	1	1
9	ΓCA			
10				
11	.TTA	TGGGCGTAA/	1	1
12	TTA	TGGGCGTAA/	1	1
13	TTA	TGGGCGTAA/	1	1
14				
15	TCA	TGGGCTTAAA	1	1
16	.CTA	TGGGCGTAA/	1	1
17	ΓCA	TGGGCTTAAA	1	1
18				
19	iCGT			
20				
21	TTA	TGGGCGTAA/	1	1
22	ΓCA			
23	TCA	TGGGCGTAA/	1	1
24				
25	.TCA	TGGGCGTAA/	1	1
26	.ACA	TGGGCGTAA/	1	1
27				
28	.TCG	TGGGCGTAA/	1	1
29	TCA	TGGGCGTAA/	1	1
30				
31	.TCA	TGGGCGTAA/	1	1
32	.TGA	TGGGCGTAA/	1	1
33	ΓCG	TGGGCTTAAA	1	1
34				
35	.TCA	TGGGCGTAA/	1	1
36	.TCA	TGGGCGTAA/	1	1
37	.TCA	TGGGCGTAA/	1	1
38				
39	.TCA	TGGGCGTAA/	1	1
40	TCA	TGGGCGTAA/	1	1
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42	.TCA	TGGGCGTAA/	1	1
43	.TCA	TGGGCGTAA/	1	1
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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Comamonas
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Zoogloea
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Azonexus
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Thauera
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Dechloromon
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Actinobacteri	Actinobacteria		Ornithinococci	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	

Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillales Reyranella
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Proteobacteria Betaproteobacteria Rhodocyclales Rhodocyclaceae
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteria Flavobacterium
Bacteria	Actinobacteria Actinobacteria Micrococcales Intrasporangia Tetrasphaera
Bacteria	Proteobacteria Betaproteobacteria B1-7BS
Bacteria	Proteobacteria Betaproteobacteria Rhodocyclales Rhodocyclaceae Denitratisoma
Bacteria	Proteobacteria Gammaproteobacteria Xanthomonas Xanthomonadaceae
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillales Defluviicoccus
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillaceae
Bacteria	Proteobacteria Betaproteobacteria Burkholderia Oxalobacteria Massilia
Bacteria	Bacteroidetes Sphingobacteriia Sphingobacteriia env.OPS 17
Bacteria	Acidobacteria Acidobacteria Subgroup 4
Bacteria	Cyanobacteria Melainabacteres Obscuribacterales
Bacteria	Proteobacteria Betaproteobacteria
Bacteria	Planctomycetes BD7-11
Bacteria	Planctomycetes OM190

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Bacteria	Verrucomicro	Opitutae	Opitales	Opitutaceae	Opitutus
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae	
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28 waste
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Phaselicystidæ	Phaselicystis
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Eukaryota	Metazoa				
Bacteria	Chlorobi	Ignavibacteriæ	Ignavibacteriæ	BSV26	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae	Haliangium
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Stenotrophon
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Bacteroidetes	Flavobacteriæ	Flavobacteria	Flavobacteria	Chryseobacte
Bacteria	Verrucomicro	OPB35 soil group			

Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Ferruginibacte
Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	Planctomycet OM190
Bacteria	Proteobacteri Gammaprote Pseudomona Pseudomona Pseudomonas
Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae
Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomona Nitrosomonas
Bacteria	Planctomycet OM190
Bacteria	Bacteroidetes Flavobacterii Flavobacteria Flavobacteria Elizabethkingi
Bacteria	Proteobacteria
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Ferruginibacte
Bacteria	Acidobacteria Holophagae Subgroup 7
Bacteria	Proteobacteri Alphaproteob Caulobacteri Hyphomonad Woodsholea
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Actinobacteri Actinobacteri Micrococcale Microbacteriaceae
Bacteria	Proteobacteri Alphaproteob Rhizobiales
Bacteria	Acidobacteria Acidobacteria Subgroup 4
Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclaceae
Bacteria	Proteobacteri Gammaprote Xanthomona Xanthomonadaceae
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonada Leptothrix
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae

Bacteria	Proteobacteria Gammaproteobacteria	Thiothrix
Bacteria	Actinobacteria Actinobacteria Micrococcales Microbacteriales Leucobacter	
Bacteria	Proteobacteria Betaproteobacteria Hydrogenophiles Hydrogenophilaceae	
Bacteria	Proteobacteria Betaproteobacteria	
Bacteria	Cyanobacteria Chloroplast	
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillaceae Defluviicoccus	
Bacteria	Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae	
Bacteria	Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadaceae	
Bacteria	Proteobacteria Alphaproteobacteria Caulobacteriales Caulobacteriaceae Phenyllobacter	
Bacteria	Bacteroidetes Flavobacteriales Flavobacteriaceae Flavobacteriaceae Flavobacterium	
Bacteria	Acidobacteria Acidobacteria Subgroup 4	
Bacteria	Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae	
Bacteria	Proteobacteria Gammaproteobacteria	
Bacteria	Proteobacteria Betaproteobacteria Neisseriales Neisseriaceae	
Bacteria	Actinobacteria Actinobacteria	
Bacteria	Planctomycetes Planctomycetes Planctomycetes Planctomycetes Planctomyces	
Bacteria	Proteobacteria Alphaproteobacteria Rhodobacterales Rhodobacteraceae Rhodobacter	
Bacteria	Acidobacteria Acidobacteria Subgroup 3 SJA-149	
Bacteria	Chloroflexi	
Bacteria	Proteobacteria Betaproteobacteria Burkholderiales Burkholderiaceae Chitinimonas	
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillaceae Dongia	
Bacteria	Acidobacteria Acidobacteria Subgroup 3	

Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	DS-100
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Actinobacteri	Actinobacteri	PeM15	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadae Comamonas
Bacteria				
Bacteria	Proteobacteria			
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga Ferruginibacte
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	DEV007
Bacteria	Planctomycet	OM190		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia Bradyrhizobiu
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Polyangiaceae Byssovorax
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Leptospiraceae Turneriella
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona Nitrosomonas
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Nocardioideae Nocardioide
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae

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Bacteria	Chloroflexi	KD4-96		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia Bosea
Eukaryota	Basidiomycot	Tremellomyc	Tremellales	Trichosporon; Trichosporon
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga; Ferruginibacte
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobacteraceae
Bacteria	Acidobacteria	Holophagae	Subgroup 10	ABS-19
Eukaryota	Heterolobose	Tetramitia		Naegleria
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	B79
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona; Nitrosomonas
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera; SM1A02
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona Novosphingol

Bacteria	
Bacteria	Proteobacteri Alphaproteob Rhizobiales
Bacteria	Proteobacteri Alphaproteob Rhodobacteri Rhodobacteraceae
Bacteria	Acidobacteria Acidobacteria Subgroup 3 Elev-16S-1166
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Flavisolibacte
Bacteria	Gemmatimon Gemmatimon Gemmatimon Gemmatimonadaceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Proteobacteri Alphaproteobacteria
Bacteria	Proteobacteri Alphaproteob Caulobactera Caulobactera Brevundimon
Bacteria	Acidobacteria Holophagae Holophagales Holophagaceae Geothrix
Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	OC31
Bacteria	Proteobacteri Betaproteoba Rhodocyclace Rhodocyclace Thauera
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Schlesneria
Eukaryota	Euglenozoa Kinetoplastea Metakinetopl Neobodonida Neobodo
Bacteria	Proteobacteri Alphaproteob DB1-14
Bacteria	Chlorobi Chlorobia Chlorobiales SJA-28
Bacteria	Actinobacteri Actinobacteri Micrococcale Intrasporangiaceae
Bacteria	Proteobacteri Gammaprote Xanthomonas Xanthomonas Thermomona
Bacteria	Acidobacteria Acidobacteria Subgroup 4
Bacteria	Proteobacteri Alphaproteob Rhodospirilla Acetobactera Acidocella



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Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Plasticicumula
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56
Bacteria	Verrucomicro	OPB35	soil group	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Azonexus
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteri
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	SD04E11
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria Flavobacteriu
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Devosia
Bacteria	Cyanobacteri	Melainabacte	Obscuribacterales	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Proteobacteri	Alphaproteobacteria		

Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae	Ensifer
Bacteria	Spirochaetae	Spirochaetes	Spirochaetales	Leptospiraceae	Turneriella
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		Rhodoplanes
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclales	Rhodocyclaceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Nitrosomonadaceae	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	
Bacteria	Actinobacteri	Actinobacteri	Micrococcales	Microbacteriaceae	
Bacteria	Bacteroidetes				
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Chryseobacte
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Bacteria	Proteobacteri	Gammaprote	Chromatiales	Chromatiaceae	Nitrosococcus
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacte	Micropruina

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Bacteria	Planctomycet OM190
Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Candidatus Ac
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pirellula
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Proteobacteri Alphaproteob Caulobactera Hyphomonad Hirschia
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Chloroflexi Anaerolineae Anaerolineale Anaerolineaceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacteriales
Bacteria	Proteobacteri Gammaprote Xanthomonas Xanthomonas Candidatus Cc
Bacteria	Proteobacteri Alphaproteob Rhodobacter Rhodobacteraceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Proteobacteri Alphaproteob Rhodospirilla Rhodospirilla Defluviicoccus
Bacteria	Proteobacteri Betaproteoba Burkholderial Alcaligenaceae
Bacteria	Proteobacteri Betaproteoba Nitrosomonas Nitrosomonadaceae
Bacteria	Proteobacteri Gammaprote Xanthomonas Xanthomonas Stenotrophon
Bacteria	Armatimonadetes
Bacteria	Verrucomicro OPB35 soil group
Bacteria	Proteobacteri Alphaproteob Rhizobiales Methylobacter Meganema
Bacteria	Proteobacteri Alphaproteob Rickettsiales mitochondria
Bacteria	Proteobacteri Betaproteoba Burkholderial Burkholderiac Cupriavidus
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae

Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Proteobacteria			
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	KD3-93
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Planctomycet	OM190		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobactera
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae

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Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Proteobacteri Betaproteobacteria
Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 6
Bacteria	Acidobacteria Holophagae Subgroup 10 ABS-19
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri Alphaproteob Rhizobiales MNG7
Bacteria	Bacteroidetes Sphingobacte Sphingobacteriales
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Sphingobacteriaceae
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Eukaryota	Euglenozoa Kinetoplastea Metakinetopl Eubodonida Bodo
Bacteria	Actinobacteri Actinobacteri Micrococcale Microbacteri Leucobacter
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae Runella
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycetaceae
Bacteria	Proteobacteri Alphaproteob Sphingomona Sphingomona Sphingomona
Bacteria	

Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla	Defluviicoccus
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Xanthobacteraceae	
Bacteria	Planctomycet	OM190			
Bacteria	Armatimonadetes				
Bacteria	Acidobacteria	Holophagae	Subgroup 7		
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Sphingomona
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla	Ferrovibrio
Bacteria	Proteobacteri	Betaproteoba	Neisseriales	Neisseriaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Alcaligenaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 17		
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteria	Massilia
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	JTB255 marine benthic grou	

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Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla	Defluviicoccus
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Bacteria	Proteobacteri	Alphaproteob	DB1-14		
Bacteria	Candidate division	BRC1			
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20	
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiracea	Nitrospira
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Bacteroidetes				
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimon
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Pedomicrobiu
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	F0723	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteria				

Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria Flavobacteriu
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimon Gemmatimon
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Hyphomicrob
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada Comamonas
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas Rhodanobacte
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	RB41
Bacteria	Proteobacteri	Alphaproteob	Caulobacteria	Caulobacteria Phenylobacte
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria Cloacibacteriu
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Eukaryota	Tubulinea	Arcellinida	Echinamoebida	Echinamoeba
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales	
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	NS9 marine group



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8	Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymenophorea
9	Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteria Stella
10	Bacteria	Proteobacteri	Alphaproteob	Caulobacteria	Caulobacteria
11					Brevundimon
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15	Bacteria	Proteobacteri	Gammaprote	Chromatiales	Chromatiaceae Rheinheimera
16					
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19	Bacteria	Chloroflexi		Ardeenticatenia	
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22	Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	
23	Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera
24					CL500-3
25	Bacteria	Proteobacteri	Alphaproteobacteria		
26					
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28	Bacteria	Actinobacteri	Actinobacteri	PeM15	
29	Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
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35	Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
36	Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae
37	Bacteria	Planctomycet	Phycisphaera	WD2101 soil group	
38					
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45	Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
46					
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49	Bacteria	Proteobacteri	Alphaproteobacteria		
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52	Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56
53					
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56	Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Candidatus Cc
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Bacteria	Proteobacteri	Betaproteobacteria
Bacteria	Proteobacteri	Alphaproteob Rhizobiales
Bacteria	Proteobacteri	Alphaproteob Rhizobiales Bradyrhizobia Bosea
Bacteria	Proteobacteri	Alphaproteob Caulobactera Caulobactera Phenylobacte
Bacteria	Chloroflexi	TK10
Bacteria	Actinobacteri	Actinobacteri Propionibacte Propionibacte Propionicicell
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonade Comamonas
Bacteria	Proteobacteri	Alphaproteobacteria
Bacteria	Proteobacteri	Betaproteoba Burkholderial Oxalobacteraceae
Bacteria	Planctomycet	Planctomycet Planctomycet Planctomycetaceae

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Bacteria	Proteobacteri	Gammaprote	Xanthomonadales
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Comamonada Comamonas
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Burkholderiac Pandoraea
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale Rhodocyclace Denitratisoma
Bacteria	Proteobacteri	Gammaprote	Thiotrichales Thiotrichacea Thiothrix
Bacteria	Actinobacteri	Acidimicrobi	Acidimicrobiales
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal Rhodospirillal Candidatus Al
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3 SJA-149
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales Bradyrhizobia Bosea
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale Anaerolineaceae
Eukaryota	Basidiomycot	Tremellomyc	Tremellales
Bacteria	Firmicutes	Clostridia	Clostridiales Peptostrepto Incertae Sedis

Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pirellula
Bacteria	Proteobacteri Betaproteoba SC-I-84
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Schlesneria
Bacteria	Candidate division BRC1
Bacteria	Verrucomicro OPB35 soil group
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Reyranelia
Bacteria	Proteobacteri Betaproteobacteria
Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte NS11-12 marine group

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	DA111
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Pedomicrobiu
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellaceae
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	SM2D12
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteriaceae
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Proteobacteri	Gammaprote	Pseudomonadales	
Bacteria	Proteobacteria			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Pir4 lineage

Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae	
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria					
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Hyphomonad	Woodsholea
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae	
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Nocardioidac	Nocardioides
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Hyphomonad	Woodsholea

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Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacte	Propionibacte	Propionibacte
Bacteria	Proteobacteri	Alphaproteob	Caulobacteri	Hyphomonadaceae		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomycet
Eukaryota	Cercozoa	Novel Clade	Gran-3			
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Singulisphaera	
Bacteria	Proteobacteri	Gammaproteob	Enterobacteri	Enterobacteriaceae		
Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexaceae	Roseiflexus	
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrion	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Brucellaceae		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteria	Roseomonas	
Bacteria	Elusimicrobia	Elusimicrobia				
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10		

Bacteria	Planctomycet Planctomycet Planctomycet Planctomycetaceae
Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonac Candidatus Cc
Bacteria	Proteobacteri Alphaproteob Rhizobiales
Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Proteobacteri Alphaproteobacteria
Bacteria	Acidobacteria Acidobacteria Subgroup 6
Bacteria	Proteobacteri Betaproteoba TRA3-20
Bacteria	TM6
Bacteria	Proteobacteri Gammaprote Methylococc Methylococc Methylosarcir
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Gemmata
Bacteria	Proteobacteri Gammaprote Pseudomona Pseudomona Pseudomonas



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Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Sphingopyxis
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Comamonas
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Sphingobacte	Sphingobacte
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Rhodobacter
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae	Candidatus Rf
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Armatimonadetes				
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderia	Limnobacter
Bacteria	Cyanobacteri	Melainabacte	Obscuribacterales		
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiaceae	Rickettsia
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae	Simkania
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae	

Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Deltaproteobacteria		
Bacteria	Chloroflexi	Chloroflexia	Chloroflexale	Roseiflexacea Roseiflexus
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrobiaceae
Bacteria	Proteobacteri	Deltaproteob	Desulfobacte	Desulfobulba Desulfobulbus
Bacteria	Actinobacteri	Acidimicrobii	Acidimicrobia	Acidimicrobia CL500-29 mar
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida Neobodo
Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymeno Tetrahymena
Bacteria	Proteobacteri	Betaproteoba	Hydrogenoph	Hydrogenophilaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga Niabella
Bacteria	Proteobacteri	SPOTSOCT00m83		
Bacteria	Proteobacteria			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ Variovorax

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Bacteria	Proteobacteri	Gammaprote	Enterobacteri	Enterobacteriaceae
Eukaryota	Metazoa			
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales I Candidatus Ca
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob
				Hyphomicrob
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas Candidatus Cc
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteri
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Gemmata
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia Bradyrhizobiu
Bacteria	Proteobacteri	Gammaprote	Pseudomonas	Moraxellacea Acinetobacter
Eukaryota	Gracilipodida			Filamoeba
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera SM1A02
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada Aquabacteriu
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion Bdellovibrio
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Armatimonadetes			
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacte Microlunatus

Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobactera	Massilia
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Bacteroidetes	vadinHA17			
Bacteria	Proteobacteri	Gammaprote	Legionellales	Coxiellaceae	
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales I	Candidatus Cc
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteriæ	Leucobacter
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	Verrucomicrobiaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteræ	Rhodobacteræ	Amaricoccus
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10	
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera	Caulobacter
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Chloroflexi				
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		

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Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	PHOS-HE51
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona Sphingomona
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Devosia
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Dokdonella
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Armatimonadetes			
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	
Bacteria	Actinobacteri	Acidimicrobii	Acidimicrobia	Acidimicrobia CL500-29 mar
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida Neobodo
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Hyphomicrob

Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Candidatus Al

Bacteria Proteobacteri Alphaproteob Rhodobacter Rhodobacter Defluviimonas  
Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Pir4 lineage

Bacteria Actinobacteri Thermoleoph Gaiellales

Bacteria Planctomycet Phycisphaera WD2101 soil group

Eukaryota Tubulinea Arcellinida Echinamoebida Vermamoeba

Bacteria Proteobacteri Betaproteoba Burkholderiales

Bacteria Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae  
Bacteria Chlorobi Chlorobia Chlorobiales SJA-28

Bacteria Actinobacteri Actinobacteri Micrococcale Dermabacter Brachybacteri  
Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadaceae

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Bacteria      Bacteroidetes Sphingobacte Sphingobacte NS11-12 marine group

Bacteria      Bacteroidetes Sphingobacte Sphingobacte WCHB1-69

Bacteria      Bacteroidetes Flavobacteriiz Flavobacteria NS9 marine group

Bacteria      Proteobacteri Gammaprote Xanthomonac Xanthomonac Stenotrophon

Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacteriaceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales I Candidatus O
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Eukaryota	Ascomycota	Sordariomyce	Microascales	Microascaceae
Bacteria	Proteobacteri	Gammaprote	Pseudomona	Pseudomona Pseudomonas
Bacteria	Actinobacteri	Actinobacteri	Actinomyce	Actinomyce Actinomyces
Bacteria	Actinobacteri	Actinobacteri	Micromonos	Micromonos Micromonos
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteri Mesorhizobiu
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangiaceae



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Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomonadaceae
Bacteria	Proteobacteri	Deltaproteob	GR-WP33-30	
Bacteria	Acidobacteria	Holophagae	Subgroup 7	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirillaceae
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Spirochaetaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Denitratisoma
Bacteria	Proteobacteri	Gammaprote	Pseudomonas	Pseudomonas Pseudomonas
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Betaproteoba	Hydrogenoph	Hydrogenoph Thiobacillus
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Acetobacteria Roseomonas
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga Flavitalea

Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae
Bacteria	Proteobacteri	Deltaproteob	Desulfobacte	Desulfobacte
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	NS9 marine group
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae Kaistia
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Candidatus Cc
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae
Bacteria	Proteobacteri	Alphaproteobacteria		
Bacteria	Cyanobacteri	Chloroplast		
Bacteria	Proteobacteria			
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Dermatophilaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Xanthobacter Labrys
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadales Incertae

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Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Thioclava
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Novosphingol
Bacteria	Actinobacteri	Actinobacteri	Corynebacter	Mycobacteria	Mycobacteriu
Bacteria	Proteobacteri	Gammaproteobacteria			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Verrucomicro	Verrucomicro	Verrucomicrobiales	Haloferula	
Bacteria	Chlorobi	Ignavibacteri	Ignavibacteri	BSV26	
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium se
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	TA18			
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Sphingomona
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacte	Microlunatus
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Leptospiraceae	Leptospira
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Eukaryota	Ciliophora	Intramacronu	Conthreep	Colpodea	Platyophrya

Bacteria	Proteobacteri	Gammaprote	Legionellales	Coxiellaceae	Coxiella
Bacteria	Bacteroidetes				
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae	
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales		Sphingomona
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Rhodanobact
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangi	Phycococcus
Bacteria	Proteobacteri	Gammaprote	Thiotrichales	Thiotrichacea	Thiothrix
Bacteria	Proteobacteri	Gammaprote	Methylococcc	Methylococcc	Methylocaldu
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149	

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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacter
				Methylobacter
Bacteria	Proteobacteri	Gammaproteob	Xanthomonas	Xanthomonas
				Rhodanobacter
Bacteria	Actinobacteri	Thermoleoph	Solirubrobact	480-2
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteri
				Microbacteri
Bacteria				
Bacteria	Bacteroidetes	Sphingobacter	Sphingobacter	Saprospiraceae
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteri
				Leucobacter
Bacteria	Chlorobi	Chlorobia	Chlorobiales	SJA-28
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter
				Rhodobacter
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Actinobacteri	Actinobacteri	Micrococcales	

Bacteria	Proteobacteria: Betaproteobacteria: Burkholderiales: Oxalobacteraceae
Bacteria	Bacteroidetes: Sphingobacteriales: Sphingobacteriales: Chitinophagaceae
Bacteria	Planctomycetes: Planctomycetes: Planctomycetes: Planctomycetes: Planctomyces
Bacteria	Proteobacteria: Alphaproteobacteria: Rhizobiales
Bacteria	Cyanobacteria: Chloroplast
Bacteria	Planctomycetes: Phycisphaerales: Phycisphaerales: Phycisphaerales: Phycisphaerales: Phycisphaerales
Bacteria	Planctomycetes: Planctomycetes: Planctomycetes: Planctomycetes: Gemmata
Bacteria	Acidobacteria: Acidobacteria: Subgroup 4
Bacteria	Proteobacteria: Betaproteobacteria: Burkholderiales: Comamonadaceae: Comamonas
Bacteria	Actinobacteria: Actinobacteria: Frankiales: Nakamurellaceae: Nakamurella

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Bacteria	Planctomycet OM190
Bacteria	Chloroflexi Anaerolineae Anaerolineae Anaerolineaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 17
Bacteria	Actinobacteri Actinobacteri Micrococcale Microbacteri Microbacteriu
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonade Xylophilus
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillaceae
Bacteria	Proteobacteri Betaproteoba SC-I-84

Bacteria	Proteobacteri	Betaproteoba	Burkholderiales
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri	Gammaprote	Xanthomonac Xanthomonadales Incertae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales F0723
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales JG35-K1-AG5
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Pir4 lineage
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycetaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Isosphaera
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3
Bacteria	Actinobacteri	Actinobacteri	Propionibacte Propionibacteriaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Gemmata
Eukaryota	Ascomycota		
Bacteria	Proteobacteri	Alphaproteob	Sphingomona Sphingomona Sphingomona
Bacteria	SHA-109		



Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiales	Hyphomicrobiales
Eukaryota	Discosea	Flabellinia	Vannellida		

Bacteria	Actinobacteri	Acidimicrobi	Acidimicrobiales
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycetaceae

Bacteria Verrucomicro Opitutae Opitutales Opitutaceae Opitutus

Bacteria      Proteobacteria

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16 Bacteria Proteobacteria Gammaproteobacteria Xanthomonadaceae Xanthomonas Dokdonella  
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19 Bacteria Cyanobacteria Melainabacteriales Obscuribacteriales  
20 Bacteria Planctomycetes Planctomycetes Planctomycetes Planctomycetaceae  
21 Bacteria Firmicutes Clostridia Clostridiales Clostridiaceae Clostridium se  
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31 Bacteria Proteobacteria Betaproteobacteria SC-I-84  
32 Bacteria Proteobacteria Betaproteobacteria Burkholderiales Burkholderiaceae Lautropia  
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37 Bacteria Proteobacteria Betaproteobacteria Burkholderiales Oxalobacteraceae  
38 Bacteria Proteobacteria Betaproteobacteria Burkholderiales Comamonadaceae Comamonas  
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41 Bacteria Proteobacteria Betaproteobacteria Nitrosomonadaceae Nitrosomonadaceae  
42 Bacteria Proteobacteria  
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51 Bacteria Bacteroidetes Sphingobacteriales Sphingobacteriales Chitinophagaceae Ferruginibacter  
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Eukaryota	Chlorophyceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae Haliscomenot
Bacteria	Chloroflexi Anaerolineae Anaerolineale Anaerolineaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri Deltaproteob Bdellovibrion Bdellovibrion Bdellovibrio
Archaea	Euryarchaeot Methanomicr Methanomicr Methanoregu Methanolinea

Bacteria	Proteobacteri	Gammaprote	Legionellales	Coxiellaceae	Coxiella
Bacteria	Acidobacteria	Acidobacteria	Subgroup 6		
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales		
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Zoogloea
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Nocardioidea	Marmoricola
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	Clostridium se
Bacteria	Proteobacteri	Gammaprote	Aeromonada	Aeromonada	Aeromonas
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga	Flavitalea
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Pelomonas

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Gammaproteobacteria		
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Dechloromon
Bacteria	Proteobacteri	Gammaprote	Pseudomona	Moraxellacea Acinetobacter
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ Comamonas

Bacteria Acidobacteria Acidobacteria Subgroup 3

Bacteria Proteobacteria Alphaproteobacteria Rhizobiales

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Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Meganema
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	

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Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillal	Reyranella
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadales	Incertae
Bacteria	Caldiserica	Caldisericia	Caldisericales	Caldisericaceae	Caldisericum
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Blastopirellula

Archaea Euryarchaeot Methanomicr Methanosarci Methanosaet Methanosaet

Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Reyranela  
Bacteria Proteobacteri Betaproteoba Burkholderiales

Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Ferroviario

Bacteria Chloroflexi Anaerolineae Anaerolineae Anaerolineaceae

Bacteria Proteobacteri Alphaproteob Rhizobiales

Bacteria Actinobacteri Actinobacteri Micrococcale Microbacteriaceae

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Bacteria	Actinobacteri	Acidimicrobii	Acidimicrobia	Acidimicrobia	Candidatus M
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Steroidobacte

Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
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Bacteria	Firmicutes	Erysipelotrich	Erysipelotrich	Erysipelotrich	Turicibacter
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Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Eukaryota	Ascomycota	Saccharomyc	Saccharomyc	Incertae Sedi	Candida
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Defluviicoccus
Bacteria	Proteobacteri	Betaproteoba	B1-7BS		
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Gallionellaceae	Gallionella
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20	

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Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Sphingobium
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales		
Eukaryota		Chlorophyceae			
Bacteria	Proteobacteri	Alphaproteobacteria			
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	CCU22	

Bacteria Proteobacteri Gammaprote Gammaproteobacteria Incertae Sedis

Bacteria Proteobacteri Alphaproteob Rhizobiales Hyphomicrob Devosia

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Pirellula

Bacteria Firmicutes Bacilli Bacillales Bacillaceae Bacillus

Bacteria Proteobacteri Gammaprote Xanthomonadales

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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Gammaprote	Enterobacteri	Enterobacteri Escherichia-St
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae Clostridium se
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria Chryseobacte

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Flavisolibacte

Bacteria Proteobacteri Gammaprote Xanthomonac Xanthomonac Lysobacter

Bacteria Armatimonadetes

Bacteria Chloroflexi Caldilineae Caldilineales Caldilineaceae

Bacteria Chloroflexi Ardentificatonia

Bacteria Actinobacteri Actinobacteri Micrococcale Intrasporangiaceae

Bacteria Firmicutes Bacilli Lactobacillale Streptococcae Lactococcus

Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclaceae

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadaceae

Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclaceae

Bacteria Proteobacteri Alphaproteob Rhizobiales B142

Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Reyranelia



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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Chloroflexi	Thermomicro	JG30-KF-CM45	
Bacteria	Firmicutes	Clostridia	Clostridiales	PeptostreptoIncertae Sedis
Bacteria	Proteobacteri	Deltaproteob	GR-WP33-30	
Bacteria	Verrucomicro	Spartobacteri	Chthoniobact	FukuN18 freshwater group
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobiaceae
Bacteria	Actinobacteri	Thermoleoph	Solirubrobact	480-2
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Rhodoplanes

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19 Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Thauera  
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37 Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillac Defluviicoccus  
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41 Bacteria Proteobacteri Alphaproteob Rhodobacter Rhodobacter Rubellimicrob  
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51 Bacteria Proteobacteri Gammaprote Legionellales Coxiellaceae Aquicella  
52 Bacteria Bacteroidetes Flavobacteriia Flavobacteria NS9 marine group  
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Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteri	Agromyces
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Hyphomicrob

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9 Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Reyranela  
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13 Bacteria Proteobacteri Betaproteoba Nitrosomona Nitrosomona Nitrosomonas  
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Bacteria      Acidobacteria Acidobacteria Subgroup 3    SJA-149

Bacteria      Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces

Bacteria Proteobacteri Deltaproteob Bdellovibrion; Bdellovibrion; Bdellovibrio

Bacteria Chloroflexi

Bacteria Proteobacteri Alphaproteob Rhizobiales Methylosul

Bacteria Chloroflexi KD4-96

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae

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Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Defluviicoccus
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Acidobacteria	Holophagae	Subgroup 7	

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tag	Flocs Control 1	Flocs Control 2
TCAACTGGTTGTTGGGTCTTAAGTCACTCAGTA	105	174
TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAG	64822	11841
CCGACTCGGATTCAGATGAATCAAAAAGTTCAT	82	1101
<b>GATACTTGTGTTGGAGGTATTGACCCCTTCAG</b>	<b>291</b>	<b>251</b>
TCAACTAGTTGTTGCGGTGAGGAGACTCATTGAG	15627	15566
CCGACTTGGGATTGGAGGCGTGCACTTTCCGCC	35313	17284
TCAACTGGTTGTTGGGAGGGTTTCTTCTCAGTA	7075	33750
CCGACCAGGGATCGAGGACAGTCCCATGGTTGA	2823	4530
TCAACTAGGTGTTGGGTGGGTAAAACCATTTAG	6154	6077
TGCACTTGGTGTGTTGGGCCGATTAGGTTCAGTGC	3	0
TCAACTAGTTGTCGGATCTTAATAGATTTGGTA	3853	3059
CGAACTGGATGTTGGGCTCAACTTGGAGCTCAG	3711	7488
TCGACTAGTCGTTGCGAGCAGCAATGCACTGAG	3871	2018
ATGACTCGATGTTGGCGATACACAGCCAGCGTC	0	4
CCAAGTAGGGATATGTGGACGTTTGTGTTGAAGA	6573	6209
TACACTAGACTGGTGCGGTTTTGACGCCGTATC	329	620
GATACTAGCTGTTGGAGGAACTTCAGTGGCTA	0	2
TATACTTGGTGTAAGTGGACTCAACCCTAGTTG	29	13
GATACTAGCTGTTGGGAGTAATTTCAGTGGCTA	402	668
ATTACTCGTTGCTGGGAGGTAACCTTTCAGTGAC	4755	4342
ATGACTCGATGTTGGCGATATACAGCCAGCGTC	4694	4802
CGCACTAGACCGGTGCGGTTTTGACGCCGTATC	5417	3299
CCGACTAGGGATGAGTGAACGTTGCATTATCGA	2604	6731
CGAACTGGATGTTGGTCTCAACTCGGAGATCAG	3180	9777
TCGACTAGGTGTTGCGGAAGGAGACTTCTTGAG	2279	5578
ATGGCTGGATGTTGGCGATACACCGTCAGCGTC	0	0
ATGACTTGGTGTGTGCGGTTTTAAGTCCCGGCG	16	17
TCAACTAGTTGTCGGGTCTGTTTAAGGATTTGG	2835	1682
CCGACTAGCGATCCGCCGGCGTGGTTTCGATGA	3989	2249
CCGACTAGGGATCGGTCCACGTTATTTTTTGAC	832	14567
ATTACTCGATGTGTGCGATACACGGCACGCGTC	957	869
ATTACTCGCTGCTAGATGGCAACGTTTAGTGGC	4	7
AGCACTAGACGTCGGGCGGGTGACCGTCCGGTG	232	500
CTAACGATGGACGCGGGGAATCAGAACATCACA	0	0
ATTACTCGATGTTGGCGATACACAGCCAGCGTC	18	60
ATTACTCGACATACGCGATACACAGTGTGTGTC	2014	2315
ATCACTCGATGTTGGCGATACACAGCCAGCGTC	21	12



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4	TATGCTAGACCGGTGCGGTTTTGACGCCGTATC	1844	3245
5	AATGCTAGACGTTGGCGAGCATGCTCGTCAGTG	67	87
6	CCGACCGGGGATGGGGAGAGGTAATACCTTAAC	3772	1732
7	CCGACCAAGGATAAGAGGTCGTAATTATCTTGA	1826	2609
8	TGAACTTGCGTGGTGGGTAAACTCCATCAG	1272	1985
9	CTAACTCGTTTTTGGGGCGTAAGTTTCAGAGAC	1099	8394
10	AGAACTAGGTGTCGTGGGTGTTGACCCCCGCGG	1392	1027
11	CTTACTCGACGTACGGCCCTGGCGGCTGTGCGT	1614	2222
12	ATTACTCGTTTTTGGGTTTTATGATTCAGAGAC	0	0
13	CCGACTCGGATTCAGATGAATATTAAGTTCAT	161	3969
14	ATTACTCGACATACGCGATACACTGTGTGTGTC	1389	2440
15	AGCACTAGACGTCGGGTGGGTGACCGTCCGGTG	458	479
16	ATCACTAGATTTTGGCCGTATGGTCAGAGTCCA	0	0
17	TACGCTAGATCGGTGCGGGTTTGACCCCGTATC	955	2624
18	AGAACTGGACGTTGGGAGGAATTCGCCTCTTAG	1039	2171
19	GATACTCGACATCAGCGATACACTGTTGGTGTGTC	1289	1461
20	ATTACTCGATGTTGGCGATACACGGCCAGCGTC	5	6
21	TCAACTAGTTGTCGGGTCTTATTGGGCTTGTA	1540	1034
22	TCTACTAGTTGTCGGGTCTTAATTGACTTGTA	277	5686
23	ATTACTCGCTGCTGGGAGGTAACTTTCAGTGGC	364	268
24	TAAACTTGCGTCGGTGGCTTAAACTCCATCGG	118	44
25	CATACTTGGTGTGAGCCATTCATTTGGTTCGTG	1356	1606
26	TTCACTAGTGTTGCGGGTATTTATTTATCTGCA	1082	986
27	TCGACTAAGGATGATAAAATATTAATGAATGA	94	38
28	CTGACTTGGTGCCCCCGGTTTAAAGTCCGGGGG	684	1832
29	CTAACGATGGACGCGGGGAATCAGTCTCTTTTT	0	0
30	CCGACTAGGGATCGGTGGACGTTGCATAGCATG	10	2769
31	CACACTAGGTCTTGGCGGATTCGACCCCCCAG	789	835
32	ATTACTCGGTGCTAGCGATATACGGTTAGTGCC	2	11
33	CCGACTCAGGATTGGCAGACGTCTTTACCGACT	6	42
34	CTGACTTGGTGTTCAGGTTTTAAATCTTGGGG	1284	1285
35	CCAACTAGGGATACGTGGACGTTTGTTCGAAGA	1298	1084
36	TCAACTGGTTGTTGGACGGCTTGCTGTTCACTA	1075	682
37	CTAACGATGGACGCGGGGAATCAGATCACTTTG	0	0
38	AACACTAGATGTTACGGGTATTGACCCCTGTAG	671	1755
39	GATACTAGCTGTTGGGAGCAATTTCACTGGCTA	0	3
40	AGAGCTAGTTGTCGGCACGCATGCGTGTCGGTG	719	704
41	TACGCTGAGTTAGAGCGGCTCTGACGCCGTTTCG	849	1204
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ATTACTCGCTGCTAGAGGGCAACTTTTAGTGGC	1300	473
TACGCTAGACTGGTGCGGTTTTGAAGCCGTATC	470	459
GATACTAGGCGTATCGGGTATCGACCCCTGATG	610	1255
TCAACTAGTTGTCGGGCCTTAATAGGTTTGTA	725	924
CAAACCTGGTGTAGGCAGTTCAGTCTGTCTGTG	975	1208
AGCACTAGACGCTGGTGGGGTGACCTGCCGGTG	3	6
CCAACTAGTTGTTGGGGAAGGAGACTTCCTTAG	558	1310
TTTACTTGCTGTTTGGCTTTCGGGCTGAGTGGC	0	0
CCGACTTGGTGTTCGCGGTTTTAAGTCCGGGGG	765	965
CTAACGATGGACGCGGGGAATCAGTCTCTCTT	0	0
CCGACCAGCGATTGGGAGACGTTACATGGATGA	1047	429
CTAACGATGGACGCGGGGAATCAGAAAGAAATT	0	0
AGTGCTAGATGCTGTGGGTATTGACCCCCGCGG	6	15
TCAACTAGTTGTTGGATCCGTTTAAGGATTTGG	1165	878
CGCACTAGGTGACGGGACCTCTCACGGTCTCGC	453	1037
GATACTCGACATACGCGATACACTGTGTGTGTC	731	544
ATCACTAGATTTTGGCCGTATAGTCAGAGTCCA	0	0
TAAACTCGACATTAGCGATATACAGTTAGTGTC	680	814
CCGACCAGGGATTGGGAGACGTTAAATTTTATA	1088	225
CCGACTAGGGATCGGTCCACGTTATTTTCTGAC	297	2718
TCGACTAGCCGTTGGAATCCTTGAGATTTTAGT	48	2462
CATACTCGCTGTTGGGTTATAGATTACGCGGCT	0	0
TCAACTAGTTGTTGGATCCATTTAAGGATTTAG	691	773
AATGCCAGCCGTTGGGGAGCTTGCTCTTCAGTG	469	334
CGAACTAGGTGTTGGGGAAGGAGACTTCTTTAG	439	888
CGAACTGGATGTTGGGTGCAATTTGGCACGCAG	217	397
TCAACTGGTTGTTGGAGGGGTTTCTCTTCAGTA	537	913
CCGACTGGGTGTGGGAGGTGAACACCTTCTGTG	0	4
CTCACTTGCTGTTCCCGATTACTCGGGAGTGGC	2	0
CCGACCAGGGATCGGAGAGTGTTACATGGATGA	501	685
AATGCCAGACGTCGGGCAGCATGCTGTTCCGGTG	395	392
AGCACTAGACGCTGGGGGGGTGACCTTTCGGTG	9	10
CTAACGATGGACGCGGGGAATCAGAAAGAATAC	0	0
ATTGCTAGTTGTCGGGAAGTTTACTTCTCGGTG	0	0
ATCACTCGAGATCGGCGATATACGGTCGGTCTC	17	29
GGTGCTGGATGTCGGGGGGCTTGCCCTTCGGTG	440	717
CTAACGATGGACGCGGGGAATCAGATCACAATC	0	0
GATACTCGACATACGCGATATACTGTGTGTGTC	438	612

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4	ATTACTAGATTTTGGCCGCAAGGTCAGAGTCCA	0	0
5	AATGCCAGTCGTCGGCAAGCATGCTTGTCGGTG	671	371
6	GATACTCGACATTTGCGATACACTGTAAGTGTC	460	447
7			
8	CGAACTGGACGTTGGTCTCAACTTGGAGATCAG	0	0
9	AACACTTGGTGTGGAGGGAGTTGACCCCTTCCG	481	538
10			
11	CGCATTTGCTGTGGGCGGAATCGACCCCGCCCG	8	8
12	TCGACCAGACGTCGGGGGTGTCAACCCCTCCGG	0	0
13	AGAGCTAGGTGTCGTGGGTGTTGACCCCGCGG	54	49
14			
15	TCGACTGGGTGTCGGCGATTAAAAACGTCGGT	243	562
16	AGCACTAGGTGTTGGTCCCTTTGGGGCCAGTGC	274	690
17			
18	GATGCTGGATGTCGGGGGGCTTGCCCCTCGGTG	0	0
19	CCGACCAGGGATATGAGGTAATTAATAGATTAT	0	8
20			
21	AATGCCAGACGTCGGCAAGCATGCTTGTCGGTG	291	67
22	CTAACGATGGACGCGGGGAATCAGAGAGAAGAA	0	0
23			
24	GCGACCGAGATTCAGGAAATGCCCAAGATGGCT	266	828
25	GGTACTAGGCGTCGGGGGGAGCGACCCCTCGG	353	430
26			
27	AGTGCTAGACGTCGGGGGGTTCCTCTCGGTGT	0	0
28	CCAGTTAGGGATTGGCAGGGTCTCGTTACGTCC	0	0
29			
30	TGAACTTGGCGTCGGTGGCTTAAACACCATCGG	289	201
31	AGGACTAGGTATTGGCTCGCAAGAGTCGGTGCC	502	337
32	CTAACTCGTTTTTGGGACGTAAGTTTCAGAGAC	175	1495
33			
34	AGTGCTAGTTGTCGGCATGCATGCATGTCGGTG	215	609
35	GGTGCTAGGTGTCGCGGGCTTTGACCCTCGCGG	293	510
36			
37	TCAACTAGTTGTTGGATCTTAATAGATTTGGTA	220	190
38	CATACTTGGTGTGGGTGATTCATTTTATCCGTG	225	229
39			
40	ATAACTAGCTGTCCGGGCTCTCAGAGCTTGGGT	0	0
41	TACTACTAGACCGGTGCGGTTTTGACGCCGTATC	288	492
42			
43	AGAACTAGGTAGTGGGTCCGACCTGGGCACACT	212	561
44	GATACTCGACATTTGCGATATACTGTAAGTGTC	82	41
45	CCAAGTGTCTTTTAGATGCGGTTACTCATATGA	87	77
46			
47	GGTGCTTGGTGTGCGGGGTATCGACCCCTCCGG	242	464
48	CCAACCAAAGATAAGAGGTTGTAAATACAAAAA	349	211
49			
50	AATACTCGGTGTCGGGTGCGAAGATTCGGCGCC	422	414
51			
52	TCAACTAGTTGTCGGGTCTTATTAGATTTGGTA	318	345
53	AATGCCAGCCGTCGGAAAGCTTGCTTTTCGGTG	0	4
54			
55	GATGCTAGGCGTTGGCAGACTCAATCCTGTCCG	0	0
56			
57	AGTACTAGGTAGAGGAGGCCTCGTCGCCTTCTC	0	0
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59	AGTGCTAGATATTTAGATATTTATTCTGAGTGT	0	0
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4	TGTGCTAGACGTTGGGAAGCCTAGCTTCTCAGT	13	20
5	ATAACTAGCTGTCCGGGCACATGGTGCTTGGGT	28	64
6	CTCATTAGGTATGGGGGGTATCGACCCCTCCCG	78	571
7	ATCACTCGATGTGTGCGATACACAGCACGCGTC	259	418
8	AGTACTAGGTGTAGGAGGAGTGAAATCCTTCTG	221	423
9	CTCACTCGACGTACGGTAGGAATATTGTGCGTC	0	0
10	GATACTTGGTGTTGGAGGTATTGACCCCTTCAG	63	67
11	CATACTAGGCGTAGCGGAATTTCAATTCTGCTG	0	2
12	ATTACTCGTTGCTGGGGAGCAATTTCCAGTGAC	262	456
13	GGCACTAGGTCCTTGGGGGAGCGACCCCGTGAG	176	200
14	ATCACTAGATTTTGGTCGCAAGATCAGAGTCCA	224	576
15	TCAACTGGTTGTTGGGAATTCATTTTCTCAGTA	543	166
16	AGTGCTAGATGTTGGGGTTTTACCTCAGTGTCG	0	0
17	GGCGCTAGGTGTGGGACTCATTCCACGAGTTCC	11	12
18	GGCACTAGCTTGGGGTCTCCCTGTGTGATCCCA	95	86
19	ATAACTAGCTGTCCGGGCACTTGGTGCTTGGGT	122	145
20	CCGACCAGGGATTGGGGGCGGTTAAAGTTCTAT	38	43
21	AACACTTGGTGTTCCGGGAGTTGACCCCGGAG	150	755
22	GGTACTAGGCGTCGGGGGGAGCGACCCTCCCGG	205	392
23	AGTGCTAGATGTTGGTTGACTTATCAATCGGTG	0	0
24	TTTACTTGCTGTGTGATCTTCGGATTGCGTGGC	41	21
25	TATGCTTGATGTTGGGGTAGCAATACCTCAGTG	7	20
26	GATGCTAGCCGTTGGACAGCTTGCTGTTCAAGT	85	434
27	CATACTTGGTGTTGGGCAGTTCATTCTGTCCGTG	220	348
28	CCGACCAAGGATCATGAGATGTTAAATATAAAT	422	16
29	CGCACTAGACTGGTGCGGTTTTGACGCCGTATC	39	49
30	ATCGCTGGGTGTGGGGGGTTTTACTCCCCCG	229	201
31	TCGACTAGGTGTGCGCGCCTAAAAACCGTCGGT	90	490
32	CATACTTGGTGTTGAGTCCTTCATTGGATTCTG	137	260
33	TCAACTAGTTGTCGGATCTTAATAGGTTTGGTA	96	130
34	CGGACTTGGTGTTGGGCAGTTCAGTCTGTCTGTG	209	189
35	CGCACTAGGTCGGGGAGGCTTGACGCCCTCCTG	0	6
36	CACGTTTGGTGTTGGGCGCAATCGACCGCGTCCG	234	186
37	GATACTCGACATTTGCGATACACAGTAAGTGTC	227	167
38	CGCACTGGATCGGAGCAACTCTCACGTTGTTTC	0	0
39	AGTGCTGGATGTGCGGAAGCCTAGCTTTTCGGT	140	392
40	TGTGCTGGATCACGGCGGCTCTGACGCCGTCCG	170	308
41	TATACTTGGTGTAATTGGAATCAACCCTAATTG	0	0
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4	TTTACTTGCTGTTTCTGGGCAACTGGGAGTGGC	124	243
5	CGAACTGGATGTTGGGTGCAACTAGGCACTCAG	16	31
6	CCGACCAGCCATTTCGGAGACGTTACATTTTATG	109	56
7	CCGACTTGGTGTCCCCGGTTTTAAGTCCGGGGG	167	278
8	TACATTGTATGGTGGGAATCTTGCATTTTCACT	11	624
9	AATGCCAGTCGTCGGGCAGCATGCTGTTCCGGTG	10	5
10	AGTACTAGGTGTGGGTGGAGTCAAATCTATCCG	179	251
11	ATTGCTAGTTGTCTGGGCTGCATGCAGTTCGGTG	27	62
12	AGTGCTAGGTGCTGCGGGTATTGACCCCTGCGG	223	247
13	TGCACTAGGTGTTGGGGACTTCGTCTTCAGCGC	0	0
14	TCAACTAGTTGTCTGGATCTGTTTAAGGATTTGG	22	7
15	AATACTAGGTGTTGGTGGCTTTAACCCCACTAG	0	0
16	ATCACTCGTCATTGGCGATATACGGTCAGTGAC	0	0
17	AATGCCAGCCGTCGGGGAGCTTGCTCTTCGGTG	28	105
18	ACCCCCATGAATTGGGGAGTATTTTGGTTCTTT	0	0
19	TGTGCTGGATGTTGGGTGGCCTAGCCATTCACT	7	15
20	TATACTAGTTGTTGGTGGTTTCAACGCCATCAG	115	180
21	TGCGCTGGATGTTGGGTGACCTAGTCACTCAGT	133	217
22	AATACTAGGCGTAGGGAGAGTCAAATCTTTCTG	76	299
23	GATACTCGACATACGCGATACACAGTGTGTGTC	332	166
24	AATGCTAGACGTTGGGGAGCTTAGCTCTTCAGT	0	0
25	AATACTCGGTGTTGGTCCGCAAGGATCAGCGCC	174	291
26	GCCCCCATGAATTGGGGAGTATTTGGTATCAGG	0	0
27	TTCCTAGTTTTGCGGGATGTTTTATTCTGCA	16	144
28	CACACTTGGTGTGAGCGATTCAATTCGTTCTGTG	152	290
29	ATAACTAGCTGCCAGGGCTCTTAGAGCTTTGGT	7	6
30	AGTGCTAGTTGTTAGCCCGGCTTGAGCCGGGTT	0	0
31	TACATTGTATGGTGGGGATCTTGCATTCTCACT	0	0
32	CCAACTAGATGTTTCGGTTGGGGAAACTCAACAG	0	0
33	CTGACTAGGTGTCTGGCGATTAAAAACCGCCGGT	95	346
34	ACACCCATGAATTGGGGAGTACTTTGGTCGCCT	0	0
35	AACACTCGACGTTGGCCCTGTATGGGGTCAGTG	0	0
36	AGCACTAGACGTTGGGCGGGTGACCGCCCGGTG	2	9
37	GATACTAGCTGTTTGGAGCAATCTGAGTGGCTA	286	138
38	GGTGCTAGACGTTGGCGGGCTTGCTCGTCAGTG	217	216
39	AATGCCAGCCGTTAGTGGGTTTACTCACTAGTG	102	367
40	ATCACTCGATGTTGGCGATACACTGTCAGCGTC	172	229
41	GGCACTAGGTCCTTGGGGGAGCGACCCCTTGAG	181	228
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4	AGAACTAGGTATCGTGGGTGTTGACCCCCGCGG	169	211
5	TCAACTAGTTGTCGGACCTTAATAGGTTTGGTA	127	210
6	GGTGCTGGATGTCGGGGGGCTTGCCCCTCGGTG	144	239
7			
8	TCAACTGGCTGTTGGGAGAGAAATCTTTCAGTA	0	0
9	TCAACTGGTTGTTGGGTTTTAATTAACCTCAGTA	171	227
10			
11	CTTACTCGTTGTTTGGCTTTCGGGCTGAGTGAC	0	0
12	ATTACTCGATGTGTGCGATACTGTACGCGTC	173	246
13	TCTACTAGTTGTCGGGACTTAATTGTCTTGGTA	0	0
14			
15	CACACTAGGTTTTGGAGGATTCGACCCCTTCAG	87	114
16	TCGACTAGTTGTTGGGGAAGGTAACCTCCTTAG	36	54
17			
18	AGAGCTAGCCGTTGGAGGATTTATCCTTCAGTG	0	0
19	CACGTTTGCTGTAAGAGGAATCGACCCCTTTTG	160	153
20	CTAACTCGTTTTTGGTATTTTCGGTATCAGAGAC	20	508
21			
22	CACACTAGGTCTTGGCGGATTCGACCCACCAG	82	111
23	AATATTAATTGTCGAATTTTCGGTAATTTAGTT	174	192
24			
25	TGCACTAGACTGGTGCGGTTTTGACGCCGTATC	136	174
26	CTAACGATGGACGCGGGGAATCAGAACACAAAA	0	0
27			
28	CAAACCTGGTGTGCGCCCTTCATTGGGTGCGTG	205	173
29	AATACTTGGTGTCTGGAGGTTTAATACTCCGGG	136	75
30			
31	TCTACTAGTTGTTGGGGTAGCAATACCTTAGTA	0	0
32	CCAACCAAAGATAAGAGGTTGTAAATATTATAA	126	94
33			
34	GATACTAGCTGTTGGAGGTAACCTCAGTGGCTA	0	0
35	TTTACTTGCTGTTTGGCTTTCGGGCCGAGTGGC	148	130
36			
37	GATGCTAGCCGTCGGCAAGCTTGCTTGTCGGTG	61	74
38	TCGACTAGTTGTTGGGGAAGGAACTTCCTTAG	96	234
39			
40	CCGACTAGGGATCGGTGGATGTTTTTATTGACG	222	93
41	TCAACTAGTTGTCGGGCCTTATTGGGCTTGGTA	112	114
42			
43	GGCACTAGCTTGGGGTCTCCCTGTGGGATCCCA	96	172
44	TAAACTCGACATTAGCGATATACTGTTAGTGTC	52	174
45			
46	AACACTTGGTGTGGTGGGAGTTGACCCCTGCCG	168	112
47	GAAGCTAGCCGTCGGCAAGTTTACTTGTCGGTG	32	54
48			
49	ATTACTCGTTCTCGGCGATATACGGTCGGGGAC	79	90
50			
51	CCGACCAGTGATTGGGCGACGTTGCATGGATGA	2	6
52			
53	AGTGCTAGTTGTTGGGAAGTTTACTTCTCAGTG	0	0
54			
55	TCAACTAGTTGTCGGGCCTTAATAGGCTTGGTA	145	90
56			
57	GGCACTGGGTAGGGGGCTCGCCGATGGGCTCCC	76	88
58			
59	CGTGCTGGACGTTGGCCAGCCTAGCTGGTCGGT	6	21
60			
	CACGTTTGCTGTAAAAGGAATCGACCCCTTTTG	122	139

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4	TGTGCTGAATCACGGCAGCTCTGACGCTGTCGG	160	115
5	TCAACTGGCTGTTGGGAGAGCAATCTCTTAGTA	0	0
6	TACGTTGAGTTAGAGCGGCTCTGACGCCGTTCTG	97	177
7	TCGACTGGTTGTTGGGGGTTTGACACTCTCAGT	148	140
8	ATTACTCGCTGCTGGGGGGCAACCTTCAGTGGC	82	38
9	TCAACTGGTTGTTGAGGGGGTTCCTCCTCAGTA	93	169
10	CCGACTAGGGATTGGTGGGTGTTATTAGCGACT	4	15
11	TGCACTAGATCGGTGCCGGTTTGACCCGGTACC	11	10
12	AATGTAAAAAAAAAATAATTTTTATTTTATTT	0	0
13	CACGCTTGATTACGACGGCTCTGACGCCGCCGG	96	120
14	TCAACTAGCTGTCTGTAGATTAAGGTTTATAGG	179	102
15	CATACTAGATCCGGGAGACACTCATCGTAATCC	91	187
16	TGCACTTGGCCTGGGAGGATTCGACCCCTTCCG	143	120
17	TCAACTAGTTGTCGGACCTTATTGGGTTTGTA	134	110
18	CGCATTTGCTGTGAGCGGAATCGACCCCGCTCG	80	86
19	CACATTGGACCGGTGCTGCTCTGACGTAGTATT	0	0
20	AGAACTAGACGGTGGGGAGGTCACCTCTCGCTG	0	0
21	CGAACTAGGTGTTGGGGAAGGAGACTTTCTTAG	74	145
22	ATCACTCGAGATTGGCGATATACGGTCAGTCTC	2	7
23	AGCACTAGACGTCGGGCGGGTGACCGCCCGGTG	0	0
24	GGCACTGGGCAGGGGGGATACCTATGGTCTCT	63	170
25	GGTGCTAGCCGTTGGAAAGCTTGCTTTTCAGTG	0	0
26	TCGACTAGTTGTTTCGGAGCAGCAATGCACTGAG	121	158
27	TGTGCTAGTTGCTGGATCGCTTAGCGTTTCAGT	0	0
28	TTTACTTGCTGTTTCGGGCTTAGGCTTGAGTGGC	65	74
29	TCAACTGGTTGTTGGGGAAGGTAACCTCCTTAG	76	129
30	ATTACTCGCTGTTGGCGATACACTGTCAGCGGC	94	54
31	GATACTCGACATCAGCGATACACAGTTGGTGTC	25	40
32	GGAAGTAGATGTAGGGACCATTCCACGGTTTCT	66	160
33	GATGCTAGCCGTTGGGGGGATACCCTTCAGTGG	115	75
34	ATTACTCGTTGTTGGCGATATACTGTCAGCGAC	54	71
35	TTTACTTGCTGTTTGTTCCTTCGGAATGAGTGGC	79	90
36	CCGGTTAGGGATTGGCAGGGTATCGTTACGTCT	0	0
37	AGAGCTAGCCGTTGGAGGGTTTACCCTTCAGTG	61	181
38	CCGACTCAGGATGGGCAGTCCGTTGTTTCCGAC	0	0
39	AGAACTAGACGTTGGGAGGGTCAGCCTCTCAGT	84	142
40	TACTAGACCGGTGCGGCTCTGACGCCGTATT	64	122
41	GATACTAGATGTTGAACAGATCGACCTGTGCAG	0	2
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4	CCGACCAGGGATATGAGGTATATAAAATATTAT	0	0
5	CCGACCAGGGATATGAGGTAAATAAAATATTAT	0	5
6	AACACTTGGTGTGGGGGGAGTTGACCCCTTCCG	6	24
7	TAACTGGACCGGTGCGATTTTGACGTTGTATC	5	21
8	AGCACTGGAGGAGGGAGGCTTCGGCCTTCTTTC	160	43
9	CAGACTCGGTGTCCACTCTCGCAAGGGAGGGGG	2	13
10	AATGCCAGCCGTCGGGAAGCTTGCTTTTCGGTG	0	0
11	TGTGCTAGACGTTGGGGGGTTCGCCCTCCGGTGT	6	2
12	GATGCTAGCCGTTGGGGGGTACCCTCCAGTGG	0	0
13	GATACTAGCTGTTGGGGGTAACCTCAGTGGCTA	101	101
14	ATGACTGGGTGTGCGGCGATTAAAAACCGTCGGT	66	134
15	AGAGCTAGCCGTCGGCAAGTTTACTTGTCGGTG	86	46
16	TATACTCGACATCAGCGATACACTGTTGGTGTC	19	122
17	AATACTAGGTGTAGGTCGTGTCAAACGGTCTG	34	75
18	CCGACCAGGGATATGAGGTAGAAATTGATTAT	0	2
19	GGTGCTAGGTGTGCGGGGCATTGACCCCTGCGG	0	0
20	CGAACTGGATGTTGGGTGCAACTTGGCACCCAG	0	0
21	CCGACTAGGGATTGGGAGGTTACTTACCTCTCA	120	92
22	GATGCTAGCCGTTGGCGAGCTTGCTCGTCAGTG	61	105
23	AATGCCAGCCGTTGGGGAGCTTGCTCCTCAGTG	0	10
24	TCAACTAGTTGTGCGGGGAAGCAATTCCTTGGA	106	95
25	TATGCTTGGTGTGTTGGCTCTTTAGAGTCAGTGCC	0	0
26	TCAACTAGGTGTTGGGAGGGTTAAACCCTTTAG	49	14
27	TATGCTTGGTGTGTTGGGGCAGCAATGCTTCAGTG	0	91
28	ATAACTCGCTGTTGGTGTTTTGCATCAGTGGCT	170	56
29	GGTGCTAGGTGTGCGGGGCTTTGACCCCTGCGG	27	214
30	AATACTAGGTGTGAGTGGTGTCAAAGCCATTTCG	0	0
31	GAAGCTAGCCGTTGGCAAGTTTACTTGTCGGTG	62	87
32	CTAACTCGATGTTTGGGCGTAAGTTTGAGCATC	0	21
33	GATACTAAGTGTGCGGCGGGTTACCGCCGGTGCC	44	79
34	TCAACTAGTTGTTGGGCCTTAATAGGCTTGGA	14	39
35	CGGACTTGGTGTAGGCAGTTCAGTCTGTCTGTG	58	110
36	ATTACTCGATGTTTGGCGATACACTGTAAGCGTC	85	42
37	GGTGCTAGATGTGCGGGAGCTTGCTCTTCGGTG	74	114
38	CTAACTCGTTTTTGGGTTTTTCGGATTCAGAGAC	3	406
39	AATACTAGACGTTGGGGTTAACTCAGTGTCGC	0	0
40	GGAAGTAGATGTAGGGCCTGTTCCACGGGTTCT	2	5
41	GGCACTTGATGTGCGGGGTTTCTACCCCTGCGG	63	114
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4	TTTACTTGCTGTTGGGGGCAACCTTAGTAGCGA	0	0
5	TCAACTAGCTGTTGGGGCCTTCGGGCCTTGGTA	0	0
6	GGTGCTAGGCGTCGGGGGGAGCGACCCCTTCGG	82	78
7	ATGACTAGTTGTTGGAGGAGTTAAATCCTTTAG	85	100
8	TGCGCTAGACGTTGCCGGACCTAGTTCGGCAGT	5	20
9	AATACTAGGTGTAGGTGGTGTCAAACTATCTG	11	18
10	CCAGCTGGATGTTTCGTACCTCGAAAGGGGTATG	0	0
11	AGCACTGGGTAGAGGTGGTAGCTGATGCCTCCT	0	0
12	GATACTAGTTGTTTGGAGCAATCTGAGTGACTA	2	4
13	AATGCTAGTTGTCAGTAAGTATACTTATTGGTG	78	117
14	CCGACCAGGGATCCGGAGAAGTTACGTGGATGA	33	4
15	CAGACTAGGCGTGGGGGGAGTTGACCCCTCCG	44	65
16	GGCGCTAGGTGTGGGGAACATTCCACGTTCTCC	92	63
17	TCAACTAGTTGTTGGATGGGTAAAACCATTTAG	0	0
18	AACACTCGCTGTTGGCGATAAACGGTCAGCGGC	0	0
19	GATACTAGCTGTTTCGGAGCAATCTGAGTGGCTA	149	98
20	GGCACTGGACGCCGGAGGGGTGACCTTTCGGTG	0	3
21	ATTACTCGATGTTGGCGATATACTGTCAGCGTC	91	56
22	CTTACTTGCTGTTCCCGATTTATCGGGAGTGGC	0	0
23	TCAACTGGTTGTTGGGTCTTGACTGACTCAGTA	101	38
24	CCGACTATGAATAGGATATCGTTTTAAGAAGGG	87	47
25	CCGACCAAGGATTCGGAGAAGTTACGTGGATGA	101	35
26	CACACTTGGTCGGAGAGGTTAGACGCCTTTCCG	48	117
27	ATTACTCGCTGCTAGGAGGTAACTTTTAGTGGC	70	13
28	TGTGCTAGTTGTTGGGCAGCTTAGCTGTTCACT	0	0
29	AGAGCTAGTTGTCAGTAAGCATGCTTATTGGTG	0	0
30	TGCACTAGGGAGAGGATGGGTCCTAACTCATTC	0	0
31	AGCGCTAGACGTTGGACGGAATGTTCACTGTCTG	80	76
32	TATGCTTGGTGTTGGGTCGCAAGACTCAGTGCC	0	0
33	GGTGCTAGATGTTGGGAGGCTTGCTTCTCGGTG	51	98
34	GATACTAGCTGTTGGATTTATTTTCAGTGGTTA	0	0
35	TTTACTCGACGTCCGGCCCCTGCGGCCGTGCGT	69	69
36	ACACCCATGAATTGGGGAGTACCTCCCGACGTG	0	0
37	CCGACTCGGATTCAGATGAATCAAAAAAGTTCA	0	0
38	GGTGCTAGATGTTGGGAAGCTTGCTTCTCGGTG	55	76
39	TTTACTTGCTGTTCTGCACTACGCGGGAGTGG	43	78
40	TCAACTGGTTGTTGGGTCTTCACTGACTCAGTA	11	12
41	AATGCTAGGTGTTGGGGATTACTCCTCAGTAC	0	0
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CACACTTGGTGTGGGCCATTCAATTTGGTCTGTG	64	81
ATTGCTAGTTGTTGGGAAGTTTACTTCTCGGTG	21	75
AGCGCTAGACGTGGGGCAGGTGACTGCTCGGTG	69	63
ATCACTAGATTTTGGTCGCGAGATCAGAGTCCA	124	32
ATTACTCGTTGTTGGCGATACACTGTCAGCGAC	48	64
CACGCTTGGTGTGGGAAGGTTGACCCCTTCTG	0	0
AGCACTGGATCGGAGAGCCCTCCATAGCTTTCC	19	34
CATATTTGGTGTGGGTCATTGAGTTGATCCGTG	42	86
CTAGCTGGGTGTTGAGGGGGGAAACCCCTCGG	74	69
ATTACTCGACATACGTGATACACTATGTGTGTC	0	0
AGCACTGGGCGGAAGGAAGTTCGCTTCTTTCTG	0	0
ATTACTCGTTGTTGGCGATATAAAGTCAGCGAC	12	14
TAACTTGGTGTGCGGTGGCTTAACTCCTTCGG	0	0
CTGACTTGGTGTCCCCGGTTTTAAGTCCGGGGG	49	59
TTTACTTGCTGTTTGGGCTATATGCCTGAGTGG	41	82
TGTGCTAGACGTGCGGAAGCCTAGCTTCTCGGT	38	41
AACACTAGGTGTGGGTGGGTTCAAAACCATCTG	47	64
TCAACTAGGCGTAGGAGGTTATAAACCCCTTCT	69	80
AATACTCGGCATCTGGTGGCCGATCTTCGGCGG	45	63
TCAACTGGTTGTTGGGAAGGTTCTTCTCAGTA	22	63
TCAACTGGGTGTGCGGTAGTTTTACTAGCGGT	49	82
CCGACTCGGATTCAGATGAATCAAAAGTTCATT	0	0
GAAGCTAGCCGTCAGTCAGCTTGCTGAGTGGTG	50	79
TTCACTAGGCGTTGGGGTCGCAAGACCTCAGTG	0	0
TCAACTAGCCGTTGGGAGCTTTAAAGTTCTTAG	39	74
AGTGCTAGCTGTTGGGTCCTTGAGGCTCGATGG	20	93
TATACTAGATGTTGGGGGTTTCAACGCCCTCAG	0	30
CCGACCAGGGATCGGAGACAGTTACATGGATGA	57	39
AGTGCTAGGTGTCGTGGGTATTGACCCCCGCGG	2	186
TGCGCTGGATGTTGGGGCTCTTAGAGCTTCAGT	36	61
TGTGCTAGACGTGCGAAGGCTTGCCTTTCGGTG	0	0
CTTACTCGACGTCCGCCCCCTGCGGTGCTGCGT	62	64
TTAACTGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
GGCGCTAGGTGTGGGATCCATTCCACGGGTTCC	40	85
ATTACTCGATGTGTGCGATATACAGCACGCGTC	50	70
ACAAC TAGATGTTGGGAGGGTCTGCCTTCCGGT	32	65
GATACTAGGCGTAAGAGGTATCGACCCCTCTTG	22	84
AGCACTAGACGTGCGGCGGGTGACTGCTCGGTG	35	74

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4	TGTGCTAGCTGTTGGTGCTTACGGCATCGGCGG	0	0
5	TCAACTGGTTGTTGGGCCTTCGCTGGCTCAGTA	5	9
6	TCGACCAGACGTCGGGGGAGTCAACCCCTCCGG	14	89
7	AATGCTTGGTGTCTGGAGTGTTAATTCTCTGGG	47	43
8	TCAACTAGGTGTTGGGAGGGTTAAACCTTTAGT	21	6
9	GATGCTAGATGTCGCGGGTATTGACCCCTGCGG	32	63
10	TCAACTAGCCGTTGGGATCATTGAAGGTCTTAG	13	13
11	AGAGCTAGTTGTCGGCATGCATGCATGTCGGTG	30	78
12	CACACTAGATCGGAGTCGCTCTGACGCGCCTCT	0	2
13	TCAACTAGTTGTCGGGTCTGTTCAAGGATTTGG	25	10
14	ATCACTCGTGATTGGCGATATACGGTCAGTCAC	0	0
15	CGAACTGGATGTTGGGTGCAACTTGGCACTCAG	29	100
16	AGCACTAGTCCGTGGGGACTTTCACATCCTCTC	20	38
17	CCGACCAGGGATTCTGAAGATATCCTTTATTTAA	0	0
18	GACACTAGGTGTAGGTAGAGTTAAATCTATCTG	6	26
19	CGCACTGGACCGGTGCGGTTTTGACGCCGTATC	58	38
20	AATACTTGGTGTCTGGAGTTTTTATCCTCCGGG	60	36
21	GACCCTAAATTTAATTTAAGCGAAAGCGCAAAG	88	31
22	GATACTAGCTGTTGGGGGCAACTTCAGTGGCTA	66	32
23	AGCACTGGGGGAGGGAGGTTTCGGCCTTCTTTC	26	72
24	GGTACTAGGCGTTCGGGGGGAGCGACCCTCTCGG	27	58
25	ACCCCCATGAATTGGGGAGTATTTGGTCGGTCA	0	2
26	TCGACCAGGCGTTCGGGGGTATCAACCCCTCGG	4	17
27	AGTACTAGGTGTTCGGGGGTATCGACCCCTCGG	28	53
28	ATCACTCGTTGCTGGGGGGTAACCTTCAGTGAC	11	5
29	GATACTAGGCGTATGGGGTATCGACCCCCCATG	19	88
30	CTCACTAGGTGTTGGGGAAGCGATTCTTGGA	12	93
31	GGTGCTAGGTGTTCGCGGGCTTTGACTCCTGCGG	74	34
32	CCGACCAGAGATTGTAAGACGTTGAATATAAAG	57	40
33	CCGACCAGGGATATGAGGTAATATTTGTTTTAT	0	0
34	TCAACTAGTTGTTGGGGATTCAATTCCTTAGTA	56	93
35	AGTGCTAGTTGTTGGGGGGTTTACCTCTCAGTG	0	0
36	GATACTTGGTGTGTGGGGTTCTCAAAGTCCCCG	29	50
37	AGGACTAGGTATCGGCAATTTATTGTCGGTGCC	47	44
38	TCGACCAGACGTCGGAGGTATCTATCCCTTCGG	28	59
39	GGTGCTAGCCATATCGGGTGTTGACCCTTAGGT	13	53
40	CACACTAGATCGGTGCGGTTTTGACGCCGTATC	47	56
41	GGTGCTAGGTGTCAGGGGCTTTGACCCCTCTGG	21	55
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4	AGTGCTAGTTGTCGGGGTCTTTGACTTCGGTGG	0	0
5	GATACTCGACATTTGCGATAAACTGTAAGTGTC	44	21
6	CCGACCAGGGATATGAGGTATTTAGATTATTAT	0	10
7			
8	CCGACCAGGGATATGAGGTAGAAATTATTATAT	0	0
9	CACGTTTGCTGTAAGAGGAATCGACCCCTCTTG	39	53
10	AGAACTAGATGTTGGGAGGGTTTTGCCTCTCAG	24	60
11	AGTGCTAGATGTTGTGGGTATTGACCCCCGCAG	0	0
12	GGTGCTAGACGTTGGCGAGCTTGCTCGTCAGTG	27	45
13	ACACCCATGAATTGGGGAGTTTGTTGCGGGGTT	0	0
14	TTTACTTGCTGTTCTGCATTAAGTGGGAGTGG	13	25
15	CCGACCAGGGATATGAGGTAAATAGTATATTAT	0	0
16	CGAACTGGATGTTGGGTTCAACTTGGAACCCAG	0	0
17			
18	CGAACTAGCTTTTTGGTTTAGGATTAGGAGGCT	94	26
19	TCAACTAGTTGTTGGGAGGGTTTCTTCTCAGTA	3	2
20	AGCACTAGACCGGAGAACCCTCCACAGTTTTTC	0	7
21	TCAACTGGTTGTTGGGTGGGTTTCTACTCAGTA	0	0
22	CCGACTAGGGATCGGGCGGCGTTTCAATTAAGTA	20	53
23	TCAACTGGTTGTTGGGTCTTAATTGACTCAGTA	0	0
24	GATACTAATTGTGAGAGGTATCGACCCCTCTCG	0	0
25	ATTACTCGATGTTGGCGATACACTGTCAGCGTC	50	24
26	AGTGCTAGACGTTGGAGGGTATCCTTCAGTGTT	0	0
27	TCTACTAGTTGTCGGGTTTTAATTAAGTTGGTA	29	92
28	AGTGCTAGACGTTGGGAAGCTTAGCTTTTCAGT	19	31
29	AATACTAGGTGTGGGTGGAGTGAAATCCATCTG	42	54
30	TGCGCTAGGTGTAGGAGGTATCGACCCCTTCTG	11	5
31	ATCACTGGGTGTTCTGGGGAGCGATCTCTGAGTA	12	55
32	TATACTAGTTGTTGGCGGTTTCAACGCCGTCAG	0	0
33	CACACTTGGTGTGGGTGATTCATTTATCCGTG	39	37
34	TCAACTGGTTGTTGGGTTTTAACTGACTCAGTA	0	0
35	TCAATTGGTTGTTGGGTCTTAAGTACTCAGTA	0	0
36	TCAACTGGTTGTTGGGTCTTAAGTACTTAGTA	0	0
37	GATACTAGATGTCGGGGGTTCTTACCCCTCCGG	0	0
38	CCGACTAGGGATCGGTCCACGTTATTATTGAC	16	132
39	TATACTAGGTGCGGGAGGTATCGACCCCTTCCG	0	0
40	CCAACCAAAGATAAGAGGTTGTAAAAATTATAA	16	13
41	GGTGCTAGGTGTCACGGGTATTGACCCCTGTGG	3	4
42	CCGACTAGGGATCGGACGATGTTATTTCTTGAC	14	141
43	GGCACTAGGTAGGGGGCTCGCCGATGGGCTCCC	5	10
44			
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4	AATGTTAGCCGTTGGGGAGTTTACTCTTCGGTG	0	2
5	GGCACTGGCTAGAGGTGACCCTGCGTCGTCTCT	18	42
6	AGTGCTAGGCGGTGGAGGATTTTGACCCCTTCG	14	54
7	CTTACTCGTTGTTTGTCTTCGGGATGAGTGAC	0	0
8	AATGCTAGACGTGGTGGGTCTTGACCCCCGCCG	0	0
9	TCAACTGGTTGTTGAGTGGGTTTCTACTCAGTA	25	39
10	ATCACTGGGTGTTCTGGGGAGCGATCTCTGGGTA	0	0
11	GATGCTAGCCGTCAGCAAGCATGCTTGTTGGTG	32	47
12	TCAACTAGTTGTCGGGTCTTAATAGGCTTGTA	49	19
13	CCGACCAGGGATATGAGGTAAAAAGTATTATTA	0	0
14	TGCACTAGGTGCTGGGGCGGATGCCTCAGTGCC	0	0
15	TCAACTAGCCGTTGGGTTCGTAAATGAGCTTAG	38	22
16	GGTGCTCGGTGTCGCGGGTATCGACCCCTGCGG	23	37
17	TCTACTAGTTGTTGGTGGAGTGAAATCCATCAG	0	0
18	GATGCTAGCTGTTCTGGGGGTTCCTCCCTGAGTAG	0	89
19	ATCACTCGATGTTGGCATTATGTCAGCGTCCA	8	77
20	CCGACCAGGGATCCGGAGAGTTTGCATGGATGA	8	10
21	TACTACTGGGTGTTGAGTCGGGGGAAGCTCGACGG	0	0
22	GACTACTAGGTGTTGGTGGTATCAACCCCGCCAG	30	36
23	TCAACTGGTTGTTGGGAATTTACTTTCTCAGTA	0	0
24	TCAACTGGTTGTTGGGTCTTAAGTATTGAGTA	0	0
25	GGTACTTGGTGTGGAGGTATTGACCCCTTCAG	0	0
26	AGCACTGGAGGGGGGCGGGTTCGCCCTTCCCC	17	44
27	AACACTAGGTGTGAGCGGTGTCAAAGCCGTTG	33	42
28	CCGACCAGGGATATGAGGTAAATAATTAGATTA	0	0
29	TCAACTGGCTGTTGGGAGAGCAATCTCTTGTA	0	0
30	CCAACCAAAGATAAGAGGTTGTAAATACAAGAG	8	5
31	GGTGCTAGATGTCACGGGCTTTGACCCCTGTGG	6	39
32	AGTGCTAGACGTTGGGAAGCCTAGCTTTTCAGT	4	13
33	CTGACTTGGTGTCCCGGGTCTTAAGTCCCGGGG	35	18
34	GATACTTGGTGTGTGGGGTATTAAGTCCCTACG	14	13
35	CGCATTAGACCGGTGCAGGTCTGACCCTGTATT	17	28
36	TGCGCTAGACGTTGACGGACCTAGTTCGCCAGT	15	30
37	CCGACCAGGGATATGAGGTATATAAATTATTAT	0	0
38	CGAACTGGATGTTGGGTGCAACTAGGCACCCAG	0	0
39	TATGCTTGGTGTGGATCTTTGATTGAGTGCCG	0	0
40	CACGTTTGCTGTGGGCGGATTCGACCCCGTCCG	26	34
41	GGCGCTAGGTGTGGGACTCATTTACGAGTTCT	19	41
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4	AATGCCAGACGTCGGCAGGCATGCCTGTCGGTG	0	0
5	AGCACTTGGTAGAAATCGCTCCGATGGCGACTT	25	26
6	TCAACTAGGTGTTGGGTGGGTAAACCATTTAG	24	19
7	ATTACTCGACATTGGCGATAAACTGATCAGTGT	0	0
8	TCGACCAGGCGTCGGAGGTATCAACCCCTTCGG	16	29
9	AGAACTGAGCGGGGGGAGGCTTGCCTCTCCCGG	9	10
10	GATGCTAGCTGATGGGACTTCTACCGTCTCGTT	0	3
11	AGTGCTAGATGTCGGGGAGCTTAGCTCTTCGGT	19	48
12	CGGACTTGGTGTGGGCAGTTCAGTCTGTCCGTG	13	10
13	CCGACCAGGGATCGGGGAACGTTATCGTCGACG	49	4
14	AACACTAGGTGTAGGTGATGTGAAAGTTATCTG	0	0
15	ATCACTCGATGTTGGCGATACACGGCCAGCGTC	17	27
16	AGAACTAGACGATGGTGTCTTGAGGCATCAGT	26	4
17	CGCACTAGATCGGTGCAGGTCTGACCCTGTATC	27	24
18	TGTGCTGGGCGTCGGGGGGCTTGCCCCTCGGTG	17	27
19	TGCACTTGGCCTGGGAGGATTAGACCCCTTCCG	29	28
20	GGCGCTAGGTGTGGGGCTCTTCCACGAGTTCC	13	25
21	AGTACTAGTGGGGAGGTCCGCGAGGGCTTCTC	20	28
22	AATACTAGGTGTCTGGGCGTGTCAAAACGGTCGG	14	37
23	AGTGCTAGATGTCGGATTTTCGGATTTCGGTGTC	0	0
24	AGCGCTGGGTGTAGGGGGTATGAACCCCCCTG	12	37
25	TCAACTGGTTGTTGGTCTTAACTGACTCAGTAA	0	0
26	CCAACCAAAGATAAGAGGTTGTAAATACAAGAA	22	20
27	AATGCTAGCCGTTGGTCAGCATGCTGATCGGTG	0	0
28	TATACTTGGTGTAGCCGGACTCAACCCTGGCTG	47	17
29	CATGCTAGATGTCGGTCTGTCAAAGGATCGGTG	0	0
30	TATACTTGATGTAGTTGGGCTCAACCCTGACTG	2	2
31	TTTACTTGCTGTTTGCCCCTTGAGGGTGAGTGG	25	69
32	CGCACTAGGTCTGGGGAGGCTGACGCCCTCCTGG	0	0
33	AATACTAGGCGTAGGTGGAGTGAAATCCATCTG	21	27
34	CCGACTAGGGCTGAGTCTTTTTAGATTTCGGACC	0	0
35	ATCACTCGTGATCGGCGATATACGGCCGGTCAC	15	43
36	TCAACTGGTTGTTGGGTATTTACTTACTCAGTA	0	0
37	GATGCTCGCCCTATGGAGGTCTTAAAGCCTTTG	14	48
38	TCAACTAGTTGTCGGGTCTTAATTGACTTGGTA	16	23
39	CGCATTTGAGGTGGGAGGATTCGACCCCTTCCG	13	47
40	AGTACTGAATTGAAGGGTCCTTCATAGCCCTTC	5	12
41	CGAACTGGATGTTGGGAGCAACTAGGCTCTCAG	25	17
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4	GGCGCTAGGTGTGGGGCTCATTCCACGAGCTCT	0	0
5	TTTACTTGCTGTTTGTATTTCCGGTATGAGTGGC	8	21
6	TCGACTAGCCGTTGGGATCCTTGAGATCTTAGT	4	77
7	CCGACCAGGGATATGAGTAGTATATTTCAATTAG	0	3
8	TCAACTAGTTGTCGGATCTTAACTGATTTGGTA	4	8
9	ATTGCTAGTTGTCGGCACGCATGCGTGTCGGTG	24	36
10	CATACTTGGTGTAGTTGGACTCAACCCCGACTG	37	6
11	CCGACCAGGGATATGAGTAGTATATTTCAATTA	0	13
12	TCAACTGGTTGTTGGTTCTTAACTGACTCAGTA	0	0
13	TCAACTGGTTGTTGGGAATTAGTTTTCTCAGTA	0	33
14	GGTGCTGGGTGTCGCGGGTATTGACCCCCGCGG	5	25
15	GGCACTGGGCAGGGGGGATACTTATGGTCCTCT	28	16
16	AATACTAGATTTGGTGGGTCTTGACCCCCGCCG	49	5
17	GATGCTAGCCGTCGGATAGCTTGCTATTCGGTG	26	24
18	GATGCTAGGTGTTGGCGGATTTAACCCTGCCAG	24	27
19	TAGATTAGGTGTCGGGGGAGTCGAACCCCTTCGG	0	0
20	AGTACTAGGTGTTGGGGGTATCGACCCCCTCAG	8	8
21	GATGCTAGGTGTGGGTGGTATTGACCCCATCCG	11	30
22	GGCGCTAGGTGTGGGGAACCTTCCACGTTCTCC	15	23
23	CAGACTAGGCGTGGGGGGACTTGACCCCCTCCG	12	21
24	CCGACCAGGGATGGGCGGGCGTTGAATCCTGAG	10	38
25	CTAACTCGATGTTTGGATTAGGTTTGAGCATC	6	42
26	AGCACTAGTCCGTGGGAACCCTCACATTTTCTC	13	41
27	TTTACTTGCTGTTCCGGCTTATGTTGGAGTGGC	0	2
28	AGTGCTAGTTGTTGGGTCTTAGAACTCAGTGA	0	16
29	CCGACCAGGGATATGAGGTAATTGTTATTATAT	0	0
30	CACACTAGGTGACGCGAACTCTGACGTTTGCGC	0	0
31	TCAACTAGCCGTTGGGAGCCTTGAGCTCTTAGT	12	10
32	TTGGCCTAGGATCGGAGGATGTTAATAGACGAC	0	0
33	TCTACTAGCTGTTTCGTGACCTTGTGTCGTGAGT	0	0
34	GATGCTAGGTGTTGTGGGTATTGACCCCTGCAG	12	42
35	AGCACTGGATTGGAGGGTCCTCCATAGCCTTCC	7	28
36	CTTACTAGCTGTTTGGTAGGAATATTGAGCGGC	6	73
37	CGAACTAGGTGTTGGGGGAGGAGACTTCCTTAG	0	7
38	AGTACTAGGTGTAGGGGGAGTGAAATCCTTCTG	18	25
39	GGCACTAGGTGTGGGTCTCAACCAACGAGATCC	0	5
40	GGGACTAGGTGCTTGGGGGAGCGACCCCTCGAG	33	9
41	AGAGCTAGCCGTTGGGAAGTTTACTTCTCAGTG	0	0
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4	AGTGCTAGCCGCTGGGACTGTTACCGTCTCGGT	6	13
5	CACACTAGGTCTTAGCGGATTGACCCCACTAG	21	25
6	AATGCCAGTCGTCGGGCAGTATACTGTTCCGGTG	21	18
7	ACACCCATGAATTGGGGAGTATTTGGTAGGCCGG	0	0
8	GATGCTAGCTGTTGGGGGGTTACCTCTCAGTAG	0	0
9	AGTGCTAGACGTTGGCCCCTTCGGGGTCAAGTGT	29	18
10	TCAACTGGTTGTTGGGAGGGTTCCTTCTCAGTA	13	32
11	TGTGCTAGTTCTTGGGCAGCTTAGCTGTTCCGGG	0	0
12	AGTGCTAGACGTTGGGGAACTTAGTTCCTTGGT	0	0
13	GGGACTAGGTGCTTGGGGGAACGACCCCCCGGG	0	0
14	CACACTAGATGACGGGGCCTCTCACGGCGCCGC	11	29
15	GATACTAGGTGTGGGAGGTATCGACTCCTTCCG	0	0
16	CACACTTGGTGCAGACGGGCTCAACCCTGTCTG	17	36
17	AATGCTAGCCGTTGGGAAGTTTACTTCTCCGTG	0	0
18	AGAACTAGGTAGTAGACTTGACTTGGGTTTACT	18	21
19	CTGACTTGGTGTCCCCGGTTTTAAGTCCAGGGG	21	23
20	CCGACTAGGGATTGGAAGGCTACGTACCTTTCA	0	0
21	TATGCTTGGTGTCTGGGGTAGAAATATCTCGGTG	0	70
22	GATACTTGTGTTGGTGGTATTGACCCCATCAG	6	28
23	AGTACTAGTGGGGAGGGAGTTCGCCTCCTTTCC	12	20
24	CCGACTAGGGATCGGACGATGTTACATTTTTGA	0	25
25	GGCGCTAGGTGTGGGGCTCGTTCCACGAGTTCC	6	17
26	AGAACTAGATGTTGGGAGGTATAACCTCTCAGT	0	0
27	GGTACTAGCTTGGGGTCTCCCTGTGTGATCCCA	0	0
28	TTAACTAGGTGTTGGGAGGGTTAAACCTTTTAG	10	2
29	TCAACTAGCTGTTGGTCATATGAATGTGATTAG	16	21
30	AATACTCGGCATCTGGCGGCCGATCTTCGGCGG	0	0
31	TCAACTGGTTGTTGGGTCTTAACCGACTCAGTA	0	0
32	CGAACTGGACGTTGGGCACACTTAGGTGCTCAG	7	8
33	GGGACTAGGTGCTTGGGGGAACGACCCCTCGAG	0	0
34	CCGACCAGGGATATGAGTAGTATATTTCAACAG	0	5
35	TCAACTAGTTGTCGGGTCTTATTGGACTTGCTA	14	11
36	CATACTTGGTGTGGGAGGATTCGACCCCTCCTG	0	0
37	AATGCTTGGTGTCTGGGGTTTTATATTCCCCGG	36	13
38	CACACTAGGCTTGAGGACCTCTTACGGATCTCG	12	23
39	CACGTTTGGTGTGGGAGGATTCGACCCCTTCCG	26	14
40	TATGCTTGGTGTGGGATTTATCTCAGTGCCGA	0	6
41	TACGCTAGATCGGTGCGGTTTTGACGCCGTATC	15	18
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4	ATAACTAGATGTTTGC	0	0
5	ATACTAGACGTGCGGTGGGTGACCGCTCGGTG	7	27
6	AGCACTGGAGGGGAGGGGCTTCGGCCTTTTCCC	7	9
7			
8	CCAAGTAGCGATTAGCTGCTGTTAATTAAACGA	6	37
9	CCGACTTGGATTGAGATGAATCAAAAAGTTCAT	0	0
10			
11	AATACTCGGCATCTTTCGACCGAGCTTCGGCCG	13	20
12	CCGACTAGGGATGAGTGAGCGTTGCATTATCGA	15	30
13	CTGACTTGGTGTCCCGGGTTTGAAGTCCCGGGG	19	19
14			
15	ATAACTCGCTGCTGGGGGGTAACCTTCAGTGGC	16	17
16	GGCACTAGGTGCTTGGGGGAGCGACCCCCTGAG	22	16
17			
18	TACGCTAGATCGGTGCAGGTCTGACCCTGTATC	14	12
19	GTGACTAGGTGTGGCTGGCTCAAGGGCTGGTCG	9	13
20			
21	CCGGCGGGGCGCGGGGGGGGCCGAGGGAGGCGCT	0	0
22			
23	TATACTAGATGTAGTCGGACTCAACCCCGACTG	22	12
24	GAAGCTAGCCGTTGGCAGGTTTACCTGTCGGTG	0	0
25	ATCACTAGACGTTAGTCTCACTCTGTGAGATTA	29	5
26	GGCACTAGGCAAGGGAGGTACCTATGTCTTTCC	0	0
27			
28	TCAACTAGTTGTTGGATCTATTTAAAGATTTGG	14	17
29	TCAACTGTTGTTGGGTCTTAACTGACTCAGTAA	0	0
30			
31	TGTACTTGATGTAGCTAGGCTCAACCCTGGCTG	21	13
32	TATACTAGGTGTAGCCGGACTCAACCCTGGCTG	0	0
33	AACACTGGGCGGGAGAAGGTTGCTTTTCCGG	6	14
34	GGTACTAGGTTTGGTGGGTCTTGACCCCCGCCG	7	23
35			
36	GGTACTAGGCTTCGTGGGAATTGACCCCTGCGG	0	0
37	CGCACTAGGTTCTGAAGGTCTCTGACGATCCTCG	5	9
38			
39	GATACTAGACGTGGTGGGTCTTGACCCCTGCCG	0	0
40	CCAACCAAAGATAAGAGGTTGTAAAAACAAGAA	7	3
41			
42	CCAACCGAGTATTTGGGAAGACACTATCCCAGC	0	0
43	GGTACTAGGTGTTGACCGTATCGACCCGGTCAG	0	0
44			
45	ATAACTAGCTGTCCGGGTACTTGGTACTTGGGT	17	38
46	TCAACTGGTTGTTGAGAGGGTTCCTTCTCAGTA	18	8
47	AGTGCTAGTCGTTGGGGGTACCCATTCCCTCAG	0	0
48			
49	CTGACTCGGATTGAGATGAATCAAAAAGTTCAT	0	0
50	CCGACTGTAGATTAGAAGACGTTATTCAAGGAA	12	12
51			
52	AATACTCGATGTTGGCGATATACAGTCAGCGTC	6	31
53	GGTACTAGGTGTCTGGGGGAGCGACCCCCTGGG	24	12
54			
55	TATACTTGATGTAGTTAGGCTCAACCCTGACTG	0	2
56	TCAACTGGTTGTTGGGAGTTTCTTCTCAGTAAC	0	37
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AGTACTGGGCGGGAGGGGGTTTCCCTTTTCTGC	11	18
AATGCTAGGTGTTGGTGGGTACCATCAGTGCC	0	0
AATACTCGTTGTTGGAGGTATTGACCCCTTCAG	0	0
CCGACCAAGTTTTTCGAGGAATTCTATTGTTACC	0	0
TTTACTTGCTGTTCCGACTTAGGTTGGAGTGGC	23	16
ATCACTGGGTGTTGGGAGAGCGATCTTCTAGTA	0	4
AGTGCTAGACGCTGTGGGTATTGACCCCTGCGG	0	0
CCAGCTGGGTGTTCAAGTTGGGGAAACCAACGG	0	2
CCGACTCGGATTCGGATGAATCAAAAAGTTCAT	0	0
CCGACCAGGGATATGAGTTGTTAAGATTATGTG	27	2
CCGACCAGGGATATGAGGTATTTAAAAGATTAT	0	0
TCAACTAGGTGTTGGAGGGTTAAACCTTTTAGT	8	2
CCGACTCGGATTCAGATGAATTA AAAAGTTCAT	0	0
GATGCTAGGTGTTGGAGGACTTAACCCCTCCTG	0	5
TCACTGGGTGTTCAAGTCGGGGAAGCCTGACGG	0	0
TCACTAGATCGGTGCCGGTTTGACCCGGTACC	3	0
TCAACTAGCCGTTGGGTCCATTGAAGGGCTTAG	0	0
CGCACTTGCTGTAAGAGGATTCGAACCCTTTTG	21	4
CCGACCAGGGATATGAGGTATTATATTATTTAT	0	0
CACACTAGGTCTTGACGGATTCGATCCCGCCAG	0	0
CCGACCAGGGATATGAGGTAAAAAGATTATTAT	0	0
TACGCTAGACTGGTGCGGTTTTACGCCGTATC	8	18
AGTGCTAGTTGTTGGGAAGTTAGTTCTCGGTGA	0	23
CCGACTAGGGATCGGACGATGTTATTTTTTGAC	0	6
CGAACTGGACGTTGGGAGCAACTTGGCTCTCAG	13	13
CCGACTAGGGATGGGTGAACGTTGCTTATCGAC	0	0
GGTGCTAGCCATATCGGGTGTTGACCCAAAGGT	0	0
AGTGCTGGGTGTTGTGGGTACGACCTGCAGCG	0	0
TCAACTGGTTGTTGGGGATTAATTTTCTCAGTA	8	24
AACACTAGACGTTGGGCGGGTGACCGCCCGGTG	0	0
GATACTAGGTGTAGGAGGTCATTAACCCCTTCT	7	20
TCAACTGGTTGTTGGGTCTTAGCTGACTCAGTA	0	0
CCGACTCGGATTCAGATGAATCAAAAGGTTCAT	0	0
CCGACCAGGGATATGAGGATCTTTATTTATACT	0	0
GGCGCTAGGTGTGGGGCTCATTCCACGAGTTCC	6	16
AATGCTAGCTGATGGGGCTTCTACCGCTTCGTT	0	0
CCGACCAGGGATATGAGGTATTTAATAGATTAT	0	9
CATACTTGGTGTTGGGTCTTCACTGGATCCGTG	0	0

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4	CTTACTCGTTGTTTGATCTAAGGATTGAGTGAC	4	8
5	TAAACTTGGCGTTGGTGGCTTAAACACCATCAG	0	0
6	AGTGCTAGTTGTCGGCAGGCATGCCTGTCGGTG	0	29
7	CCAACTGGGTGTTCTGTCTCCCGCAAGGGAGGGG	0	0
8	CCGACTCGGGATCGGCTGGAATAAATGTCCAGT	0	0
9	TCGACTAGGTGTTCTGGTGAGGAGACTCATTGAG	17	7
10	GGCACTAGGTGTGGGGAACATTCCACGTTCTCC	10	17
11	TCGACTAGGTGTTCTGGGGAGGAGACTCCTTGAG	4	10
12	TCGACTGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
13	AGCACTGGGCGGGAGAAGGTTGCCTTTTCCGG	8	17
14	TCAACTAGCCGTTGGAATCCTTGAGATTTTAGT	0	60
15	AGAGCTAGACGTCGGGCGGCTTGCCGTTCTGGTG	10	16
16	TCAACTAGGTGTTGGGAGGGTTAACCTTTTAGT	10	0
17	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAGT	2	0
18	CGTATTTGAGGTGGGAGGATTCGACCCCTTCCG	9	13
19	CCGACCAGGGATATGAGGATTTTTATTTATACT	0	0
20	CCGACCAGGGATATGAGTAGTATATTTCACTAG	0	8
21	GAAGCTAGCCGTTGGTAAGTTTACTTATCGGTG	0	0
22	GATACTAGGTGTCCGGGCTTCTGGCCTGGGTGC	0	0
23	CCGACTAGGGATTGGCGGACGTTTTTGCATGAC	0	0
24	CACACTAGATCGGTGCGGGTTTCACCCCGTATT	16	11
25	CCAACTAGATGTTCTGGCTGGGGAAACCCAGCAG	0	3
26	CCAACTGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
27	AGTGCTAGATGTCTGGGGGGCTTGCCCTTCGGTG	11	14
28	GGCACTAGGCCCTTGGGGGAGCGACCCCTGAG	0	0
29	CCGACTCGGATTTAGATGAATCAAAAAGTTCAT	0	2
30	TCAATTAGGTGTTGGGAGGGTTAAACCTTTTAG	5	0
31	TCAACTAGGTGGTGATTGTGTCGATCCAAGCAC	0	0
32	CAAATTAAGATTAGTTTTTTTTAAACAAGTCTT	6	49
33	TCGACTAGCCGTCGGGCTCATTATTGAGAGTTT	21	3
34	TCGACTTTGGATTAGGAAATATTACATGGATGA	22	6
35	ATCGCTAGCTTTTCGGAGTATCGACCCTCTGAG	0	0
36	AGCGCTAGGTGTTGTGGGTGTTGACCCCCGAG	15	13
37	TTTACTCGTTGTGCGGGAGCAATTTTGCGCAAC	0	0
38	GGTACTAGGTGTGGACTTACATGGGTTCACAG	9	18
39	GGTACTAGGTAGTGGACTTACATGGGTTCACTG	8	15
40	AGTGCTAGATGTTGGGGCTTTTTGGTCTCGGCG	0	0
41	TATACTTGGTGTAGCTGGACTCAACCCCGGCTG	0	3
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4	AGTACTAGGTGTAGGGGGTATCGACCCCCTCTG	13	18
5	ATTACTCGTTGTTGGCGATATGACAGTCAGCGA	24	2
6	TCAACTGGTTGGGTCTTAAGTACTCAGTAACG	0	0
7	AATGCTAGTTGTTAGGAAGTTTACTTCTTAGTG	10	7
8	CGAGCTGGATGTCTGGAGGGCTTGCCCTTCGGTG	5	16
9	AGAACTAGATGTTGGAGGGGGGAACCCTGCAGTA	4	3
10	TAGACTAGATGTGCGCGTCACTACGGTGACGTG	0	0
11	AGAACTAGGTGTCTAGGTGTTGACCCCTGCGG	0	36
12	TTCACCTCGCTGTTGGATTTTACATTCAGTGGCT	0	0
13	CCGACTCGGATTCAGATGAATCAAAAAGTTTAT	0	0
14	AATGCTAGACGTTGGGACCCCTAGGGTTTCAGT	0	0
15	TCAACTGGTTGTTGGGTCCTAACTGACTCAGTA	0	2
16	AATACTCGGCATCTTTCGACCGATTTTCGGCCG	8	18
17	AGTGTTTTATATACATATTTGTATATGATAGTT	0	23
18	GGCACTGGGTAGAGGGCTCTCCGATGGGCTCTC	6	9
19	ATTACTCGCTGTTTTCGATACACAGTAAGCGGC	13	21
20	TCAACTAGGTGTTGGGAGGGTTAACTTTTTAG	10	0
21	AGTGCTAGATGTCTGGCTCCTTTAGGGGTCGGTG	0	0
22	AGCACTTATCTGGGGATCCTCCCATAGGTTCCC	0	0
23	CGCATTTGCTGTAAGAGGAATCGACCCCTTTTG	14	14
24	GATGCTAGGCGTCTGGGGGTATCGACCCCCCGG	9	25
25	GATACTTGTGTTAGTGGTATTGACCCCACTAG	0	0
26	GGTGCTAGATGTCTGGGGGGCTTGCCCTTCGGTG	6	23
27	TCAACTGGTTGTTGGAAGGGTAACCTTTTAGTA	0	0
28	GGTGCTAGCTGTTCTGGGGGTTCCCCCTGAGTAG	6	5
29	ATAGCTAGATGTGTGAGGTATTGACCCCTTACG	0	0
30	TATACTTGGTGTAAGTGAATCAACCCTAGTTG	13	5
31	ATAACTAGCTGTCCGGGTTTCATAGAACTTGGGT	14	14
32	CCGATTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
33	CCGACCAGGGATATGAGGATTCTTATTTATACT	0	0
34	GGTACTTGGTAGAAATCGCTCCGATGGCGACTT	7	15
35	TCAACTGGTTGTTGGGTCTTAAGTACTCGGTA	0	0
36	AGCACTGGGCGGGAGGGGGTTTCCCTTTTCTGC	0	2
37	AGAACTGGACGTTGGGAGGAATTTGCCTCTTAG	5	14
38	CCGACCAGGGATATGAGTTGTTAGGATTACATG	21	0
39	TCAACTGGTTGTTGGGTCTTAAGTACTGACCCAGTA	0	0
40	TCAACTAGGTGTCCACTCGGCCACGGTCGAGGG	10	11
41	GATGCTAGCCGTCGGTGGGCATGCCCTTCGGTG	7	10
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4	TCAACTAGGTGTTGGGAGGGTTAACCCCTTTAG	3	1
5	CACACTAGACCGATGCGGCTCTGACGCCGTATT	0	0
6	GATGCTAGACGTAAGAGGTATCGACCCCTCTTG	13	11
7	AATGTAAAAAAAAAATAATTTTTATTTTATTTT	0	0
8			
9	GATGCTAGATGTACGGGTATTGACCCCTGTGG	8	16
10	TACGCTAGATCGGCCAGGCTCTGACGTCTGGCT	2	14
11	AGCACTAGACTGTGGGGACCCTCACATCCTCTC	2	6
12	AGAACTAGGTAGTAGACTTGACATGGGTTTACT	9	16
13	ATAACTAGCTGTCCGGGCTCATAGAGCTTGGGT	8	17
14			
15	TCAACCGGTTGTTGGGTCTTAAGTACTCAGTA	0	0
16	TATGCTTGGTGTGGGGCAGCAATGTTCCAGTG	2	0
17			
18	TATACTTGGTGTAGTTGGACTCAACCCCGACTG	0	0
19			
20	CGAACTAGATGTGCGGGAGGGTCAGCCTCCCGGT	9	8
21	GGTACTAGGTTGCGGGCTTACATGGGCTCGCAG	9	9
22			
23	CCGGTTAGGGATTGGCAGGGTTTCGTTACGTCT	0	0
24	AATACTAGGTGTAGGTGGTGTCAAAGCTATCTG	3	6
25	GGCACTAGACGCCGGGGGGGTGACCTTTCGGTG	0	0
26			
27	GATACTAGGCGTCAAGGGTATCGACCCCTTGG	0	0
28			
29	CCGACCAGGGATATGAGTTGTTAGGATTATATG	13	0
30	TATACTTGGTGTAAATCGGACTCAACCCTGATTG	10	4
31			
32	GGCACTAGGTGTGGGACCCTTCCACGGGTTCGG	8	10
33	TGTGCTGGATGTTGGGGCTCCTAGAGTCTCAGT	10	5
34	TCGACTGGTTGTTGGGGAAGGAACTTCCTTAG	7	16
35			
36	GGTACTAGATTTGGTGGGATTTGACCCCTGCCG	11	4
37	ATAACTCGATGTTGGCGATAGACAGCCAGCGTC	0	25
38			
39	GGTACTAGGTTTGGTGGGTCTTGACCCCTGCTG	0	19
40	CACACTAGACCGGTGCGGTTTTGACGCCGTATC	12	14
41	ATTACTCGCTGTTGGCGATAGACAGCCAGCGGC	15	3
42			
43	AGTGCTAGGTGTCACGGGCTTTGACTCCTGTGG	0	0
44			
45	AATGTTAGCCGTCGGCAAGCATGCTTGTCGGTG	0	0
46	AGTGCTAGACGTTGGGAGGTTACCTTTCAGTGT	20	4
47	CCGACCAGGGATATGAGGTAGAAATTATATTAT	0	0
48			
49	TGTGCTGGATGTTGGGCGGCCTAGCCGTTCACT	2	19
50	AGTGCTAGATATCGGGAGTTTTCTTTCGGTTT	16	2
51			
52	AGCACTAGGTGTCGCGGGTATTGACCCCTGCGG	9	7
53	ATAACTAGTTGTTTCGGTCACTTGGTGACTGAGT	0	25
54	CCGACCAGGGATATGAGGTAATAATTATTATAT	0	0
55			
56	ATTACTAGCTGTTTGCTTAAGTAAGTGGCTAAG	0	0
57			
58			
59			
60			

TTTACTTGCTGTTCCGCCCCTGGGCGGAGTGGC	7	13
CCGACTAGGGATGGGTGAACGTTGACTTTAACG	16	13
TCAACTAGCCGCTAGTCTCGCTTTAGAGATTGG	0	0
CCGACCAGGGATATGAGGATTTTTATTTATGCT	0	0
CATACTTGGTGTGGGCCGTTCAAGTCGGTCTGTG	6	9
CCGACTAGGGATTGGCAGGGCCTTCTAAACCT	0	2
TCAACTGGTTGTTGGGTCTAAACTGACTCAGTA	0	0
TCTACTTGCTGTTGGGGGTAAAACCTTAGTAGC	0	0
AGCACTAGTTATCGGAGGTATTGACTCCTTCGG	5	2
ATAACTAGCTGTCCGGGTTTCATGGAATTTGGGT	7	30
GGCACTAGGTGTGGGGACTTATCAACGGTCTCC	0	0
TCAACTGGTTGTTGGGTCTCAACTGACTCAGTA	0	0
TCTACTAGTTGTTGGGTCTTAATTGACTTAGTA	0	0
TCAACTGGTTGTTGGGACTTAACTGACTCAGTA	0	0
CCGACCGGGGATGGGGAGAGGTAATACCATAAC	14	2
TGAACTTGGCGTAGGTGGGTCAAATCCATCTG	8	4
AGCACTAGATCGCTGGGGAGCTATCTTTGGCGG	0	8
GGTGCTAGATGTCGGGAAGCTTAGCTTCTCGGT	4	14
TCAACTGGTTGTTTGGTCTTAACTGACTCAGTA	0	0
TCAACTAGGCGTAGGAGGTTATTGACCCCTTCT	3	6
CGCACTAGGTGCGGGGAGGCTTCACGCCCTCCCG	0	14
AACACTGGAGGAAGGGGGCTTCGGCCTTCTTTC	13	14
TCTACCAGTTGTTTGAGGTATCAACCCCTCGAG	0	0
TCAACTGGTTGTTGGGTCTTAACTAACTCAGTA	0	0
CCAAGTCTTTTAGATGCGGTTATTTATATGA	0	8
TCAACTAGGTGTTGGAAGGGTTAAACCTTTTAG	5	6
AACACTAGGTGTAGGTGGTGTCAAAACCATCGG	5	10
GATACTAGTTGTTTGAGTAATCTGAGTGACTA	0	0
ATCACTAGACGTCTGTTTTGCTTAGCAAAATAG	7	14
CCGACTGTAGATTAGAAGACGTTAATCAAAGGA	5	8
AGAGCTAGTCGTCGGGCGGCATGCCGTTCCGGTG	2	7
CACACTAGGTGACGCAATCTCTGACGATGGCGC	4	9
ATTACTCGCTGCTGGAGGGCAACTTTCAGTGGC	0	0
TCAACTAGCTGTCTGATACATTAGATATTGGGT	0	0
TCGATTAGGAAGTGGTTTATATCACTTTCGAAG	0	20
CCGACCAGGGATATGAGTAGTATATTTCATTG	0	8
GGCACTAGATGTGGGCGGTGTCGACTCCGTCCG	0	2
ATTACTCGTTGCTGGAAGGTAACCTTTCAGTGAC	16	4

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3			
4	CACGCTTGGTGTGGGGGGTTGACACCCTCTGTG	6	16
5	GGCGCTAGGTGTGGGGCTTTCCACGAGTTCCGT	3	13
6	TGCTAGGTGTTGGGGTGTAGACTTCAGCGCC	0	0
7	TCAACTAGGTGTTGGGAGGGTTAAATCTTTAG	5	1
8	CCGACCAGGGATATGAGGTAGAATTTGATATAT	0	0
9	TCAACTAGGTGTTGGGAGGGTTTAACTTTTAG	6	0
10	AGCACTAGATCGGGGGCCTCCACAGGTTCTTG	6	12
11	GATGCTAGATGTTGGTAACGTCAAGTTATCAGT	0	0
12	CCGACCAGGGATATGAGGTATATAGATTATTAT	0	0
13	CATACTAAGTGTCTGCCTGTAAAAGGGTGGGTG	7	5
14	CCAACTAGGGATGTGGACGTTTGTGTTGAAGACT	7	0
15	AATACTTGGTGTCTGGAGTTATTAGTGCTCCGG	12	9
16	TCCACTAGATTGTGGCGCTTTTAAACGGCGTCAT	0	0
17	CCGACCAGGGATCAGCGGATGTTGCTTTTAGGA	0	0
18	CCGACTAGGGATTGGTGGACGTTTTTTTTATGA	0	0
19	GGTGCTAGATGTCGGGGGGCTTGCTCTTCGGTG	3	6
20	CCGACTAGGGATCGGTTGTTGTTCTTTATTGA	3	23
21	AATGTTAGCCGTCGGCATGCATGCATGTCGGTG	0	0
22	ATTGTTAAACGTTAACGCTAAGCAATCCGCCTG	0	14
23	GATACTAGGTGTAGGCGGTCATTTACCCCGCCT	4	13
24	TAGACCAGATGTGGGGGGTATCGACCCCTCCG	3	14
25	AGTGCTAGATGTTGGTGAAGGAATTCATCAGTG	11	0
26	CCGACTAGGGATGGGTGAACGTTGCTTCTTCGA	0	0
27	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAG	0	1
28	CCGACAAGGGATTGGCGGAGTCTCGTTTTGTCT	0	0
29	CCGTCTTTGAATGGGGAAGCGATTTAAGTTTGA	11	5
30	CATACTTGGTGTAGCTGGACTCAACCCCGGCTG	5	0
31	TACTACTAAACGTTTCAGTCTTGGAACAAGACGG	0	0
32	AGCACTAGACGTCAGGCGGGTGACTGCCTGGTG	0	0
33	GGCACTGGGCAGGGGAAGCACCTATGTCTTTCC	4	7
34	AGCACTAGATCGCTGGGGAGCTATTCCTTGGCG	6	2
35	ACAAGTGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
36	GATGCTAGCCGTTGGGAAGCTTGCTTCTCAGTG	0	4
37	CCGACTAGGGATCGGGTGTGTTCTTTTTTTGA	9	5
38	CGAACTGGATGTTGGGCACACTTAGGTGCTCAG	5	9
39	GATACTTGTGTTAGAGGTATTGACCCCTTTAG	0	15
40	GGTGCTAGCTGTTGGGGGGTTACCTCTGAGTAG	3	3
41	TCAACTGGTTGTTGGGCCTTAACTGACTCAGTA	0	0
42			
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GTGACTAGGTGTGGCTGGCTTAAGGGCTGGTCG	2	7
CACATTTGCTGTAAGTGGAATCGACCCCACTTG	11	3
TCAACTGGTCGTTGGGTCTTAAGTACTCAGTA	0	0
GGTACTCGGTGTGCGGGGTATCGACCCCTGCGG	4	8
ATAACTCGCTGTTGGCGATATACTGTCAGCAGC	5	3
CACATTTGCTGTGGGCGGAATCGACCCCGCCCCG	8	8
TCAACTGGTTGTTGGGAGGTTTCTTCTCAGTAA	0	14
TCAACTGGTTGTTGGGTCTTAACAGACTCAGTA	0	0
CCGACCAGGGATTGGAAGACGTTAATTTAAAAA	3	7
AGTGCTAGACGTTGGGCAGGTGACTGCTCGGTG	8	5
AGTGCTAGATGTGGGTACTTTGTATCCGTGTGCG	0	0
AGAACTAGATGTTGAGAGGGTAAGCCTCCCAGT	8	6
TATACTCGACATATGCGATACACTGTATGTGTC	4	6
CACACTTGGTGTGGGGGGGATTTCGACCCCTCCCCG	0	0
AGTGCTAGATTTTCGGGAAATTTTATTTCTCGGT	0	0
GGAAGTGTGTTGGGGTCTTTCCACGGATTCC	3	8
AATACTAGCTGACTGGCGATAAGCTGGGTGGCG	5	4
AGAACTAGCTGTTGGAGGGGATACCTTTTCAGTG	12	5
ATGACTTGGTGTGTCGGGTTTTTCAGTCCCGATG	6	0
CCGACTAAGGATCGGCAGGGGTCGGTTAGCGAC	7	5
CACACTAGATCGGTGCAGGTTTACCCCTGTATT	2	0
TCAACTGGTTGTGCGGGTCTTAAGTACTCAGTA	0	0
TATACTTGGTGTAGCTGGTCTCAACCCCGGCTG	7	5
AGGACTAGACGTTGGAGGGGTAAGCCTTTTCAGT	9	7
TCGACTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
AGAACTGGATGAGGGGCTGGGTAAACCACTCC	0	15
AACACTTGTGTTAGGAGGTATTGACCCCTCCTG	0	14
TCAACTGGTTGTTGGGAATTCACCTTCTCAGTA	0	15
GATACTAGCTATTTGGGAATTCGTTCCCTGAGTG	0	0
CCGACTCAGATTCAGATGAATCAAAAAGTTCAT	0	0
CCGACTAGGGATCGGACGGTGTTATTTTTTGAC	4	18
GACACTCGGCCTGTGGGCGGTGTAAGTGCCGCC	2	11
TAGATTAGGTGTGCGGAGGAGTCGAACCCTTCGG	0	2
CATACTTGGTGTAAAGTCCTTCATTGGATTTGTG	4	10
AGCACTAGTCGTGGTAGGAATAACGCCTGCCG	0	15
CCGACTAGGGATCGCGCGGTGTTGATTACGACC	0	9
TCAACTAGCCGTTGGTCTTATTGATAAGATTAG	3	5
TCGACTGGTTGTTGGGGGAGTCTGTCCCTCAGT	4	14



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2			
3			
4	CGAACTAGCTTTTTGGCTTTGAGGTTGAGAGGC	0	0
5	GATGCTAGCCGTCAGGAAGCTTGCTTCGTGGTG	9	2
6	GGTGCTAGATGTCGGGGAGCTTAGCTTCTCGGT	7	2
7			
8	TCAACTAGTTGTCGGGTTCTATTGGACTTGTA	5	7
9	AATGCTAGCCGTCGGTGAGCATGCTCTTCGGTG	0	0
10			
11	CCGACCAGGGATGGGGAGAGGTAATACCTTAAC	13	2
12	CCGACCAGGGATATGAGGATTCTTATTTATGCT	0	0
13	CCGACCAGGGATATGAGTTGTTAAGATTATATG	6	2
14			
15	CCGACCAGGGATATGAGTTGTTATGATTATATG	13	4
16	GGCGCTAGATGTGGGGACCATTCCACGGTTTCC	6	4
17			
18	TCAACTAGGTGTTGGGGGGGTTAAACCTTTAG	4	0
19	CACATTAGACGTGAGGGGTATCGACCCCCTTCG	2	17
20	ACAACTGGATGTCGGGAGGGTTTGCCTTCCGGT	4	5
21			
22	AATGCCAGCCGTCGGGGAGCTTGCTCCTCGGTG	6	2
23	AATGCCAGCCGTTGGGGTGCATGCACTTCAGTG	0	20
24			
25	AATGCTAGATGTCAGGCCTTTCGGGGTTTGGTG	0	0
26	AGTGCTTGGTGTGGCGGGTATCGATCCCTGCCG	3	4
27			
28	GGCACTAGGTGTGGGTCTCAACCAACGGGATCC	0	0
29	TCAACTAGTTGTTGGGGAAGCAATTCTTGTA	5	0
30	AATACTGATTGTTGAGTAGATTTCTATTCAGTG	3	12
31			
32	AGAACTAGACGATGGTGCTTAGAGGCATCAGT	11	2
33	TCAACTGGTTGTTGGGTCTTAACTGACACAGTA	0	0
34			
35	TGTACTTGATGTAGCTGGGCTCAACCCTAGCTG	5	6
36	AGTACTAGACTTTGGGCTTTTGTTGAGAGTCGC	0	0
37			
38	TCAACTGGATGTTGGGTCTTAACTGACTCAGTA	0	0
39	TCTACTTGCTGTTGGGGGTAGAACCTTAGTAGC	9	0
40	TCAACTAGGTGTTGGGGGGGTTAAACCTTTAG	0	0
41			
42	AGCACTAGACGTTGGGCGGGTGACCGTCCGGTG	4	12
43	CGAACTAGCTTTTTGTCTTTAAGGTTGAGAGGC	0	0
44	CCGACTCGGACTCAGATGAATCAAAAAGTTCAT	0	0
45			
46	ACAACTAGGTGTCGGGCATCTAAGGATGTTCCG	0	0
47	TCGATTTGGAGGCTGTGTCCTTGAGACGTGGCT	0	0
48			
49	GATGCTAGGTGTGGGAGGTATCGACCCCTTCCG	0	0
50	AACACTGGAGGACGGGGGCTTCGGCCTTCGTTT	0	3
51			
52	GATACTAGGCGTTAGGGGTATCGACCCCCCTAG	3	7
53	CCGACCAGGGATATGAGGTATTATTTTATTTAT	0	11
54	TCGACTAGGTGTTGGGAGGGTTAAACCTTTAG	4	0
55			
56	AGTACTAGCTGTCGGAGGTTACCCCTTCGGTG	6	5
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1			
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3			
4	AGCACTAGACGCCGGGGGGGTGACTTTTCGGTG	4	8
5	CCGACCAGGGATATGAGGTAGAAATTGATATAT	0	0
6	GATACTAGGTGTGGAGGGTATCGACCCCTCTG	0	0
7	AGAACTAGATGTTTGTGGTTTAATAACTGTGAG	0	0
8	TGTGCTTGTCTGCTGGGGAGTTCACTCTTCGGTG	0	0
9	CTAGCTGGGTGTTTCAGGGGGGAAACCTCTCGG	0	0
10	GCCCCCATGAATTGGGGAGTTATTGAGCTGGCG	0	0
11	GGCACTAGGCAGGGGGGATACTTATGGTCCTCT	9	3
12	AGCACTGGACGGGAGGGGCTTCGGCCTCTCCGG	5	7
13	AGTACTGGCCCTTGGAGGTATTGACCCCTTCAG	0	0
14	GATGCTAGGTGTTGGCAGATCTAACCCTGCCAG	3	9
15	AGTACTAGTGGGGAGAGGCTTCGCGCCTTTTCC	2	3
16	TCAACTAGGTGTTGGGAGGGTAAACCTTTTAGT	0	0
17	GGCGCTAGGTGTGGGGATTGTTTCCACGATCTC	3	7
18	ATCGCTGGGTGTGGGGGGTTTTTACTCCCTCCG	4	0
19	CCAACTAGGTGTTGGGAGGGTTAAACCTTTTAG	5	0
20	TATACTAGATGTTGGCGGTTTCAACGCCGTCAG	0	2
21	TATACTAGATGTTGGTGGTTTCAACGCCATCAG	0	0
22	TACACTTGATGTAGCTGGTCTCAACCCAGTTG	0	3
23	AGCACTAGGTGTGGGGGGTTTTGACCCTCCGTG	0	0
24	CCGACTCGGATTCAGATGAGTCAAAAAGTTCAT	0	0
25	CTAACTCGATATAGGGACGAATGAGTTTCTGTG	0	0
26	CTAACTCGTTTTTGGGACGCAAGTTTCAGAGAC	9	3
27	ATCACTCGTCATTGGCGATACACGGTCAGTGAC	0	4
28	TTTACTTGCTGTTTGGCCTTTGGGTTGAGCGGC	0	0
29	CCGACATAGGAATACATAATAGTAGGACTAAAG	9	4
30	AATGCTAAACGTTGGGTTGTTTACAACCTCAGTG	0	0
31	TCAACTGGTTGTTGGGTCTTACTGACTCAGTAA	0	0
32	TGCGCTAGGTGTTGGAGGTATCGACCCCTTCAG	0	0
33	TGTGCTAGACGTCGGGAGGCTTGCCTCTCGGTG	4	3
34	AGCACCAGACGCCGGGCGGGTGACCGCCCGGTG	3	7
35	TCAACTAGGTGTTGGGAGGGATAAACCTTTTAG	1	0
36	TCAACTAGGCGTTGGGAGGGTTAAACCTTTTAG	4	0
37	TGCGCTGGATGTTGGGGCCCTTAGGGTCTCAGT	2	10
38	CGAACTAGCTTTTTGATTTAGGATTAGGAGGCT	0	2
39	CCAACTAGGCGCTGGTGGTGATAAGCCATCGGT	7	2
40	TACACTTGGTGTGGTTCTTTATGGATCAGTGC	0	0
41	AATACTCGGCATCTGGCGGCCGATTTTCGGCGG	0	0
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4	CGAACTGGATGTTGGGCTCAATTTGGAGCTCAG	3	3
5	ATCACTAGATGTTAGGTCCGCTTTAGGGCTTAG	0	0
6	CCGACTAGGGATCCGTCAGCGTTCTACGTGACT	13	3
7	CTTACTCGATATTCGCCCTTCGGGGTGAGTGTC	3	6
8	AATATTTTATGTTTATATCTTTGTATATGAATA	3	7
9	AGCACTGAATTGAAGGGTCCCACATAACCCTTC	3	6
10	AGTGCTGGGTGTCCGGCGTATGCTGGGTGCCGT	2	5
11	CGAACTGGATGTTGGGTTCAACTTGGAACCTCAG	4	5
12	AGTGCTAGATGTTGGGAACGTAGTTCTCAGTGT	0	0
13	CCGACTCAGGATCGGTGGGCTGTATATTGTGGC	0	0
14	CCAGCTCGACGTTACACCCGCACCGCGGTGGGG	0	0
15	CCGACCAGGGATATGAGGATTTCTATTTATACT	0	0
16	CCGACTAGGGATTGGCGAATGTTTTTTAATGA	0	0
17	CCGACTCGGATTCAGATGAATCAAAAAGTTCAA	0	0
18	AGTACTAGATTGTAGACTAATCATGGGTTTACA	6	2
19	TCGACTTGGGATTGGAGGCGTGCACTTTCCGCC	7	2
20	AAGACTAGATGTTGGTAGGGTAAACCTATCAGT	9	3
21	CACGCTTGGTGTGGGAGGGTTCGACCCTTTCTG	0	0
22	TCAACTGGTTGTTGGGTCTTAACTGTCTCAGTA	0	0
23	TCAACTGGTTGTGGGTCTTAACTGACTCAGTAA	0	0
24	TCAACTAGGAGTTGGGAGGGTTAAACCTTTTAG	0	0
25	GGCGCTAGGTGTGGGACTCTTTTCACGAGTTCT	2	5
26	TCGACTAGCCGTTGGGATCCTTGAGATCATAGT	0	26
27	ACAACTAGGTGTGGGAGGTGTGCACTCCTCCCG	5	8
28	AATACTCGTTGTTGGCGATATACAGTCAGCGAC	0	0
29	TCAACTAGTTGTTGGGCTTTAAAAAGCTTGGTA	0	5
30	CATACTTGGTGTAGTCGGTCTCAACCCCGACTG	0	0
31	ACCCCCATGAATTGGGGAGTTTTTTGTGGAGGTG	0	0
32	TCTACTAGCCGTTGGGGCCTTTGAGGCTTTAGT	0	5
33	TCAACTAGGTGTAAACCTTTTAGTGCCGTAGC	0	0
34	CCGACTCGGATTCAGACGAATCAAAAAGTTTCAT	0	0
35	CCGACCAGGGATATGAGGATTTCTATTTATGCT	0	0
36	AGAACTGGGCGTTGGAAGGTTTTACCTTTTAGT	3	3
37	GATGCCAGCCGTTGGACAGCTTGCTGTTCAGTG	0	0
38	CATACTTGGTGTGAGCCATTCAGTTGGTTCGTG	0	0
39	AGTACTAGTGGGAAGAGGCTTCGCGCTTTTTCC	4	6
40	AATACTAGATGTTGGTCATATTGATCAGTGTCG	0	0
41	TCGACTGGTTGTTGGGGGAAATTGTCCCTCAGT	0	0
42			
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3			
4	ATCACTAGATGTTTGGCGATACACTGTAAGCGTC	4	7
5	AGCACTAGATGGAAGGGTCCTCCATAGCCTTTC	5	3
6	AGTGCTAGATGTCGGGGAGCTTGGCTTTTCGGT	0	7
7			
8	TGCACTAGGTGCTGGGGCGGATGCTTCAGTGCC	0	0
9	CCGACCGAGGGCCCCGGAGGAGTTACGTACGACC	9	0
10	ATGGCTGGGTGTTGGCGATACACCGTCAGCGCC	0	0
11			
12	AGCACTAGATCGGGGGCCTCCACAGGCTCCTGG	2	3
13	CCGACTCGGATTCAGATGGATCAAAAAGTTCAT	0	0
14			
15	CTTACTAGTTGTTTGGATGAGAATCTGAGTGAC	0	0
16	CCGACTAGGCGCTGGTGGTTTGAACGCTGCCAG	0	3
17			
18	CCGACTCGGGTTCAGATGAATCAAAAAGTTCAT	0	0
19	CCGGCGGGGCGCGGGGGGGCCGAGTGGGGCGGC	0	0
20	CAAACCTGGTGTGGTGGCGTAAAAACCATCAG	0	0
21			
22	ATAACTCGTTGTTGGCGATACACAGTCAGCGAC	6	5
23	GGCACTAGGTGTGGGGAGCCGTCAACGCTCTCT	0	4
24			
25	AATGTTAGATGTCGGGAGGTTACCTCTCGGTGT	0	0
26	TCAACTGGTTGATGGGTCTTAAGTACTCAGTA	0	0
27			
28	GAAGCTAGCCGTTGGTGGGTTTACTCATCGGTG	0	0
29	CGAACTAGCTTTTCGGTTTAGGATTGGGAGGCT	8	6
30			
31	ATAACTAGCTGTCCGGGCCTTTAGGCTTGGGTG	0	0
32	CCGACTCGGATTCTGATGAATCAAAAAGTTCAT	0	2
33	TCGACTAGTTGTTGGGGAGTCTGTCCCTCAGT	0	0
34			
35	AGTGCTAGTTGTTGGGTTTTTAAAGTCTCAGTGA	2	0
36	TCAACTAGTTGTCGGGCCTATTTAGGTTTGGTA	5	4
37			
38	TCAACTGGCTGTTGGGTCTTAAGTACTCAGTA	0	0
39	TATGCTGAATCGGAGCGGCTCTGACGCCGTTCT	0	0
40	CTAACTCGATGTTGGGAATGCAAATTTTCAGCG	0	0
41			
42	TCAACTAGTTGTCGGATCCATTTAAGGGTTTGG	3	3
43	CCGACTCGGATTCTGATGAATCAGAAAGTTCAT	0	0
44			
45	CTGACTTGGTGTCTCGGGTATTAATTCCCGGGG	4	4
46	GATACTAGATGTTCCGAGAGTTAACCCTCTGAG	0	0
47			
48	AGAGCTAGCCGTTGGCAGGTTTACCTGTCGGTG	0	0
49			
50	TCAACTAGGTGTTGGGGAAGGTGACTTCCTTAG	2	4
51	AGCGTTGAATGTTGGGAGACTTAAAGTCTTTC	3	4
52	CAGATTAGCTTTTCGGAGTATCGACCCTTCGAG	0	3
53			
54	CTAGCTAGATGTCTGGGCCGCGCAAGCGGAGTG	0	0
55			
56	TATACTTGGTGTAGCTGGACTCAACCCAGCTG	6	5
57			
58	TCAACTAGGTGTTGGGAAGGTTAAACCTTTTAG	2	0
59			
60			

1			
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3			
4	GATACTTGTTGTTGGAGGTATTGACCCCTTTAG	0	0
5	AGTACTAGGTGTGGGTTGAGTGAAATCAATCTG	2	8
6	AGTACTAGACGTTGGTGACGAGAGTTACGAGTG	8	0
7			
8	CCGACTCGGATTCAGAAGAATCAAAAAGTTCAT	0	0
9	TCCACTAGATTGTGGTGGCTCTGACGCCATCAC	2	2
10	ATTACTCGCTGCTAGATGGCAACATTTAGTGGC	3	2
11	ATAATTTTAATTTTTGAGCGGATTTATAGAGGA	7	3
12	CAGACTAGGCGTAGGTGGACTTGACCCCATCTG	0	0
13			
14	AGAACTAGGTAGTAGGCTTGACATGGGCTTACT	4	8
15	CACACTAGACCGGTGCCGCTCTGACGCGGTATC	0	5
16	ATCACTAGGTGTTGGGGGGGTTAAACCCTTCGG	0	0
17			
18	ATGACTAGACCTGTGGTGGTGCTAAGCCTCTGG	4	5
19	GAAGCTAGCCGTCGGCAAGCATGCTTGTCGGTG	0	0
20			
21	TCAACTAGGTGTTGGGAGGGTTAAACCTCTTAG	4	0
22	CACACTTGGTGTGAGCCATTCAATTTGGTTCGTG	3	9
23	CACACTAGGTATGGGAGGAATCGACCCCTTCCG	0	0
24			
25	TATACTTGGTGTAACCGGACTCAACCCTGGTTG	5	2
26			
27	AGAACTAGGTGTCGTGGGTGTTGATCCCCGCGG	0	0
28			
29	CCGACCAGGGATATGAGTTGTTAAGATTGTATG	7	0
30	TGCGCTGGATGTTGGGGGGCATAGCCCTTCAGT	3	2
31	TCAACTGGTTGTTGGGTCTTAACTGACTCAGAA	0	0
32			
33	TCGACTTGAGAGTTGTGCCCTTGAGGCGTGGCT	0	13
34	TGTGCTAGCCGTCGGTCAGCTTGCTGTTTCGGTG	0	0
35			
36	TGTACTGGATCGCAGAGACTAATACGTCATTGT	0	0
37			
38	TCAACTGGTTGTTGGGTCTTATCTGACTCAGTA	0	0
39	ATAACTAGCTGTCCGGGTGCATGGCACTTGGGT	8	2
40	CACACTAGGTCTTGGTGGATTTCGACCCACCAG	0	0
41			
42	CCGACTTGGGATTGGAGGCGTGCACCTTCCGCC	5	3
43	CAGACTTGGTGTGCGCTCTTCATTGAGTGTGTG	4	4
44	ACAACTAGGCGCTGAGGGACTCAACCCCCGCGG	3	5
45			
46	TAACTGGTTGTTGGGTCTTAACTGACTCAGTAA	0	0
47	AGTGTTGAATGTTGGGGGACTTAAAAGTCTTTC	2	3
48			
49	TCTACTGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
50	CTAACTCGATGTTTGGTTGAAAGATTGAGCATC	0	5
51			
52	CTAACTCGACATGTGATCTACGGATTGTGTGTC	5	6
53	TATACTTGGTGTAACCTGGACTCAACCCAGTTG	6	3
54	TCGACTGGCTGTCGGGGGGCTTGACCCCTCGG	0	4
55			
56	CTGACTTGGGATTGGAGGCGTGCACTTTCGCC	2	5
57			
58			
59			
60			

TCAACTGGTTGTTAGGTCTTAAGTACTGACTCAGTA	0	0
TTTACTTGCTGTTTGGGCCATGTGCCTGAGTGG	0	0
CCGACTCAGGATTGACAGACGTCTTTACCGACT	0	2
TTTACTTGCTGTTTCGGACGCAAGTCGGAGTGGC	4	0
AGCACTAGCTGGGAGGGACGTAGGTCCTTCCCA	0	4
AGCACTAGATCGCTGGGGAGCTATTCTTTGGCG	0	0
GGCACTAGGTGTGGGACCCATTCCACGGGTTC	2	4
ATTACTGGACATTTGCGATATACAGTGAGTGTC	0	10
TGCGCTAGACGTTGGTGGACCTAGTTCACCGGT	0	8
GGCACTAGGTAGGGGGGTACCCAATGCCTCCCT	0	0
AGTACTGGGCGGGAGGAGGTTTCTCTTTCTGC	2	4
TCAACTAGTTGTCGATCTAATAGATTTGGTAA	3	5
CGAACTAGGGAGAGGGTGTTCTTAGACACTCTT	0	0
CCAACTAGGGATACGTGGAAGTTTGTTCAAGA	3	3
AGCACTAGGCCGGAGGGCTGCACAGCCTTTCGG	0	3
AGCACTTGATCGAGGGCCCCCATAGGCTCTC	5	2
GATGCTAGATATCGGGAGTATCGACCCTCCCGG	0	0
CCGACCAGGGATATGAGTTGTTATGATTATGTG	6	4
TCAGCTAGGTGTTGGGAGGGTTAAACCTTTTAG	0	0
GCGACTAGTTGTTGGGGTAGAAGTACCTTAGTA	2	4
TCAACTAGGTGTTGGGAGGGTTAAATTTTTTAG	0	0
TCGACTAAGGATGATAAAATATTAAGAATGAT	0	0
AGTGCTAGATGTCGGGAAGCTTGGCTTTTCGGT	2	5
CGGACTTGGTGTGCGCCCTTCATTGGGTGCGTG	3	5
GGTACTAGATGTCAGAAGTTCTTACCCTTCTGG	6	5
CCGACTCGGATCCAGATGAATCAAAAAGTTCAT	0	0
AGTGCTAGTTGTCGGGGCCTTAGGTCTCGGTGG	0	0
TCAACTGGTTGTTGGACGGCTTTCTGTTCACTA	3	0
AGTGCTAGGTGTTGGGGGTATTGACCCCCCAG	7	0
TCAACTAGTTGTCGGGCCTTATTAGGCTTGTA	3	0
AGTGCTAGACGTTGGACGGTTACCGTTCAGTGT	11	0
TCACTGGTTGTTGGGTCTTAAGTACTCAGTAA	0	0
AGCACTGGGTAGGGGGGCTCGCCGATGGGCTCTC	0	0
CCGACTAGGGATCGGTCCACGTTATTTTTGACT	0	19
TCAACTAGGTGTTGGGAGGGTTAAACCTTTTTA	0	0
TCGACTAAGGATGATAAAATATTAAGAATGATT	0	0
CGTACTAGATAGCGGCTCGTTCCGACGAGCCGC	0	0
CTAACTCGTTTTTGAATGTAAGTTTCAGAGAC	0	0

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4	CCGACTTGGGATTGGAGGCGTGCACTTCCGCCT	9	2
5	TCAACTGGTTGTTGGGAATTAACCTTCTCAGTA	5	9
6	CCGACTCGGATTCAGATGAATCAAAGTTCATTT	0	0
7	ACAAC TAGGTGTTGGGAGGGTTAAACCTTTTAG	5	3
8	CCGACTTGGGATTGGAGGCGTGCACTTCCCGCC	4	3
9	TCAACTGGTTGTTGGGTCTCTTCTGACTCAGTA	0	0
10	TCAACTGGTTGTTGGGAGGGTTTCTTTTCAGTA	0	3
11	CCGACTCGGATTCAGATGAATCAAAGAGTTCAT	0	0
12	AGCACTGGAGGAGAGGGGCTTCGGCCTTTTTCC	3	7
13	GATACTAGGTGTCCGGGCCTCTGGCCTGGGTGC	4	0
14	CCGACCAGGGATATGAGTTGTTATGATTGTATG	5	0
15	TGCACTTGGTGTGTTGGGCTGATTAGGTTCAGTGC	0	0
16	CCGACCAGGGATATGAGTTGTTATAATTATATG	5	0
17	CCGACTCGGATTCAGGTGAATCAAAAAGTTCAT	0	0
18	AGAGCTAGCCGTTGGCAAGTTTACTTGTCGGTG	0	0
19	TCAACTGGTTGTTGAGAGGGTTTCTTCTCAGTA	4	3
20	GATACTAGGCGTAAGAGGTATCTACCCCTCTTG	3	3
21	AGCACTAGTCTGTGGGGACTCTCACATCCTCTC	2	3
22	AGGACTAGGTGTCGGGTCGTAAGACTCGGTGCC	4	4
23	TCAACTGGTTGTTGGGAGGGTTTCTTCTTAGTA	3	2
24	TCAACTAGCCGTTGGGGTCCTTGAGACTTTAGT	0	0
25	CCGACTAGGGATCGGTCCACGTTATTTTTTTGA	0	14
26	GGTGCTAGCTGTCAGCGGGCTTGCTCGTTGGTG	0	0
27	TCAACTAGGTTTTGGGTGGGTAAAACCATTTAG	0	4
28	TCAACTAGGTGTTGTGAGGGTTAAACCTTTTAG	0	0
29	TGCGCTGAATGTTGGGGTTCCTAGAACCTCAGT	4	4
30	AGAACTAGGTGTCGTGGGTGTTGACCCCTGCGG	0	3
31	GGCACTAGGTAGCGGGCCTCCATGGGCCCGCTG	2	2
32	GGCACTGGGTAGGGGGCTCTCCGATGGGCTCCC	0	2
33	GGTGCTTGTGCTTGTGAGTGTAACCCCTCGCAG	0	0
34	GGAAGTAGTTGTGGGGTCCATTCCACGGATTCC	0	0
35	CCGACTTGGATTGGAGGCGTGCACTTCCGCCT	7	5
36	CCGACCAGCGATTGGGCGACGTTGCATGGATGA	0	2
37	AATGCCAGTCGTCGGGAGGCTTGCCTCTCGGTG	0	0
38	AGTGTTAGATGCTGTGGGTATTGACCCCTGCGAG	0	0
39	AGCACTGGGTAGGGGGCTCGCCGATGGGCTCCC	0	0
40	TCAACTAGGTGCTGGGAGGGTTAAACCTTTTAG	0	0
41	CCGACTTGGGATTGGAGGCGTGCACTTTCTGCC	3	1
42			
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3			
4	CCGACTTGGGATTGGGGGCGTGCACTTTCCGCC	0	7
5	AGAACTAGTTGTTGGCCCTTTTAAGGGTCAGTG	5	2
6	AGAACTAGATGTTGGAGGGGAGACCCTGCAGTA	0	0
7			
8	TCAACTAGGTTGGGAGGGTTAAACCTTTTAGTG	0	0
9	GGTACTAGGATTGGTGGGTCTTGACCCCTGCTG	3	0
10	GATACTAAATGCTGTCAAAAACAGTGTTGTAGC	0	0
11			
12	TCAACTAGTTGTTGGGCCTTATTGGGCTTGTA	4	4
13	CCGACTCGGATTCAGATAAATCAAAAAGTTCAT	0	0
14			
15	AGCACTAGACGCTGGGCGGGTGACCGCCCGGTG	2	3
16	CCGACTAGGGATCGGTCCACGTTAATTTCTGAC	0	5
17			
18	GGCGCTAGGTGTGGGGCTCATTCCACGAGTTCT	2	2
19	CACACTTGGTGTTGGGCCTTTTTGGCTCAGTGC	0	0
20	CCAACTAGGGATATGTGGATGTTTGTGAAGA	3	3
21			
22	AGTGCTAGACGTCGGATCTTTAAGATTCGGTGT	0	0
23			
24	TCAACTAGGTGTCGGGAGGGTTAAACCTTTTAG	0	0
25	GATACTCGTTATTGGGGTTTCGACTTCAGTGAC	0	0
26	GGAAGTGGTGTGGGTCTCATTCCACGAGATCC	0	5
27			
28	TACTAGACTGGTGCGGTTTTGATGCCGTATC	0	0
29	ATTACTCGACGTGCGCGATACACAGTGCGCGTC	0	4
30			
31	TCTGTTGGCTATAGGGAGTATCGACCCTCTCTG	0	0
32	TCAACTGGTGTTGGGTCTTAAGTACTCAGTAA	0	0
33	CCGACTTGGAAATTGGAGGCGTGCACTTTCCGCC	4	6
34	ATTACTCGATGTGTGCGATACACAGTACGCGTC	0	8
35			
36	CCGACTCGGATTCAGATGAAACAAAAAGTTCAT	0	0
37			
38	TCAATTAGTTGTTGCGGTGAGGAGACTCATTGAG	3	2
39	CATGCTGGCTGTGCGAGGTATTCACCCCTTCGG	0	10
40	CCGACCAGCGATTAGGAGACGTTGAATACAAAA	0	0
41			
42	TCAACTGGTTGTTGGGTCTAACTGACTCAGTAA	0	0
43	TCAACTAGTTGTGCGGGGATTCATTTCTTGTA	0	2
44			
45	GATACTTGTGTTGGAGGTATTGACCCTTTCAG	0	0
46	CTGACTGGGCGTCTGCTGGTGTGCTCTTGC	3	3
47	ATTACTCGATGTTGGCGATACACAGTCAGCGTC	0	0
48			
49	TACTAGACCGCAGAGGTTTGACACCCTTGTTG	0	0
50	TGTGCTAGGTGTTGCGGGAATCAACCCCCGCAG	0	0
51			
52	AATACTAGGTGTGGGAGGTTTCGACCCCTTCCG	0	0
53	AGAACTGGGTGTAGGGGGTATGAACCCCCCTG	0	4
54	CGCGCTAGATCGGTGCGGGTTTGACCCCGGATC	0	5
55			
56	TGTACTTGATGTAGATTGGCTCAACCCTTCTG	4	2
57			
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3			
4	GACACTTGGTGTGGAGGTATTGACCCCTTCAG	0	0
5	AATACTAGGCGTAGGTGGAGTTAAACCCATCTG	0	0
6	AGTGCTAGATATTGGAAGCATGACTTTTCAGTTT	0	0
7			
8	TCAACCAGGTGTTGGGAGGGTTAAACCTTTTAG	0	1
9	AGAACTAGCCGTTCCGGTCCTGTATGGGATTGAG	0	2
10	GTGACTAGGTGTGGGGAGCGTACAGCATCCTCG	0	3
11			
12	GACGCTAGGTGTTGGCAGATCTAACCCTGTCCG	0	0
13	AACACTTGGTGTGCCGGGAGTTGACCCCCGGCG	0	3
14			
15	GATACTAGCTGTTGGGGGTAACTCAGTGGCTA	4	4
16	AGAACTGGCTGTTGGGAGGGACTTCCTCTTAGT	0	5
17			
18	TCAACTAGGTTTTGGGAGGGTTAAACCTTTTAG	0	0
19	AGTGCTAGGTATCGGGAGAATTTCTTTCGGTTC	0	0
20			
21	AGTACTAGGTGTGGGTGGAGTGAAATCCATCTG	2	4
22	TCAACTGGTTGCTGGGTCTTAACTGACTCAGTA	0	0
23	TTAACTAGTTGTTCCGGTGAGGAGACTCATTGAG	5	3
24	GGCGCTAGGTGTGGGGAACATTTCCACGTTCTC	0	8
25			
26	TCAACTGGTTGTTGGGTCTTAACTGACTCAGTG	0	0
27			
28	TCAACTAGGTGTTGGGTGGGAAAAACCATTTAG	0	0
29	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAT	0	0
30			
31	CCGACTCAGGATTGGCGGTGTACTTCAACGTCT	0	0
32	ATCACTCGCTGCTGGGGGGTAACCTTCAGTGGC	7	0
33	ATTACTCGCTGCTAGGGGGCAACCTTTAGTGGC	0	0
34			
35	CACACTTGGTGTGGGAGGATTCGACCCCTTCCG	5	9
36	TCAACTAGGTGTTGGGAGGGTTAGACCTTTTAG	0	0
37	CCGACTCGGAATCAGATGAATCAAAAAGTTCAT	0	0
38			
39	CCAATTGGGGATCGGTACAGGATTTTAAATGAC	4	3
40	GATGCTAGCCGTCAGGAAGCTTGCTTCTTGGTG	3	0
41			
42	ATAACTAGCTGTCGGGGCACTTGGTGCTTCGGT	0	4
43	CACACTAGGTCTTGGC GGATTGACCCCCCCCA	0	0
44			
45	TATACTTGGTGTAACCTGGATTCAACCCTAGTTG	0	0
46	AGTGCTAGATGTCGGAAGATTTTCTTTCGGTTT	7	3
47			
48	TATACTCGTTGTTTGAGAGTAATCTTGAGCGAC	3	2
49	CCGACTCGGATTCAGATGAATCAAAAAGCTCAT	0	0
50			
51	TCTACTAGTTGTTGGGGGAGTTAAATCCCTTAG	0	0
52	TCAACTGGTTGGGGTCTTAACTGACTCAGTAAC	0	0
53	CCGACTCGGATTCAGATGAATCAAAAATGTTCAT	0	2
54	ATCACTAGATGTTGGCGATACACTGTCAGCGTC	0	7
55			
56	TTAACTCGATATTTATTCTACGGAGTGAGTGTC	0	0
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4	CCGACCAGGGATCGAGGATAGTCCCATGGTTGA	0	0
5	CCAACCTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
6	GGCGCTAGGTGTGGGGGTCCTTCCACGATCTCC	0	4
7	TCTACTAGTTGTCGGGGATTCTGTTTCCTTGGTA	0	0
8	CCGACCAGCGATCGGGAGACGTCGCATGGATGA	3	2
9	TCAACTAGTTGTTGGGTCTTAACTGACTCAGTA	0	0
10	ATTACTCGTTTTTGGGTTTATGATTGAGAGACT	0	0
11	ATAACTGGTTGTGCGCGATATACAGTGCGCGAC	0	0
12	AGAGCTAGCCGTTGGGGGGTTTACCCTTCAGTG	0	0
13	TGCACTGGGTGTCGGGCCGTAGGGCTCGGTACC	0	0
14	CGCACTTGCTGTAAGCGGATTGAAACCGTTTG	4	0
15	TTCATTTGCTATTTCGGAGTATCGACCCTCTGAG	0	0
16	CCGACTCGGATTCAGATGAATCGAAAAGTTCAT	0	0
17	GGCACTAGATGTCGGACCTTCTTACCGGTTCCG	0	0
18	TCAACTGGTTATTGGGTCTTAACTGACTCAGTA	0	0
19	TCAACTAGGTGTTGGGTGGGTAAACCATTTAGT	0	2
20	CCGACTAGGGATCGGTGGGTGTTTTTATGACC	0	0
21	CCGACCAGGGATATGAGGATCTTTATTTATGCT	0	0
22	AATACTCGGTGTCGCCTTCTTTGAGGGCGGTG	0	0
23	CATACTAGGTGACGGGCGCTCTGACGCATCCGC	0	3
24	GTCCTAGATGTCGGGAGTTCTTACCCTCTCGG	0	4
25	TCAACAGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
26	TAGACCCGGTCTTGGGCGATTGACCCGCTCAG	2	5
27	CCAACCAAAGATAAGGGTGGGAAAAACAGGAGA	2	4
28	GGCGCTAGGTAGTGGTCGTTCTTATGCGGTCAC	0	4
29	AGTGCTAGATGTCGCGGTCAAGACCATCGCGGT	5	2
30	AGTGCTAGACGCTGGCGGATTGACCCCGTCGGT	0	0
31	GATACTTGTTGTTGGAGGTATTGACCTCTTCAG	0	0
32	AGCACTGGGCGGGAGGAAGTTCGCTTCTTTCTG	0	0
33	TCAACTGGTTGTTGGGAGGGCTTCTTCTCAGTA	0	4
34	CTAACTCGTTTTTGGAGCGTAAGTTTCAGAGAC	0	5
35	CCGACTAGGGATCGATGGGTGTTATTAATGACC	0	0
36	TCAACTGGTTGTTGGGAAGGTTTCTTCTCAGTA	3	0
37	CCGACCAGAGATCAGAGGATGTTGAATGGAAGA	5	0
38	CCGACCAGGGATATGAGGATTTCAATTTATGCT	0	0
39	TCAACTGGTTGTTGGGTCTTACTGACTCAGTA	0	0
40	ATTACTCGATCTGTGCGATACACTGTACGGGTC	0	7
41	CATACTAAGTGTCTGCCTATAAAAGGGTGGGTG	0	2
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4	CCGACTAGGGATCGGTGGGTGTTATTAATGACC	0	6
5	CCATCTAGCGATCCGATAGGGTCTATCTAGCCT	0	0
6	TTTACTTGCTGTGCGGTCTTAGGATTGCGTGGC	0	0
7			
8	TCAACTAGTTGTCTGGATTTTAATAGATTGTTGTA	2	2
9	TCAACTGGTTGTTGGAGGGTTTCTTCTCAGTAA	2	7
10	AGAGCTAGCCGTTGGGATGTTTACATCTCAGTG	0	0
11			
12	TCAACTAGTTGCTCGGTGAGGAGACTCATTGAG	2	3
13	CACATTTGCTGTGGGCGGAATCGACCCCTGCCCCG	4	0
14			
15	CTGACTTGGTGTCTCGGTTTTAAATCCGGGGG	4	0
16	CCAACTTGGGATTGGAGGCGTGCACTTTCCGCC	6	0
17			
18	TCAACTAGTTGTTTCGGTGAGGAGACTCATCGAG	3	0
19	CGAGCTGGATGTCGGGGGACTTGTCCCTCGGTG	0	2
20	TCATCTGGTTGTTGGGTCTTAACTGACTCAGTA	0	0
21			
22	CTAACGATGGACGCGGGGAATCAGTCTCTTTAT	0	0
23			
24	AGCACTAGGTGTGGGAGGTTTTGACCTTCCGTG	0	0
25	GGTACTAGGTGTTGGAGGATTCTACCCCTTCAG	0	0
26			
27	TCAACTAGTTGTTTCGGTGAGGAACTCATTGAG	2	0
28	ATGACTCGATGTTGGCGATATATAGCCAGCGTC	6	0
29	GTCACTCGGTGCCGGCGATATACAGCCGGTGCC	0	4
30			
31	AGCACTGGGTGGAGGGTCCTCCATAGCCTTCC	0	4
32	GATACTCGATGTTGGGCGGTATAGCTCAGTGTC	0	0
33			
34	AGTGCTGGATGTCGGGAAACCTAGCTTTTCGGT	0	4
35	TCAACTGGTTGTTGGATCTTAACTGACTCAGTA	0	0
36	TCGACTGGTTGTTGGGAGATTTATTCTCTTAGT	6	3
37	CCGACCGGGGATGGGGAGAGGTAATATCTTAAC	0	2
38			
39	AATACTGATTGTTGAATAGATTTCTATTCACTG	0	4
40	AGAACTAGGTGTCGTGGGTGTTGATTCCCGCGG	0	0
41			
42	TCAACTGGTTGTTGGGAGGGTTTTTCTCAGTA	2	3
43	CCGACTTGGGATTGGAGGCGTGCACTTTCCGCT	4	4
44			
45	ACAACTAGTTGTTTCGGTGAGGAGACTCATTGAG	1	0
46	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTGG	0	0
47			
48	CACACTAGGTCTTGGCGGATTGACCCCCCAGG	4	0
49			
50	GATACTTGTGTTGGAGGTATTGACCCCTCAG	0	0
51			
52	TCAACTGGGTGTTGGGAGGGTTAAACCTTTTAG	0	0
53	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTCA	1	1
54	GGTGTTTGTGTTGGAATGTTAACCTTTTCACT	0	0
55			
56	TCAACTAGTTGTTTCGGTGAGGAGACTTATTGAG	1	0
57			
58	GATACTTGATGTTGAAGGTATTGACCCCTTCAG	0	0
59			
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4	GATATTTGTTGTTGGAGGTATTGACCCCTTCAG	0	0
5	TCAACTAGGTGTTGAGAGGGTTAAACCTTTTAG	5	0
6	CCGACTAGGTGTTCACTTTCCGACAGGGAAGGG	0	0
7			
8	CCGACCAGGGATATGAGGACTTTTATTTATACT	0	0
9	AGTGCTAGATGTCGCGGGAGTTCGCTCTTCGGTG	3	0
10			
11	CCGACCAGGGATATGAGTTGTTAGGATTGTACG	3	0
12	CCAACCAAAGATAAGGGTGGGAAAAACAAAGAG	3	0
13	GATACTCGATGTAGCTGGTATTGACCCCGGCTG	0	3
14	CCGACTCGGATTCAGATGAATCATAAAGTTCAT	0	0
15			
16	CTCGCTAGGGATTGGGAAATTAAATTTTCAGTC	0	2
17			
18	GAAGCCAGCCGTCGGGCAGCATGCTGTTTCGGTG	0	2
19	GACACTAGATGGGTGGTGAGCTATCGCTGCCTG	2	0
20			
21	GGCACTAGACGCCGGAGGGGTGACCTTTCGGTG	0	0
22	CACATTAGACCGGTGCGGTTTTGACGCCGTATC	0	3
23	CATACTAGGTGTAGGAGGGCTCAACCCTTCTG	0	3
24	AGTGCTAGATGTCGCGGGAGCTTAGCTTTTCGGT	2	4
25			
26	CCGACTTGGGATTGGAGGCGTGACTTTCCGCC	7	2
27			
28	CCGACCAGGGATATGAGGTATTCTTTTTCTAT	0	5
29	CCGACCAGGGATATGAGTAGTATATTTCAATTG	0	0
30			
31	CCGACTAGGGATTGGTGGTTGTCCATTTGGACT	0	0
32	CATACTAGGTGTAGGAGGGATCAACCCCTCTG	2	3
33	TCAACTAGGTGTTGGGAGGGTTGAACCTTTTAG	0	0
34			
35	AATGCTAGCTGATGGAGCTTCTACCGCTTCGTT	0	0
36	AATGCTAGCCGTTGGGGTGCATGCACCTCAGTG	0	7
37			
38	TCAATTGGTTGTTGGGAGGGTTTCTTCTCAGTA	0	4
39	GGCACTAGGTGTGGGACTCATTCCACGAGTTCC	3	5
40	TCAACTAGCTGTTGGTTCATATTAATGTGATTAG	0	0
41			
42	AGCACTAGACCGAAGAATCTCCACGATTTTTTG	0	5
43	CAGACTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
44			
45	GATACTTGTGTTGGAGGTATCGACCCCTTCAG	0	0
46	TTAACTGGTTGTTGGGAGGGTTTCTTCTCAGTA	0	5
47			
48	CGCACTAGGTCGGGAAGGCTTGACGCCCTCCTG	0	0
49	AGTGTTAAACGTTAGAATTTCTAATGTTACAGC	0	0
50	CTGACTAGGGATCGGTCCACGTTATTTTTTGAC	0	8
51			
52	TCAACTAGGTGTTGGGAGGGCTAAACCTTTTAG	0	0
53	CCGACTAGGGATTGGTGGGCGATTATTATATGT	4	0
54			
55	TCGACCAGACGTCGGAGGTATCTATCCCTCCGG	0	0
56	GATACTCGATGTGGCTGGTATTGACCCCGGCTG	2	0
57			
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4	GATACTTGTTGTTGGAGGTATTGACTCCTTCAG	0	0
5	GATACTAGTCGTCGGGACACCTAATCGTCTCGG	0	0
6	TCAACTAGGTGTTGGGAGAGTTAAACCTTTTAG	2	0
7	GAACTTGTTGTTGGAGGTATTGACCCCTTCAG	0	0
8	CCAATTAGGGATATGTGGACGTTTGTTGAAGA	5	0
9	AATACTTGGTGTCTGGAGTTTCAATACTCCGGG	2	0
10	CACACTAGATCGGTGCAGGTCTGACCCTGTATC	0	0
11	CCGACTAGGGATCAGGCAAGGAGTTTTTTGACT	0	0
12	ACGACTGGGTGTTGCGGGTATTGACCCCGCGG	0	2
13	CATACAAGCTGTAGTGGGGTTTTCTCCTGCTG	0	0
14	TTCCTAGATGTAGGAGGTATTGACCCCTTCTG	0	0
15	TTCTCTTGCTTTTCGGAGTATCGACCCTCTGAG	0	0
16	TCAACTAGGTGTTGGGTGGTAAAACCATTTAGT	5	0
17	TGCACTAGGTGCTGGGGCGGACGCTTCAGTGCC	0	0
18	CCGACTAGGGATTGGTCCACGTTTTTTCTGAC	0	0
19	GATATTAGGTGTGGGAGGTATCGACTCCTTCCG	2	3
20	TCGATTTGGAGGTTGTTCCCTTGAGGAGTGGCT	0	0
21	TGCATTAGGTGTAGGAGGATTCGACCCCTTCTG	2	3
22	AGCACTAGACGCTGGGGGGTGACCTTTCGGTGT	0	0
23	CAGATTAAGGGATGGAAGGAAAGAAATAAGATT	5	2
24	ATACTAGCTGTCCGGGCACATGGTGTGTTGGGT	2	0
25	AATACTAGGTTTTGGGCCCGTCAACGGTCCAGA	0	0
26	GGTACTAGGTAGTGGACCGGACATGGGTTCACT	4	2
27	GGTACTAGATGTGGGAGGTGTCGACTCCTTCCG	4	2
28	CTAACTAGGGATATGTGGACGTTTGTTGAAGA	3	4
29	GGCACTAGGTGTGGGGATCATCCTTGTTTCTG	0	4
30	CTGACCAGGGATCGAGGACAGTCCCATGGTTGA	0	0
31	TCAACTGGTTGTTGGGGAAGGAACTTCCTTAG	2	5
32	ATCACTCGATGTTGGCGATATACAGCCAGCGTC	0	0
33	CCGACCAGGGATATGAGTAGTATATTTCAATAG	0	0
34	TCAACTGGTTGTCGGGAGGGTTTCTTCTCAGTA	0	5
35	AGCACTAGGTAGCGGCCGGATCCGACCGGTGCG	0	5
36	TTAACTAGGTGTTGGGTGGGTAAAACCATTTAG	0	0
37	CTAACTCGTTTTTGGAGCGCAAGCTTCAGAGAC	2	4
38	TCAACTGGTTGTTGGGAGGGTTCTTCTCAGTAA	0	4
39	CCGACTAGGGATGAGTGAACGTTGCATTTTCGA	0	0
40	CCGACCAGGGATATGAGTAGTATATTTCAATTA	0	0
41	GGTACTGGGTAGAAAGCGCTCCGATAGCGCCTT	0	5
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3			
4	AACACTAGCCGTTGGAGGTACCCATTCCTTCAG	0	0
5	TCAACTAGTTGATCGGTGAGGAGACTCATTGAG	2	0
6	ATTGCTAGTTGTCGGGATGCATGCATCTCGGTG	0	0
7	GGTGCTAGGTGTCTCGGGTATTGACCCCCGAGG	0	0
8	TCTACTAGGTGTTGGGAGGGTTAAACCTTTTAG	1	0
9	TCGACTAGTTGTTTCGGTGCAGCAATGCGCTGAG	0	6
10	GATGCTAGCCGTCAGCCAGCATGCTGGTTGGTG	0	0
11	GATGCTAGCCGTTGGATAGCTTGCTATTCGGTG	0	0
12	AATACTAACTGTATGCGATATACTGTATGCGGT	0	0
13	CCGACTCGGATTCAGATGAACCAAAAAGTTCAT	0	0
14	TCAACTAGTTGTTTCGGTGAGGGGACTCATTGAG	3	0
15	GGTACTAGATTTGGTGGGATTTGACCCCTCGCCG	5	0
16	ATTACTCGATGTGTGCGATATACTGTACGCGTC	0	2
17	GGTACTAGGTAGTGGACTTGACATGGGTTCACT	2	0
18	AGCACTGGAGGAGAGGGGCTTCGGCCTTTCTCC	2	0
19	TAAACTTGCGTCGGTGGCTTAAACACCATCGG	0	0
20	TGGACCAAGGATCCGAGGACGTTACATGGATGA	0	0
21	AGTGCTAGACGTTGGGGATTTTTCTTCAGTGT	3	2
22	TCAACTGGTAGTTGGGTCTTAACTGACTCAGTA	0	0
23	CCGACTCGGATTCAGATGTATCAAAAAGTTCAT	0	0
24	TCAACTGGTTTTGGGTCTTAACTGACTCAGTAA	0	0
25	AATGCCAGCCGTTGGAAAGTTTACTTTTCAGTG	0	3
26	GATACTAGATGTTTGGAGAATTAACCCTCCGAG	0	0
27	AGCACCAGACGCCGGTGGGGTGACCTGTCGGTG	0	2
28	AGTGCTAAGTGTTAGGGGGTTTCCGCCCTTAG	0	3
29	ATCACTCGTTGTTGGCGATACACCGTCAGCGAC	0	0
30	CCGACTCGGATTCAGATGAATCAAAAAGTTCAC	0	0
31	CGAACTGGATGTTGGGTTCAACTTGGAGCTCAG	0	2
32	TCAACTAGCCGTCAGGTCCGCTTTAGGGCTTGG	0	0
33	CTGACTAGCGATCCGCCGGCGTGTTTCGATGA	3	0
34	CCGACTTGGGATTGGAGGCGCGCACTTTCGCC	3	1
35	AGCACTGGACCGGAGTTGTGCACACGATTCGG	2	0
36	TCAACTAGTTGTCGGGTCTTGTTGGGCTTGTA	2	3
37	TCAACTAGGTGTTGGGTGGTTAAAACCATTTAG	0	0
38	AATGCTAGTTGTTGGTAAGTTTACTTATCAGTG	0	0
39	AGCACTAGGTGTTGGATCCTTTAGGATTCGGTG	0	4
40	CCGACCGGGGATAGGGAGCACTGGTGAACTAG	0	2
41	AGTGCTAGATGTCGGGGAGCTTGCTCTTCGGTG	0	2
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4	GAAGCCAGCCGTCGGCCAGCATGCTGGTCGGTG	0	0
5	CCGACTAGGGATCGGTGGATGTCGCTTTTGA	0	3
6	AATGCTTGGTGTGGCGGGTATCGATCCCTGCCG	0	0
7	GGTGCTAGGAGGTGGGGCTCCTCGGCCTCTCCT	0	0
8	AGCACTAGACGCTGGGCGGGTGACCGTCCGGTG	0	3
9	AGAACTGGACGTTGGGAGGAATTCTCCTCTTAG	0	3
10	CGAACTGGATGTTGGGAGCAACTTGGCTCTCAG	0	2
11	CGAACTGGATGTTGGTCTCAACTTGGAGATCAG	2	3
12	CCGACTGGAGTGGGGGAGTCACTAAAAAATATA	2	4
13	GATACTCGACATTAGCGATACACTGTTAGTGTC	0	3
14	TCAACTAGTCGTTTCGGTGAGGAGACTCATTGAG	0	1
15	TCAACTAGTTGTTTGGTGAGGAGACTCATTGAG	3	1
16	GATGCTAGCCGTTGGGCAGCTTGCTGCTCAGTG	2	0
17	TCAACTGGTTGTTGGGTCTTAACGACTCAGTAA	0	0
18	CCGACTGGACGTGCACTACTACGGTAGGGCGTG	3	0
19	AATGCTAGTTGTTGGGGACTTAGTCTTCAGTGA	0	0
20	GATACTCGTTGTTGGAGGTATTGACCCCTTCAG	0	0
21	TCAACTTGGTGTGGGAGGGTTAAACCTTTTAG	0	0
22	TGTACTAGATGTTTCGGTTGACTACGGTTGATTG	0	0
23	GATACTAGATGTCGGGGGTCTGTCCCCTCGGTA	0	6
24	GATACTTGATGTTGGAGGTATTGACCCCTTCAG	0	0
25	AGTATTGAATGTTGGGAAAAGTTTTATTTTCTT	2	0
26	CCGACTAAGGATCGGAAGGGTTTCAACAGCCCT	0	0
27	GGTACTTGTTGTTGGAGGTATTGACCCCTTCAG	0	0
28	GATACTTGTTGTTGGAGGTATTTACCCCTTCAG	0	0
29	GATACTTGTTGTTGGAGGCATTGACCCCTTCAG	0	0
30	CCAACTAGGTCTTTTTTAGAGACACAATTCAAT	0	0
31	TCGACTAGGGATCGGTCCACGTTATTTTTTGAC	0	8
32	TGCACTTGGTGTGAGCCGATTAGGTTCAGTGC	0	0
33	ATGACTCGATGTTGGCGATACACAGCTAGCGTC	0	0
34	ATCACTCGATGTACACACTTGATGTGTGTGTCT	4	0
35	CCGACTAGGGATCGGATGGGTTGTTATTTTAGC	0	0
36	CCGACTCGGATTCAGATGAATCAAAAAGATCAT	0	0
37	ATTGCTAGTTGTTGGGGTGCTTGACCTCGGTG	0	0
38	TCCACTAGAGTGTGGCACCCTGACGGTGTCAT	0	0
39	CTAACGATGGACGCGGGGAATCAGTCTCTTTTG	0	0
40	CCGACTAGGGATCGGGCGATGTTGAATATATAT	2	0
41	CCGACTAGGGATGAGTGAACGTTGCTTTATCGA	5	0
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4	CCGACATAGGAATACGTAATAGTAGGACTAAAG	3	0
5	TCAACTAGGTGTTGGGAGGGTTAAGCCTTTTAG	1	1
6	AGTGCTAGCCGTTGGGACTTTTCAGTCTCAGTGG	0	0
7			
8	CCAACTCGGTGTTTGGTCCGGGGAACCGGACTG	0	0
9	ATCACTAGATGTCGGCGATACACAGTCGGTGTC	2	0
10	GAAGCTAGCCGTCGGGGAGCATGCTCTTCGGTG	0	0
11			
12	TGCACTTGGTGTGGCCGATTAGGTTTCAGTGCC	0	0
13	GGTGCTAGCCGTTGGGAAGCTTGCTTCTCAGTG	0	0
14			
15	CCGACTTGGGATTGGAGGCGTGCACTTTTCGCC	5	0
16	TCAACTAGGTGTTAGGAGGGTTAAACCTTTTAG	0	0
17			
18	TCAACTAGTTGTCGGGCCTTATTAGGTTTGTA	0	0
19	GATGCTAGGCGTGAGGGGTATCGACCCCCCTTG	0	0
20	CCGACTCGGATACAGATGAATCAAAAAGTTCAT	0	0
21			
22	TATGCTAGACGTGAGGGGACTTCGTCCTTTTCGT	0	3
23	GGTACTTGGCAGCGGGAGAACCTATGTCTTTTCG	0	2
24	ACAAGTAGATGTTGGGAGGGTCTGCCTCTCGGT	3	2
25			
26	GAAGCTAGCCGTTGGTAAGCATGCTTATCAGTG	0	0
27			
28	TCAACTAGGTGTTGGGTGGGTAAACCTTTTAG	2	1
29	CCGACCAGGGATATGAGGTATTTAGTATAGTAT	0	0
30	AGCACTAGGTGTTGGCCCCGTTAGGGGTTCAGTG	0	0
31			
32	TCAACTGGTTGTTTCGGTGAGGAGACTCATTGAG	1	3
33	CCGACTTGGGATTGGAGGTGTGCACTTTCCGCC	4	2
34			
35	TCAACTAGGTGTTGAGGGTTAAACCTTTTAGTG	0	0
36	AGAACTAGGTGTCGTGGGTGACCCCCGCGGTGC	0	0
37	AGCGCTAGACGTTGGGCAGGTGACTGCTCGGTG	2	3
38			
39	CGCACTAGACCGGTGCGGGTTTGACGCCGTATC	2	3
40	TCAACTGGTTGTTGGAGGGGTTCCCTTTTCAGTA	0	3
41			
42	TGCACTTGGTGTGGGCCGATTAGGCTCAGTGC	0	0
43	CCGACTGTAGATTAGAAGACGTTATTACAAGGA	2	2
44			
45	TATACTTGGTGTAAGTGGACTTAACCCTAGTTG	0	0
46	AGAACTGGGTGTAGGAGGGGTTAGAGCCTTCTG	3	2
47	GGTACTAGGCTTTGTGGGAATAGACCCCTGCAG	0	0
48			
49	GGTACTAGGTGTGGGGGACATTCCACGTTCTCC	0	2
50	GATACTAGCTGTTTGGAGTAATCTGAGTGGCTA	4	3
51	ATGACTGACTGAAGTGGGAGTAGATGTAGCTAA	4	3
52			
53	AATACTAGGTGTAGGGGTTGTCATGACCTCTGT	0	2
54	CGCACTAGACCGATGCAGGTCTGACCCTGTGTT	0	0
55			
56	AAGACTCGATGTTGGCGATATACAGCCAGCGTC	2	3
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4	CCGACTCGGATTCAGATGAATCAAAAAGTACAT	0	0
5	ATGACTCGATGTTGGCGATACACAGCCAGTGTC	0	0
6	TGCTAGACCGGTGCGGTTTTGACGCCGTATC	0	5
7	ACAAGTAGGCGCTGAGGGTCTCAACCCCCGCGG	0	5
8	CCGACCAGGGATATGAGTTGTTAGGAATATACG	0	3
9	AACTGGTTGTTGGGTCTTAAGTACTAGTAAC	0	0
10	AGCATTTGATTTAGTGTAACTCTTATATTATT	0	4
11	ATCACTAGATGTCGGGGGTCTTACCCCTCCGGT	0	4
12	CGGACCAGGGATTGGGAGACGTTACGTGGATGA	0	0
13	ATGACTCGACCTGTGCGGGGCTCAATCCCCCGT	0	5
14	CCGACTAGGGATCGGTTACGTTATTTTTTAC	0	5
15	TCAACTGGTTGTTGGGGGAGTGAAATCCCTTAG	3	0
16	CCGACTAGGGATCGGTGGAAGTCGATTTTACT	0	0
17	AATGCCAGCCGTCGGGCAGCATGCTGTTCCGGT	0	0
18	CCAAGTAGTTGTTCCGGTGAGGAGACTCATTGAG	1	3
19	TCAACTAGTTGTTGGGAGGGTAAACCTTTTAG	0	0
20	ATGGCTGGATGTTGGTGATACACCGTCAGCGTC	0	0
21	TCAACTAGGTGTTGGGAGGATTAAACCTTTTAG	3	0
22	GATACTCGATGTTGGGGCTTCGGCTTCAGTGTC	0	0
23	CCGACTCAGGATTGGCGGGGTGTCGTTTATGACC	0	0
24	CGCACTAGACCGGTGCGGTTTTGACGCTGTATC	0	0
25	GATACTTGTGTTGGAGGTTGACCCCTTCAGTG	0	0
26	AGAACTAGGCGTTGGAAGGTTTTACCTTTTAGT	0	0
27	TAACTAGGTGTTGGGAGGGTTAAACCTTTTAGT	0	0
28	TGTGCTGGGCGTCGGGGGGCTTGCCCCGCGGTG	0	3
29	TCAACTAGGTGTTGGGAGGGTTACCTTTTAGTG	3	0
30	TCAACTAGGTGTTGGGGGGTTAAACCTTTTAGT	0	0
31	TAACTCGATATTTATTCTTCGGAGTGAGTGTC	0	0
32	CCGACTTGGGATTGGAGGCGTGCACTTTCCACC	0	0
33	CCGACTCGGTTTCAGATGAATCAAAAAGTTCAT	0	0
34	CGCACTTGCTGTGAGCGGAATCGACCCCGCTCG	0	0
35	GATACTTGTGTTGGAGGTATTGACCCTTCAGT	0	0
36	CCGACTCTGATTCAGATGAATCAAAAAGTTCAT	0	0
37	TCAACTGGTTGTTGGACGTCTTGCTGTTTCACTA	0	0
38	TAGACAAGATGTGGGGGGTATCGACCCCTCCG	0	0
39	GTCCTAGCTGTCGGGAGAACTTACCTCCCGG	0	0
40	GATACTTGTGTTGGAGGTATTGATCCCTTCAG	0	0
41	ATGGCTGGATGTTGGCGATACATCGTCAGCGTC	0	0
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4	CCAACTAGGAATACGTGGACGTTTGTTCGAAGA	4	0
5	CCGACTCGGATTCAGTTGAATCAAAAAGTTCAT	0	0
6	TCAACTAGTTGTCGGGTCTGTTTAAGGATTGGT	0	0
7	ATTACTCGTTGCTGGAGGTAACTTTCAGTGACC	2	0
8	AGTGCTGGATATCAGTAGCGAAGCTATTGGTTT	0	0
9	TCAACTAGGTGTGGGAGGGTTAAACCTTTTAGT	0	0
10	TCAACTAGGTGTTGGGTGGGTAAAACCATTTAC	0	0
11	CCGACTCGGATTCAGATGAATCAAGAAGTTCAT	0	0
12	TAAACTCGACATTAGCGATACACAGTTAGTGTC	0	2
13	CCGACTCGGATTCAGATGAATCAAAAAGTCATT	0	0
14	GGTACTAGATAGTAGACTTGATATGGGTTTACT	0	2
15	AGCACTGGGTTGGAGGGTTCTCCACGACCTTCC	0	2
16	CTAACTCGTTTTTGGGGCGCAAGCTTCAGAGAC	0	0
17	CCGACTAGGGATTAGCAGACGTTTCATTGATGA	0	0
18	AGAACTTGACGTCGGTTTGCTCTGCAAGTCGGT	0	2
19	AGAACTAGGCGTTGGAAGGTTTTACCTTCTAGT	6	0
20	ATGGCTGGATGTTGGCGATATACCGTCAGCGTC	0	0
21	CCAACTAGGATATGTGGACGTTTGTTTGAAGAC	2	0
22	CCGACTTGGGATTGGAGGCGTGCAATTTCCGCC	1	2
23	AGAACTAGACGTTGGGAAGCTTGCTTCTTAGT	4	0
24	ATAACTCGTTGTTGGCGATATACAGTCAGCGAC	2	0
25	CGAACTGGATGTTGGGCTCAACTTGGAGCTTAG	3	0
26	ATTACTCGTTGCTGGGAGGTAACTTTCAGTGGC	3	0
27	CGCACTAGACCGGTGCGGTTTTGATGCCGTATC	1	0
28	CCGACCAGGGATCGAGGACAGTTCCATGGTTGA	0	2
29	GATGCTAGCCGTCAGCGAGCTTGCTCGTTGGTG	0	0
30	CCGACTAGGAATGAGTGAACGTTGCATTATCGA	0	0
31	ATGACTCGATGTTGGCGATACATAGCCAGCGTC	0	0
32	TCAACAAGGTGTTGGGAGGGTTAAACCTTTTAG	0	0
33	GAAACTAGGCGTGGCTTGATCGACCCGAGCCG	0	0
34	AATGCTAGCCGTTGGATAGCTTGCTATTCAGTG	0	3
35	CCGACCAGGGATCGAGGACAGTCTCATGGTTGA	0	0
36	TCAACTAGTTGTTTCGGTGAGGAGACTCATTGAT	0	0
37	TCAACTAGTTGTCGGGTCTTTGGGCTTGGTAAC	0	2
38	CCATCTTGGAATTGGGCGGATATATTATGATTC	0	2
39	TCAACTAAGTGTTGGGAGGGTTAAACCTTTTAG	3	0
40	CCGACTAAGGATCGGCAGAGGTCGTTAGCGACA	0	0
41	AGTACTAGCTGACTGGTTAAGACTGGGTGGCGA	0	2
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**ScholarOne Support 1-434/964-4100**

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3			
4	CACACTGGATGCCGAAACTCTGACGTTGCCGG	0	0
5	CCGACTTGGGATTGGAGGCGTGTATTTCCGCC	0	0
6	CCGACTTGGTGTTCGCGGGTTTAAAGTCCGGGGG	0	0
7			
8	TACACTAGACTGGTGCGGGTTTGACGCCGTATC	0	0
9	CACGTTTGCTGTGAGAGGATTCGACCCCTTTCG	0	0
10			
11	CCGATTTGGGATTGGAGGCGTGCACTTTCCGCC	0	0
12	CCGACTTGGGATTGGAGGCGTGCTCTTTCCGCC	3	0
13	ATGACTTGGTGTGTTGGGTTTAAAGTCCCGGCG	0	0
14			
15	GGTACTGGGTAGAAAGCGTTCCGATGACGCCTT	0	0
16	CCGATCGGGGATGGGGAGAGGTAATACCTTAAC	3	0
17			
18	GTCACTCGGTGTTGGCGATACACAGCCAGCGCC	3	0
19	TCAACTAGGTGTTGGGTGAGTAAACCATTAG	3	0
20	CGAACTGGATGTTGGGCTTAACCTGGAGCTCAG	2	0
21			
22	AGTGCTGGGTGTAGGGGGTCATCACCCCCCTG	0	0
23			
24	GATACTTGTTGATGGAGGTATTGACCCCTTCAG	0	0
25	TCAACTAGTTGTTGCGCGAGGAGACTCATTGAG	1	1
26	CCGACTCGGGATCGGTGGTCGTTCAATCAATGA	0	0
27			
28	ATGACTCGATGTTAGCGATACACAGCCAGCGTC	0	0
29	CCGACTCGGATTCAGATGAATAAAAAGTTCATT	0	0
30			
31	GGTACTAGGTAGTGGACTTACATGGGTTCCCTG	0	0
32	CCGACCAGGGATATGAGTAGGTTATTTCAATTA	0	0
33	CCGACTAGGGATGAGTGAACGTTGAATTATCGA	0	0
34			
35	CCAACTAGGGATACGTGGATGTTTGTTCAAGA	0	0
36	TATGCTAGACCGGTGCGGTTTTGATGCCGTATC	0	0
37			
38	TATACTAGACTGGTGCGGTTTTGACGCCGTATC	0	0
39	ATCTCTAGCTTTGAGGAGTATCGACCCTCTTCG	0	0
40	ATTACTCGATGTTGGCGATACGCGGCCAGCGTC	0	0
41			
42	CCGGTTAGGGATTGGCAGGGTTTCGTTATGTCT	0	0
43	TCAACTAGCTGTTGGTTATATGAATATAATTAG	5	0
44	ATTACTAGATTTTGGCCGTAAGGTCAGAGTCCA	0	4
45			
46	CCGACTCGGATTCAGATGAATCAAAAAGTTCGT	0	0
47	CCGACTTGGGATTGGAGGCGTACACTTTCCGCC	4	0
48			
49	TCTACTAGCCGTTGGGGGACTTGATCCTTTAGT	0	0
50	ACCCCCATGAATTGGGGAATTTTGGTCGGTGT	0	2
51			
52	TCAACAAGTTGTTGCGGTGAGGAGACTCATTGAG	0	2
53	TCGACTAGTCGTTGCGGAGCAGCAATGTACTGAG	0	0
54	GGTGCTAGGTGTACGGGTCATGACCCTGTGGT	0	0
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56	CCGACTAGGGATGGGTGAACGTTGATTTTACG	0	0
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4	AGTGCTGGGTGTCCGACATCTGTTGGGTGCCGT	0	2
5	TCGACTAGTTGTTCCGGTGAGGAGACTCATTGAG	2	0
6	CGAACTGGACGTTGGTCTCAACTCGGAGATCAG	2	0
7	TGAACTGGATGTTGGGCTCAACTTGGAGCTCAG	2	0
8	TCAACTGGTTGTTGGACGGCTTGTGTTTCAGTA	0	0
9	TACGCTAGATCGGTGCGGGTTTGACTCCGTATC	0	0
10	ATTACTCGATGTGTGCGATACATGGCACGCGTC	0	0
11	TCAACTAGTAGTCGGATCTTAATAGATTTGGTA	0	3
12	ATCACTTGATGTTGGCGATACACAGCCAGCGTC	0	0
13	TCAACTGGTTGTTGGGAGGGTCTCTTCTCAGTA	0	1
14	AGTGCTGGATGTCGGGAAGCCTATCTTTTCGGT	0	0
15	TCGACTAGTCGTTTCAGAGCAGCAATGCACTGAG	2	0
16	TCAACTGGTTGTTGGGTCTTAACTGACTCAGCA	0	0
17	GGTACTAGGTGTTGTGGGAATTGACCCCTACAG	0	3
18	AGTACTAGGTGTGGGTGGAGTCAAATCCATCTG	0	3
19	CCGATTAGGGATGAGTGAACGTTGCATTATCGA	0	3
20	CCGACCAGGGATATGAGTTGTTAGGAATATGCG	0	3
21	TGCACTTGGTGTGGGACGATTAGGTTCAGTGC	0	0
22	TCAACTGGTCGTTGGGAGGGTTTCTTCTCAGTA	0	1
23	GGTACTAGGTGTGGGTTTCCTTCCTTGGGATCC	0	3
24	AGAACTAGCCGTTCCGGTCCCGTATGGGATTGAG	3	2
25	ATAACTCGCTGTTGGCGATACACAGCCAGCGGC	3	2
26	AGCACTAGACGCTGGGTGGGTGACCGTCCGGTG	3	2
27	GGCACTAGGTGTTCCGGGTATTGACCCCCTGAG	0	2
28	CGAACTGGATGTTGGGCTCAACTTGGAGTTCAG	0	2
29	TACTACTAGACTGATGCGGTTTTGACGCCGTATC	0	0
30	TCAACTGGTTGTTGGGAGGGTTTCTTCAGTAAC	0	2
31	CCGACTCGGATTCAGATGATTCAAAAAGTTCAT	0	0
32	AATGCTAGCCGTTGGCCAGCTTGCTGGTCAGTG	2	3
33	AGAACTGGGTAGTGGTCCGGGCATGGGATCACT	2	3
34	CGTGTTGGACGTTGGCGAGCCTAGCTCGTCGGT	0	0
35	AATACTAGGTGTTGGATACATTTGTATCCAGTG	0	3
36	TCAACTGGTTGTTGGGAGGGTTTCTTCTCGGTA	1	3
37	ATGACTCGATGTTGGCGATACAGCCAGCGTCCA	3	0
38	GATACTAGGCGCTGTGCGTATCGACCCGTGCAG	0	0
39	CTAACTCGTTTTTGGGCTTTAGGGTTCAGAGAC	0	0
40	TCTACTAGTTGTTGGTGGAGTAAAATCCATGAG	0	0
41	GGCACTAGGTGTGGGGGACATTCCACGTTCTCC	0	3
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CCAACCAAAGATAAGGGTGGGAAAAACAAAAG	0	3
TCTACTAGTTGTTGGGTCTTAATTGACTTGGTA	0	3
TGCATTTGGTGTGGGCCGATTAGGTTCAGTGC	0	0
AATGCCAGACGTCGGGTAGCATGCTATTCGGTG	0	0
TCAACTAGTTGTTTCGGTGAGGAGATTCATTGAG	0	2
AGTGCTAGCTGTTGGGGGGTTACCTCTCAGTGG	0	0
CTAACTCGATGTTGGAGGTGAAAACTTTCAGCG	0	0
TCAACTAGTTGTTTCGGTGTGGAGACTCATTGAG	1	0
TCAACTAGATGTTGGGAGGGTTAAACCTTTTAG	0	0
CCGACTCGGATTCAGATGAATAAAGTTCATTTG	0	0
TGTGCTAGATGTCGGGGTTTTAAACTTCGGTGT	0	0
GATGCTAGATGTTGGTAATTTTCGGTTATCAGTG	0	0
TGCTAGGTGTGGGAGGTATCGACCCCTTCCG	0	0
TACACCAGACTGGTGCGGTTTTGACGCCGTATC	0	0
CCGACTAGGGATCGGACGGTGGTTTTTTTATGC	0	5
TCAACCGTTGTTGGGAGGGTTTCTTCTCAGTA	0	5
CTTACTCGACGTCCGGCCCCTGCGGTCTGTCGT	0	5
TCAACTAGGTGTTGGGAGGGTCAAACCTTTTAG	0	1
TCAACTAGTTGTCGGATCTTAATAGATTGGTAA	3	0
CCAACCAGGGATCGAGGACAGTCCCATGGTTGA	0	0
TGCGCTTGGTGTGGGCCGATTAGGTTCAGTGC	0	0
TCCACTAGATTGTGGCACTTTTAACGGTGTCAT	0	0
TCAACTAGGTGTTGGGAGGGTAAAACCTTTTAG	0	0
ATGACTTGGTGTGTTCGGGTTTTAATTCCCGGCG	0	0
CCGACTCGGTTTCAGATGAATCAAAAAGTTCATT	0	0
AATGTAAAAAAAAAAAAATAATTTTTATTTTATT	0	0
GAAGCTAGCCGTTGGTGGGTTTACCCATCGGTG	0	0
CTAACGATGGACGCGGGGAATCAGAAAGAATCA	0	0
CCGACCCGGATTTCAGATGAATCAAAAAGTTCAT	0	0
ATTACTCGCTGCTAGATGGCAACGTTTATGTTG	0	0
AGCACTGGGTGAGGGGACTTCCACATCCTCTC	0	0
TCAACTAGATGCAGGGGGTGTGATCCCCTCTG	0	3
CCGACCAGGGATCGAGGACAGTCCCATGGTTAA	0	0
ATCACTAGATTTTGGTCGTATAGTCAGAGTCCA	0	0
GATACTAGCTGTTGGGAGTAATTTTCGGTGGCTA	0	0
TCAACTAGCTGTTTCGGTGAGGAGACTCATTGAG	0	1
GATACCAGCTGTTGGGAGTAATTTTCAGTGGCTA	0	0
ATCACTCGATGTTGGCGATACACAGCCAGCGTT	0	0

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4	TCAACTAGGTGCTGGGTGGGTAAAACCATTTAG	0	0
5	GATACTTGTCGTTGGAGGTATTGACCCCTTCAG	0	0
6	GATACTAGCTGTTGGAGGAACTTCGGTGGCTA	0	0
7	CCGACTAAGGATCGGCAGAAAGTCATTTTTGACT	0	0
8	CGAACTAGCTTTTTGGTTTTAGGATTGGGAGGC	0	0
9	TGCACTTGGTGTGGGGCCGATTAGGTTCAGTGT	0	0
10	TCGACTAGGGATCGGTGGACGTTGCATAGCATG	0	0
11	AGTACTAGATATCGGGATTTATTTCCGGTGTCGC	0	0
12	CCAGCTAGGGATATGTGGACGTTTGTGTTGAAGA	0	0
13	GGTACTAGCTAGTAGGGTTCACATGACTTTACT	0	0
14	GATACTTGTTGGAGGTATTGACCCCTTCAGTGA	0	0
15	CTTACTCGACGTACGGCCCTGGTGGCTGTGCGT	0	0
16	GATACTAAATGCTGTCAAAAACAGTGTTGAAGC	0	0
17	TCAACTAGTTGTTCTGTGAGGAGACTCATTGAG	0	0
18	CTTACTCGACGTCCGGCCCCTGTGGTTCGTGCGT	2	0
19	GGCACTAGGTGTGGGGAGCATTTTCACGTTCTCC	2	0
20	TATACTTGGTGTAATCGGACTCAACCCCGATTG	2	0
21	TTGACTAGGTGTCGACGGTCTAAACCCCGCCGG	2	0
22	CTGACTTGGTGTTCAGGTTTTAAGTCCTGGGG	2	0
23	CCGACTTGGGATTGGAGGCATGCACTTTCCGCC	2	0
24	CCAACTAGGAATATGTGGACGTTTGTGTTGAAGA	2	0
25	CCGACTAAGGATCGGCAAAGGTCATTATTGACA	0	0
26	TCATCTAGGTGTTGGGAGGGTTAAACCTTTTAG	0	0
27	ATGACTTGATGTTGGCGATATACAGCCAGCGTC	0	0
28	AACACTGGAGAAAGGGGGCTTCGGCCTTCTTTC	0	0
29	GATACTTGTTGTTGGAGATATTGACCCCTTCAG	0	0
30	TCAACAGGTGTTGGGAGGGTTAAACCTTTTAGT	0	0
31	ATGACTCGATGTTGGCGATACACGGCCAGCGTC	0	0
32	TACTACTAGACTGGTGTGGTTTTGACGCCGTATC	0	0
33	ATTACTCGACATTGGCGATACACAGTCAGTGTC	0	0
34	TCAACTAGTTGTCGGGTCTTATTAGGCTTGGTA	0	0
35	GATGCTAGCCGTCGGTCAGCTTGCTGATCGGTG	0	0
36	TCAACTAGGTGTTGGGAGGGTTAAACCTTCTAG	0	0
37	GGCACTAGCTTGGGGTCTCCTGTGTGATCCCAG	0	0
38	TGTACTTGATGTACCTAGGCTCAACCCTGGGTG	0	0
39	TCAACTAGGGATATGTGGACGTTTGTGTTGAAGA	0	0
40	CCGACTGGAGTGGAGGAGTCACAATTCATACTC	0	0
41	GGTACCAGGTGTGGACTTGCATGGGTTCACAG	0	0
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4	CCGACTTAGGATTGGAGGCGTGCACTTTCCGCC	3	0
5	TCAACTAGTTGTTGGGTCTTAATAGACTTGGTA	0	0
6	CCGACCAGGGATATGAGTTGTTAAGATTACATG	4	0
7	ATAACTAGCTGTCCGGGCACTTGGTGCCTGGGT	4	0
8	TCAACTAGGTGTTGGGTGGGTATAACCATTTAG	4	0
9	CCGACCAGGGGATGGGGAGAGGTAATACTTTAAC	4	0
10	CCGACTCGGATTCATGAATCAAAAAGTTCATTT	0	0
11	CCGACCAGGGATATGAGTAGGTTATTTCAATAG	0	0
12	TCAACTGGTTGTTGGGAGGGTTTCTTCACAGTA	0	0
13	CCGACTAGGGATTGGAGGATGTTCTTTTGATGA	0	0
14	AATACTAGGTGTCTGGGGTCAAACCTAGGTGCC	0	0
15	CCGACTGTAGATTAGAAGACGTTAATCAAGGAA	2	0
16	CCGACTAGCAATCCGCCGGCGTGTTTCGATGA	2	0
17	CCGACCAGGGGATGGGAGAGGTAATACCTTAACC	2	0
18	ATTACTCGTTGCTGGGAGGTAATTTTCAGTGAC	3	0
19	CGCATTTGCTGTGGACGGAATCGACCCCGTCCG	0	0
20	CCGACTAGGGATATGTGGACGTTTGTGTTGAAGA	0	0
21	CCAACTAGGGATATGTGGACGTATGTTTGAAGA	0	0
22	CCGACTAGGGATTGGGGAGTCATCAAGCTCCCC	0	0
23	AGCACTAGGTGTCGGGGGTATCGACCCCTCGG	2	0
24	CGCACTAGACCAAGTGCGGTTTTGACGCCGTATC	2	0
25	TATGCTAGACCGGTGTGGTTTTGACGCCGTATC	2	0
26	TATACTAGGTGTAGCTGGACTCAACCCAGTTG	2	0
27	TTTACTAGTGTTGCGGGTATTTATTTATCTGCA	2	0
28	TTTACTTGCTGTTGGGGGCAACCTAAGTAGCGA	2	0
29	GATGCTAGCCGTCAGCAGGCTTGCTGTTGGTG	2	0
30	CCGACTAGCGATCCGCCGGCGTGTTTGTATGA	0	0
31	CGAACTGGATGTTGGGCTCAACTGGGGCTCAG	1	0
32	CCGACTCGATTGAGATGAATCAAAAAGTTCATT	0	0
33	CCGACTCAGGATCGGTGGGCTGTTTTTAGTGGC	0	0
34	CTTACTCGACGTACGGTCCTGGCGGCTGTGCGT	0	0
35	GATACTTGTTGTTGGAGGTATTAACCCCTTCAG	0	0
36	TCAACTGGTTGTTGGGAGGGTTTCTTCTCAGCA	0	1
37	TTTACTTGCTGTTGCGTCTTCGGATTGAGTGGC	0	0
38	GATACTAGCTGTTGGAGGAACTTCAGTAGCTA	0	0
39	CATATTTGAGGTGGGGGGATTGACCCCTTCCG	0	2
40	CCAACTAGCGATTAGCTGCTGTTAAAAACGACA	0	2
41	ATCTCTCGGTTTTTCGGAGTATCGACCCTCTGAG	0	2
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5	CCGACTTGGGGTTGGAGGCGTGCACTTCCGCC	0	2
6	TCTACTAGTTGTCGGGTTTTAATTGACTTGGTA	0	2
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8	TCAACTAGGAGTTGGGTGGGTAAAACCATTTAG	0	0
9	ATTACTCGACATACGCAATACACAGTGTGTGTC	0	0
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11	ATTACTAGGTGTTAGTGGTATCAAGCCCACTAG	0	0
12	CGAACTGATGTTGGGCTCAACTTGGAGCTCAGT	0	0
13	TCGACTGGTTGTTGGGAGGGTTTCTTCTCAGTA	0	2
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15	CGCACTAGACCGGTGCGGTTTTGACGCCGTATT	0	2
16	AGTGCTAGACGTTGGGGTTATAAACTTCAGTGT	0	2
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18	TCAACTGGTTGTTGGGAGGTTTTCTTCTCAGTA	0	1
19	GATACTAGCTGTTGGGGGTAATTTCAGTGGCTA	0	0
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21	TAAACTTGGCGTTGGTGGCTTAAACTCCATCGG	0	0
22	TACACTAGACTGGTGCGATTTTGACGTCGTATC	0	0
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24	TTCACTAGTGTTGCGTGTATTTATTTATCTGCA	2	2
25	CCGACTTGGGATTGGAGGCGTGCGCTTCCGCC	2	2
26	AGTACTGGGTGTGGGTGGAGTCAAATCCATCTG	2	2
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28	GGTGCTAGCTGTTCCGGGGTTACCCTTGAGTAG	2	2
29	AGCACTAGACGCTGGGCGGGTGACCGGCCGGTG	2	2
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31	CCGACTAGGGATGGGTGAACGTTGAATTTACGA	0	2
32	TACACTTGGTGTTTGCGGTTCCATCCGTAGGCAC	0	2
33	ACAAC TAGACGTTGGGAGGGTAAGCCTCACAGT	0	2
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35	ATGACTCGATGTTGGCGATATACAGCCAGCATC	0	2
36	GATGTTAATTCTTGACTTTTTTGCTTTTTTTTA	0	2
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38	TGCACTTGGTGTTGGGTGCGATTAGGTTCAGTGC	0	0
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41	ATTACTCGACATACGCAATACACTGTGTGTGTC	0	2
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8	ATGACTCGATGTTGGCGTTACACAGCCAGCGTC	0	0
9	ATGACTTGGGGTGTGCGGGTTTAAAGTCCCGGCG	0	0
10	AGCACTAGATGTCGGGCGGGTGACCGTCCGGTG	0	0
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20	CCGACTAGGGATCGGTCCACGTTATTCTCTGAC	0	4
21	GATACTTGGTGTGTGGGGTATTTAGTCCCCACG	0	4
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25	ATCACTAGATTTTGGCTGTATGGTCAGAGTCCA	0	0
26	ATGACTTGGTGTGTGCGGGTTTAAAGTCCCGGTG	0	0
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30	TCAACTAGTTGTTTCGGTGAGGAGGCTCATTGAG	0	0
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38	AGCACTGGATTGAAGGGTCCTCCATAGCCTTTC	0	2
39	AGAACTAGGTGTCGTGGGGGTTGACCCCCGCGG	0	2
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5	AGAACTAGGTGTCGTGGGTGTTGACCCCGCGGT	2	0
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7	ATACTCGATGTTGGCGATACACAGCCAGCGTCT	0	0
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9	TGCACTCGGTGTTGGGCCGATTAGGTTCAGTGC	0	0
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12	ATGACTCGATGTTGGTGATACACAGCCAGCGTC	0	0
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20	CCAAGTGGTCTTTTTTAGAGACACAATATTAT	0	0
21	AGTGCTAGACGTTGGGGCCCCTAGGGCTTCGGT	0	0
22	ATTACTCGATGTGTGCGATACACGGCATGCGTC	0	0
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24	TATACTTGGTGTAACCGGACTCAACCCCGGTTG	0	0
25	TACTACTGGACTGGTGCGGTTTTGACGCCGTATC	0	0
26	TGTACTTGGTGTTGGGCCGATTAGGTTCAGTGC	0	0
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32	TCAACTAGTTGTCGGGTCAGTTTAAGGATTG	0	2
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35	TCAACTAGTTGTCGGGTTTGTGTTAAGGATTG	0	0
36	ATTACTTGCTGCTAGATGGCAACGTTTAGTGGC	0	0
37	AGTGCTAGATATTTAGATATTATTCTGAGTGTC	0	0
38	ATGGTTGGATGTTGGCGATACACCGTCAGCGTC	0	0
39	GGTGCTAGGTGTCGCGGGCTTTGATCCCTGCGG	0	0
40	GATACTTGTGTTGGAAGTATTGACCCCTTCAG	0	0
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CCAACCAGCAATCAGCCTGAGTTGTCTATTGAC	0	0
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4	CCGTCTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
5	TCAACTAGTTGTTCCGGTGAGGAGACTCAATGAG	0	1
6	ACAACTGGTTGTTGGGAGGGTTTCTTCTCAGTA	0	0
7	TCAACTAGTTGTTCCGGTGGGGAGACTCATTGAG	0	0
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9	TTCGTTAGATGTGGGAGGTATCGACCCCTTCCG	0	0
10	TCGACTAGTCCTTCGGAGCAGCAATGCACTGAG	0	0
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12	GATACTAGCTGTTGGGAGAAATTTCAAGTGGCTA	0	0
13	CCGACCAAGTGATCGAGGACAGTCCCATGGTTGA	0	0
14	AGCACTGGGTAGGGGGTCCGCCCATGGACTCCC	0	0
15	ATTACTCGATGTTGGTGATACACAGCCAGCGTC	0	0
16	GATACTTGTTGCTGGAGGTATTGACCCCTTCAG	0	0
17	GATACTTGTTGTTGGAGGAATTGACCCCTTCAG	0	0
18	CCGACTCGTATTCAGATGAATCAAAAAGTTCAT	0	0
19	CCGACTTGGGATTGGAGGCGTGCACTTACCGCC	0	1
20	TACGCTAGATCGGTGCGGGTTTGGCCCCGTATC	3	0
21	CCGACCGGGATGGGGAGAGGTAATACCTTAACC	3	0
22	CCGACCAAGGATAAGAGGTCGTAATTATCTTGT	3	0
23	GGCACTAGGTGTGGGGATCTATCGACGGTCTCC	3	0
24	CCGACCGGGGATAGGGAGAATGGTGAGACCAGA	3	0
25	TCAACTAGTTGTCGGGTCTGTTTAAGGATTTGT	3	0
26	ATCACTCGATGTGTGTGATACACAGCACGCGTC	3	0
27	TCTACTAGTTGTTGGGTGCGCAAGTGCTTG GTA	3	0
28	AGCACTGGGTGGAGGGTCCTCCATAACCTTCC	3	0
29	CCAACTAGGGATATGTGGACGTTTGTTTGAAGT	3	0
30	CTTACTCGACGTACGGCCCTGGCGCCTGTGCGT	3	0
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32	TGAACTTGGCGTTGGTGGGTAAACTTCATCAG	3	0
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36	TCAACTAGTTGTCGAGTCTTATTGGGCTTG GTA	0	0
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38	ATTACTCGCTGCTAGAGGGCAACCTTTAGTGGC	0	0
39	CACGTTTG GTGTGGGCAGGTT CAGACCCTGTCC	0	0
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41	TCGACTAGGTGTTCCGGGAAGGAGACTTCTCGAG	0	0
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5	ATCGCTGGGTGTGGGGGGTTTTACTCCCCCGT	0	0
6	GGAAGTGGGTAGGGGGGCTCTCCGATGGGCCCCC	0	0
7	ATGACTCGATGTTGGCGTTATACAGCCAGCGTC	0	0
8	CGAACTGGATGATGGGCTCAACTTGGAGCTCAG	0	0
9	GATGCTAGCTGATGGGACTTTTACCGTCTCGTT	0	0
10	TCGACTCGGATTCAGATGAATATTAAAGTTCAT	0	0
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13	GATACTAGTTGTTGGAGGAACTTCAGTGGCTA	0	0
14	TCGACTAAGGATGATAAAATATTAAAAATGATT	0	0
15	CCAGTTAGGGATTGGTAGGGTCTCGTTACGTCC	0	0
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17	TCGACTAGTCGTTTCGGAGCAGCAATGCATTGAG	0	0
18	CTGACTTGGTGCCCCCGGTTTAAAGTCCGGGGT	0	0
19	ATTACTCGATATGTGCGATACACGGCACGCGTC	0	0
20	AGCACTGGGCGGGAGGAGGTTTCCTTTTCTGC	0	0
21	ATCACTAGATTTTGGTCGTATGGTCAGAGTCCA	0	0
22	CGAACTGGATGTTGGCCTCAACTTGGAGCTCAG	0	0
23	TCATCTAGTTGTTTCGGTGAGGAGACTCATTGAG	0	0
24	TCAACTAGTTGTTTCGGAGAGGAGACTCATTGAG	0	1
25	AGTGCTAGTTGTCTGGGCCCTTAGGGTTCGGTGG	0	0
26	ATGACTTGGTGTGTCTGGATTTTAAAGTCCCGGCG	0	0
27	TCGACTAGACGTTTCGGAGCAGCAATGCACTGAG	0	0
28	CCGACCAGGGATATGAGTAGCATATTTCAATTA	0	0
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35	ACGACTAGGTGTGGGAGCGTGACAACGGTCCCG	0	0
36	CCAAGTGGGATATGTGGACGTTGTTTGAAGAC	0	0
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41	ATTACTCGACATACGCGATACACAGTGTGCGTC	0	0
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5	GGCGCTAGGTGTGGGGATCCTTCCACGATCTCC	0	0
6	TCAACTGGTTGTTAGGAGGGTTTCTTCTCAGTA	0	0
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8	TCAACTGGTTGTTGGGAGGGTTTTCTTCTCAGT	0	0
9	TCAACTAGTTGTCGGGTCCTATTGGGCTTGGA	0	0
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11	TCAACTGGATGTTGGGAGGGTTTCTTCTCAGTA	0	0
12	CCAACTAGGGATATGTGGACGTTTGTGAAGACT	0	0
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24	CCGACTGGGGATGAGTGAACGTTGCATTATCGA	2	1
25	CCGACTTGGGATTGGAGGCGTGCACTATCCGCC	2	1
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8	AGAACTAGCTGTCAGGGCCTTTTAGGCTTTGGT	0	0
9	TCTACCAGTTGTTAGAGGTATTAACCTCTAG	0	0
10	GGTACTAGAGTTTGGGGGAGTTGACCCCTCCGG	0	0
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18	CCGACTTGGGACTGGAGGCGTGCACTTTCCGCC	0	2
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30	CCGACTTGGATTCAGATGAATATTAAGTTCAT	0	3
31	ATGACTAGGTGTTGGAAGAGTTGACCCTTTCAG	0	3
32	CCGACTAGGATCGGTCCACGTTATTTTTTACT	0	3
33	TCAACTAGTTGTTGGGGATTCATTTTCTCAGTA	0	3
34	CCGACTAGGGATCGGTCCACGTTTTTTTACTG	0	3
35	CCGACCAGGGATCGGTCCACGTTATTTTTTACT	0	3
36	CCGACTAGGGATTGGTCCACGTTATTTTTTACT	0	3
37	TCGATTAGCCGTTGGAATCCTTGAGATTTTAGT	0	3
38	AGAACTGGATGAGTGTGGAGTTAAATCCATGCG	0	3
39	ATACTAGCTGTTGGGGCTCTTAGAGTTCCAGT	0	3
40	AATACTTAAATTTTAATTTTTTTTAGTAAGTG	0	3
41	TCAACTGGTTGTTGGGAGGGTTTCTTCTCAGTG	0	3
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**ScholarOne Support 1-434/964-4100**

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4	TCAACTAGTGTTGGGAGGGTTAAACCTTTTAGT	0	0
5	AATGCTAGCCGTTGGGGGGTTTACTCCTCAGTG	0	0
6	ATTACTAGATTTGGCCGCAAGGTCAGAGTCCAA	0	0
7	AGTGCTAGCTGTCGGGTTGCATGCAACTCGGTG	0	0
8	AGCACTAGACGTCGGGCGGTTGACCGTCCGGTG	0	0
9	ATAACTCGATGTTGGCGATACACAGCCAGCGTC	0	0
10	TGCACTTGGTGTGTTGGGCCGATTAGGTACAGTGC	0	0
11	TCAACTAGGGGTTGGGAGGGTTAAACCTTTTAG	0	0
12	GATACTAGCTGATGGAGGAACTTCAGTGGCTA	0	0
13	TATACTTGGTGTAAGTGGACTCAGCCCTAGTTG	0	0
14	CCGACTCGGATTCAGATGAATCAAAAAGTCCAT	0	0
15	AAGACTTGGTGTGTCTGGGTTTTAAGTCCCGGCG	0	0
16	TCAACTAGTTGTCAGATCTTAATAGATTTGGTA	0	0
17	TCAACTAGTTGTTCTGGTGAGAAGACTCATTGAG	0	1
18	TCAACTGGTTGTTGAGTCTTAACTGACTCAGTA	0	0
19	ATGACTTGGTGTGTCTGGGTTTCAAGTCCCGGCG	0	0
20	TAAACTTGGCGTCGGTGACTTAACTCCATCGG	0	0
21	AATGTTAGCCGTCGGGCAGTATACTGTTCTGGTG	0	0
22	ATTACTCGCTGCTGCGAGGTAAGTTTCAGTGGC	0	0
23	ATGACTCGATGTTGGCGATACTCAGCCAGCGTC	0	0
24	GATACTAGCTGTTGGGAGTAATTTAGTGGTTA	0	0
25	TATACTTAGTGTAAGTGGACTCAACCCTAGTTG	0	0
26	CCGACTAGGGATTAGCAGACGTTTTATTGATGA	0	0
27	ATTACTCGATGTTGGCGATACACGGTCAGCGTC	0	0
28	TCAACTAAGGATGATAAAATATTAAATGAATGA	0	0
29	AATGCTAGACGTTGGCGAGCATGCTCGTCAGCG	0	0
30	TCAACTGGTTGTTGGGTAACTGACTCAGTAAC	0	0
31	ATTTTTTATATTTACATAAATAAATCCACCAGA	0	0
32	AATACTAGGTGTAGGAGGTATCGACCCCTTCTG	0	0
33	CCGACTCGGATTCAGATGATCAAAAAGTTCATT	0	0
34	CCGACTCGGATTCAGATGAATCAAAAAGTTCCTT	0	0
35	AATGCTAGCTGTTGGGTTTTTAAACTCAGTGG	0	0
36	TCAACCAGTTGTTCTGGTGAGGAGACTCATTGAG	0	0
37	TTAACTAGTTGTCGGATCTTAATAGATTTGGTA	0	0
38	TATACTCGGTGTAAGTGGACTCAACCCTAGTTG	0	0
39	GATACTAGCTGTTGGGAGTGATTTAGTGGCTA	0	0
40	ACGACTCGATGTTGGCGATACACAGCCAGCGTC	0	0
41	CCGACTCGGATTCAGATGAATCAAATAGTTCAT	0	0
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4	CCGACACGGATTCAGATGAATCAAAAAGTTCAT	0	0
5	TCAACTAGTTGTCGGATCTTAATGGATTTGGTA	0	0
6	GATACTAGCCGTTGGGAGTAATTTTCAGTGGCTA	0	0
7	ATGACTCGATGTTGGCGATGCACAGCCAGCGTC	0	0
8	CCGACTCGGATTAAGATGAATCAAAAAGTTCAT	0	0
9	TCAACTAGTAGTTCGGTGAGGAGACTCATTGAG	0	1
10	AGCACTAGACGTCGGGTGGGTGACCGTTCGGTG	0	0
11	CCGACCAAGGATGAGAGGTAAGAAAAGAAAGTA	0	0
12	AGCACTGGACGTCGGGTGGGTGACCGTCCGGTG	0	0
13	GGCACTAGGTGTGGGAGGGAGTCAACCCCTTCC	0	0
14	TCGACTAGTCGTTTCGGAGCAGCAATGCACTGGG	0	0
15	TATACTAGGTGTAAGTGGACTCAACCCTAGTTG	0	0
16	AATGCTAGATGTTGGCGAGCATGCTCGTCAGTG	0	0
17	TATACTTGGTGTAAGTGGACTCAACCCTAGTCG	0	0
18	TCAACTGGTTGTTGGGTCTTAAGTGGCTCAGTA	0	0
19	GATACTAGATGTCGGGAGTTCTTACCCTCTCGG	0	0
20	AGAACTAGATGTTGGATGGCGTAGCCATTTAGT	0	0
21	TATACTTGGTGTAAGTGGACTCAACCTTAGTTG	0	0
22	GATATTAGCTGTTGGGAGTAATTTTCAGTGGCTA	0	0
23	ATTACTCGATGTTAGCGATACACAGCCAGCGTC	0	0
24	TGCACTTGGTGTTTGGCCGATTAGGTTCAGTGC	0	0
25	AATACTCGATGTTAGCGATATACAGTTAGCGTC	0	0
26	ATGGCTCGATGTTGGCGATACACAGCCAGCGTC	0	0
27	ATAACTAGCTGTCCGGACACATGGTGCTTGGGT	0	0
28	GATACTAGCTGTTTGGTAGCAATACTGAGTGGC	0	0
29	TCAACTAGTCGTCGGATCTTAATAGATTTGGTA	0	0
30	TACTACTAGACTGGTGCGGTTTTGACGCTGTATC	0	0
31	GATACTCGCCGATGGTGGTTTTAGAGCCATTGT	0	0
32	ATTACTCGCTGCTAGATGGCAACGTTTCAGTGGC	0	0
33	ATGACTCGACGTTGGCGATACACAGCCAGCGTC	0	0
34	TGTGCTGGATTACGGCGGCTCTGACGCCGTCGG	0	0
35	TCAACTAGGTGTTGGCTGGGTAAAACCATTTAG	0	0
36	ATCACTCGAGATCGGCGATACGGTCGGTCTCCT	0	0
37	TGAACTTGGTGTTGGGCCGATTAGGTTCAGTGC	0	0
38	ATGGCTGGATGTTGGCGATACACCGTCAGCCTC	0	0
39	GATGATAGGCGTTGGCAGACTCAATCCTGTCCG	0	0
40	CTAACGATGGACACGGGGGAATCAGTCTCTTTT	0	0
41	ATTACTCGATGTTGGCAATACACAGCCAGCGTC	0	0
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4	GGTACTAGACGCCGGGGGGGTGACCTTTCGGTG	0	0
5	TCAACTAGGTGTTGGGTGGGTGAAACCATTAG	0	0
6	CCGACTAGGGATCGGATGGGTAGTTATTTTAGC	0	0
7	TGCACTTGGTGTGGGCCGATTAGATTCAGTGC	0	0
8	TACTAGACTGGTGCGGTTTTGACGCCGTATT	0	0
9	TCGACTAAGGATGATAAAATATTAAATAATGAT	0	0
10	ATCACTCGATGTTGGTGATACACAGCCAGCGTC	0	0
11	CCAGTTAGGGATTGGCAGGGTCTCGTTACGTCT	0	0
12	ATGACTCGATGTTGCGGATACACAGCCAGCGTC	0	0
13	CTAACGATGGACGCGGGAATCAGTCTCTTTTT	0	0
14	ATTACTCGATGTGTGCAATACACGGCACGCGTC	0	0
15	GATACTAGCTGTTGGGAGTAATTTCAAGTGGCTG	0	0
16	TCAATTAGTTGTCGGATCTTAATAGATTGGTA	0	0
17	CTAACGATGGACGCGGGAATCGGAAAGAAATT	0	0
18	CCGACTAGGGATCAGCGGATGTTATTTTACGA	0	0
19	TGCACTTGGCGTTGGGCCGATTAGGTTCAAGTGC	0	0
20	TGCACTTGGAGTTGGGCCGATTAGGTTCAAGTGC	0	0
21	TGCACTTGGTGTAGGCCGATTAGGTTCAAGTGC	0	0
22	CCGACTCGGATTCAGATGAATAAAAAAGTTCAT	0	0
23	CGCACTTGGTGTGGGCCGATTAGGTTCAAGTGC	0	0
24	TACTCTAGACTGGTGCGGTTTTGACGCCGTATC	0	0
25	TGCTCTTGGTGTGGGCCGATTAGGTTCAAGTGC	0	0
26	CCGACCAGGGATCGAGGACAGTCCTATGGTTGA	0	0
27	GATACTAGCTGTTGGAGGAACTTCAGTGGCTG	0	0
28	GGTGCTAGATGTTGGGAAGCTTGCTTTTCGGTG	0	0
29	CCGACTCGGATTCAGATGAATATTAAGTTCATT	0	0
30	TCGACTAGGTGTTGCGGAAGGAGACTTCTTGGG	0	0
31	AGAACTAGGTGTCGTAGGTGTTGACCCCCGCGG	0	0
32	TCGACCAAGGATAAGAGGTCGTAATTATCTTGA	0	0
33	TTCACTAGTGTTGCGGGTATATTTATCTGCA	0	0
34	GAAACTCGACATCAGCGATACACTGTTGGTGTC	0	0
35	TATACTAGAAGTAGGAGGGCTCAACCCCCCTG	0	0
36	CCGACTGTAGATTAGAAGACGTTAATTAAAGGA	0	0
37	TACTACTAAACATCAGTACCTCCTCGAGAGGTAT	0	0
38	CCGACTAGGGATCGGACGATGTTATATTTTGAC	0	0
39	CGAACTGGATGTTGGGCTCAACTTGAGCTCAGT	0	0
40	ATTACTCGACATACGCGATACACTGTGTGTCTG	0	0
41	GGTGCTCGGTGTCGGGGGTATCGACCCCTCCGG	0	0
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4	GATACTTGTTGTTGGAGGTTTGACCCCTTCAGT	0	0
5	CCGACTTGGCATTGGAGGCGTGCACTTTCGCC	0	0
6	CCGACCAGGGATCGGAGAGTGTTACGTGGATGA	0	0
7	ATTACTCGACATACGCGATACTGTGTGCGTC	0	0
8	AGCACTGGAGGGGAGGGGCTTCGGCCGTTTCCC	0	0
9	ATTACTCGTTGCTGGGAGGAACTTTCAGTGAC	0	0
10	CCGACCAGGGATATGAGGTAAATAAAATAGTAT	0	0
11	CGCACTAGGTGACGGGACCACTCACGGTCTCGC	0	0
12	CCAAGTAGGGATATGTGGACGTCTGTTTGAAGA	0	0
13	TCAACTAGTTGTCAGGTCTGTTTAAGGATTTGG	0	0
14	CGAACTGGATGTTGGGATCAACTTGGAGCTCAG	0	0
15	AGTACTAGTTGTCGGCATGCATGCATGTCGGTG	0	0
16	AGAACTGGACGTTGGGAGGAATTCGCCTCCTAG	0	0
17	TGAACTTGGCGTTGGTGGGTAAACTCCATCGG	0	0
18	CCGACTATGGATCGGTGGACGTTGCATAGCATG	0	0
19	CCGACCAGGGATATGAGGTAAAGAATTGATTA	0	0
20	CCGACTAGGGATCGGTGGACATTGCATAGCATG	0	0
21	CCGACCAGGGACCGAGGACAGTCCCATGGTTGA	0	0
22	AATGCTAGCCGTTAGTGGGTTTACTCACTAGTG	0	0
23	CCGACCAAGGATTGGGAGACGTTACATGGATGA	0	0
24	CCGACTCGGGATCGGACGATGTTACATGACTC	0	0
25	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTA	0	0
26	AATGTCAGCCGTTAGTGGGTTTACTCACTAGTG	0	0
27	TATGCTAGACCGGTGCCGTTTTGACGCCGTATC	0	0
28	AATGCTTGGTGTCTGGAGTTTTAAGTCTCCGGG	0	0
29	GGTACTTGGTGTGTTGGTGGTATTGACCCCATCAG	0	0
30	GATACTAGGCGTATCGGGTATCGACGCCTGATG	0	0
31	TGCGCTAGGTGTAGGAGGTGTCGACCCCTTCTG	0	0
32	CTTACTCGACATACGGCCCTGGCGGCTGTGCGT	0	0
33	TGGACTTGGCGTTGGTGGGGTAAAAGCCATCAG	0	0
34	TCGACTAGCCGTTTCGGAGCAGCAATGCACTGAG	0	0
35	GGTACTAGGCGTCGGGGGAGCGACCCCTCGGT	0	0
36	GATACTTGTTGTTGGAGGTATTGACCCCTTCA	0	0
37	AACACTTGGTGTTCGGGGAGTTGACCCCGGAGT	0	0
38	TCGACTAGGTATCGGCGCCTAAAAACCGTCGGT	0	0
39	ATTACTCGACGTGTGCGATACACGGCACGCGTC	0	0
40	AAGACTGGCTGTTGGGGGCCTAAGGGTTCTTAG	0	0
41	AGTGCTAGATGTCGGGGGGAAACCTTCGGTATC	0	0
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4	AGCACTAGGTGTCGGTCGTAAGATCGGTGCCAA	0	0
5	CCGACTAGGGATCGGTGGACGATGCATAGCATG	0	0
6	TCAACTGATTGTTGGGAGGGTTTCTTCTCAGTA	0	0
7	TCAACTGGTTGTTGGGAGGGTTAAACCTTTTAG	0	0
8	ATTACTCGTTTTTGGGGTTTATGATTCAGAGAC	0	0
9	AGAACTAGGTGTAGACTAGACATGGGTTTACA	0	0
10	AGTGCTAGATGTCGGAACATATGTTTCGGTAT	0	0
11	TCAACTAGCTGCTGGGGCCTTCGGGCCTTGGA	0	0
12	TCAACTAGGTGGGGAGGGTTAAACCTTTTAGTG	0	0
13	ATTACTCGTTTTTGGGGTTTATGATTTAGAGAC	0	0
14	CCGTCTAGGGATCGGTCCACGTTATTTTTTGAC	0	0
15	TCAACTAGTTGTCGGATCTTAATAGAATTGGTA	0	0
16	TGAACTGGATGTTGGGTGCAATTTGGCACGCAG	0	0
17	TCAACTGGTGTGGGAGGGTTAAACCTTTTAGT	0	0
18	ACAACTAGGGATATGTGGACGTTTGTTGAAGA	0	0
19	ATTACTCGACATACGCGATACACTGTTTGTGTC	0	0
20	TAAACTCGACATTAGCGCTATACTGTTAGTGTC	0	0
21	GGCACTAGGTGTGGGATCCTTCCACGGATTCCG	0	0
22	AATGCCAGCCGTTGGGAAGTTTACTTTTCAGTG	0	0
23	ATTACTCGACATACGCGATACACTGGGTGTGTC	0	0
24	CCAACTAGGTGTTGGGGAAGGAGACTTCCTTAG	0	0
25	GGAAGTAGATGTAGGGGCCATTCCACGGTCTCT	0	0
26	TCAACTGGTTGTTGGAAGGGTTTCTTCTCAGTA	0	0
27	CCGACTAGGGATGAGTGAACGTTTCATTATCGA	0	0
28	ACTACTCGTTTTTGGGTTTTATGATTCAGAGAC	0	0
29	AGAACTAGGTAGTGGTTCGACCTGGGCACACT	0	0
30	GTGACTAGGTGTGTGGGGCGATAACAAGCCCCG	0	0
31	TCAACTAGTTGTTGGATCCGTTTAAGGATTTGT	0	0
32	CCAACTGGATGCCTGTGATCCGAAAGGGTTGTG	0	0
33	CGCACTACACCGGTGCGGTTTTGACGCCGTATC	0	0
34	CCAACCAAAGATAAGAGGTTGTAAATACAAAAT	0	0
35	GATACTTGTTGTTGGAGGTAATGACCCCTTCAG	0	0
36	CCAACTAGGGGTACGTGGACGTTTGTTCAAGA	0	0
37	ATTACTCGTTTTTGGGTTTTGTGATTCAGAGAC	0	0
38	CGGACCAGGGATTGGAGAGAGTTACCGAATGAC	0	0
39	TTCCTAGTGTTGCGGGTATTTATTTATCTGTA	0	0
40	AGTGCTAGTTGTTAGCCCGGCTTGAGCTGGGTT	0	0
41	TAACTGGTTGTTGGACGGCTTGCTGTTCAAGTA	0	0
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4	TTAACTAGTTGTCGGGTCTGTTTAAGGATTTGG	0	0
5	AATACTAGCTGTTGGGAGCAATTTCAAGTGGCTA	0	0
6	GATACTCGACATTTGCGATACACTGTAAGTCTC	0	0
7	CTGACCAAGGATAAGAGGTCGTAATTATCTTGA	0	0
8	CACGTTTGCTGTAAGAGGAATCGATTCCTTTTG	0	0
9	TCAACTAGGTGTTGGGAGGGTTAAACCTTAGTG	0	0
10	TCAACTGGTTGTTGGAGGGTTTCTCTTCAGTAA	0	0
11	TCAACTAGGTGTAAAACCATTTAGTACCGGAGC	0	0
12	CCAACTAGGGATATGTGGACGTTTCGTTTGAAGA	0	0
13	AGGACTAGGTGATGGATGAGTTAACTCATTTG	0	0
14	TCAACTAGGTGTTGGTGGGGTTAAACCCATTAG	0	0
15	CCGACCAGGGATTAGGAGACGTTAAATTTTATA	0	0
16	TTTACTTGCTGTTTGGCCTTTGGGTTGAGCGGT	0	0
17	ATTACTCGATGTGTGCGATACACTGTACGTGTC	0	0
18	TCAACAAGTTGTCGGATCTTAATAGATTTGGTA	0	0
19	CCGACTCGGGATCGGTGAGCGTGATTTTTTTTG	0	0
20	CCGACTAGCGATCCGCCGGCGTGGTTTCGTTGA	0	0
21	CCGACTAGGGATCGGTGGATGTTTTATTGACGC	0	0
22	GATACTCGACATACGCGATACACTGTGTGTCTG	0	0
23	GATACTTGTTGTTGAAGGTATTGACCCCTTCAG	0	0
24	CGAACTGGATGTTGGGCTCAACTTGTAGCTCAG	0	0
25	TCAACTAGTTGTCGGATCTATAGATTTGGTAAC	0	0
26	GATACTAGCTGTTGGGAACAATTTCAAGTGGCTA	0	0
27	CCGACCAAGGATCATGAGATGTTAAAATAAATG	0	0
28	CCAACTGGGATACGTGGACGTTTGTTTGAAGAC	0	0
29	CCGACTAGCGATCCGCCGACGTGGTTTCGATGA	0	0
30	CGCACTAGACCGGCGCGGTTTTGACGCCGTATC	0	0
31	AATGCCAGTCGTCGGCGAGCATGCTTGTCGGTG	0	0
32	GGTACTGAGTAGTGGACTGACATGGGTTCACTG	0	0
33	TCGACTAGCCGTTTCGGTCCATTTAAGGGTTGAG	0	0
34	ATTACTCGCTGCTAGAAGGCAACTTTTAGTGGC	0	0
35	AATGCCAGCCGTTGGGGAGCTTGCTCTTAGTG	0	0
36	ATGACTCGATGTTGGCGATGTACAGCCAGCGTC	0	0
37	CGAACTGGATGTTGGTCTTAACTCGGAGATCAG	0	0
38	CCAACTAGCGATCAGGTGGTGGTTTTTTTAGCC	0	0
39	TACGCTGAGCTAGAGCGGCTCTGACGCCGTTTCG	0	0
40	TTTACTTGCTGTTTGGTTTTTCGGACTGAGTGGC	0	0
41	CCGACCGGGCATGGGGAGAGGTAATACCTTAAC	0	0
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4	TATACTTGGTGTAGCTGGAATCAACCCCGGCTG	0	0
5	GGTACTAGATTTGGTGGGATTTGACCCCGCCG	0	0
6	TGTGCTAGATGTTGGGCGGCCTAGCCGTTCACT	0	0
7	CCGACTCGGATTCAGATGAATATTAAAGTTCAC	0	0
8	CTGACTTGGTGTGCGCAGGTTTTAAGTCCTGCGG	0	0
9	ATGACTCGATGTTGACGATATACAGCCAGCGTC	0	0
10	TGAACTTGGCGTTGGTGGGTCAAACCTCCATCAG	0	0
11	ATTACTAGTTTTTTGGGTTTTATGATTCAGAGAC	0	0
12	GGTACTAGGTAGTAGACTAGACATGGGTTTACT	0	0
13	CCGACTAGCGATCCGCGGGCGTGTTTCGATGA	0	0
14	TCAACTAGTTGTTTCGGTGAAGAGACTCATTGAG	0	0
15	ATTACTAGGTGTGAGTGGTATCAAGCCCACTCG	0	0
16	CCGACCGGGGATGGGGAGAGGTAGTACCTTAAC	0	0
17	GATACTTGTTGTTGGAGGTATAGACCCCTTCAG	0	0
18	AATGCCGGTTCGTCGGCAAGCATGCTTGTCGGTG	0	0
19	CATACTTGGTGTGAGTCCTTCATTGGATTCTG	0	0
20	CCGACTAGCGATCCGCCGGCGTGTTTAGATGA	0	0
21	CCAACTAGGGGTATGTGGACGTTTGTGTTGAAGA	0	0
22	TCAACTAGTTGACGGATCTTAATAGATTTGGTA	0	0
23	AGTGCTGGATGTCGGGAAGCCTACCTTTTCGGT	0	0
24	TCAACTAGGTGAGGGTTAAACCTTTTAGTGCCG	0	0
25	CTGACTTGGTGTTCAGGTTTTAAATCTTGGAG	0	0
26	AAGACTAGAAGCTGGTTGGATAAAACCGGTCGG	0	0
27	TCAACTAGTTGTCGGGTCTTAATAGACTTGTA	0	0
28	CCGACTTGCGGTTCCCGGTTTTAAGTCCGGGGG	0	0
29	ATGACTGGGTGTCGGTGATTAAAAACCGTCGGT	0	0
30	GATTCTCGACATACGCGATACACAGTGTGTGTC	0	0
31	AACACTTGGGTGGTGGGAGTTGACCCCTGCCGT	0	0
32	AGCACTAGACGTCGGGTGGGTGACCGTCCAGTG	0	0
33	ATTACTCGTTGTTGGCGATATAAAGCCAGCGAC	0	0
34	TTCACTAGTGTTGCGGGCATTATTTATCTGCA	0	0
35	TTTACTCGTTTTTTGGGTTTTATGATTCAGAGAC	0	0
36	ATCACTCGATGTGTACGATACACAGCACGCGTC	0	0
37	CCGACTAGGGATCGGGCGATCTCAATCTTATGT	0	0
38	TCAACTAGGGTTTGGGAGGGTTAAACCTTTAG	0	0
39	TCAACTAGGTGACCTTTTAGTGCCGTAGCTAAC	0	0
40	AATACTAGGCGTAGGAGGAGTCAAATCTTTCTG	0	0
41	TATACTTGGTGTAATTGGACTCAACCCTAGTTG	0	0
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4	GATACTAGGTGTCCGGGATGTAAACCTCCTGGG	0	0
5	GATGCTAGCTGTTGGAGGAACTTCAGTGGCTA	0	0
6	TGTGCTTGTGCTGGGAGGTTACCTCTCGGTG	0	0
7	ATTACTAGCTGTTGGGTTTTAAATTCAGTGGC	0	0
8	ATGACTCGATGTTGGCGATACACAGCCAGCATC	0	0
9	TGCACTTGGTGTGGCCCGATTAGGTTCAGTGC	0	0
10	TCAACTAGTTGTTCAGTGAGGAGACTCATTGAG	1	0
11	GATACCTGTTGTTGGAGGTATTGACCCCTTCAG	0	0
12	GATACTTGTGTTGGAGGTATTGACCCCTACAG	0	0
13	GATACTAGCTGTTGGGAGTAATTCCAGTGGCTA	0	0
14	GATACTAGCTGTTGGAGGAGACTTCAGTGGCTA	0	0
15	TGCACTTAGTGTTGGGCCGATTAGGTTCAGTGC	0	0
16	AGCGTTGAATGTTGGGGGACTTAAAAGTCTTTC	2	0
17	TCTACTAGTTGTCGGGTCTTAATTGACTTGATA	2	0
18	ATCACTCGATGTGTGCGATACACGGCACGCGTC	2	0
19	TCGTCTAGTTGTTCGGAGCAGCAATGCACTGAG	2	0
20	AATGTTGAATATTGGAATAATAAAATTTTAGTT	2	0
21	ATTACTCGTTGCTGGGAGGTAACTTTTAGTGAC	2	0
22	TCAACTAGGTGTTGGGTGGGTAAAACCATTTAT	2	0
23	TCGACTAGTTGTTTGAAGCAGCAATGCACTGAG	2	0
24	AATGCTAGTTGTCAGTATGTATACTTATTGGTG	2	0
25	GGCACTAGGTGTGGGACTCTATCGACGGGTTCC	2	0
26	TCAACTGGTTATTGGGAAGGTTCTTCTCAGTA	2	0
27	CCAACTAGGGATATGTGGACGTTTGTTCGAAGA	2	0
28	TCAACTAGTTGTCTGATCTTAATAGATTGGTA	2	0
29	CCGACCAGGGTTCGGAGACAGTTACATGGATGA	2	0
30	CAAACCTAGGGATACGTGGACGTTTGTTCGAAGA	2	0
31	GGGACTAGGTGTGGGACTTGACATGGGTTTACA	2	0
32	AGTGCTGGATTTCGGGAAGCCTAGCTTTTCGGT	2	0
33	ATTACTTGACATACGCGATACACAGTGTGTGTC	2	0
34	ATCACTGGGTGTTGGGGAAGCGATTCTTGGTA	2	0
35	TCAACTAGTTGTCGGGTCTGTTTAAGGATTGA	2	0
36	CCGACCAGGGATATGAGTTGTTATGGTTGTATG	2	0
37	TCAACTAGTTGTCGGATCTTAAAAGATTGGTA	2	0
38	AATACTAGATGTTGGTCCTTTTAAGGATCAGTA	2	0
39	TTTACTTGCTGTTTGTCTTCGGTATGAGTGGC	2	0
40	TGTGCTAGACGTTGGAGGGTAACCTTCGGTGTC	2	0
41	TACTACTAGACCGGTGCGGTTTTGACGCCGCATC	2	0
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7	CACGTTTGGTGTGGCGCAATCGACCGCGTCCGC	2	0
8	AATGCCAGTCGTCGGGTAGCATGCTATTCCGGTG	2	0
9	TATGCTAGACCGGTGCGGTTTTGACGCCGTATA	2	0
10	CCGACTAGGGATCGGGCAATGTTGTTTACTGAC	2	0
11	CCAATAAAAAATATATGGACGTTTGTGTTGAAGA	2	0
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15	CCGACTAGCGATCAGCCGGCGTGGTTTCGATGA	2	0
16	CCGACTATGAATAGGATATTGTTTTAAGAAGGG	2	0
17	CCGACTAGGGATCGGTCCACGTTATTTTATGAC	2	0
18	TCGACCAGGGATCGGAGAGTGTTACATGGATGA	2	0
19	CGAACTGGTTGTTGGTCTCACTCGGAGATCAG	2	0
20	AGCACTAGGTGTTGGGGGTATTGACCCCCCAG	2	0
21	ATCGCTGGGTGTAGGGGGTTTTTACTCCCCCG	2	0
22	TCAACTAGGTGTTGGGAGGGTAAAACCATTAG	2	0
23	CCGACTAGGGAGGAGTGAACGTTGCATTATCGA	2	0
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25	TTTACTTGCTGTTTCGGTCTTAGGCTTGAGTGGC	2	0
26	TCGACTAGTCGTTTCGGAGCAGCAATGCGCTGAG	2	0
27	TACGCTGAGTTAGAGCGGCTCTGACGCTGTTTCG	2	0
28	GGCGCTAGGTGTGGGGCCCATTCACGAGTTCC	2	0
29	TCGACTCGTCGTTTCGGAGCAGCAATGCACTGAG	2	0
30	TACGCTGAGTTAGAGCGGCTTTGACGCCGTTTCG	2	0
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32	CCGACCAGGGATATGAGTTGTTAGGATTATGTG	2	0
33	GGCACTAGCTTGGGGTCTCCCTGTGGAATCCCA	2	0
34	AACACTAGATGTTACGGATATTGACCCCTGTAG	2	0
35	CCGACATAGGAATACATAATAGTGGGACTAAAG	2	0
36	AATACTGATTGTTGGGTAGGTGTCTATTCAGTG	2	0
37	AGTGCTAGATGTTAGGGCTTAGGCCTTAGTATC	2	0
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39	CCAACCAAAGATATGAGGTTGTAAATACAAGAA	2	0
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41	TACGCTGAGTTAGAGCGGCTCTGACGCCATTTCG	2	0
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5	CCGACCAGGGATATGAGGTATTTTAGAATATAT	2	0
6	CCAACCAAAGATAAGGGTGGGAACAATAAAAGA	2	0
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16	GCGACCGGGGATGGGGAGAGGTAATACCTTAAC	2	0
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22	CACACTAGGTCTTGGCGGACTCGACCCCCCAG	2	0
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25	CCGACCAGGGATCGGGGAACGTTAACGTCGACG	2	0
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29	CCGACCGGGGATGGGGTGAGGTAATACCTTAAC	2	0
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43	CCCCTAGGGATATGTGGACGTTTGTTTGAAGA	0	0
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56	CGTACTAGGTGACGGGACCTCTCACGGTCTCGC	0	0
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6	AGAACTAGGTGTCGTGGGTGTTGACCCCCGAGG	0	0
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9	TCGACTGGGTGTGCGGCGATTAAAAAACCGTCGG	0	0
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33	TCAACTGGTTGTTGGAGGGGTTTCGCTTCAGTA	0	0
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40	AGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAG	0	0
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43	AGAACTAGGTGTCGTGGGTGTTCACTCGGACGA	0	0
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51	CCGACTCGGATTCAGATGAATATTAAATTTTCAT	0	0
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56	GGCACTAGGTCCTTGGGGAGCGACCCCGTGAGG	0	0
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5	CCGAATAGGGATGAGTGAACGTTGCATTATCGA	0	0
6	TCGACTAGTTGTTTCGGAGTAGCAATGCACTGAG	0	0
7	ATTACTCGACGTACGCGATACTGTGTGTGTC	0	0
8	TGCTAGATTGGTGCGGTTTTGACGCCGTATC	0	0
9	ATTACTTGATGTTGGCGATACTGTCAGCGTC	0	0
10	TACGCTGGATCGGTGCGGGTTTGACCCCGTATC	0	0
11	CCAACTAGGGATATATGGACGTTTGTGTTGAAGA	0	0
12	GGCGCTAGGTGTGGGGAACCTTTCACGTTCTCC	0	0
13	ATAACCAGCTGTCCGGGCACTTGGTGCTTGGGT	0	0
14	TCAACTTGTTGTTGGGAGGGTTTCTTCTCAGTA	0	0
15	AGAACTGGCTGTTTGATAGTTTAAAAGCTATTG	0	0
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17	CCGACTTGGGTTTGGAGGCGTGCACTTTCGCC	0	0
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20	GATGCTAGCCGTTGGCAAGCTTGCTTGTCGGTG	0	0
21	TCAACTAGGTGTTGGGTGGGTAAAACCATTTGG	0	0
22	CCGACTAGGGATCAGCGGGCGTTGTTTAGCGAC	0	0
23	AGCGCTGGGTGTAGGGGGTATGAACCCCCCG	0	0
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32	CGCACTAGGTGACGGGACCTCTCACGTTTCGC	0	0
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5	TATACTTGGTGTAACCTGGACTCGACCCTAGTTG	0	0
6	GATACTAGCTGTTGGGAGTAATTTTAGTGGCTA	0	0
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8	ACGACTCGATGTTGGCGATATACAGCCAGCGTC	0	0
9	AACACTAGATGTTATGGGTATTGACCCCTGTAG	0	0
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11	CCGACTAGGGATGAGTGAACGTTGCATTATCAA	0	0
12	TATACTTGATGTAGCTGGGCTCAACCCTAGCTG	0	0
13	CTGACCGGGGATGGGGAGAGGTAATACCTTAAC	0	0
14	ATAACTAGCTGCCGGGGCACATGGTGTTTCGGT	0	0
15	GGTACTAGGCGTCGAGGGGAGCGACCCTCCCGG	0	0
16	CGAACTGGATGTTGGGCTCAACCTGGGAACTGC	0	0
17	TATGCTAGACTGGTGCGGTTTTGACGCCGTATC	0	0
18	CCGACTTGGTGTTCCCGGTTTAAAGTCCGGGGGT	0	0
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21	TCGACTAGGTGTTCCGGGAAGAGACTTCTTGAGT	0	0
22	CCGACCAGGGATATGAGGTAAAAGAATATTTAT	0	0
23	CCGACTAGGGATGAGTGAATGTTGCATTATCGA	0	0
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25	CCGACTCGGATTCAGATGAACATTAAAGTTCAT	0	0
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37	CCGACTAGCGATCCGTCGGCGTGTTTCGATGA	0	0
38	CCAACTAGGGATATGTGGACGTTTGTTCGAAGA	0	0
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40	CCAACTAGGGATACGTGGACGTTTGTTCGAGGA	0	0
41	CCGACCAAGGATAAGAGGTCGAAATTATCTTGA	0	0
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5	CGCATTGCTGTGAGCGGAATCGACCCCGCTCGT	0	0
6	TCAACTGGTTGTTGGAGGGGTTTCCTTTCAGTA	0	0
7	CCAACTAGTTGTTGGGGAAGGAGACTTCCTTAA	0	0
8	TTCACTAGTGTTTCGGGTATTTATTTATCTGCA	0	0
9	AGTACTAGGTGTAGGCGGAGTGAAATCTGTCTG	0	0
10	TGTGCTGGATCACGGCAGCTCTGACGCCGTCGG	0	0
11	CCGACTAGTGATCCGCCGGCGTGTTTCGATGA	0	0
12	TACGTTGAGTTAGAGCAGCTCTGACGCCGTTTCG	0	0
13	CGCACTAGACCGGTGCGGTTTCGACGCCGTATC	0	0
14	ATTACTAGCTGCTAGAGGGCAACTTTTAGTGGC	0	0
15	GATACTAGGCGTATCGGGTATCGACCTCTGATG	0	0
16	AGAACTAGGTATCGTGGGTGTTGACCCCGCGGT	0	0
17	CACACTAGGTCTTAGTGGAATTCGACCCCACTAG	0	0
18	TATGCTAGACCGGTGCAGTTTTGACGCCGTATC	0	0
19	CCAACTAGGGATATGTGGACGTTTGTTTAAAGA	0	0
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21	AATACTAGGCGTAGGTAGAGTCAAATCTTTCTG	0	0
22	CTAACTCGTTTTTGGGGCGTAGGTTTCAGAGAC	0	0
23	CCGACTTGAGATTGGAGGCGTGCACTTTCGCC	0	0
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27	GGTACTAGGTAGCGGCCTGTCATGGGGTCGCTG	0	0
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7	TCAACTGGTTATTGGGAGGGTTTCTTCTCAGTA	0	0
8	GCGACTGAGATTCAGGAAATGCCCAAGATGGCT	0	0
9	CCGACTAGGGATGAGTGAACGTTGCGTTATCGA	0	0
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12	AGAACTACGTGTCGTGGGTGTTGACCCCCGCGG	0	0
13	GGAAGTGGCGTGGGTCTCATTCCACGAGATCC	0	0
14	GATGCTAGGCGTATCGGGTATCGACCCCTGATG	0	0
15	GGTGCTAGGTGTCGCGGGCTTTTACCCTCGCGG	0	0
16	CGAACC GGATGTTGGGCTCAACTTGGAGCTCAG	0	0
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22	AGGACTGGATAGTGGGATTACATGGTCTCACTG	0	0
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25	CGAACTAGATGTCGGGAGGGTCAGCCTCTCGGT	0	0
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39	TCATCTGGTTGTTGGGAGGGTTTCTTCTCAGTA	1	1
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41	TCAACTAGTTATTTCGGTGAGGAGACTCATTGAG	0	1
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6	CCGGTTAGGGATTGGCAGGGCTTCGTTACGTCT	0	0
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9	ATTACTCGATGATGGCGATACACAGCCAGCGTC	0	0
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11	ACCACTCGATGTTGGCGATACACAGCCAGCGTC	0	0
12	TGCACTTGGTGTGGGCCGATTAAGTTCAGTGC	0	0
13	ATTACTCGATGTGCGCGATACACGGCACGCGTC	0	0
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16	ATGACTTGGTGTGTGCGGGTTTTAGGTCCCGGCG	0	0
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22	ATCACTAGATTTTGGCCGTATGGTCAGAGTCGA	0	0
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26	CCGACCAGGGATCGAGGACAGTCCCATGGCTGA	0	0
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40	TCAACTGGTTGTTGGGGATTCAATTCTTCAGTA	0	2
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46	CTGACTAGGGATCGGTCCACGTTATTATTTGAC	0	2
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49	AACGCTAGATCGGTGCGGGTTTGACCCCGTATC	0	2
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53	CCGACTCGGATTCAGTTGAATATTAAAGTTCAT	0	2
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56	AGAACTAGAGGTTGGAATGCAAATTCTTGTCTC	0	2
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5	ATCACTCGGTGTTGGCGATACACGGCCAGCGTC	0	2
6	ATCACTCGACATTGGCGATATACGGTCAGTGTC	0	2
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9	GATACTAGATGTTTCGAGGAATTAACCCCTTGAG	0	2
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11	TCAACTAGTTGTCGGACCTTTGGGTTTGGTAAC	0	2
12	CCGACCAAGGATAGGAGGTCGTAATTATCTTGA	0	2
13	AGTGCTAGCTGTAGGGAGCTATAAGTTCTCTGT	0	2
14	ACGACTAGCCGTTGGAATCCTTGAGATTTTAGT	0	2
15	GGCACTAGGTGTGGGGAACCTCCACGTTCTCCG	0	2
16	CCGACTAGGGATCGGACCACGTTATTTTTTGAC	0	2
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18	TGAACTTGGCGTTGGTGGTTTAAACTCCATCAG	0	2
19	AGCTCTAGACGTCGGGTGGGTGACCGTCCGGTG	0	2
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21	CTAACTCGTTTTTGGGACATAAGTTTCAGAGAC	0	2
22	AGTGCTAAGTGTTGGGGGTCGAACCTCAGTGCT	0	2
23	GGAGCTAGTTGTCGGCATGCATGCATGTCGGTG	0	2
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26	TCAACTAGTTGTTGGGTGAGGAGACTCATTGAG	0	2
27			
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29	AGCGCTAGGTGTTGGGGGTATTGACCCCCCAG	0	2
30	CCGACCAAGATAAGAGGTCGTAATTATCTTGA	0	2
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33	AGAACTAGATGCATGTTGACTGAGGTTGATGTG	0	2
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36	ATGACTCGATGTTGGCGATATACAGTCAGCGTC	0	2
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38	CTGACTTGGTGTTCCAGGTTAAATCTTGGGGTG	0	2
39	CTGACTTGGTGCCCCCGGCTTAAAGTCCGGGGG	0	2
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41	TACGCTAGATCGGTGCGGGTTTGACCCTGTATC	0	2
42	ATGACTCGATGTTGGCAATATACAGCCAGCGTC	0	2
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45	CTCATTAGGTATGGGGGTATCGACCCCTCCCGT	0	2
46	CCGACTAGGGATAGGTCCACGTTATTTTCTGAC	0	2
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49	GATGCTAGGCGTTGGGGGTATCGACCCCTCCAG	0	2
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52	CCAACCTCGTTTTTGGGGCGTAAGTTTCAGAGAC	0	2
53	CTAACTCGTTTTTGGGGCGTAGTTTCAGAGACT	0	2
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CCA	ACTAGGGATACGTGGACGTTTGTTGAAGA	0	2
GAT	ACTAAGTGTGACGGGTACCGCCGGTGCC	0	2
ATT	ACTCGACATTTGCGATACACAGCAAGTGTC	0	2
CCG	ACTCGGATTGAGATGAATATTAAGTTCAT	0	2
CCG	ACTAGGGATCGGTCCACGTTACTTTCTGAC	0	2
GGT	ACTAGGTGTTGGTCCCTTTGGGGCCAGTGC	0	2
TCA	ACTAGTTGTCGGATCTTAATAGATTTGGTT	0	2
CCA	ACTAAGGATATGTGGACGTTTGTTGAAGA	0	2
CGA	ACTGGATGTTGGTCCCACTCGGAGATCAG	0	2
TCA	ACTAGTTGTTGCTGAGGAGACTCATTGAG	0	2
TTT	ACTTGCTGTTTGCCCCTCGAGGGTGAGTGG	0	2
ATT	ACTCGACATATGCGATACACTGTGTGTGTC	0	2
AAC	ACTAGATGTTACGGGTATTAACCCCTGTAG	0	2
GAT	ACTAAGTGTGTCGGGTACCGCCGGTGCC	0	2
CCG	ACCAGGGATATGAGGTATTCTTTTTTCTA	0	2
TAT	GTTAGACCGGTGCGGTTTTGACGCCGTATC	0	2
AAT	GCTTGGTGTCTGGAGTGATAATTCTCTGGG	0	2
TCA	ACTAGCTGTTGGTCATATTAAGATGATTAG	0	2
CCG	ACTAGGGATTGGTCCACGTTATTTTCTGAC	0	2
AAC	ACTTGGTGTCCCGGGAGTTGACCCCCGGAG	0	2
AGC	ACTTGTTGGGGATCCACCCATAGGTTCCC	0	2
CCG	ACTGGGCGACAAGAAGTGGACCTTTGGGAG	0	2
CCA	ACTAGGGATATGTGGACGTTTGCTGAAGA	0	2
TCG	ACTAGGTGCTCGGGAAGGAGACTTCTTGAG	0	2
TAT	GCTAGACCGGTGCGGGTTTGACGCCGTATC	0	2
CAG	ACTAGGGATGAGTGAACGTTGCATTATCGA	0	2
CAA	ACTTGGTGTAGACAGTTCAGTCTGTCTGTG	0	2
CCG	ACTAGGGATCGGAGGTCGTTGTTTCATGAC	0	2
CCG	ACTAGGGATGAGTGAACGTTGCTTAATCGA	0	2
CCG	ACTAGGGATCGGTCCACGTATTTTTTGA	0	2
CTT	ACTCGACGTACGGCCCTGGCGGCTGTGTGT	0	2
TACT	TTGTATGGTGGGAATCTTGCAATTTTCACT	0	2
TAT	GCTAGACGTGGGGAGGCTTAGCCTCTTTGT	0	2
CGA	ACCGGATGTTGGTCTCAACTCGGAGATCAG	0	2
TCA	ACTAGTTGTACGGTGAGGAGACTCATTGAG	0	2
ATG	ACCCGATGTTGGCGATATACAGCCAGCGTC	0	2
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9	TCGACTGGGTGTGCGCGATTAAAACTGTCGGT	0	2
10	CGGACTGGATGTTGGTCTCAACTCGGAGATCAG	0	2
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25	ATGGCTGGATGTTGGCGATACTCCGTCAGCGTC	0	0
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8	CCGACCAGGGATCGAGGACAGTCCATGGTTGAC	0	0
9	TCAACTAGTTATTGGATGGGTAAAACCATTTAG	0	0
10	AGTGCTAGACGTTGGGGCCCCTAGGGCTTCAGT	0	0
11	GATACTAGCTGTTGGAGGAATCTTCAGTGGCTA	0	0
12	TATATTTGGTGTAACCTGGACTCAACCCTAGTTG	0	0
13	ACCCCATGAATTGGGAGTATTTTGGTTCTTTG	0	0
14	TCAACTAGGTTTGGGAGGGTTAAACCTTTTAGT	0	0
15	TGCACTTGGTGTCGGGCCGATTAGGTTTCACTGC	0	0
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22	TCAACTAGTTGTCGGATCTTAATAGATTAGGTA	0	0
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8	ATAACTAGCTGTCCGGACTCATAGAGTTTGGGT	0	0
9	AGATCTAGGTGTCGTGGGTGTTGACCCCCGCGG	0	0
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13	TCGACTAAGGATGATAAAATATTAAATGAAAGA	0	0
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22	CCAACCTCGGATTCAGATGAATAAAAAAGTTCAT	0	0
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7	GATACTAGGTGCTGGGCTTACTTTGGTCGGCTC	0	0
8	CGCATTGCTGTGGGCGGAATCGACCCAGCCCC	0	0
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37	ATTACTCGATGCTAGATGGCAACGTTTAGTGGC	0	0
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27	ATTACTCGCTGCTGGGAGGTAGCTTTCAGTGGC	0	0
28	ATTACTCGCTGCTAGATGGCAACGGTTAGTGGC	0	0
29	ATGACTCGATGTTGGCTATACACAGCCAGCGTC	0	0
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43	ATTACTCGCTGCTAGATGGCAACGTGTAGTGGC	0	0
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56	CCGACTGGATTCAGATGAATCAAAAAGTTCATT	0	0
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5	TCAACTAGATGTAGGGGGTGTTGATCCCCTCTG	0	0
6	ATTGCTAGTTGTCGGGAAGTTTACTTTTCGGTG	0	0
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9	AATGCCAGCCGTCGGGAAGCTCGCTTTTCGGTG	0	0
10	ACCACTAGATTTTGGCCGTATGGTCAGAGTCCA	0	0
11	AGTGCTAGATGTTGGTTGACTTATCAATCGGTA	0	0
12	ATTACTCGCTGCTGGGAAGTAACTTTCAGTGGC	0	0
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15	CATACAAGTCGTAGCTGGGATTGACTCCGGCTG	0	0
16	TCGACTAGTCGTTTCGGAGGCAGCATCAACGTGC	0	0
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33	TGCACTGGGGAGAGGATGGGTCCTAACTCATTC	0	0
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42	ATGGCTGGATGTTGGCGATACACCGTCAGCGCC	0	0
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CCA	A	T	A	G	G	T	G	T	G	G	G	T	A	A	A	C	A	T	T	A	G	0	0											
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A	G	C	A	C	T	A	G	A	C	G	T	T	G	G	G	C	G	G	G	T	G	G	C	C	G	C	C	C	G	G	T	G	0	0
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C	C	G	A	C	C	A	G	G	G	A	T	T	G	G	G	A	G	A	C	G	T	T	A	A	A	T	T	G	G	A	T	G	0	0
T	A	T	A	C	T	T	G	G	T	G	T	A	A	C	T	G	G	A	C	T	A	G	T	T	G	0	0	0	0	0	0	0	0	
T	A	C	A	C	T	A	G	A	C	T	G	G	T	G	C	G	G	T	T	T	T	G	A	C	G	T	C	G	T	A	T	C	0	0
C	T	A	A	C	G	A	T	G	G	A	C	G	C	G	G	A	A	T	C	A	G	A	A	C	A	T	C	A	C	A	0	0	0	0
T	C	A	A	C	T	A	G	T	T	G	T	T	C	G	G	T	G	A	G	G	A	C	T	C	A	T	A	G	A	G	0	0	0	0
G	G	C	A	C	T	A	G	C	T	T	G	G	G	G	T	C	C	C	T	G	T	G	T	G	G	T	C	C	C	A	0	0	0	0
A	A	T	G	C	C	A	G	C	G	G	T	T	G	G	G	A	G	C	T	T	G	C	T	T	C	A	G	T	G	0	0	0	0	
A	G	T	G	C	T	A	G	T	T	G	T	C	G	A	C	A	T	G	C	A	T	G	C	A	T	G	T	C	G	G	T	0	0	0
C	C	A	A	C	T	G	T	C	T	T	T	T	A	G	A	T	G	C	G	G	T	T	A	C	C	C	A	T	A	G	A	0	0	0
T	C	G	A	C	T	A	T	G	G	A	T	G	A	T	A	A	A	A	T	A	T	T	A	A	A	T	G	A	A	T	G	0	0	0
G	A	T	A	C	T	A	G	C	T	G	T	T	G	G	G	A	G	T	A	A	T	C	T	C	A	G	T	G	G	C	T	A	0	0
T	C	G	A	C	G	A	A	G	G	A	T	G	A	T	A	A	A	A	T	A	T	T	A	A	A	T	G	A	A	T	G	0	0	0
T	C	G	A	C	T	A	A	G	A	A	T	G	A	T	A	A	A	A	T	A	T	T	A	A	A	T	G	A	A	T	G	0	0	0
C	T	A	A	C	G	A	T	G	G	A	C	G	C	G	G	G	A	A	T	C	A	G	A	C	T	C	T	T	T	0	0	0	0	

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4	CCAACCAGGTTTCATCTGGGGACTTTTATGAGT	0	0
5	CCGACCAGGGATATGAGGTAAAAAAGTATTTA	0	0
6	TCAACTAGCTGTTTGAAACATTAGATTTTGAGT	0	0
7	CCGACCAGGGATCGAGGACAGTCCCACAAGGTT	0	0
8	CCGGAGCTAACGCGTTAAGTCAGCCGCCTGGGG	0	0
9	TCGACCAGACGTCGGGGGTGTCAACCCCTCTGG	0	0
10	ATGGCTTGGTGTGTCTGGGTTTTAAGTCCCGGCG	0	0
11	TCAACTGGTAGTTGGGTCTTAATTGACTCAGTA	0	0
12	TCAACTGGTTGCTGTGTCTTAAGTACTCAGTA	0	0
13	GATAATTGTTGTTGGAGGTATTGACCCCTTCAG	0	0
14	TCAACTAGGTGTTGGGTGGGTAAAACCATATAG	0	0
15	GATACTTGTTCTTGGAGGTATTGACCCCTTCAG	0	0
16	GATACTAGTTGTTGGAGGTATTGACCCCTTCAG	0	0
17	TCAACTAGGTGTTTGGAGGGTTAAACCTTTTAG	0	0
18	GATACTTGTTGTTGGATGTATTGACCCCTTCAG	0	0
19	GATACTTGTTGTTGGAGGTATTGTCCCCTTCAG	0	0
20	GATACTTGTTGTTGGAGGTATTGACACCTTCAG	0	0
21	GATACTTATTGTTGGAGGTATTGACCCCTTCAG	0	0
22	TCAACTAGTTGTTGCGGTGAGGAGACCCATTGAG	0	0
23	CCGACTTGGGATTGGAGGCGTGCACCTTACGCC	0	0
24	CGAACTGGATGTTGGGCTCAACTTGGAACCTCAG	0	0
25	GATACTAGCTGTTGGGAGCAAATTCAGTGGCTA	0	0
26	CGAGCTGGATGTTGGGCTCAACTTGGAGCTCAG	0	0
27	TCAACTAGGTGATGGGAGGGTTAAACCTTTTAG	0	0
28	GATACTTGTTGTTGTAGGTATTGACCCCTTCAG	0	0
29	CCGACCTGGGATTGGAGGCGTGCACCTTCCGCC	0	0
30	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAC	0	0
31	TCAACTAGGTGTTGGGTGGGTAAAACTATTTAG	0	0
32	TCAACTGGTTGGGGGTCTTAAGTACTCAGTAA	0	0
33	TCAACTGGTTGTTGGGTCTTAATTGACTAAGTA	0	0
34	CCAAGTGGGATATGTGGGCGTTTGTTTGAAGA	1	0
35	CGAACTGGATGTTGGTCTCAACTCGGTGATCAG	1	0
36	CGCACTAGACCGGTGCAGTTTTGACGCCGTATC	1	0
37	TCAACAGGTTGTTGGGAGGGTTTCTTCTCAGTA	1	0
38	CGCACCAGACCGGTGCGGTTTTGACGCCGTATC	1	0
39	ATTACTCGATGCTGGGAGGTAACCTTTCAGTGAC	1	0
40	CCAACCAGGGATATGTGGACGTTTGTTTGAAGA	1	0
41	CGAACTGGACGTTGGGCTCAACTTGGAGCTCAG	1	0
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4	CCGACTTGGGATTGGTGGCGTGCACTTTCCGCC	1	0
5	CCAAGTGGTTGTTGGGAGGGTTTCTTCTCAGTA	1	0
6	TCAACTAGTTGTTCCGGTGCAGGAGACTCATTGAG	1	0
7	CGCACTAGACCGGTGCGGTTTTGACACCGTATC	1	0
8	CGGACTTGGGATTGGAGGCGTGCACTTTCCGCC	0	0
9	TCAACTAGGTGTTGGGTGGGCAAAACCATTAG	0	0
10	TCAACTAGGTGTTGGGAGGGTTAATCCTTTTAG	0	0
11	CCGCCTTGGGATTGGAGGCGTGCACTTTCCGCC	0	0
12	GTTACTTGTGTTGGAGGTATTGACCCCTTCAG	0	0
13	TCAACTAGGTGTTGGGTGGGTAAAACCTTTAG	0	0
14	TCAACTGGGTGTTGGGTGGGTAAAACCATTAG	0	0
15	GATTCTTGTGTTGGAGGTATTGACCCCTTCAG	0	0
16	TCAACTAGGTGTTGGGTAGGTAAAACCATTAG	0	0
17	CCGACTTGGGATTGGAGGCGTGCACTTTCTCC	0	0
18	CCGACTTGGGATTGGAGGCGTGCACTTTCCGCC	0	0
19	TCAACTGGTTGTTGGGAGAGTTTCTTCTCAGTA	0	0
20	CCGACTTGGGATTGAAGGCGTGCACTTTCCGCC	0	0
21	ATTGCTCGTTGCTGGGAGGTAACCTTTCAGTGAC	0	0
22	CCGACTTGGGATTGGAGGCGTGCAATTTCCGCC	0	0
23	ATTACTCGACATACGCGATACACGGTGTGTGTC	0	0
24	TCAACTAGGTGTTGGGTGTGTAAAACCATTAG	0	0
25	CCGACTTGGGATCGGAGGCGTGCACTTTCCGCC	0	0
26	CGAACTGGATGTTGGGCTCAACTTGGAGCTCGG	0	0
27	CCGACTTGGGATTGGAGGCGTGCACTTTCAGCC	0	0
28	TCAACTGGTTGTTGGGAGTGTTTCTTCTCAGTA	0	0
29	TCAACTGGTTGTTGGGAGGGTTTCTTATCAGTA	0	0
30	TCAACTAGTTGTTCCGGTGAGGAGACTCGTTGAG	0	0
31	TCAACTAGGTGTTGGGTGGGTAAAACCATTAG	0	0
32	TCAACTGGTTGTTGGGAGGGTTTCTTCTGAGTA	0	0
33	TCGACTAGGTGTTCCGGAAGGAGACTTCTGGAG	0	0
34	TCAAGTGGTTGTTGGGAGGGTTTCTTCTCAGTA	0	0
35	ATTACTCGTTACTGGGAGGTAACCTTTCAGTGAC	0	0
36	CCGACTAGCGATCCGCCGGCGTGGGTTTCGATGA	0	0
37	GCGACTTGGGATTGGAGGCGTGCACTTTCCGCC	0	1
38	CCGACTAGGGATCGGTCCACGTTACTTTTTGAC	0	1
39	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAA	0	1
40	CGAACTGGATGTTGGTCTCAACTCGGAGATTAG	0	1
41	CCAAGTAGGCATATGTGGACGTTTGTGTTGAAGA	0	1
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4	CGAGCTGGATGTTGGTCTCAACTCGGAGATCAG	0	1
5	CGAACTGGATGTTGGCCTCAACTCGGAGATCAG	0	1
6	CCAACTAGGGATGAGTGAACGTTGCATTATCGA	0	1
7	CCGACTAGGGATCGGTCCACGTTTTTTTTTGAC	0	1
8	TCAGCTGGTTGTTGGGAGGGTTTCTTCTCAGTA	0	1
9	CAAACCTGGATGTTGGTCTCAACTCGGAGATCAG	0	1
10	CTAACTCGTTTTTGGGGTGTAAGTTTCAGAGAC	0	1
11	CCGTCTTGGGATTGGAGGCGTGCACTTTCGCC	0	1
12	TCAACTAGTTGTTTCGATGAGGAGACTCATTGAG	0	1
13	TCAACTGGTTGTTTGGAGGGTTTCTTCTCAGTA	0	1
14	TCGACTAGGTGTTTCGGGAAGGAGTCTTCTTGA	0	1
15	CGAATTGGATGTTGGTCTCAACTCGGAGATCAG	0	1
16	TCAACTGGTTGTTGGCAGGGTTTCTTCTCAGTA	0	1
17	CGAACTGGATGTTGGTCTCAACTCGGAGATCAG	0	1
18	TCAACTGGTTGTTGGCAGGGTTTCTTCTCAGTA	0	1
19	CGAACTGGATGTTGGTCTCAACTCGGAGATCAG	0	1
20	TCAACTGGTTGTTGGCAGGGTTTCTTCTCAGTA	0	1
21	CGAACTGGATGTTGGTCTCAACTCGGAGATCAG	0	1
22	CTAACTCGTTTTTGGGGCGTAAGTTTCTGAGAC	0	1
23	CCGACTTGGGATTGGAGGCGTGAACTTTCGCC	0	1
24	CCGACTTGGGATTGGAGACGTGCACTTTCGCC	0	1
25	CCGACTAGGGATCGGTCCACGTTATTTTTGTC	0	1
26	CCGACTAGGGATCGGTCCACGTTATTTTTGAC	0	1
27	CGAACTGGATGTTGGGCTCAACTTTGAGCTCAG	0	1
28	CTAATTCGTTTTTGGGGCGTAAGTTTCAGAGAC	0	1
29	TCAACTGGTTGTTGGGAGGGTTTCTTCCCAGTA	0	1
30	CCGACTTGGGATTGGAGGCTTGCCTTTCGCC	0	1
31	CTAACTCGTTTTTGGGGCGTAAGTTTCAGAGAC	0	1
32	CCGACTTGGGATCGGTCCACGTTATTTTTGAC	0	1
33	CGAACTGGATGTTGGTGTCAACTCGGAGATCAG	0	1
34	TCAACTAGTTGTTTCGGTGAGGAGACTCACTGAG	0	1
35	CGAACTGGATGTTGGTCTCAACTCTGAGATCAG	0	1
36	CGAACTGGATGTTGGTCTCAACTCGGAAATCAG	0	1
37	CCGACTAGAGATCGGTCCACGTTATTTTTGAC	0	1
38	CCGACTCGGGATTGGAGGCGTGCACTTTCGCC	0	1
39	CCGACTTGGGATTTGAGGCGTGCACTTTCGCC	0	1
40	TCTACTAGTTATCGGGTCTTAATTGACTTGGTA	0	1
41	CGAACTGGATGTTGGGCTCAACTTGGTGCTCAG	0	1
42	CCGACTTGGGATTGGAGGCGTGCACTTTCGCC	0	1
43	TCAACTGGTTCTTGGGAGGGTTTCTTCTCAGTA	0	1
44	GATACTAGCTGTTGGGAGTAACCTCAGTGGCTA	0	0
45	CCGACCAGGGATCGAGGACTGTCCCATGGTTGA	0	0
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4	CCGACTCGGATTCAGATGAATCAAAAAGTTCAG	0	0
5	GATACTAGCTGTTGGTGGAACTTCAGTGGCTA	0	0
6	GATACTAGCTGTTGGAGGAAATTTAGTGGCTA	0	0
7	GATACTAGCTGTTGGAGGAACTTCATTGGCTA	0	0
8	TCAACTAGTTGTCGGATCTTAATAGATTTGGCA	0	0
9	GATACTAGATGTTGGAGGAACTTCAGTGGCTA	0	0
10	CCGACCAGGGTTCGAGGACAGTCCCATGGTTGA	0	0
11	CCGACCAGGGATCGAGGACAATCCCATGGTTGA	0	0
12	CCGACTCGGATTCAGATGAATCAAAAAATTCAT	0	0
13	GATACTAGCTGTTGGGAGTAATTTAGTAGCTA	0	0
14	CCGACCAGGGATCGAGGACAGTCCACGGTTGA	0	0
15	AATACTTGGTGTAACCTGGACTCAACCCTAGTTG	0	0
16	GATACTAGCTGTAGGAGGAACTTCAGTGGCTA	0	0
17	ATTACTCGATGTTGGCGATATACAGCCAGCGTC	0	0
18	ATGACTCGATGTTGGCGATACACACCCAGCGTC	0	0
19	CCGACTCGGATTCAGATGAATCAAAAAGTTGAT	0	0
20	TACTACTAGACTGGTGCGGTTTTAACGCCGTATC	0	0
21	ATGACTCAATGTTGGCGATACACAGCCAGCGTC	0	0
22	AGTGCTAGACGTTGGCGAGCATGCTCGTCAGTG	0	0
23	ATTACTCGATGTTGGCGATACACAGCTAGCGTC	0	0
24	CCCACTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
25	ATTACTCGCTGCTGGATGGCAACGTTTAGTGGC	0	0
26	CCGACTCGGATTCAGATGAATCAAAAAGTTCAT	0	0
27	TCAACTAGTTATCGGATCTTAATAGATTTGGTA	0	0
28	CCGACTCGGATTCAGATGAATCAAAAATTCAT	0	0
29	AATGCTAGACGTTGGCGAGCATGCTCGTCGGTG	0	0
30	ATTACCCGATGTTGGCGATACACAGCCAGCGTC	0	0
31	ATTACTCGACGTTGGCGATACACAGCCAGCGTC	0	0
32	TCAACTAGTTGTCGGATCTTAATAGATTTGGAA	0	0
33	ATGACTCGATGTTGGCGATACGCAGCCAGCGTC	0	0
34	ATTACTCGATGTGTGCGATACACGGCACACGTC	0	0
35	ATGACTCGATGTTGGCGATACACAGTCAGCGTC	0	0
36	CCGACCAGGGATCGAGGGCAGTCCCATGGTTGA	0	0
37	AATGCTAGACGTTGGTGAGCATGCTCGTCAGTG	0	0
38	TACATTAGACTGGTGCGGTTTTGACGCCGTATC	0	0
39	TCGACTAGTCGTTCCGAGCAGCCATGCACTGAG	0	0
40	ATTACTCACTGCTAGATGGCAACGTTTAGTGGC	0	0
41	TACTACTAGACTGGTGCGGTTTTGACGCCGAATC	0	0
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4	TACTAGACTGGTGCGGTTTTGACGCCATATC	0	0
5	TATACTTGTTGTAAGTGGACTCAACCCTAGTTG	0	0
6	CCGACCAGGGATCGAGGACAGTCCCATTGTTGA	0	0
7	CCGACAAGGGATCGAGGACAGTCCCATGGTTGA	0	0
8	CCGACTCGGATTCACATGAATCAAAAAGTTCAT	0	0
9	CCGACCAGGGATCGAGGACAGTGCCATGGTTGA	0	0
10	ATGACTCGATGTTGGCGATACACAGCCAGCGTT	0	0
11	CACACTAGACTGGTGCGGTTTTGACGCCGTATC	0	0
12	TGCACTTGGTGTGGGCCGATTAGGTTCAGTAC	0	0
13	CCGACCAGGGATCGAGAACAGTCCCATGGTTGA	0	0
14	GATGCTAGCTGTTGGGAGTAATTTCAAGTGGCTA	0	0
15	GATACTAGCTGTTGGAGGGAACCTTCAGTGGCTA	0	0
16	CCGACCTGGGATCGAGGACAGTCCCATGGTTGA	0	0
17	ATGACTTGGTGTGTGCGGTTTTAAGTCCCAGCG	0	0
18	TACTAGGCTGGTGCGGTTTTGACGCCGTATC	0	0
19	CTAACGATGGACGCGGGGAATCAGAACATCATA	0	0
20	TATGCTTGGTGTAACTGGACTCAACCCTAGTTG	0	0
21	TACGCTAGACTGGTGCGGTTTTGACGCCGTATC	0	0
22	AATACTCGCTGCTAGATGGCAACGTTTAGTGGC	0	0
23	CCGACCAGGGATCGAGGACAGTCCCATGGTTGG	0	0
24	TGCACTTGGTGTGGGCCGATTAGCTTCAGTGC	0	0
25	TGCACTTGGTATTGGGCCGATTAGGTTCAGTGC	0	0
26	CCGTCCAGGGATCGAGGACAGTCCCATGGTTGA	0	0
27	TACTAGACTGGTGCGATTTTGACGCCGTATC	0	0
28	TCGACTAGTAGTTCGGAGCAGCAATGCACTGAG	0	0
29	ATTACTCGATGTTGGCGATACACAGCCAGCGTT	0	0
30	TGCACTTGGTGTGGGCCGATTAGGTTCAGTGA	0	0
31	ATGACTCGATGTTGGCGATACACAGCCAGCGAC	0	0
32	TTGACTCGATGTTGGCGATACACAGCCAGCGTC	0	0
33	CCGACCAGGGATCGAGGACAGTCCCATGATTGA	0	0
34	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTTG	0	0
35	TCGACTAGTCGTTTCGGAGCAGCAATGCACTAAG	0	0
36	TCGACTAGTCGTTTCGGAGCAGCAATGCACTGTG	0	0
37	GTTACTAGCTGTTGGGAGTAATTTCAAGTGGCTA	0	0
38	TATTCTTGGTGTAACTGGACTCAACCCTAGTTG	0	0
39	TCAACTAGGTGTTGGGAGTGTTAAACCTTTTAG	0	0
40	GATACTAGCTGTTGGAGGAACTTCAGAGGCTA	0	0
41	TATACTTGGTGTAACTGGACACAACCCTAGTTG	0	0
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GGTACTAGCTGTTGGAGGAACTTCAGTGGCTA	0	0
GATACTAGCTGTTGGAGCAAACCTTCAGTGGCTA	0	0
CCGACTAGGGATCGAGGACAGTCCCATGGTTGA	0	0
GATACTAGCTGTTGGGAGTAAATTCAGTGGCTA	0	0
ATTACTCGGTGCTAGCGATATACGGCTAGTGCC	0	0
GATACTAGCTGTTGGAAGAACTTCAGTGGCTA	0	0
TGCACTTGGTGTGGGCCGATTAGGTTTCAGAGC	0	0
GATACTAGCTGTCGGGAGTAATTTTCAGTGGCTA	0	0
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For Peer Review



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Flocs Control 3	Flocs Treated 1	Flocs Treated 2	Flocs Treated 3
125	35	56	8
23745	83948	72725	71784
270	313	695	67
6514	27800	30207	36646
14431	11012	10907	11774
17235	9209	4232	9894
33561	7788	9966	2682
4603	3133	2569	2492
6657	8212	6742	5833
3	5	4	4
4792	3338	2585	3277
11670	6187	3755	5421
2078	1653	1620	2670
0	4	4	6
6028	5187	4066	4741
579	381	378	290
2	0	3	2
20	13	7	20
329	279	417	240
5561	4002	2424	3570
4052	2838	2304	2975
4013	3331	2036	3847
4512	2944	3273	1973
5599	1038	1410	977
3707	2793	3882	2172
0	7	4	2
20	50	68	29
1234	656	786	2182
4260	2944	1223	3373
1226	87	1417	54
986	561	515	590
4	3	2	2
449	194	270	256
2	0	0	2
49	29	24	16
2585	2225	1844	1849
10	23	10	23

2781	2391	1837	1451
89	43	43	49
2471	1268	1030	2635
2830	1837	1196	1349
2155	2067	2538	1581
2755	107	288	12
1179	955	749	1010
2554	1525	1421	1611
0	3191	4738	2298
1480	1404	3626	159
2727	1577	1350	802
506	270	277	350
0	0	0	0
1854	1354	1597	807
2148	1459	1294	1168
1285	978	945	780
7	5	3	5
1796	1144	939	1248
1910	81	924	23
320	183	151	236
86	204	135	155
1258	993	855	939
1643	1414	826	1170
102	85	20	76
433	410	482	551
0	0	0	0
203	192	3562	12
638	560	420	449
5	0	3	0
73	180	415	211
922	825	717	1060
992	786	651	990
752	1161	1146	1039
2	0	0	0
1191	960	988	492
2	436	405	3291
675	524	530	348
1109	788	685	671

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3				
4	1140	908	451	1116
5	424	363	274	300
6	858	583	788	551
7				
8	1028	708	720	597
9	862	664	541	686
10				
11	5	2	5	5
12	909	717	857	578
13	0	0	3	0
14				
15	1149	772	548	689
16	3	0	0	0
17				
18	715	591	298	1003
19	0	0	0	0
20				
21	13	7	14	4
22	825	328	337	836
23	825	553	604	382
24				
25	522	446	356	538
26	0	0	0	0
27				
28	753	537	333	429
29	535	360	125	771
30	588	62	545	29
31				
32	1025	47	537	18
33	0	0	0	0
34				
35	781	411	439	555
36	703	558	238	337
37	575	479	511	350
38				
39	751	831	665	596
40	645	370	477	510
41				
42	0	0	0	0
43	2	5	2	2
44				
45	714	472	519	394
46	604	491	535	281
47	13	10	5	4
48				
49	0	0	0	0
50	2	0	2	0
51				
52	19	19	13	14
53	694	298	430	403
54	0	0	0	0
55				
56	448	512	423	357
57				
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0	0	0	0
671	417	232	344
570	369	323	410
0	0	0	0
516	410	312	326
4	12	6	9
0	0	0	0
104	58	36	30
428	233	231	213
531	332	350	201
0	0	0	0
0	0	2	0
78	60	45	55
0	0	0	0
310	336	347	117
420	392	266	295
0	0	0	0
0	0	0	0
221	472	449	325
374	293	226	381
503	21	51	2
522	83	101	80
414	279	222	287
488	322	154	251
280	181	122	193
0	0	0	0
350	300	309	224
355	331	332	169
27	19	19	52
248	136	71	116
372	334	273	221
429	315	112	361
351	244	215	228
404	286	254	248
3	0	0	0
0	0	0	0
0	0	0	0
0	0	0	0

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3				
4	35	20	18	15
5	53	24	26	15
6	275	295	426	99
7	329	295	227	193
8	371	229	219	245
9	0	0	0	0
10	73	52	32	76
11	0	0	0	0
12	356	216	240	140
13	186	296	113	108
14	285	227	230	121
15	339	224	115	213
16	0	0	0	0
17	11	8	5	6
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For Peer Review

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Granules Control 1	Granules Control 2	Granules Control 3	Granules Treated 1
28	25	21	22
64220	71374	68312	46456
78580	77929	72797	219109
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3459	3269	2152	2724
11425	13966	5815	12115
5389	4770	5273	4347
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6963	4075	5047	5471
13239	9690	4144	8993
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7898	8177	5830	6638
5071	6813	11744	3733
5550	7603	9446	3498
3467	6400	10974	2273
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718	379	274	321
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3838	6076	4866	3527
6426	5354	3182	5046
2646	2609	2568	1680
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7240	4700	540	5626
5413	2639	2491	3047
2669	5075	3365	2162
7579	3223	820	4924
538	117	41	224
4951	4568	1484	3677

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25	781	726	224	424
26	2255	2549	1877	1841
27	243	238	166	180
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31	1247	1923	2447	960
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33	230	230	221	156
34	163	145	38	108
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36	3032	1807	917	1699
37	1140	657	725	772
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39	1422	2498	1790	878
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43	417	1374	3096	323
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793	1407	712	1102
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602	1099	707	460
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18	206	347	374	78
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30	355	233	232	214
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103	65	42	62
185	194	156	123
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Granules Treated 2	Granules Treated 3	tag	use	taxon_level
21	13	TCAACTGGTT	long	f
64244	71247	TCAACTAGGT	long	g
155188	221988	CCGACTCGGA	tag	g
751	575	GATACTTGTT	long	g
4086	5891	TCAACTAGTT	long	g
0	2	CCGACTTGGGATTGGAGGCGTGCAC	TTTTCC	
7	7	TCAACTGGTT	long	f
5518	9131	CCGACCAGG	long	g
2339	2458	TCAACTAGGT	long	f
10014	6147	TGCACTTGGT	tag	g
4080	5309	TCAACTAGTT	long	g
7	7	CGAACTGGA	long	g
3633	4536	TCGACTAGTC	long	g
6889	3917	ATGACTCGAT	long	g
4	0	CCA	ACTAGGGATATGTGGACGTTTGT	TGTTGA
5594	6261	TACACTAGAC	tag	g
5105	10480	GATACTAGCTGTTGGAGGAACTTC	AGTTGG	
5729	9989	TATACTTGGT	tag	g
4205	9673	GATACTAGCT	long	g
0	0	ATTACTCGTT	long	f
219	371	ATGACTCGAT	long	f
9	0	CGCACTAGACCGGTGCGGTTTTG	ACGCCGT	
2	0	CCGACTAGGGATGAGTGAACGTTG	CATTAT	
7	13	CGAACTGGA	long	f
0	5	TCGACTAGGTGTT	CGGGAAGGAGACTTCT	
4639	4779	ATGGCTGGA	long	g
4147	3232	ATGACTTGGT	long	o
2000	2658	TCAACTAGTTGTCGGGTCTGTTT	AAGGATTT	
0	0	CCGACTAGCC	long	p
0	0	CCGACTAGG	long	g
2561	1272	ATTACTCGAT	long	f
3518	556	ATTACTCGCTGCTAGATGGCAACG	TTTAGTC	
2826	2398	AGCACTAGAC	long	g
3217	3545	CTAACGATGGACGCGGGAATCAG	AACATC	
2040	730	ATTACTCGAT	tag	f
66	52	ATTACTCGAC	long	f
2787	1416	ATCACTCGAT	long	f

0 TATGCTAGACCGGTGCGGTTTTGACGCCGT,  
2246 2595 AATGCTAGAC long f  
6 0 CCGACCGGGGATGGGGAGAGGTAATACCT  
210 376 CCGACCAAGGATAAGAGGTCGTAATTATCT  
114 201 TGAACCTGGC tag g  
0 0 CTAACCTCGTTTTTGGGGCGTAAGTTTCAGAC  
1119 1437 AGAACTAGG long o  
4 3 CTTACTCGACGTACGGCCCTGGCGGCTGTG  
4 4 ATTACTCGTT long g  
0 0 CCGACTCGGA long f  
27 17 ATTACTCGAC long f  
1522 1535 AGCACTAGAC long g  
2250 1086 ATCACTAGAT long f  
36 30 TACGCTAGATCGGTGCGGGTTTGACCCCGT,  
0 2 AGAACTGGA long f  
517 311 GATACTCGAC long f  
2078 1679 ATTACTCGAT tag f  
199 200 TCAACTAGTT long g  
0 0 TCTACTAGTT long f  
1565 1452 ATTACTCGCT long f  
1604 2244 TAAACTTGGC tag f  
193 177 CATACTTGGT long f  
119 42 TTCACTAGTGTTGCGGGTATTTATTTATCTG  
1486 1188 TCGACTAAGGATGATAAAATATTAAATGAA  
600 644 CTGACTTGGTGCCCCCGGTTTAAAGTCCGG  
1713 1690 CTAACGATGGACGCGGGGAATCAGTCTCTT  
50 122 CCGACTAGGGATCGGTGGACGTTGCATAGC  
646 825 CACACTAGGT long g  
1048 3145 ATTACTCGGTGCTAGCGATATACGGTTAGT  
1829 3115 CCGACTCAGGATTGGCAGACGTCTTTACCG,  
3 8 CTGACTTGGTGTTCCAGGTTTTAAATCTTGG  
64 46 CCAACTAGGC long c  
20 15 TCAACTGGTT tag g  
1361 1433 CTAACGATGGACGCGGGGAATCAGATCACT  
12 15 AACACTAGATGTTACGGGTATTGACCCCTG  
718 50 GATACTAGCT long g  
422 231 AGAGCTAGTT long g  
29 14 TACGCTGAGTTAGAGCGGCTCTGACGCCGT

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0	0	ATTACTCGCT	long	f
668	329	TACGCTAGACTGGT	GCGGTTTTGAAGCCGT	
96	247	GATACTAGGC	long	o
55	75	TCAACTAGTT	long	g
7	9	CAAACCTGGT	long	o
955	1449	AGCACTAGAC	tag	g
0	0	CCAACCTAGTT	long	c
1141	957	TTTACTTGCTGTTT	GGCTTTCTGGGCTGAGTG	
0	0	CCGACTTGGTGTT	CCCGGTTTTAAGTCCGGC	
1050	1135	CTAACGATGGACG	CGGGGAATCAGTCTCTC	
124	152	CCGACCAGCC	long	p
1024	1030	CTAACGATGGACG	CGGGGAATCAGAAAGA	
1025	688	AGTGCTAGAT	tag	g
0	0	TCAACTAGTTGTT	GGATCCGTTTAAGGATTT	
109	99	CGCACTAGGTGAC	GGGACCTCTCACGGTCT	
284	159	GATACTCGAC	tag	f
1179	794	ATCACTAGATTTT	GGCCGTATAGTCAGAGTC	
106	127	TAAACTCGAC	long	f
140	299	CCGACCAGGGATT	GGGAGACGTTAAATTT	
0	2	CCGACTAGGC	tag	o
0	0	TCGACTAGCC	long	g
798	456	CATACTCGCTGTT	GGGTTATAGATTACAGCGC	
0	0	TCAACTAGTTGTT	GGATCCATTTAAGGATTT	
109	109	AATGCCAGCC	long	g
63	134	CGAACTAGGT	long	g
5	0	CGAACTGGA	long	g
22	29	TCAACTGGTT	long	g
769	461	CCGACTGGGTGT	GGGAGGTGAACACCTTCT	
607	1319	CTCACTTGCTGTT	CCCGATTACTCGGGAGTG	
0	0	CCGACCAGGGAT	CGGAGAGTGTTACATGG	
72	77	AATGCCAGAC	long	f
651	778	AGCACTAGAC	tag	g
671	759	CTAACGATGGACG	CGGGGAATCAGAAAGA	
489	194	ATTGCTAGTT	long	g
573	532	ATCACTCGAG	long	f
0	4	GGTGCTGGA	long	g
697	754	CTAACGATGGACG	CGGGGAATCAGATCAC	
4	3	GATACTCGAC	long	f

873 465 ATTACTAGATTTTGGCCGCAAGGTCAGAGT(

0 2 AATGCCAGTC tag f

8 8 GATACTCGAC long f

292 620 CGAACTGGA( long g

0 0 AACACTTGGT tag g

481 602 CGCATTGCT tag c

405 1090 TCGACCAGACGTCGGGGGTGTCAACCCCTC

503 474 AGAGCTAGGTGTCGTGGGTGTTGACCCCG

93 134 TCGACTGGGTGTCGGCGATTAAAAACCGTC

0 0 AGCACTAGGTGTTGGTCCCTTTGGGGCCAG

471 543 GATGCTGGA tag f

452 682 CCGACCAGGGATATGAGGTAATTAATAGAT

245 523 AATGCCAGAC long f

479 510 CTAACGATGGACGCGGGGAATCAGAGAGA

0 23 GCGACCGAGATTCAGGAAATGCCCAAGATC

8 5 GGTACTAGG( long f

436 614 AGTGCTAGAC tag f

377 285 CCAGTTAGGGATTGGCAGGGTCTCGTTACG

27 35 TGAACCTGGC tag f

0 2 AGGACTAGG tag p

0 0 CTAACCTCGTTTTTGGGACGTAAGTTTCAGAC

95 62 AGTGCTAGTT tag f

0 0 GGTGCTAGG long o

81 80 TCAACTAGTTGTTGGATCTTAATAGATTTGG

119 131 CATACTTGGT long f

275 323 ATAACCTAGCT long f

0 0 TACACTAGACCGGTGCGGTTTTGACGCCGT/

0 0 AGAACTAGG long g

343 175 GATACTCGAC long g

239 331 CCAACTGTCT long p

0 0 GGTGCTTGG tag o

22 21 CCAACCAAAGATAAGAGGTTGTAAATACAA

0 0 AATACTCGGT tag f

0 0 TCAACTAGTT long g

334 348 AATGCCAGCCGTCGGAAAGCTTGCTTTTCG(

399 277 GATGCTAGGCGTTGGCAGACTCAATCCTGT(

335 486 AGTACTAGGTAGAGGAGGCCTCGTCGCCTT

433 566 AGTGCTAGATATTTAGATATTTATTCTGAGT

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4	332	335 TGTGCTAGAC long	f
5	229	139 ATAAGTAGCT long	o
6	0	0 CTCATTAGGT tag	o
7			
8	8	0 ATCACTCGATGTGTGCGATACACAGCACGC	
9	3	0 AGTACTAGGT long	f
10			
11	304	486 CTCACTCGAC long	f
12	316	334 GATACTTGGT tag	g
13	262	761 CATACTAGGCGTAGCGGAATTTCAATTCTGC	
14			
15	0	0 ATTACTCGTT long	f
16	92	50 GGCAGTAGGT long	f
17			
18	0	0 ATCACTAGAT tag	f
19	0	0 TCAACTGGTT long	f
20			
21	285	364 AGTGCTAGATGTTGGGGTTTTACCTCAGTG	
22	220	335 GGCGCTAGG tag	o
23	172	190 GGCAGTAGCT tag	c
24			
25	130	114 ATAAGTAGCT long	f
26	233	292 CCGACCAGGGATTGGGGGCCGTAAAGTTC	
27	0	0 AACACTTGGTGTTCCGGGAGTTGACCCCCG	
28			
29	4	3 GGTACTAGGT long	f
30			
31	382	397 AGTGCTAGATGTTGGTTGACTTATCAATCGC	
32	219	296 TTTACTTGCT long	f
33	290	331 TATGCTTGAT long	f
34			
35	67	92 GATGCTAGCC tag	o
36	0	0 CATACTTGGT long	o
37	0	0 CCGACCAAGGATCATGAGATGTTAAATATA	
38			
39	197	301 CGCACTAGACTGGTGCGGTTTTGACGCCGT	
40	0	0 ATCGCTGGGT long	o
41			
42	5	2 TCGACTAGGTGTCGGCGCCTAAAACCGTC	
43	61	55 CATACTTGGT long	o
44			
45	164	198 TCAACTAGTT long	g
46	46	46 CGGACTTGGT long	o
47			
48	265	224 CGCACTAGGTCGGGGAGGCTTGACGCCCTC	
49	28	20 CACGTTTGGT tag	g
50	71	90 GATACTCGAC tag	f
51			
52	217	375 CGCACTGGATCGGAGCAACTCTCACGTTGT	
53	0	0 AGTGCTGGA long	g
54	0	0 TGTGCTGGAT long	g
55			
56	288	405 TATACTTGGTGTAATTGGAATCAACCCTAAT	
57			
58			
59			
60			

0 TTTACTTGCTGTTTCTGGGCAACTGGGAGTC  
103 572 CGAACTGGA1long f  
152 186 CCGACCAGCCATTCCGAGACGTTACATTTTA  
0 CCGACTTGGTGTCCCCGGTTTTAAGTCCGGC  
8 23 TACATTGTAT1long c  
182 213 AATGCCAGTC1long f  
0 0 AGTACTAGGT1long f  
14 7 ATTGCTAGTT1long g  
6 2 AGTGCTAGGT1long g  
463 301 TGCACTAGGTGTTGGGGACTTCGTCTTCAGC  
274 200 TCAACTAGTTGTCGGATCTGTTTAAGGATT  
224 241 AATACTAGGT1long p  
288 245 ATCACTCGTC1long f  
142 159 AATGCCAGCC1long g  
186 357 ACCCCCATGAATTGGGGAGTATTTTGGTTCT  
179 188 TGTGCTGGAT1tag g  
66 69 TATACTAGTT1long g  
4 0 TCGCTGGAT1long f  
34 23 AATACTAGGCGTAGGGAGAGTCAAATCTTT  
0 3 GATACTCGAC1long f  
176 175 AATGCTAGAC1long g  
0 0 AATACTCGGTGTTGGTCCGCAAGGATCAGC  
165 47 GCCCCCATGA1tag g  
119 234 TTCCTAGTTTTGCGGGATGTTTTTATTCTGC  
0 0 CCACTTGGT1long o  
220 49 ATAAGTAGCT1long g  
162 159 AGTGCTAGTTGTTAGCCCGGCTTGAGCCGG  
233 250 TACATTGTATGGTGGGGATCTTGCACTCTCA  
224 231 CCAACTAGATGTTTCGGTTGGGGAACTCAA  
0 0 CTGACTAGGTGTCGGCGATTAAAAACCGCC  
220 67 ACACCCATGAATTGGGGAGTACTTTGGTCTG  
143 148 AACACTCGACGTTGGCCCTGTATGGGGTCA  
172 261 AGCACTAGAC1long g  
0 0 GATACTAGCT1long g  
4 2 GGTGCTAGAC1long g  
16 18 AATGCCAGCC1long g  
0 0 ATCACTCGAT1tag f  
0 0 GGCACTAGGT1long f



1			
2			
3			
4	0	0	AGAACTAGGTATCGTGGGTGTTGACCCCCG
5	4	5	TCAACTAGTTGTCGGACCTTAATAGGTTTGC
6	0	0	GGTGCTGGATGTCGGGGGGCTTGCCCCCTCC
7			
8	181	245	TCAACTGGCT long f
9	0	0	TCAACTGGTT long f
10			
11	188	143	CTTACTCGTTGTTTGGCTTTCGGGCTGAGTG
12	5	2	ATTACTCGAT tag p
13	237	87	TCTACTAGTT long f
14			
15	67	97	CACACTAGGTTTTGGAGGATTCGACCCCTTC
16	120	166	TCGACTAGTT long f
17			
18	104	119	AGAGCTAGCC long g
19	0	0	CACGTTTGCT long c
20	0	0	CTAACTCGTT long g
21			
22	82	77	CACACTAGGT tag g
23	0	0	AATATTAATTGTCGAATTTTCGGTAATTTAG
24	0	0	TGCACTAGACTGGTGCGGTTTTGACGCCGT
25			
26	198	222	CTAACGATGGACGCGGGGAATCAGAACAC
27	0	0	CAAACCTTGGT long f
28	0	0	AATACTTGGT long o
29			
30	304	128	TCTACTAGTT long g
31			
32	7	12	CCAACCAAAGATAAGAGGTTGTAAATATTA
33	130	302	GATACTAGCT long g
34	0	0	TTTACTTGCTGTTTGGCTTTCGGGCCGAGTG
35			
36	68	86	GATGCTAGCC long f
37	0	0	TCGACTAGTT long f
38			
39	0	0	CCGACTAGGGATCGGTGGATGTTTTTATTGA
40	7	5	TCAACTAGTTGTCGGGCCTTATTGGGCTTGC
41	0	5	GGCACTAGCTTGGGGTCTCCCTGTGGGATC
42			
43	0	0	TAAACTCGAC long f
44	0	3	AACACTTGGT tag g
45			
46	60	79	GAAGCTAGCC long f
47	41	36	ATTACTCGTT long g
48			
49	150	58	CCGACCAGTGATTGGGCGACGTTGCATGGA
50	144	87	AGTGCTAGTT tag f
51	0	0	TCAACTAGTT tag g
52			
53	51	45	GGCACTGGG tag f
54	126	126	CGTGCTGGACGTTGGCCAGCCTAGCTGGTC
55			
56	0	0	CACGTTTGCT long c
57			
58			
59			
60			

0 TGTGCTGAAT long g  
275 189 TCAACTGGCTGTTGGGAGAGCAATCTCTTAC  
10 5 TACGTTGAGTTAGAGCGGCTCTGACGCCGT  
0 TCGACTGGTT long f  
42 38 ATTACTCGCTGCTGGGGGGCAACCTTCAGT  
3 5 TCAACTGGTTGTTGAGGGGGTTCTCCTCAC  
60 107 CCGACTAGGCT long o  
144 123 TGCCTAGATCGGTGCCGGTTTGACCCGGT  
122 157 AATGTAAAAAATAATTTTTATTTAT  
11 10 CACGCTTGATTACGACGGCTCTGACGCCGT  
0 TCAACTAGCTGTCTGTAGATTAAGGTTTATA  
0 CATACTAGATCCGGGAGACACTCATCGTAA  
0 TGCCTTGGCCTGGGAGGATTGACCCCTT  
0 TCAACTAGTTGTCGGACCTTATTGGGTTTGC  
45 36 CGCATTTGCT tag c  
121 134 CACATTGGACCGGTGCTGCTCTGACGTAGT  
95 211 AGAACTAGAC long g  
3 2 CGAACTAGGTT tag g  
95 254 ATCACTCGAG tag f  
114 108 AGCACTAGACGTCGGGCGGGTGACCGCCCC  
0 GGCCTGGGCT tag c  
112 87 GGTGCTAGCC long f  
0 TCGACTAGTT long g  
133 137 TGTGCTAGTT long o  
31 84 TTTACTTGCTGTTGGGCTTAGGCTTGAGTG  
11 4 TCAACTGGTT long f  
4 12 ATTACTCGCT long f  
55 75 GATACTCGAC tag f  
0 2 GGAACTAGAT long f  
0 GATGCTAGCCGTTGGGGGGATACCCTTCAG  
28 39 ATTACTCGTT tag f  
0 4 TTTACTTGCT long f  
49 43 CCGGTTAGGCT long g  
3 7 AGAGCTAGCC long g  
78 174 CCGACTCAGGATGGGCAGTCCGTTGTTTCC  
0 AGAACTAGAC tag o  
18 28 TCACTAGACCGGTGCGGCTCTGACGCCGT  
78 74 GATACTAGAT long c

1			
2			
3			
4	87	212	CCGACCAGGGATATGAGGTATATAAAATAT
5	113	184	CCGACCAGGGATATGAGGTAAATAAAATAT
6	109	107	AACACTTGGTGTGGGGGGAGTTGACCCCTT
7			
8	104	89	TAACTGGACCGGTGCGATTTTGACGTTGT/
9	0	0	AGCACTGGA(long)g
10			
11	93	131	CAGACTCGGTtagk
12	129	79	AATGCCAGCClongo
13	115	114	TGTGCTAGACtagf
14			
15	151	148	GATGCTAGCCGTTGGGGGGTTACCCTCCAG
16	0	0	GATACTAGCTlongg
17			
18	0	0	ATGACTGGGTGTCGGCGATTAAAAACCGTC
19	30	31	AGAGCTAGCC(long)g
20	25	34	TATACTCGACATCAGCGATACTGTTGGTC
21			
22	60	30	AATACTAGGTGTAGGTCGTGTCAAAACGGT
23	92	162	CCGACCAGGGATATGAGGTAGAAATTGATT
24	87	148	GGTGCTAGG(long)g
25	0	0	CGAACTGGA(long)g
26			
27	0	0	CCGACTAGGGATTGGGAGGTTACTTACCTC
28			
29	8	11	GATGCTAGCClongg
30	71	96	AATGCCAGCClongf
31			
32	0	0	TCAACTAGTTtagf
33	89	104	TATGCTTGGTlongk
34	43	41	TCAACTAGGTGTTGGGAGGGTTAAACCCTT
35	63	64	TATGCTTGGTtagf
36			
37	0	0	ATAACTCGCTGTTGGTGTTTTGCATCAGTGG
38			
39	0	0	GGTGCTAGG(long)o
40	83	86	AATACTAGGTlongf
41			
42	10	16	GAAGCTAGCC(long)g
43	90	129	CTAACTCGATGTTTGGGCGTAAGTTTGAGC/
44	23	33	GATACTAAGTtagg
45	70	52	TCAACTAGTTGTTGGGCCTTAATAGGCTTGC
46			
47	3	0	CGGACTTGGTlongo
48	43	52	ATTACTCGAT(long)f
49			
50	0	0	GGTGCTAGATGTCGGGGAGCTTGCTCTTCG
51			
52	6	0	CTAACTCGTTlongg
53	108	140	AATACTAGAClongf
54	15	15	GGAAGTAGA(long)g
55			
56	0	0	GGCACTTGATlongc
57			
58			
59			
60			

63 95 TTTACTTGCT(long f  
0 0 TCAACTAGCT tag f  
0 2 GGTGCTAGG(long f  
0 0 ATGACTAGTT long f  
67 49 TCGCTAGACGTTGCCGGACCTAGTTCGGC  
89 60 AATACTAGGT tag f  
101 116 CCAGCTGGATGTTTCGTACCTCGAAAGGGGT  
72 78 AGCACTGGGTAGAGGTGGTAGCTGATGCC  
74 115 GATACTAGTT tag g  
0 0 AATGCTAGTTGTCAGTAAGTATACTTATTGG  
70 80 CCGACCAGG(long g  
27 19 CAGACTAGG(tag o  
0 0 GGCGCTAGG long o  
95 98 TCAACTAGTT long f  
30 0 AACACTCGCT long g  
0 0 GATACTAGCT long g  
92 89 GGCAGTGGACGCCGGAGGGGTGACCTTTCC  
0 0 ATTACTCGAT long f  
64 133 CTTACTTGCTGTTCCCGATTTATCGGGAGTG  
0 0 TCAACTGGTT long f  
0 0 CCGACTATGAATAGGATATCGTTTTAAGAAC  
0 0 CCGACCAAGGATTCGGAGAAGTTACGTGG  
0 2 CACACTTGGTCGGAGAGGTTAGACGCCTTT  
29 27 ATTACTCGCT(long f  
83 61 TGTGCTAGTTGTTGGGCAGCTTAGCTGTTCA  
85 92 AGAGCTAGTT long g  
77 77 TGCAGTGGGAGAGGATGGGTCCTAACTCA  
0 0 AGCGCTAGACGTTGGACGGAATGTTCACTG  
54 134 TATGCTTGGT long k  
0 0 GGTGCTAGAT long g  
50 61 GATACTAGCTGTTGGATTTATTTTCAGTGGT  
0 0 TTTACTCGACGTCCGGCCCCTGCGGCCGTG  
90 106 ACACCCATGAATTGGGGAGTACCTCCCGAC  
96 146 CCGACTCGGATTCAGATGAATCAAAAAAGT  
0 0 GGTGCTAGATGTTGGGAAGCTTGCTTCTCG  
53 2 5 TTTACTTGCTGTTCTGCACTACGCGGGAGT  
54 83 TCAACTGGTT long f  
55 90 44 AATGCTAGGTGTTGGGGATTTACTCCTCAGT

1		
2		
3		
4	0	0 CACACTTGGTGTGGGCCATTCATTTGGTCTG
5	6	5 ATTGCTAGTTlong g
6	0	0 AGCGCTAGACGTGGGGCAGGTGACTGCTC
7		
8	0	0 ATCACTAGATTTTGGTCGCGAGATCAGAGT
9	0	0 ATTACTCGTTlong f
10		
11	73	82 CACGCTTGGTlong f
12	42	38 AGCACTGGATCGGAGAGCCCTCCATAGCTT
13	0	0 CATATTTGGTlong o
14		
15	0	0 CTAGCTGGGTlong f
16	59	84 ATTACTCGACATACGTGATACTATGTGTG
17	74	70 AGCACTGGGlong g
18	0	0 ATTACTCGTTtag c
19		
20	47	123 TAAACTTGGTGTCTGGTGGCTTAAACTCCTTC
21	0	0 CTGACTTGGTtag o
22		
23	6	6 TTTACTTGCTGTTTGGGCTATATGCCTGAGT
24		
25	21	26 TGTGCTAGAClong f
26	16	8 AACACTAGGTGTGGGTGGGTCAAACCAT
27	4	2 TCAACTAGGClong c
28		
29	17	11 AATACTCGGClong g
30	9	18 TCAACTGGTTlong f
31		
32	0	0 TCAACTGGGTtag p
33	58	120 CCGACTCGGATTCAGATGAATCAAAAGTTC
34	0	0 GAAGCTAGClong f
35		
36	62	78 TTCACTAGGCGTTGGGGTCGCAAGACCTCA
37	2	0 TCAACTAGCCGTTGGGAGCTTTAAAGTTCTT
38		
39	0	0 AGTGCTAGCTGTTGGGTCCTTGAGGCTCGA
40	40	96 TATACTAGATGTTGGGGGTTTCAACGCCCTC
41	0	0 CCGACCAGGGATCGGAGACAGTTACATGG
42		
43	0	0 AGTGCTAGGTtag f
44		
45	4	10 TCGCTGGATlong g
46	43	54 TGTGCTAGACtag g
47	0	0 CTTACTCGACGTCCGCCCTTGCGGTCGTGC
48		
49	0	0 TTAAGTGGTTGTTGGGTCTTAACTGACTCAG
50	0	0 GGCGCTAGGlong g
51	0	0 ATTACTCGATGTGTGCGATATACAGCACGC
52		
53	0	0 ACAACTAGATGTTGGGAGGGTCTGCCTTCC
54		
55	0	0 GATACTAGGClong p
56	0	0 AGCACTAGACGTGGGGCGGGTGACTGCTCC
57		
58		
59		
60		

51 60 TGTGCTAGCT long o  
40 67 TCAACTGGTT long f  
0 0 TCGACCAGACGTCGGGGGAGTCAACCCCTC  
0 0 AATGCTTGGTGTCTGGAGTGTTAATTCTCTG  
30 25 TCAACTAGGT tag g  
0 0 GATGCTAGAT long o  
39 45 TCAACTAGCC long p  
5 8 AGAGCTAGTT long g  
41 55 CACACTAGATCGGAGTCGCTCTGACGCGCC  
38 33 TCAACTAGTTGTCGGGTCTGTTCAAGGATT  
55 57 ATCACTCGTG long f  
0 0 CGAACTGGA long f  
10 15 AGCACTAGTC long g  
49 66 CCGACCAGGGATTCTGAAGATATCCTTTATTA  
21 29 GACACTAGGTGTAGGTAGAGTTAAATCTAT  
4 0 CGCACTGGACCGGTGCGGTTTTGACGCCGT  
0 0 AATACTTGGT tag o  
2 0 GACCCTAAAT tag f  
0 0 GATACTAGCT long g  
0 0 AGCACTGGGGGAGGGAGGTTTCGGCCTTC  
0 0 GGTACTAGG tag f  
39 44 ACCCCCATGA long g  
21 73 TCGACCAGGCGTCGGGGGTATCAACCCCTC  
5 12 AGTACTAGGT tag k  
41 56 ATCACTCGTTGCTGGGGGGTAACCTTCAGT  
0 0 GATACTAGG long p  
0 0 CTCACTAGGT long o  
0 0 GGTGCTAGG tag g  
0 0 CCGACCAGAGATTGTAAGACGTTGAATATA  
57 62 CCGACCAGGGATATGAGGTAATATTTGTTT  
0 0 TCAACTAGTT long f  
51 51 AGTGCTAGTT tag f  
2 0 GATACTTGGT long f  
0 0 AGGACTAGGTATCGGCAATTTATTGTCGGT  
0 0 TCGACCAGACGTCGGAGGTATCTATCCCTC  
0 0 GGTGCTAGCCATATCGGGTGTTGACCCTTA  
0 0 CACACTAGATCGGTGCGGTTTTGACGCCGT  
0 0 GGTGCTAGG long g

1			
2			
3			
4	68	86	AGTGCTAGTTGTCGGGGTCTTTGACTTCGGT
5	0	0	GATACTCGAC long f
6	40	69	CCGACCAGGGATATGAGGTATTTAGATTAT
7			
8	61	53	CCGACCAGGGATATGAGGTAGAAATTATTA
9	0	0	CACGTTTGCT tag c
10			
11	0	0	AGAACTAGAT long o
12	42	11	AGTGCTAGATGTTGTGGGTATTGACCCCCG
13	0	3	GGTGCTAGAC long g
14			
15	57	51	ACACCCATGAATTGGGGAGTTTGTTGCGGG
16	0	0	TTTACTTGCTGTTCTGCATTAAGTGGGAGT
17			
18	43	48	CCGACCAGGGATATGAGGTAAATAGTATAT
19	36	37	CGAACTGGA long g
20	5	0	CGAACTAGCT long g
21			
22	24	20	TCAACTAGTT long g
23	27	45	AGCACTAGACCGGAGAACCCTCCACAGTTT
24			
25	54	45	TCAACTGGTT long g
26	0	0	CCGACTAGGC long o
27	0	0	TCAACTGGTT long f
28			
29	52	69	GATACTAATT long p
30	0	0	ATTACTCGAT long f
31			
32	37	67	AGTGCTAGACGTTGGAGGGTATCCTTCAGT
33	0	0	TCTACTAGTT long g
34			
35	13	21	AGTGCTAGAC long g
36	0	0	AATACTAGGT tag f
37			
38	13	19	TGCGCTAGGT tag p
39	5	12	ATCACTGGGT long o
40	34	50	TATACTAGTTGTTGGCGGTTTCAACGCCGTC
41	0	0	CACACTTGGTGTGGGTGATTCATTTATCCG
42			
43	0	0	TCAACTGGTTGTTGGGTTTTAACTGACTCAG
44	0	0	TCAATTGGTTGTTGGGTCTTAAGTACTCAG
45	0	0	TCAACTGGTTGTTGGGTCTTAAGTACTTAG
46			
47	76	38	GATACTAGATGTCGGGGGTTCTTACCCTTCC
48			
49	2	0	CCGACTAGGGATCGGTCCACGTTATTATTTG
50	37	41	TATACTAGGT long p
51	15	14	CCAACCAAGATAAGAGGTTGTAAAAATTA
52			
53	35	33	GGTGCTAGGT tag f
54	0	0	CCGACTAGGC long f
55			
56	30	25	GGCACTAGGTAGGGGGCTCGCCGATGGGC
57			
58			
59			
60			

0 AATGTTAGCC long g  
0 GGCAGTGGCTAGAGGTGACCCTGCGTCGTC  
0 AGTGCTAGG long g  
38 33 CTTACTCGTT long f  
41 50 AATGCTAGACGTGGTGGGTCTTGACCCCCG  
0 TCAACTGGTTGTTGAGTGGGTTTCTACTCAG  
42 28 ATCACTGGGT long o  
0 GATGCTAGCC long g  
2 0 TCAACTAGTT tag g  
34 60 CCGACCAGGGATATGAGGTAAAAAGTATTA  
40 38 TGCAGTGGT tag f  
0 TCAACTAGCCGTTGGGTTCGTAAATGAGCTT  
0 GGTGCTCGG long f  
36 51 TCTACTAGTT long f  
0 GATGCTAGCTGTTGCGGGGTTCCCCCTGAG  
0 ATCACTCGATGTTGGCATTATGTCAGCGTC  
0 3 CCGACCAGG long g  
46 25 TCACTGGGTGTTGAGTCGGGGAAGCTCGA  
5 2 GACACTAGG long c  
32 26 TCAACTGGTT long f  
0 TCAACTGGTT long g  
32 77 GGTACTTGGT long g  
0 AGCACTGGAGGGGGGCGGGTTGCGCCCTTC  
0 3 AACACTAGGTGTGAGCGGTGTCAAAGCCGT  
44 53 CCGACCAGGGATATGAGGTAAATAATTAGA  
44 45 TCAACTGGCT long f  
18 22 CCAACCAAAGATAAGAGGTTGTAAATACAA  
4 0 GGTGCTAGAT tag g  
24 29 AGTGCTAGAC long f  
0 CTGACTTGGTGTCCCGGGTCTTAAGTCCCGC  
16 14 GATACTTGGTGTGTGGGGTATTAAGTCCCTA  
9 10 CGCATTAGACCGGTGCAGGTCTGACCCTGT  
7 15 TGCCTAGACGTTGACGGACCTAGTTCGCC  
35 49 CCGACCAGGGATATGAGGTATATAAATTAT  
33 35 CGAACTGGA long g  
17 22 TATGCTTGGTGTGGATCTTTGATTCAGTGC  
0 CACGTTTGCT tag c  
0 GCGCTAGG long g



1			
2			
3			
4	20	25 AATGCCAGAC	long f
5	4	7 AGCACTTGGT	tag f
6	7	16 TCAACTAGGT	long g
7			
8	14	29 ATTACTCGACATTGGCGATAAACTGATCAGT	
9	0	0 TCGACCAGGCGTCGGAGGTATCAACCCCTT	
10			
11	15	30 AGAACTGAG	(long g
12	0	0 GATGCTAGCTGATGGGACTTCTACCGTCTCC	
13	0	0 AGTGCTAGAT	tag g
14	0	0 CGGACTTGGT	long f
15	0	0 CCGACCAGGGATCGGGGAACGTTATCGTCC	
16			
17			
18	37	37 AACACTAGGT	long f
19	6	5 ATCACTCGAT	tag f
20			
21	8	28 AGAACTAGACGATGGTGTCTTGAGGCATC	
22	0	0 CGCACTAGATCGGTGCAGGTCTGACCCTGT	
23	4	7 TGTGCTGGG	(tag g
24	0	0 TGCACTTGGCCTGGGAGGATTAGACCCCTT	
25	0	0 GGCGCTAGG	long g
26	0	0 AGTACTAGTG	tag g
27	3	0 AATACTAGGTGTCGGGCGTGTCAAAACGGT	
28	4		
29			
30	43	18 AGTGCTAGAT	long g
31	0	0 AGCGCTGGG	tag o
32	0	0 TCAACTGGTTGTTGGTCTTAACTGACTCAGT	
33	0	0 CCAACCAAAGATAAGAGGTTGTAAATACAA	
34			
35			
36	35	24 AATGCTAGCCGTTGGTCAGCATGCTGATCG	
37	0	0 TATACTTGGTGTAGCCGGACTCAACCCTGG	
38			
39	31	35 CATGCTAGATGTCGGTCTGTCAAAGGATCG	
40	32	48 TATACTTGATGTAGTTGGGCTCAACCCTGAC	
41	0	0 TTTACTTGCTGTTTGCCCCTTGAGGGTGAGT	
42			
43	22	26 CGCACTAGGTCTGGGGAGGCTGACGCCCTCC	
44	6	0 AATACTAGGCGTAGGTGGAGTGAAATCCAT	
45			
46	13	139 CCGACTAGGGCTGAGTCTTTTTAGATTCCG	
47	7	0 ATCACTCGTG	long f
48			
49	36	24 TCAACTGGTT	long g
50	0	0 GATGCTCGCCCTATGGAGGTCTTAAAGCCT	
51	0	0 TCAACTAGTT	(long f
52	0	0 CGCATTTGAGGTGGGAGGATTGACCCCTT	
53			
54	13	13 AGTACTGAAT	tag f
55	0	0 CGAACTGGA	(long f
56			
57			
58			
59			
60			

13 33 GGCCTAGG` long o  
8 7 TTTACTTGCTGTTTGTATTTCTGGTATGAGTG  
0 0 TCGACTAGCC long o  
19 23 CCGACCAGGGATATGAGTAGTATATTTCA  
28 9 TCAACTAGTTGTCGGATCTTAAGTATTTGG  
0 0 ATTGCTAGTT` long g  
8 0 CATACTTGGT` long g  
25 14 CCGACCAGGGATATGAGTAGTATATTTCAA`  
0 0 TCAACTGGTTGTTGGTTCTTAAGTACTCAG  
20 4 TCAACTGGTT long g  
9 3 GGTGCTGGG` tag g  
0 0 GGCCTAGG` long c  
0 0 AATACTAGATTTGGTGGGTCTTGACCCCCG  
3 2 GATGCTAGCC long g  
0 0 GATGCTAGG` tag p  
22 40 TAGATTAGGTGTCGGGGGAGTCGAACCCTT  
19 15 AGTACTAGG` long c  
0 0 GATGCTAGG` long p  
0 0 GGCCTAGG` long c  
7 3 CAGACTAGG` tag o  
0 0 CCGACCAGGGATGGGCGGGCGTTGAATCC  
10 14 CTAAGTATGATGTTTGGATTTAGGTTTGAACA  
0 0 AGCACTAGTCCGTGGGAACCCTCACATTTTC  
26 18 TTTACTTGCTGTTCCGGCTTATGTTGGAGTG  
13 23 AGTGCTAGTT tag f  
20 26 CCGACCAGGGATATGAGGTAATTGTTATTA`  
23 22 CACACTAGGTGACGCGAACTCTGACGTTTG  
6 4 TCAACTAGCC long g  
27 21 TTGGCCTAGGATCGGAGGATGTTAATAGAC  
64 14 TCTACTAGCT` long g  
0 0 GATGCTAGG` long g  
5 0 AGCACTGGA` long f  
0 0 CTTACTAGCTGTTTGGTAGGAATATTGAGCC  
21 26 CGAACTAGG` long g  
0 0 AGTACTAGGTGTAGGGGGAGTGAAATCCTT  
10 23 GGCCTAGG` long g  
3 3 GGGACTAGG` long g  
13 19 AGAGCTAGCC` long f

1			
2			
3			
4	0	5	AGTGCTAGCCGCTGGGACTGTTACCGTCTC
5	0	0	CACACTAGGT long g
6	0	0	AATGCCAGTC long f
7			
8	14	7	ACACCCATGA tag g
9	21	42	GATGCTAGCTGTTGGGGGGTTACCTCTCAG
10	0	0	AGTGCTAGACGTTGGCCCCCTTCGGGGTCAG
11	0	0	TCAACTGGTT long g
12			
13	16	24	TGTGCTAGTT long o
14	17	36	AGTGCTAGACGTTGGGGAACCTTAGTTCCTT
15	9	13	GGGACTAGGTGCTTGGGGGAACGACCCCC
16	0	0	CACACTAGATGACGGGGCCTCTCACGGCGC
17			
18	0		
19	15	16	GATACTAGGT tag p
20	0	0	CACACTTGGTGCAGACGGGGCTCAACCCTGT
21			
22	21	23	AATGCTAGCCGTTGGGAAGTTTACTTCTCCG
23	0	0	AGAACTAGGTAGTAGACTTGACTTGGGTTT
24	0	0	CTGACTTGGTGTCCCCGGTTTTAAGTCCAGC
25			
26	20	73	CCGACTAGGGATTGGAAGGCTACGTACCTT
27	0	0	TATGCTTGGT long f
28			
29	0	0	GATACTTGT tag g
30			
31	4	8	AGTACTAGTG long g
32	22	12	CCGACTAGGC long f
33	0	0	GGCGCTAGGTGTGGGGCTCGTTCCACGAGT
34			
35	12	19	AGAACTAGAT long o
36	19	35	GGTACTAGCT tag c
37			
38	11	14	TTAACTAGGTGTTGGGAGGGTTAAACCTTT
39	0	0	TCAACTAGCT tag g
40	21	19	AATACTCGGCATCTGGCGGCCGATCTTCGG
41	0	0	TCAACTGGTT long f
42			
43	6	4	CGAACTGGA long g
44			
45	14	12	GGGACTAGGTGCTTGGGGGAACGACCCCTC
46	7	17	CCGACCAGGGATATGAGTAGTATATTTCAA
47	0	2	TCAACTAGTTGTCGGGTCTTATTGGACTTGG
48			
49	32	13	CATACTTGGT long g
50	0	0	AATGCTTGGT long f
51			
52	0	0	CACACTAGGCTTGAGGACCTCTTACGGATCT
53	0	0	CACGTTTGGT long o
54	7	4	TATGCTTGGTGTGGGATTTATCTCAGTGCC
55	0	0	TACGCTAGATCGGTGCGGTTTTGACGCCGT
56			
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26 34 ATAAGTAGATGTTTGGGATACACTGTAAGCC  
0 0 AGCACTAGAC long g  
7 10 AGCACTGGAC long g  
0 0 CCAACTAGCG long p  
22 53 CCGACTTGGATTGAGATGAATCAAAAAGTT  
2 3 AATACTCGGCATCTTTCGACCGAGCTTCGGC  
0 0 CCGACTAGGGATGAGTGAGCGTTGCATTAT  
0 0 CTGACTTGGTGTCCCGGGTTTGAAGTCCCGC  
0 0 ATAAGTCGCTGCTGGGGGGTAACCTTCAGT  
0 0 GGCAGTAGG1 long k  
0 6 TACGCTAGATCGGTGCAGGTCTGACCCTGT  
2 2 GTGACTAGGTGTGGCTGGCTCAAGGGCTGC  
19 24 CCGGCGGGGCGCGGGGGGGCCGAGGGAG  
3 3 TATACTAGATGTAGTCGGACTCAACCCGAC  
3 4 GAAGCTAGC long g  
0 0 ATCACTAGACGTTAGTCTCACTCTGTGAGAT  
17 14 GGCAGTAGGCAAGGGAGGTACCTATGTCTT  
0 0 TCAACTAGTTGTTGGATCTATTTAAAGATTT  
0 0 TCAACTGTTGTTGGGTCTTAAGTACTCAGT  
0 3 TGTACTTGATGTAGCTAGGCTCAACCCTGGC  
22 23 TATACTAGGTGTAGCCGGACTCAACCCTGGC  
11 13 AACACTGGGCGGGAGAAAGGTTTCGCTTTTC  
0 0 GGTACTAGG1 tag f  
13 15 GGTACTAGGCTTCGTGGGAATTGACCCCTG  
14 17 CGCACTAGGT tag k  
10 38 GATACTAGAC tag p  
11 12 CCAACCAAAGATAAGAGGTTGTAAAAACAA  
6 3 CCAACCGAGT long g  
15 11 GGTACTAGG1 long g  
0 0 ATAAGTAGCT long f  
0 2 TCAACTGGTT long f  
10 11 AGTGCTAGTCGTTGGGGGTACCCATTCCCTC  
26 33 CTGACTCGGATTGAGATGAATCAAAAAGTT  
0 0 CCGACTGTAGATTAGAAGACGTTATTCAAGC  
0 0 AATACTCGAT tag f  
0 0 GGTACTAGG1 long f  
9 33 TATACTTGAT tag g  
0 0 TCAACTGGTTGTTGGGAGTTTCTTCTCAGTA

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2		
3		
4	0	0 AGTACTGGG(long g
5	13	13 AATGCTAGGTGTTGGTGGGTCACCATCAGT
6	11	18 AATACTCGTTGTTGGAGGTATTGACCCCTTC
7	12	22 CCGACCAAGTTTTTCGAGGAATTCTATTGTTA
8		
9	0	0 TTTACTTGCTGTTCCGACTTAGGTTGGAGTG
10	15	13 ATCACTGGGTGTTGGGAGAGCGATCTTCTA
11	9	26 AGTGCTAGACGCTGTGGGTATTGACCCCTG
12		
13	14	25 CCAGCTGGGTGTTTCAGTTGGGGAAACCCAA
14		
15	21	30 CCGACTCGGtag f
16	0	0 CCGACCAGGGATATGAGTTGTTAAGATTAT
17	21	30 CCGACCAGGGATATGAGGTATTTAAAAGAT
18	12	5 TCAACTAGGTGTTGGAGGGTTAAACCTTTA
19	25	27 CCGACTCGGATTCAGATGAATTA AAAAGTT
20	11	9 GATGCTAGGTGTTGGAGGACTTAACCCCTC
21		
22	17	27 TCACTGGGTtag f
23	6	24 TCACTAGATCGGTGCCGGTTTGACCCGGT
24		
25	14	15 TCAACTAGCC long c
26	0	0 CGCACTTGCTGTAAGAGGATT CGAACCTT
27	21	20 CCGACCAGGGATATGAGGTATTATATTATT
28	22	16 CACACTAGGTCTTGACGGATTCGATCCCGC
29	16	27 CCGACCAGGGATATGAGGTAAAAAGATTAT
30	0	0 TACGCTAGACTGGTGCGGTTTTACGCCGT
31	2	0 AGTGCTAGTTtag f
32	11	9 CCGACTAGGtag c
33	0	0 CGAACTGGAC long g
34	23	35 CCGACTAGG(long c
35	13	20 GGTGCTAGCCATATCGGGTGTTGACCCAAA
36	12	34 AGTGCTGGGTGTTGTGGGTTACGACCTGCA
37	0	0 TCAACTGGTT long f
38	13	22 AACACTAGAC long g
39	0	2 GATACTAGGTtag c
40	4	5 TCAACTGGTT long f
41	30	20 CCGACTCGGATTCAGATGAATCAAAAGGTT
42	25	8 CCGACCAGGGATATGAGGATCTTTATTTATA
43	0	0 GGCCTAGG long g
44	0	0 AATGCTAGCTGATGGGGCTTCTACCGCTTC
45	10	15 CCGACCAGGGATATGAGGTATTTAATAGAT
46	15	16 CATACTTGGT long o
47		
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11 16 CTTACTCGTT(long f  
9 13 TAAACTTGGC long f  
0 0 AGTGCTAGTT long c  
9 26 CCAACTGGGTGTTCTCTCCCGCAAGGGAG  
58 0 CCGACTCGGC long g  
0 0 TCGACTAGGT long g  
0 0 GGC ACTAGG1 long g  
0 0 TCGACTAGGT long g  
0 0 TCGACTGGTT long f  
0 0 AGCACTGGG(long g  
0 0 TCAACTAGCC tag g  
0 0 AGAGCTAGA(tag g  
9 7 TCAACTAGGTGTTGGGAGGGTTAACCTTT/  
11 5 TCAACTAGGTGTTGGGAGGGTTAAACCTTT/  
0 0 CGTATTGAGGTGGGAGGATTGACCCCTT/  
25 4 CCGACCAGG(long o  
4 9 CCGACCAGGGATATGAGTAGTATATTTAC  
4 7 GAAGCTAGC(tag g  
0 0 GATACTAGGTGTCCGGGCTTCTGGCCTGGG  
14 3 CCGACTAGG(long g  
0 0 CCACTAGATCGGTGCGGGTTTCACCCCGT/  
13 14 CCAACTAGAT tag f  
0 0 CCAACTGGTTGTTGGGTCTTAAGTACTCAG  
0 0 AGTGCTAGAT tag p  
4 22 GGC ACTAGGCCCTTGGGGGAGCGACCCCT  
14 36 CCGACTCGGATTTAGATGAATCAAAAAGTT(  
8 7 TCAATTAGGTGTTGGGAGGGTTAAACCTTT  
12 16 TCAACTAGGTGGTGATTGTGTCGATCCAAG(  
0 0 CAAATTAAAGATTAGTTTTTTTAAACAAGTC  
0 0 TCGACTAGCCGTCGGGCTCATTATTGAGAG  
0 0 TCGACTTTGG long g  
10 16 ATCGCTAGCTTTTCGGAGTATCGACCCTCTG  
0 0 AGCGCTAGG1 long g  
21 22 TTTACTCGTTGTGCGGGAGCAATTTTGCGCA  
8 3 GGTACTAGGTGTGGACTTACATGGGTTCA  
0 0 GGTACTAGG1 tag f  
12 17 AGTGCTAGATGTTGGGGCTTTTTGGTCTCG(  
6 8 TATACTTGGTGTAGCTGGACTCAACCCCGG(  
For Peer Review

1			
2			
3			
4	0	0	AGTACTAGGTtag c
5	0	0	ATTACTCGTT(long f
6	0	0	TCAACTGGTTGGGTCTTAAGTACTGACTCAGTAA
7	0	2	AATGCTAGTT long f
8	0	2	CGAGCTGGA(long g
9	2	13	AGAACTAGATGTTGGAGGGGGAACCCTGC/
10	10	11	TAGACTAGATGTGCGCGTCACTACGGTGAC
11	9	0	AGAACTAGGTGTCGTAGGTGTTGACCCCTG
12	0	14	TTCACTCGCTGTTGGATTTTACATTCACTGG
13	0	26	CCGACTCGGATTCAGATGAATCAAAAAGTT
14	16	7	AATGCTAGAC long g
15	24	0	TCAACTGGTT long f
16	11	2	AATACTCGGC long g
17	0	4	AGTGTTTTATATACATATTTGTATATGATAG
18	0	7	GGCACTGGGTAGAGGGCTCTCCGATGGGC
19	7	0	ATTACTCGCTtag f
20	0	9	TCAACTAGGTGTTGGGAGGGTTAACTTTT
21	15	18	AGTGCTAGATGTCGGCTCCTTTAGGGGTGCG
22	10	19	AGCACTTATC long g
23	14	0	CGCATTTGCT(long c
24	0	0	GATGCTAGGC(long p
25	0	21	GATACTTGTTtag g
26	12	0	GGTGCTAGA(long g
27	0	11	TCAACTGGTT long f
28	10	2	GGTGCTAGCTGTTTCGGGGGTTCCCCCTGAG
29	4	14	ATAGCTAGAT long o
30	13	0	TATACTTGGTGTAAGTGAATCAACCCTAGT
31	2	0	ATAACTAGCT long o
32	0	25	CCGATTCGGATTCAGATGAATCAAAAAGTT
33	16	5	CCGACCAGGGATATGAGGATTCTTATTTAT/
34	19	0	GGTACTTGGTAGAAATCGCTCCGATGGCGA
35	0	0	TCAACTGGTT long f
36	0	8	AGCACTGGG(long g
37	18	0	AGAACTGGA(long f
38	0	0	CCGACCAGGGATATGAGTTGTTAGGATTAC
39	0	0	TCAACTGGTT long f
40	0	0	TCAACTAGGTGTCCACTCGGCCACGGTCGA
41	0	0	GATGCTAGCC tag o
42	0		
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10 7 TCAACTAGGTGTTGGGAGGGTTAACCCTTT  
14 14 CACACTAGACCGATGCGGCTCTGACGCCGT  
0 2 GATGCTAGAC tag p  
13 13 AATGTAAAAAATAATTTTTATTTTATT  
0 0 GATGCTAGATGTCACGGGTATTGACCCCTG  
0 2 TACGCTAGATCGGCCAGGCTCTGACGTCTG  
8 8 AGCACTAGAC long g  
0 0 AGAACTAGG long g  
0 0 ATAAGCT long o  
0 0 TCAACCGGTTGTTGGGTCTTAAGTCACTCAG  
0 0 TATGCTTGGTGTGGGGCAGCAATGTTCCA  
11 8 TATACTTGGTGTAGTTGGACTCAACCCCGAC  
0 0 CGAACTAGATGTCGGGAGGGTCAGCCTCCC  
3 0 GGTACTAGGTTGCGGGCTTACATGGGCTCG  
0 0 CCGGTTAGG long f  
5 7 AATACTAGGTGTAGGTGGTGTCAAAGCTAT  
10 13 GGCCTAGAC long k  
12 15 GATACTAGGCGTCAAGGGTATCGACCCCT  
0 0 CCGACCAGGGATATGAGTTGTTAGGATTAT  
0 0 TATACTTGGT tag g  
0 0 GGCCTAGG long f  
5 3 TGTGCTGGAT tag g  
0 0 TCGACTGGTT long f  
0 0 GGTACTAGATTTGGTGGGATTTGACCCCTG  
0 0 ATAAGCT long g  
0 0 GGTACTAGGTTTGGTGGGTCTTGACCCCTG  
0 0 CACACTAGACCGGTGCGGTTTGGACGCCGT  
0 0 ATTACTCGCT long g  
20 16 AGTGCTAGGTGTCACGGGCTTTGACTCCTG  
0 6 AATGTTAGCC long g  
0 0 AGTGCTAGACGTTGGGAGGTTACCTTTGAG  
12 23 CCGACCAGGGATATGAGGTAGAAATTATAT  
0 0 TGTGCTGGAT tag g  
0 0 AGTGCTAGAT long g  
0 0 AGCACTAGG long o  
0 0 ATAAGCT long g  
10 15 CCGACCAGGGATATGAGGTAATAATTATTA  
8 15 ATTACTAGCTGTTTGCTTAAGTAAGTGGCTA



1		
2		
3		
4	2	0 TTTACTTGCTGTTCCGCCCTGGGCGGAGTC
5	0	0 CCGACTAGGGATGGGTGAACGTTGACTTTA
6	11	19 TCAACTAGCCGCTAGTCTCGCTTTAGAGATT
7	17	2 CCGACCAGGGATATGAGGATTTTTATTATC
8	0	0 CATACTTGGT tag f
9	32	0 CCGACTAGGC long f
10	0	0 TCAACTGGTT long f
11	16	10 TCTACTTGCTGTTGGGGGTAAAACCTTAGTA
12	0	0 AGCACTAGTTATCGGAGGTATTGACTCCTTC
13	0	0 ATAACTAGCT long f
14	5	7 GGCAGTAGGTGTGGGGACTTATCAACGGTC
15	0	0 TCAACTGGTTGTTGGGTCTCAACTGACTCAG
16	4	15 TCTACTAGTT long f
17	0	0 TCAACTGGTT tag f
18	0	0 CCGACCGGGGATGGGGAGAGGTAATACCA
19	0	0 TGAAGTTGGC tag g
20	0	0 AGCACTAGATCGCTGGGGAGCTATCTTTGG
21	0	0 GGTGCTAGATGTCGGGAAGCTTAGCTTCTC
22	0	0 TCAACTGGTTGTTTGGTCTTAACTGACTCAG
23	0	0 TCAACTAGGC tag c
24	0	2 CGCACTAGGTGCGGGGAGGCTTCACGCCCTC
25	0	0 AACACTGGAC long g
26	4	11 TCTACCAGTTGTTTGAGGTATCAACCCCTCG
27	0	0 TCAACTGGTT long f
28	0	7 CCAACTGTCT long p
29	2	0 TCAACTAGGT tag f
30	0	0 AACACTAGGT tag f
31	3	8 GATACTAGTTGTTTGGAGTAATCTGAGTGA
32	0	0 ATCACTAGACGTCTGTTTTGCTTAGCAAAAT
33	0	0 CCGACTGTAGATTAGAAGACGTTAATCAAA
34	0	3 AGAGCTAGTC tag g
35	0	0 CACACTAGGTGACGCAATCTCTGACGATGG
36	6	11 ATTACTCGCT tag f
37	6	24 TCAACTAGCTGTCTGATACATTAGATATTGG
38	0	0 TCGATTAGGAAGTGTTTATATCACTTTCGA
39	4	5 CCGACCAGGGATATGAGTAGTATATTTCAA
40	8	7 GGCAGTAGA tag o
41	0	0 ATTACTCGTT long f
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0 CACGCTTGGTGTGGGGGGTTGACACCCTCT  
0 GCGCTAGGTGTGGGGCTTTCCACGAGTTC  
7 TGCCTAGGTGTTGGGGTGTAGACTTCAGC  
1 TCAACTAGGTGTTGGGAGGGTTAAATCTTT  
12 CCGACCAGGGATATGAGGTAGAATTTGATA  
13 TCAACTAGGTGTTGGGAGGGTTTAACCTTT  
0 AGCACTAGATlong g  
3 GATGCTAGATGTTGGTAACGTCAAGTTATC/  
10 CCGACCAGGGATATGAGGTATATAGATTAT  
0 CATACTAAGTGTCTGCCTGTAAAAGGGTGG  
0 CCAACTAGGGATGTGGACGTTTGTGTTGAAG  
0 AATACTTGGTlong o  
12 5 TCCACTAGATTGTGGCGCTTTTAACGGCGTC  
0 CCGACCAGG(long c  
13 CCGACTAGG(long g  
0 GGTGCTAGATtag g  
0 CCGACTAGG(long g  
2 AATGTTAGCClong f  
0 ATTGTAAACGTTAACGCTAAGCAATCCGCC  
0 GATACTAGGTGTAGGCGGTCATTTACCCCG  
0 TAGACCAGATtag o  
0 AGTGCTAGATlong g  
13 7 CCGACTAGG(long g  
2 3 TCAACTAGGTGTTGGGAGGGTTAAACCTTT  
20 3 CCGACAAGG(long g  
0 CCGTCTTTGAATGGGGAAGCGATTTAAGTT  
4 5 CATACTTGGTGTAGCTGGACTCAACCCCG  
11 12 TACACTAAACGTTCACTCTTGGAACAAGAC  
6 3 AGCACTAGAClong g  
0 GGCCTGGGCAGGGGAAGCACCTATGTCTT  
0 AGCACTAGATCGCTGGGGAGCTATTCTTG  
0 ACAACTGGTTGTTGGGTCTTAAGTACTCAG  
3 4 GATGCTAGCClong g  
0 CCGACTAGG(long o  
0 CGAACTGGAtag g  
0 7 GATACTTGTTtag g  
0 GGTGCTAGCTGTTGGGGGTTACCTCTGAG  
0 TCAACTGGTTlong f

1			
2			
3			
4	0	0 GTGACTAGG1 long	f
5	0	0 CACATTTGCTGTAAGTGGGAATCGACCCCCAC1	
6	0	0 TCAACTGGTC tag	f
7	0	0 GGTACTCGG1 long	f
8	0	0 ATAACTCGCT1 long	f
9	0	0 CACATTTGCTGTGGGCGGAATCGACCCCCG1	
10	0	0 TCAACTGGTTGTTGGGAGGTTTCTTCTCAGT	
11	0	0 TCAACTGGTTGTTGGGTCTTAACAGACTCAG	
12	0	0 CCGACCAGGGATTGGAAGACGTTAATTTAA	
13	0	0 AGTGCTAGACGTTGGGCAGGTGACTGCTCG	
14	7	5 AGTGCTAGATGTGGGTACTTTGTATCCGTG1	
15	0	0 AGAACTAGA1 long	o
16	0	0 TATACTCGAC tag	f
17	8	9 CACACTTGGT long	g
18	7	6 AGTGCTAGATTTTCGGGAAATTTTATTTCTCG	
19	0	0 GGAAGTAGTT long	g
20	0	0 AATACTAGCTGACTGGCGATAAGCTGGGTG	
21	0	0 AGAACTAGCT long	o
22	0	0 ATGACTTGGT long	o
23	0	0 CCGACTAAGGATCGGCAGGGGTCGGTTAG1	
24	7	6 CACACTAGATCGGTGCAGGTTTCACCCTGT1	
25	0	0 TCAACTGGTT long	f
26	0	0 TATACTTGGTGTAGCTGGTCTCAACCCCCGG1	
27	0	0 AGGACTAGAC tag	o
28	10	11 TCGACTCGGATTCAGATGAATCAAAAAGTT1	
29	0	0 AGAACTGGATGAGGGGCTGGGTAAACCA1	
30	0	0 AACACTTGTTGTAGGAGGTATTGACCCCTCC	
31	0	0 TCAACTGGTT long	f
32	7	9 GATACTAGCTATTTGGGAATTCGTTCTTGAG	
33	10	12 CCGACTCAGATTCAGATGAATCAAAAAGTT1	
34	0	0 CCGACTAGG1 tag	c
35	6	3 GACACTCGGCCTGTGGGCGGTGTAAGTGCC	
36	4	7 TAGATTAGGTGTCGGAGGAGTCGAACCCTT	
37	0	0 CATACTTGGTGTAAGTCCTTCATTGGATTTG	
38	0	0 AGCACTAGTCGTGGTAGGAACCTAACGCCTG	
39	0	0 CCGACTAGGGATCGCGCGGTGTTGATTACG	
40	0	0 TCAACTAGCC long	g
41	0	0 TCGACTGGTT tag	o
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5 7 CGAACTAGCTTTTTGGCTTTGAGGTTGAGAC  
0 0 GATGCTAGCC long o  
0 0 GGTGCTAGA1 long g  
0 0 TCAACTAGTTGTCGGGTTCTATTGGACTTGG  
10 8 AATGCTAGCC long g  
0 0 CCGACCAGGGATGGGGAGAGGTAATACCT  
17 0 CCGACCAGGGATATGAGGATTCTTATTTATC  
0 0 CCGACCAGGGATATGAGTTGTTAAGATTAT/  
0 0 CCGACCAGGGATATGAGTTGTTATGATTAT/  
0 0 GCGCTAGA1 tag f  
6 0 TCAACTAGGT tag f  
0 0 CACATTAGAC long o  
0 0 ACAACTGGAT1 long f  
2 3 AATGCCAGCCGTCGGGGAGCTTGCTCCTCG  
0 0 AATGCCAGCC long g  
3 10 AATGCTAGATGTCAGGCCTTTTCGGGGTTTG  
2 0 AGTGCTTGGT tag o  
3 9 GGCAGTAGG1 tag g  
0 0 TCAACTAGTT1 tag p  
0 0 AATACTGATTGTTGAGTAGATTCTATTCAG  
3 0 AGAACTAGACGATGGTGTCTAGAGGCATC  
0 0 TCAACTGGTTGTTGGGTCTTAAGTACACAC  
0 0 TGTACTTGATGTAGCTGGGCTCAACCCTAGC  
7 5 AGTACTAGACTTTGGGCTTTTGTTTCAGAGTC  
0 0 TCAACTGGATGTTGGGTCTTAAGTACTCAG  
0 2 TCTACTTGCTGTTGGGGGTAGAACCTTAGT/  
2 6 TCAACTAGGT long g  
2 0 AGCACTAGAC tag g  
6 6 CGAACTAGCTTTTTGTCTTTAAGGTTGAGAG  
8 12 CCGACTCGGACTCAGATGAATCAAAAAGTT  
6 11 ACAACTAGGTGTCGGGCATCTAAGGATGTT  
3 4 TCGATTTGGA long g  
3 8 GATGCTAGG1 tag p  
6 6 AACACTGGAC long g  
0 0 GATACTAGGCGTTAGGGGTATCGACCCCCC  
3 0 CCGACCAGGGATATGAGGTATTATTTTATTT  
8 1 TCGACTAGGT long g  
0 0 AGTACTAGCT tag g

1			
2			
3			
4		0	0 AGCACTAGAC tag g
5		8	8 CCGACCAGGGATATGAGGTAGAAATTGATA
6		5	8 GATACTAGGT tag p
7			
8		4	15 AGAACTAGATGTTTGTGGTTTAATAACTGTC
9		2	0 TGTGCTTGTC long f
10			
11		8	12 CTAGCTGGGTGTT CAGGGGGGGGAAACCTCT
12		0	0 GCCCCATGAATTGGGGAGTTATTGAGCTG
13		0	0 GGCCTAGGCAGGGGGGATACTTATGGTCC
14			
15		0	0 AGCACTGGA tag g
16		0	17 AGTACTGGCCCTTGAGGTATTGACCCCTTC
17		0	0 GATGCTAGGTGTTGGCAGATCTAACCCCTGC
18			
19		0	0 AGTACTAGTG long g
20			
21		6	0 TCAACTAGGTGTTGGGAGGGTAAACCTTTT
22		0	0 GGCCTAGG tag p
23		0	0 ATCGCTGGGT long o
24			
25		3	2 CCAACTAGGTGTTGGGAGGGTTAAACCTTT
26		10	3 TATACTAGATGTTGGCGGTTTCAACGCCGTC
27			
28		4	6 TATACTAGATGTTGGTGGTTTCAACGCCATC
29		2	5 TACACTTGATGTAGCTGGTCTCAACCCCAGT
30			
31		6	5 AGCACTAGGTGTGGGGGGTTTTGACCCTCC
32		13	1 CCGACTCGGATTCAGATGAGTCAAAAAGTT
33		0	16 CTAACCTCGATATAGGGACGAATGAGTTTCTC
34			
35		0	0 CTAACCTCGTT long g
36		0	0 ATCACTCGTCATTGGCGATACACGGTCAGTC
37			
38		6	12 TTTACTTGCTGTTTGGCCTTTGGGTTGAGCG
39		0	0 CCGACATAGGAATACATAATAGTAGGACTA
40			
41		5	8 AATGCTAAAC long f
42		0	0 TCAACTGGTT long f
43			
44		8	7 TGCGCTAGGTGTTGGAGGTATCGACCCCTTC
45		2	2 TGTGCTAGAC tag g
46		0	0 AGCACCAGACGCCGGGCGGGTGACCGCCCC
47			
48		0	5 TCAACTAGGTGTTGGGAGGGATAAACCTTT
49		2	0 TCAACTAGGC tag f
50		0	0 TGCGCTGGAT long g
51			
52		2	0 CGAACTAGCTTTTTGATTAGGATTAGGAGC
53		0	0 CCAACTAGGC long f
54			
55		6	7 TACACTTGGTGTTGGTTCTTTATGGATCAGT
56		7	9 AATACTCGGCATCTGGCGGCCGATTTTCGGC
57			
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0 CGAACTGGA1long f  
0 ATCACTAGAT long p  
0 CCGACTAGGC long p  
0 CTTACTCGATATTCGCCCTTCGGGGTGAGTC  
0 AATATTTTATGTTTATATCTTTGTATATGAAT  
0 AGCACTGAATTGAAGGGTCCCACATAACCC  
0 AGTGCTGGGTGTCCGGCGTATGCTGGGTGC  
0 CGAACTGGA1tag f  
2 AGTGCTAGATGTTGGGAACGTAGTTCTCAG  
0 CCGACTCAGGATCGGTGGGCTGTATATTGT  
5 CCAGCTCGACGTTACACCCGCACCGCGGTG  
13 0 CCGACCAGGGATATGAGGATTTCTATTTATA  
0 CCGACTAGGC long c  
4 1 CCGACTCGGATTCAGATGAATCAAAAAGTT  
0 AGTACTAGATTGTAGACTAATCATGGGTTT  
0 TCGACTTGGGATTGGAGGCGTCACTTTCC  
0 AAGACTAGATGTTGGTAGGGTAAACCTATC  
5 6 CACGCTTGGTGTGGGAGGGTTCGACCCTTT  
0 TCAACTGGTTGTTGGGTCTTAACTGTCTCAG  
0 TCAACTGGTTGTGGGTCTTAACTGACTCAGT  
2 4 TCAACTAGGAGTTGGGAGGGTTAAACCTTT  
0 GGCCTAGG long g  
0 TCGACTAGCC long o  
0 ACAACTAGGT long f  
6 8 AATACTCGTT long f  
0 TCAACTAGTTGTTGGGCTTTAAAAAGCTTGC  
0 9 CATACTTGGT tag g  
0 ACCCCCATGAATTGGGGAGTTTTTGTGGAG  
0 3 TCTACTAGCC long g  
5 0 TCAACTAGGTGTTAAACCTTTTAGTGCCGTA  
4 4 CCGACTCGGATTCAGACGAATCAAAAAGTT  
10 0 CCGACCAGGGATATGAGGATTTCTATTTATC  
4 3 AGAACTGGGCGTTGGAAGGTTTTACCTTT  
4 3 GATGCCAGCC tag g  
10 4 CATACTTGGT long f  
0 0 AGTACTAGTGGGAAGAGGCTTCGCGCTTTT  
6 3 AATACTAGAT tag g  
3 8 TCGACTGGTTGTTGGGGGAAATTGTCCCTC

1		
2		
3		
4	0	0 ATCACTAGATGTTTTCGATACACTGTAAGCC
5	2	0 AGCACTAGATtag f
6	0	0 AGTGCTAGATGTCGGGGAGCTTGGCTTTTC
7		
8	3	7 TGCACTAGGTtag f
9	0	0 CCGACCGAGlong g
10		
11	8	4 ATGGCTGGGlong g
12	3	0 AGCACTAGATlong g
13		
14	10	2 CCGACTCGGATTCAGATGGATCAAAAAGTT
15	0	14 CTTACTAGTTGTTTGGATGAGAATCTGAGTC
16	5	2 CCGACTAGGCGCTGGTGGTTTGAACGCTGC
17		
18	4	13 CCGACTCGGGTTCAGATGAATCAAAAAGTT
19	3	10 CCGGCGGGGCGCGGGGGGGCCGAGTGGG
20		
21	4	5 CAAACTTGGTGTTGGTGGCGTAAAAACCAT
22	0	0 ATAACTCGTTtag p
23	0	0 GGCACTAGGlong g
24		
25	3	7 AATGTTAGATGTCGGGAGGTTACCTCTCGG
26	0	0 TCAACTGGTTGATGGGTCTTAAGTACTCAG
27		
28	0	0 GAAGCTAGCCGTTGGTGGGTTTACTCATCG
29	0	0 CGAACTAGCTTTTCGGTTTAGGATTGGGAG
30		
31	2	2 ATAACTAGCTGTCCGGGCCTTTAGGCTTGG
32	2	19 CCGACTCGGATTCTGATGAATCAAAAAGTT
33	6	9 TCGACTAGTT long o
34	0	0 AGTGCTAGTTGTTGGGTTTTTAAACTCAGT
35		
36	0	0 TCAACTAGTTGTCGGGCCTATTTAGGTTTGG
37	0	0 TCAACTGGCT long g
38		
39	6	7 TATGCTGAAT long g
40	0	10 CTAAGTTCGATGTTGGGAATGCAAATTTTCAG
41		
42	0	0 TCAACTAGTTGTCGGATCCATTTAAGGGTTT
43	1	0 CCGACTCGGATTCAGATGAATCAGAAAGTT
44		
45	0	0 CTGACTTGGTGTCTCGGGTATTAATTCCCGG
46	0	4 GATACTAGATGTTTCGGAGAGTTAACCTCTC
47	0	5 AGAGCTAGClong f
48	0	0 TCAACTAGGT long f
49		
50	0	0 AGCGTTGAATGTTGGGAGACTTAAAAGTCT
51	0	0 CAGATTAGCTTTTCGGAGTATCGACCTTCG
52		
53	6	6 CTAGCTAGATGTCTGGGCCGCGCAAGCGGA
54	0	0 TATACTTGGTGTAGCTGGACTCAACCCCAGC
55		
56	3	4 TCAACTAGGTGTTGGGAAGGTTAAACCTTT
57		
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0 GATACTTGTTGTTGGAGGTATTGACCCCTTT  
0 AGTACTAGGTGTGGGTGAGTGAAATCAAT  
0 AGTACTAGACGTTGGTGACGAGAGTTACGA  
15 CCGACTCGGATTCAGAAGAATCAAAAAGTT  
0 TCCACTAGATTGTGGTGGCTCTGACGCCATC  
0 ATTACTCGCTtag f  
0 ATAATTTTAATTTTGAGCGGATTTATAGAG  
4 2 CAGACTAGGtag o  
0 AGAACTAGGlong g  
2 0 CACACTAGACCGGTGCCGCTCTGACGCGGT  
0 4 ATCACTAGGTtag p  
0 ATGACTAGACCTGTGGTGGTGCTAAGCCTC  
3 0 GAAGCTAGCtag o  
4 0 TCAACTAGGTlong g  
0 0 CACACTTGGTlong o  
2 6 CACACTAGGTATGGGAGGAATCGACCCCTT  
0 0 TATACTTGGTtag g  
0 6 AGAACTAGGTGTCGTGGGTGTTGATCCCCG  
0 0 CCGACCAGGGATATGAGTTGTTAAGATTGT  
0 0 TCGCTGGATGTTGGGGGGCATAGCCCTTC  
0 0 TCAACTGGTTGTTGGGTCTTAAGTACTCAG  
0 0 TCGACTTGGAtag f  
5 4 TGTGCTAGCClong g  
5 7 TGTACTGGATCGCAGAGACTAATACGTCAT  
0 0 TCAACTGGTTGTTGGGTCTTATCTGACTCAG  
0 0 ATAAGTACTlong f  
5 2 CACACTAGGTCTTGGTGGATTCGACCCACG  
0 0 CCGACTTGGGATTGGAGGCGTGACCTTCC  
0 0 CAGACTTGGTtag f  
0 0 ACAACTAGGCGCTGAGGGACTCAACCCCCG  
0 0 TAACTGGTTGTTGGGTCTTAAGTACTCAGT  
0 0 AGTGTTGAATGTTGGGGGACTTAAAGTCT  
0 0 TCTACTGGTTGTTGGGTCTTAAGTACTCAG  
3 6 CTAAGTCTGATlong f  
0 0 CTAAGTCTGACATGTGATCTACGGATTGTGTC  
0 1 TATACTTGGTGTAAGTGGACTCAACCCCACT  
0 0 TCGACTGGCTGTCGGGGGGCTTGACCCCTT  
0 0 CTGACTTGGGATTGGAGGCGTGCACTTTCC



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4	0	0 TCAACTGGTT tag f
5	2	0 TTTACTTGCTGTTTGGGCCATGTGCCTGAGT
6	0	0 CCGACTCAGGATTGACAGACGTCTTTACCGA
7		
8	0	0 TTTACTTGCTGTTTCGGACGCAAGTCGGAGT
9	5	0 AGCACTAGCT long g
10		
11	0	4 AGCACTAGATCGCTGGGGAGCTATTCTTTG
12	0	0 GGCCTAGG1 long g
13	0	0 ATTACTGGAC long f
14		
15	0	0 TGCCTAGACGTTGGTGGACCTAGTTCAC
16	0	5 GGCCTAGG1 tag c
17		
18	0	0 AGTACTGGG( long g
19	0	0 TCACTAGTTGTCGGATCTAATAGATTTGGT
20		
21	3	6 CGAAGTAGGGAGAGGGTGTTCCTAGACACT
22	0	0 CCAAGTAGGGATACGTGGAAGTTTGTTCGA
23		
24	0	0 AGCACTAGG( long g
25	0	2 AGCACTTGAT tag g
26	3	9 GATGCTAGATATCGGGAGTATCGACCCTCC
27	0	0 CCGACCAGGGATATGAGTTGTTATGATTAT
28		
29	0	0 TCAGCTAGGTGTTGGGAGGGTTAAACCTTT
30	0	0 GCGACTAGTT long o
31		
32	0	0 TCACTAGGTGTTGGGAGGGTTAAATTTTTT
33	0	3 TCGACTAAGGATGATAAAATATTAAGAAT
34		
35	0	0 AGTGCTAGATGTCGGGAAGCTTGGCTTTTC
36	0	0 CGGACTTGGTGTGCGCCCTTCATTGGGTGC
37		
38	0	0 GGTACTAGATGTCAGAAGTTCTTACCCTTCT
39	0	16 CCGACTCGGATCCAGATGAATCAAAAAGTT
40	2	4 AGTGCTAGTTGTCGGGGCCTTAGGTCTCGG
41	0	0 TCACTGGTTGTTGGACGGCTTTCTGTTGAG
42		
43	0	0 AGTGCTAGG1 long g
44	0	0 TCACTAGTTGTCGGGCCTTATTAGGCTTGC
45		
46	0	0 AGTGCTAGACGTTGGACGGTTACCGTTGAG
47	0	0 TCACTGGTTG tag g
48		
49	0	6 AGCACTGGGTAGGGGGCTCGCCGATGGGC
50	0	0 CCGACTAGGGATCGGTCCACGTTATTTTTGA
51		
52	0	0 TCACTAGGTGTTGGGAGGGTTAAACCTTT
53	0	8 TCGACTAAGGATGATAAAATATTAAGAATG
54	4	4 CGTACTAGATAGCGGCTCGTTCCGACGAGC
55		
56	0	0 CTAAGTCGTT long g
57		
58		
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0 CCGACTTGGGATTGGAGGCGTGCACCTCCG  
0 TCAACTGGTT long g  
4 CCGACTCGGATTCAGATGAATCAAAGTTCA  
2 ACAACTAGGTGTTGGGAGGGTTAAACCTTT  
0 CCGACTTGGGATTGGAGGCGTGCACCTCCG  
5 TCAACTGGTT tag g  
0 TCAACTGGTT tag f  
2 CCGACTCGGATTCAGATGAATCAAAGAGTT  
0 AGCACTGGA tag g  
0 GATACTAGGTGTCCGGGCCTCTGGCCTGGG  
0 CCGACCAGGGATATGAGTTGTTATGATTGT  
4 TGCACTTGGTGTTGGGCTGATTAGGTTCA  
0 CCGACCAGGGATATGAGTTGTTATAATTAT  
12 CCGACTCGGATTCAGGTGAATCAAAAAGTT  
3 AGAGCTAGC long f  
0 TCAACTGGTT tag f  
0 GATACTAGGCGTAAGAGGTATCTACCCCTC  
0 AGCACTAGTC long g  
0 AGGACTAGGTGTCGGGTCGTAAGACTCGG  
0 TCAACTGGTTGTTGGGAGGGTTTCTTCTAG  
8 TCAACTAGCC long g  
0 CCGACTAGG long g  
2 GGTGCTAGCT long g  
0 TCAACTAGGTTTTGGGTGGGTAAAACCATTT  
3 TCAACTAGGTGTTGTGAGGGTTAAACCTTT  
0 TGCCTGAAT long g  
0 AGAACTAGG tag k  
2 GGCCTAGGTAGCGGGCCTCCATGGGCCCC  
2 GGCCTAGGTAGGGGGCTCTCCGATGGGC  
5 GGTGCTTGTGTTGTGAGTGTAACCTCG  
0 GGAAGTAGTT tag g  
0 CCGACTTGGATTGGAGGCGTGCACCTTCCG  
0 CCGACCAGCGATTGGGCGACGTTGCATGGA  
4 AATGCCAGTC long g  
6 AGTGTTAGATGCTGTGGGTATTGACCCCTG  
2 AGCACTGGG tag f  
3 TCAACTAGGTGCTGGGAGGGTTAAACCTTT  
0 CCGACTTGGGATTGGAGGCGTGCACCTTCT

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4	0	0 CCGACTTGGGATTGGGGGCGTGCACCTTTCC
5	0	0 AGAACTAGTT tag f
6	2	2 AGAACTAGATGTTGGAGGGGAGACCCTGC/
7	2	4 TCAACTAGGTTGGGAGGGTTAAACCTTTTA(
8	0	0 GGTACTAGGATTGGTGGGTCTTGACCCCTG
9	5	0 GATACTAAATGCTGTCAAAAACAGTGTTGT/
10	0	0 TCAACTAGTTGTTGGGCCTTATTGGGCTTGC
11	10	10 CCGACTCGGATTCAGATAAATCAAAAAGTT(
12	0	0 AGCACTAGACGCTGGGCGGGTGACCGCCCC
13	0	2 CCGACTAGG( long g
14	0	0 GGCGCTAGG` long c
15	5	3 CACACTTGGTGTTGGGCCTTTTTGGCTCAGT
16	0	0 CCAACTAGGGATATGTGGATGTTTGTGTTGA/
17	5	3 AGTGCTAGACGTCGGATCTTTAAGATTCCG`
18	0	5 TCAACTAGGTGTCGGGAGGGTTAAACCTTT`
19	0	6 GATACTCGTTATTGGGGTTTTCGACTTCAGTG
20	0	0 GGAACTAGG` long f
21	0	2 TACACTAGACTGGTGCGGTTTTGATGCCGT/
22	0	0 ATTACTCGAC tag g
23	2	9 TCTGTTGGCT, long p
24	0	0 TCAACTGGTGTTGGGTCTTAACTGACTCAGT
25	0	0 CCGACTTGGAATTGGAGGCGTGCACCTTTCC(
26	0	0 ATTACTCGAT` tag p
27	10	0 CCGACTCGGATTCAGATGAAACAAAAAGTT
28	3	0 TCAATTAGTTGTTCCGGTGAGGAGACTCATT(
29	0	0 CATGCTGGCTGTCGGAGGTATTCACCCCTTC
30	0	0 CCGACCAGCC` tag g
31	0	0 TCAACTGGTT long g
32	0	0 TCAACTAGTT` long f
33	0	0 GATACTTGTTGTTGGAGGTATTGACCCTTTC
34	0	0 CTGACTGGGCGTCTGCTGGTGTTTGCTCTTT
35	5	4 ATTACTCGAT` tag p
36	2	2 TACACTAGACCGCAGAGGTTTGACACCCTTC
37	2	4 TGTGCTAGGTGTTGCGGGAATCAACCCCCG
38	3	0 AATACTAGGTGTGGGAGGTTTCGACCCCTT(
39	0	0 AGAACTGGG` tag o
40	0	0 CGCGCTAGATCGGTGCGGGTTTGACCCCGG
41	0	0 TGTACTTGATGTAGATTGGCTCAACCCTTTC`
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3 GAACTTGGT tag g  
2 AATACTAGGC long p  
6 AGTGCTAGATATTGGAAGCATGACTTTTCAG  
4 TCAACCAGGTGTTGGGAGGGTTAAACCTTT  
0 AGAACTAGCC long g  
0 GTGACTAGGTGTGGGGAGCGTACAGCATCC  
4 GACGCTAGGTGTTGGCAGATCTAACCTGT  
0 AACACTTGGT tag g  
0 GATACTAGCT long g  
0 AGAACTGGC tag g  
0 TCAACTAGGTTTTGGGAGGGTTAAACCTTT  
3 AGTGCTAGGTATCGGGAGAATTTCTTTCGG  
0 AGTACTAGGT tag f  
0 TCAACTGGTTGCTGGGTCTTAAGTACTCAG  
0 TTAAGTACTGTTGTTCCGGTGGGAGACTCATT  
0 GCGCTAGGTGTGGGGAACATTTCCACGTT  
0 TCAACTGGTT long g  
0 TCAACTAGGTGTTGGGTGGGAAAAACCATT  
0 TCAACTAGGTGTTGGGAGGGTTAAACCTTT  
0 CCGACTCAGGATTGGCGGTGTACTTCAACG  
0 ATCACTCGCTGCTGGGGGGTAACCTTCAGT  
0 ATTACTCGCT tag f  
0 CACACTTGGTGTGGGAGGATTGACCCCTT  
1 TCAACTAGGTGTTGGGAGGGTTAGACCTTT  
3 CCGACTCGGAATCAGATGAATCAAAAAGTT  
0 CCAATTGGGC long g  
0 GATGCTAGCC long o  
0 ATAAGTACT tag g  
3 CACACTAGGT tag g  
3 TATACTTGGTGTAAGTGGATTCAACCCTAGT  
0 AGTGCTAGATGTGGAAGATTTCTTTCGGT  
0 TATACTCGTT tag f  
14 CCGACTCGGATTGATGAATCAAAAAGCT  
0 TCTACTAGTT long f  
0 TCAACTGGTTGGGGTCTTAAGTACTCAGT  
0 CCGACTCGG tag g  
0 ATCACTAGATGTTGGCGATACACTGTCAGC  
5 TTAAGTCTGATATTTATTCTACGGAGTGAGTG

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3			
4	0	2 CCGACCAGG	(tag g
5	0	9 CCAACTCGGATT	CAGATGAATCAAAAAGTT
6	0	0 GCGCTAGG	long g
7	0	0 TCTACTAGTT	(tag g
8	0	2 CCGACCAGCGAT	CGGGAGACGTTCGCATGG
9	0	0 TCAACTAGTT	long g
10	0	0 ATTACTCGTTTTT	GGGTTTATGATT
11	0	0 ATTACTCGTTTTT	GGGTTTATGATT
12	0	0 ATTACTCGTTTTT	GGGTTTATGATT
13	6	0 ATAAGTGGTTGT	GCGCGATATACAGT
14	6	2 AGAGCTAGC	(tag g
15	3	0 TGCACTGGGTGT	CGGGCCGTAGGGCTCGG
16	6	0 CGCACTTGCTGT	AAGCGGATTCGAAACCGT
17	0	0 CGCACTTGCTGT	AAGCGGATTCGAAACCGT
18	0	0 TCAACTGGTTATT	GGGTCTTAAGT
19	2	0 TCAACTGGTTATT	GGGTCTTAAGT
20	3	12 CCGACTCGGATT	CAGATGAATCGAAAAGTT
21	4	3 GGCCTAGATGT	CGGACCTTCTTACCGGTT
22	0	0 TCAACTGGTTATT	GGGTCTTAAGT
23	0	3 TCAACTAGGTGTT	GGGTGGGTAAACCATTT
24	0	6 CCGACTAGGGAT	CGGTGGGTGTTTTTATG
25	4	0 CCGACCAGGGAT	ATGAGGATCTTTATTTAT
26	5	0 AATACTCGGTGT	CGCCTTCTTTTGAGGGCG
27	5	0 AATACTCGGTGT	CGCCTTCTTTTGAGGGCG
28	0	0 CATACTAGGTG	ACGGGCGCTCTGACGCATC
29	0	0 GTCCTAGATGT	CGGGAGTTCTTACCCTCTC
30	0	0 TCAACAGGTTGTT	GGGTCTTAAGT
31	0	0 TAGACCCGGTCTT	GGGCGATTTCGACCCGCT
32	0	0 CCAACCAAAGATA	AAGGGTGGGAAAAACAG
33	0	0 GCGCTAGG	tag c
34	0	0 AGTGCTAGATGT	CGCGGTCAAGACCATCGC
35	0	2 AGTGCTAGAT	(tag f
36	0	0 GATACTTGTTGTT	GGAGGTATTGACCTCTTC
37	0	0 AGCACTGGG	(long g
38	2	0 TCAACTGGTTGTT	GGGAGGGCTTCTTCTCAG
39	0	0 CTAAGTCTGTTTTT	GGAGCGTAAGTTTCAGAG
40	0	0 CCGACTAGGGAT	CGATGGGTGTTATTAATG
41	6	0 TCAACTGGTT	tag g
42	0	0 CCGACCAGAGAT	CAGAGGATGTTGAATGG
43	4	0 CCGACCAGGGAT	ATGAGGATTTCAATTTAT
44	0	0 TCAACTGGTT	tag f
45	0	0 ATTACTCGAT	long f
46	0	2 CATACTAAGT	tag f
47	0		
48	0		
49	0		
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0 CCGACTAGGGATCGGTGGGTGTTATTAATG  
5 0 CCATCTAGCG tag p  
0 TTTACTTGCTGTGCGGTCTTAGGATTGCGTG  
2 0 TCAACTAGTTGTCGGATTTTAATAGATTTGG  
0 0 TCAACTGGTTGTTGGAGGGTTTCTTCTCAGT  
0 0 AGAGCTAGC tag f  
0 0 TCAACTAGTTGCTCGGTGAGGAGACTCATT  
0 0 CACATTTGCTGTGGGCGGAATCGACCCTGC  
0 0 CTGACTTGGTGTCCTCGGTTTTAAATCCGGG  
0 0 CCAACTTGGGATTGGAGGCGTGCACTTTCC  
0 0 TCAACTAGTTGTTCCGTGAGGAGACTCATC  
0 0 CGAGCTGGA tag g  
0 0 TCATCTGGTTGTTGGGTCTTAAGTACTCAG  
3 0 CTAACGATGGACGCGGGGAATCAGTCTCTT  
3 0 AGCACTAGGTGTGGGAGGTTTTGACCTTCC  
0 0 GGTACTAGG long p  
5 0 TCAACTAGTTGTTCCGTGAGGAAACTCATT  
0 3 ATGACTCGATGTTGGCGATATATAGCCAGC  
0 0 GTCACTCGGTGCCGGCGATATACAGCCGGT  
0 0 AGCACTGGG long f  
6 0 GATACTCGATGTTGGGCGGTATAGCTCAGT  
0 0 AGTGCTGGATGTCGGGAAACCTAGCTTTTC  
0 0 TCAACTGGTT long f  
0 0 TCGACTGGTT tag f  
0 0 CCGACCGGGGATGGGGAGAGGTAATATCT  
0 0 AATACTGATTGTTGAATAGATTTCTATTCA  
0 5 AGAACTAGGTGTCGTGGGTGTTGATTCCCG  
0 0 TCAACTGGTTGTTGGGAGGGTTTTTCTCAG  
0 0 CCGACTTGGGATTGGAGGCGTGCACTTTCC  
0 0 ACAACTAGTTGTTCCGTGAGGAGACTCATT  
0 0 TCAACTAGGTGTTGGGAGGGTTAAACCTTT  
0 4 CCACTAGGT long g  
0 0 GATACTTGTGTTGGAGGTATTGACCCCCTC  
5 0 TCAACTGGGTGTTGGGAGGGTTAAACCTTT  
5 0 TCAACTAGGTGTTGGGAGGGTTAAACCTTT  
0 2 GGTGTTTGTGTTGGAATGTAAACCTTTCA  
0 0 TCAACTAGTTGTTCCGTGAGGAGACTTATT  
3 2 GATACTTGATGTTGAAGGTATTGACCCCCTC

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3		
4	0	0 GATATTTGTTGTTGGAGGTATTGACCCCTTC
5	0	0 TCAACTAGGTGTTGAGAGGGTTAAACCTTT
6	2	5 CCGACTAGGTGTTCACTTTCCGACAGGGAA
7		
8	3	0 CCGACCAGGGATATGAGGACTTTTATTTATA
9	0	0 AGTGCTAGATGTCGGGGAGTTCGCTCTTCG
10	0	0 CCGACCAGGGATATGAGTTGTTAGGATTGT
11	0	0 CCAACCAAAGATAAAGGGTGGGAAAAACAA
12	0	0 GATACTCGATGTAGCTGGTATTGACCCCGG
13		
14	7	6 CCGACTCGGA long f
15	0	0 CTCGCTAGGGATTGGGAAATTAAATTTTCA
16	0	2 GAAGCCAGC tag f
17		
18	0	0 GACACTAGATGGGTGGTGAGCTATCGCTGC
19	2	4 GGCCTAGACGCCGGAGGGGTGACCTTTCC
20	0	0 CACATTAGACCGGTGCGGTTTTGACGCCGT
21	0	0 CATACTAGGTGTAGGAGGGCTCAACCCTTT
22	0	0 AGTGCTAGATGTCGGGGAGCTTAGCTTTTC
23	0	0 CCGACTTGGGATTGGAGGCGTGTACTTTCC
24	0	0 CCGACCAGGGATATGAGGTATTCTTTTTTCT
25	4	0 CCGACCAGGGATATGAGTAGTATATTTTCAT
26	0	0 CCGACTAGGC long g
27	0	0 CATACTAGGT tag f
28		
29	0	1 TCAACTAGGTGTTGGGAGGGTTGAACCTTT
30	0	0 AATGCTAGCTGATGGAGCTTCTACCGCTTC
31	0	0 AATGCTAGCC long g
32	0	0 TCAATTGGTTGTTGGGAGGGTTTCTTCTCAG
33	0	0 GGCCTAGG1 tag f
34	3	0 TCAACTAGCT tag g
35	0	0 AGCACTAGAC long g
36	6	6 CAGACTCGGATTCAGATGAATCAAAAAGTT
37	0	0 GATACTTGTTGTTGGAGGTATCGACCCCTTC
38	0	0 TTAAGTGGTT long f
39	0	2 CGCACTAGGTGCGGAAGGCTTGACGCCCTC
40	3	0 AGTGTTAAACGTTAGAATTTCTAATGTTACA
41	0	0 CTGACTAGGGATCGGTCCACGTTATTTTTTG
42	1	1 TCAACTAGGTGTTGGGAGGGCTAAACCTTT
43	0	0 CCGACTAGGGATTGGTGGGCGATTATTATA
44	0	2 TCGACCAGACGTCGGAGGTATCTATCCCTCC
45	0	0 GATACTCGATGTGGCTGGTATTGACCCCGG
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0 GATACTTGTTGTTGGAGGTATTGACTCCTTC  
2 GATACTAGTCGTCGGGACACCTAATCGTCTC  
3 TCAACTAGGTGTTGGGAGAGTTAAACCTTT  
0 GACTACTTGTT tag g  
0 CCAATTAGGGATATGTGGACGTTTGTGTTGA/  
0 AATACTTGGT tag f  
2 CACACTAGATCGGTGCAGGTCTGACCCTGT/  
0 CCGACTAGGGATCAGGCAAGGAGTTTTTTTG  
0 ACGACTGGGtag f  
0 CATACAAGCTGTAGTGGGGTTTTCTCCTGC  
0 TTCACTAGATGTAGGAGGTATTGACCCCTTC  
2 TTCTCTTGCTTTTCGGAGTATCGACCCTCTG/  
0 TCAACTAGGTGTTGGGTGGTAAAACCATT/  
0 TGCCTAGGT long f  
5 CCGACTAGG long g  
0 GATATTAGGT long p  
5 TCGATTGGG tag f  
0 TGCATTAGGTGTAGGAGGATTGACCCCTTC  
3 AGCACTAGACGCTGGGGGGTGACCTTTCGG  
0 CAGATTAAGGGATGGAAGGAAAGAAATAA/  
0 ATAAGTAGGT long f  
0 AATACTAGGT long g  
0 GGTACTAGGTAGTGGACCGGACATGGGTTTC  
0 GGTACTAGGT tag f  
0 CTAAGTAGGGATATGTGGACGTTTGTGTTGA/  
0 GGCCTAGGTGTGGGGATCATCCTTGGTTTC  
4 CTGACCAGGGATCGAGGACAGTCCCATGGT  
0 TCAACTGGTT long f  
5 ATCACTCGATGTTGGCGATATACAGCCAGC  
5 CCGACCAGGGATATGAGTAGTATATTTCAA  
0 TCAACTGGTTGTCGGGAGGGTTTCTTCTCAG  
0 AGCACTAGGT long c  
0 TTAAGTAGGTGTTGGGTGGGTAAAACCATT  
0 CTAAGTCGTT long g  
0 TCAACTGGTTGTTGGGAGGGTTCTTCTCAGT  
9 CCGACTAGG long g  
0 CCGACCAGGGATATGAGTAGTATATTTCAT  
0 GGTACTGGGtag f



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4	2	0 AACACTAGCCGTTGGAGGTACCCATTCCTTC
5	2	0 TCAACTAGTTGATCGGTGAGGAGACTCATT
6	2	2 ATTGCTAGTTlong g
7	0	3 GGTGCTAGGlong g
8	0	6 TCTACTAGGTGTTGGGAGGGTTAAACCTTT
9	0	0 TCGACTAGTT long g
10	2	0 GATGCTAGCC tag o
11	0	0 GATGCTAGCC long g
12	0	3 AATACTAACT long g
13	5	7 CCGACTCGGATTCAGATGAACCAAAAAGTT
14	0	0 TCAACTAGTTGTTCCGTGAGGGGACTCATT
15	0	0 GGTACTAGATTTGGTGGGATTTGACCCTCG
16	2	0 ATTACTCGAT tag c
17	0	0 GGTACTAGGtag f
18	0	0 AGCACTGGAC long g
19	4	2 TAAACTTGGC tag f
20	0	0 TGGACCAAG tag g
21	0	2 AGTGCTAGACGTTGGGGATTTTTCTTCAGT
22	0	0 TCAACTGGTAGTTGGGTCTTAACTGACTCAG
23	0	0 CCGACTCGGATTCAGATGTATCAAAAAGTT
24	0	0 TCAACTGGTTTTGGGTCTTAACTGACTCAGT
25	0	0 AATGCCAGCC long g
26	2	2 GATACTAGATGTTTGGAGAATTAACCCTCC
27	0	0 AGCACCAGACGCCGGTGGGGTGACCTGTCC
28	0	0 AGTGCTAAGT long g
29	0	5 ATCACTCGTT tag p
30	0	13 CCGACTCGGATTCAGATGAATCAAAAAGTT
31	0	0 CGAACTGGATGTTGGGTCAACTTGAGCT
32	0	4 TCAACTAGCCGTCAGGTCCGCTTTAGGGCT
33	0	0 CTGACTAGCGATCCGCCGGCGTGTTTCGA
34	0	0 CCGACTTGGGATTGGAGGCGCGCACTTTCC
35	0	0 AGCACTGGACCGGAGTTGTGCACACGATT
36	0	0 TCAACTAGTTGTCGGGTCTTGTTGGGCTTGC
37	0	0 TCAACTAGGTGTTGGGTGGTTAAAACCATT
38	0	3 AATGCTAGTTGTTGGTAAGTTTACTTATCAG
39	0	0 AGCACTAGGTGTTGGATCCTTTAGGATTCC
40	0	0 CCGACCGGGGATAGGGAGCACTGGTGAAA
41	0	0 AGTGCTAGAT tag g
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0 3 GAAGCCAGC tag f  
0 0 CCGACTAGG tag p  
0 5 AATGCTTGGT long o  
3 0 GGTGCTAGGAGGTGGGGCTCCTCGGCCTCT  
0 0 AGCACTAGACGCTGGGCGGGTGACCGTCCC  
0 0 AGAACTGGACGTTGGGAGGAATTCTCCTCT  
0 0 CGAACTGGA tag g  
0 0 CGAACTGGA tag g  
0 0 CCGACTGGAGTGGGGGAGTCACTAAAAA  
0 0 GATACTCGAC tag g  
2 2 TCAACTAGTCGTTCCGGTGAGGAGACTCATT  
2 2 TCAACTAGTTGTTTGGTGAGGAGACTCATT  
2 0 GATGCTAGCC long o  
0 0 TCAACTGGTTGTTGGGTCTTAACGACTCAGT  
0 0 CCGACTGGAC tag f  
0 0 AATGCTAGTTGTTGGGGACTTAGTCTTCAGT  
0 0 GATACTCGTTGTTGGAGGTATTGACCCCTTC  
3 0 TCAACTTGGTGTTGGGAGGGTTAAACCTTT  
2 4 TGTACTAGAT tag f  
0 0 GATACTAGATGTCGGGGGTCTGTCCCCTCG  
0 0 GATACTTGATGTTGGAGGTATTGACCCCTTC  
0 0 AGTATTGAATGTTGGGAAAAGTTTTATTTTC  
3 2 CCGACTAAGGATCGGAAGGGTTTCAACAGC  
0 0 GGTACTTGTTGTTGGAGGTATTGACCCCTTC  
0 0 GATACTTGTTGTTGGAGGTATTTACCCCTTC  
0 0 GATACTTGTTGTTGGAGGCATTGACCCCTTC  
0 5 CCAACTAGGTCTTTTTTAGAGACACAATTCA  
0 0 TCGACTAGGGATCGGTCCACGTTATTTTTTG  
0 2 TGCATTGGTGTTGAGCCGATTAGGTTTCAG  
2 0 ATGACTCGATGTTGGCGATACACAGCTAGC  
0 0 ATCACTCGATGTACACACTTGATGTGTGTGT  
3 6 CCGACTAGGGATCGGATGGGTTGTTATTTA  
3 6 CCGACTCGGATTCAGATGAATCAAAAAGAT  
2 0 ATTGCTAGTTGTTGGGGTGCTTGACCTCGC  
0 0 TCCACTAGAGTGTGGCACCCTGACGGTGT  
0 3 CTAACGATGGACGCGGGGAATCAGTCTCTT  
0 0 CCGACTAGGGATCGGGCGATGTTGAATATA  
0 0 CCGACTAGG long g

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4	0	0 CCGACATAGGAATACGTAATAGTAGGACTA
5	0	0 TCAACTAGGTGTTGGGAGGGTTAAGCCTTT
6	5	2 AGTGCTAGCCGTTGGGACTTTCAGTCTCAGT
7		
8	0	3 CCAACTCGGTGTTTGGTCCGGGGAACCGGA
9	0	0 ATCACTAGATGTCGGCGATACACAGTCGGT
10		
11	2	6 GAAGCTAGCCGTCGGGGAGCATGCTCTTCG
12	0	0 TGCAC TTGGTGTTGGCCGATTAGGTTCAGT
13	0	0 GGTGCTAGCC long f
14		
15	0	0 CCGACTTGGGATTGGAGGCGTGCACTTTTC
16	2	0 TCAACTAGGTGTTAGGAGGGTTAAACCTTT
17		
18	2	2 TCAACTAGTT long g
19	2	2 GATGCTAGGCGTGAGGGGTATCGACCCCC
20		
21	3	1 CCGACTCGGATACAGATGAATCAAAAAGTT
22	0	0 TATGCTAGACGTGAGGGGACTTCGTCCTTT
23	0	0 GGTACTTGGCAGCGGGAGAACCTATGTCTT
24		
25	0	0 ACAACTAGAT long o
26	2	0 GAAGCTAGCC long f
27		
28	0	0 TCAACTAGGTGTTGGGTGGGTTAAACCTTT
29	3	2 CCGACCAGGGATATGAGGTATTTAGTATAG
30	2	2 AGCACTAGGTGTTGGCCCCGTTAGGGGTCA
31		
32	0	0 TCAACTGGTTGTTCCGTGAGGAGACTCATT
33	0	0 CCGACTTGGGATTGGAGGTGTGCACTTTCC
34	0	0 TCAACTAGGTGTTGAGGGTTAAACCTTTTAC
35		
36	5	2 AGAACTAGGTGTCGTGGGTGACCCCCGCGC
37	0	0 AGCGCTAGAC tag g
38		
39	0	0 CGCACTAGACCGGTGCGGGTTTGACGCCGT
40	0	0 TCAACTGGTT long g
41		
42	2	0 TGCAC TTGGTGTTGGGCCGATTAGGCTCAG
43	0	0 CCGACTGTAGATTAGAAGACGTTATTACAA
44		
45	2	1 TATACTTGGTGTA ACTGGACTTAACCCTAGT
46	0	0 AGAACTGGGTGTAGGAGGGGTTAGAGCCT
47	0	9 GGTACTAGG tag f
48	0	0 GGTACTAGG1 long f
49		
50	0	0 GATACTAGCT tag g
51	0	0 ATGACTGACTGAAGTGGGAGTAGATGTAGC
52		
53	0	0 AATACTAGGT tag g
54	0	2 CGCACTAGAC long g
55		
56	0	0 AAGACTCGATGTTGGCGATATACAGCCAGC
57		
58		
59		
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5 0 CCGACTCGGATTCAGATGAATCAAAAAGTA  
0 4 ATGACTCGATGTTGGCGATACACAGCCAGT  
0 0 TGCCTAGACCGGTGCGGTTTTGACGCCGT  
0 0 ACAACTAGGCGCTGAGGGTCTCAACCCCCG  
0 0 CCGACCAGGGATATGAGTTGTTAGGAATAT  
0 0 AACTGGTTGTTGGGTCTTAAGTACTGACTCAGTA  
0 0 AGCATTGATTAGTGTAATCTTTATATTATT  
0 0 ATCACTAGATGTCGGGGGTCTTACCCCTCCG  
0 0 CGGACCAGG(tag k  
0 0 ATGACTCGACCTGTGCGGGGCTCAATCCCC  
0 0 CCGACTAGGGATCGGTTACGTTATTTTTTG  
0 0 TCAACTGGTT tag g  
2 5 CCGACTAGGGATCGGTGGAAGTCGATTTTG  
0 0 AATGCCAGCC tag g  
0 0 CCAACTAGTT long g  
0 0 TCAACTAGTT long f  
1 1 ATGGCTGGATGTTGGTGATACACCGTCAGC  
1 1 TCAACTAGGTGTTGGGAGGATTAAACCTTT  
0 3 GATACTCGATGTTGGGGCTTCGGCTTCAGT  
0 0 CCGACTCAGGATTGGCGGGTGTCGTTTATG  
0 0 CGCACTAGACCGGTGCGGTTTTGACGCTGT  
0 0 GATACTTGTGTTGGAGGTTGACCCCTTCAG  
0 3 AGAACTAGGCGTTGGAAGGTTTTACCTTTT  
0 0 TAACTAGGTGTTGGGAGGGTTAAACCTTTT  
0 0 TGTGCTGGG(tag g  
0 0 TCAACTAGGTGTTGGGAGGGTTACCTTTTAC  
3 0 TCAACTAGGTGTTGGGGGGTTAAACCTTTT  
0 0 TTAAGTCGAT tag g  
0 0 CCGACTTGGGATTGGAGGCGTGCACCTTTCC  
2 0 CCGACTCGGTTTCAGATGAATCAAAAAGTT  
0 0 CGCACTTGCTGTGAGCGGAATCGACCCCGC  
0 0 GATACTTGTGTTGGAGGTATTGACCCCTTCA  
1 2 CCGACTCTGATTCAGATGAATCAAAAAGTT  
0 0 TCAACTGGTT long g  
2 0 TAGACAAGATGTGGGGGGTATCGACCCCT  
0 0 GTCCTAGCTGTCGGGAGAACTTACCCTCC  
0 0 GATACTTGTGTTGGAGGTATTGATCCCTTC  
2 0 ATGGCTGGATGTTGGCGATACATCGTCAGC

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4	0	0 CCAACTAGGAATACGTGGACGTTTGTTCGA/
5	0	3 CCGACTCGGATTCAGTTGAATCAAAAAGTT(
6	0	0 TCAACTAGTTGTCGGGTCTGTTTAAGGATTC
7	0	0 ATTACTCGTTGCTGGAGGTAACTTTCAGTGA
8	0	0 AGTGCTGGATATCAGTAGCGAAGCTATTGG
9	0	0 TCAACTAGGTGTGGGAGGGTTAAACCTTTT/
10	0	0 TCAACTAGGTGTTGGGTGGGTAAAACCATT
11	0	
12	0	0 TCAACTAGGTGTTGGGTGGGTAAAACCATT
13	3	7 CCGACTCGGATTCAGATGAATCAAGAAGTT(
14	0	0 TAAACTCGACATTAGCGATACACAGTTAGTC
15	3	0 CCGACTCGGATTCAGATGAATCAAAAAGTC,
16	0	0 GGTACTAGATlong g
17	0	0 AGCACTGGGTTGGAGGGTTCTCCACGACCT
18	0	0 CTAACTCGTT long g
19	3	3 CCGACTAGGGATTAGCAGACGTTTCATTGA
20	0	0 AGAACTTGAC long g
21	0	0 AGAACTAGGCGTTGGAAGGTTTTACCTTCT/
22	2	0 ATGGCTGGATGTTGGCGATATACCGTCAGC
23	0	0 CCAACTAGGATATGTGGACGTTTGTTCGAA(
24	0	0 CCGACTTGGGATTGGAGGCGTGCAATTTCC(
25	0	0 AGAACTAGACGTTGGGAAGCTTGTCTTCTT/
26	0	0 ATAACTCGTTtag c
27	0	0 CGAACTGGATGTTGGGCTCAACTTGGAGCT
28	0	0 ATTACTCGTTGCTGGGAGGTAACTTTCAGTC
29	0	0 CGCACTAGACCGGTGCGGTTTTGATGCCGT,
30	2	0 CCGACCAGGGATCGAGGACAGTTCCATGGT
31	0	0 GATGCTAGCC long g
32	0	0 CCGACTAGGAATGAGTGAACGTTGCATTAT(
33	1	0 ATGACTCGATGTTGGCGATACATAGCCAGC(
34	0	0 TCAACAAGGTGTTGGGAGGGTTAAACCTTT
35	0	2 GAAACTAGG(tag f
36	0	0 AATGCTAGCC tag g
37	2	0 CCGACCAGGGATCGAGGACAGTCTCATGGT
38	0	0 TCAACTAGTTGTTCCGGTGAGGAGACTCATT(
39	0	0 TCAACTAGTTGTCGGGTCTTTGGGCTTGGA/
40	0	0 CCATCTTGGAATTGGGCGGATATATTATGA1
41	1	0 TCAACTAAGTGTTGGGAGGGTTAAACCTTT1
42	0	4 CCGACTAAGGATCGGCAGAGGTCGTTAGCC
43	0	0 AGTACTAGCTGACTGGTTAAGACTGGGTGG
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0 2 ATGATTTCGATGTTGGCGATACACAGCCAGC  
0 0 TCGACTGGGTGCGGGAGGGGCTCGACCCT  
0 0 GGCCTAGGtag g  
0 0 GGTACTAGGTAGCAGACTAGACATGGGTTT  
0 0 TCAGCTGGTT long g  
0 7 ATCACTGGAT tag p  
0 0 TGAAGTGGATGTTGGTCTCAACTCGGAGAT  
0 4 AAACAGTTATGATTGTTTAAATGATAAATGC  
0 3 TCGACCAGGGATCGAGGACAGTCCCATGGT  
0 3 AATACTAGAC long f  
0 0 GGCCTAGGlong f  
0 0 TCAACTGGTTGTTGGGTCTTAAGTACAGTA  
0 0 TCAACTAGGTGTAGGGAGGGTTAAACCTTT  
2 0 TCAACTAGGTGTTGGTTGGGTAAAACCTTT  
3 3 TCGACCAGACGTCGGGGTGTCAACCCCTCC  
0 0 TTTACTAGTT(long g  
0 0 AGTACTGAGCGGAAGGAAGTTCGCTTTTTT  
0 0 CCGACCAGGGATATGAGTAGTATATTTCTT  
0 0 TCGACTAGTCGTTTCGGAGCAGCGATGCACT  
0 3 CCGACTAGGGATCGGACGGGTAGTTATTTT  
0 0 ATGACTTGATGTTGGCGATACACAGCCAGC  
2 0 TTCATTAGGTTTTTCGGAGTATCGACCCTCTG  
0 0 TCAACTAGGTGTTGGGAGTTAAACCTTTTAC  
0 5 CTAACGATGGACGCGGGAATCAGAACATCA  
2 3 TCGACTAGTCGTTTCGGAGCAGTAATGCACT  
0 0 TTGACTAGGTGTTTCGGGAAGGAGACTTCTT  
2 3 CCGACTCGAATTCAGATGAATCAAAAAGTT  
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0 0 ACGACTGGTTGTTGGGGGAGTTGTCCCTCA  
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0 0 GATACATGTTGTTGGAGGTATTGACCCCTTC  
0 0 CGAATTGGATGTTGGGCTCAACTTGAGCT  
0 0 TCAACTAGCC long g  
0 0 GATACTTGTTGTTGGAGGTATTGGCCCTTC  
0 0 CCGACAAGGGATTGGTGGGGTTTCGTTATG  
0 0 CCGACCAGGGATATGAGGATTCTTACTTAT  
0 0 CCGACCGGGGATAGGGAGTCTGGTGAAAC  
0 0 TCTACTAGTTGTCGGGACTTGTTGTCTTGG

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5	0	0 CCGACTTGGGATTGGAGGCGTGATTTTCC
6	0	0 CCGACTTGGTGTTCCCGGGTTTAAGTCCGG
7		
8	2	4 TACACTAGACTGGTGCGGGTTTGACGCCGT
9	0	0 CACGTTTGCTGTGAGAGGATTGACCCCTT
10		
11	0	0 CCGATTTGGGATTGGAGGCGTGCACTTTCC
12	0	0 CCGACTTGGGATTGGAGGCGTGCTCTTTCC
13		
14	2	4 ATGACTTGGTGTTGGGTTTTTAAGTCCCG
15	0	0 GGTACTGGGTAGAAAGCGTTCGATGACGC
16	0	0 CCGATCGGGGATGGGGAGAGGTAATACCT
17		
18	0	0 GTCACTCGGT long f
19	0	0 TCAACTAGGTGTTGGGTGAGTAAAACCATT
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21	0	0 CGAACTGGATGTTGGGCTTAACTTGGAGCT
22	0	0 AGTGCTGGGTGTAGGGGGTCATACCCCCC
23	0	0 GATACTTGTTGATGGAGGTATTGACCCCTT
24		
25	0	0 TCAACTAGTTGTTGCGCGAGGAGACTCATT
26	3	0 CCGACTCGGC long g
27	3	0 ATGACTCGATGTTAGCGATACACAGCCAGC
28		
29	3	2 CCGACTCGGATTCAGATGAATAAAAAAGTTC
30	0	0 GGTACTAGGTAGTGGACTTACATGGGTTCC
31		
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33	0	0 CCGACTAGGGATGAGTGAACGTTGAATTAT
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36	0	0 TATGCTAGACCGGTGCGGTTTTGATGCCGT
37		
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39	4	0 ATCTCTAGCTTTGAGGAGTATCGACCCTCT
40	0	0 ATTACTCGATGTTGGCGATACGCGGCCAGC
41		
42	0	0 CCGGTTAGGGATTGGCAGGGTTTCGTTATG
43	0	0 TCAACTAGCT long g
44		
45	2	0 ATTACTAGATTTTGGCCGTAAGGTCAGAGT
46	1	0 CCGACTCGGATTCAGATGAATCAAAAAGTT
47	0	0 CCGACTTGGGATTGGAGGCGTACACTTTCC
48		
49	5	0 TCTACTAGCC long g
50	0	0 ACCCCCATGAATTGGGGAATTTTGGTCGG
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52	0	0 TCAACAAGTTGTTGCGGTGAGGAGACTCATT
53	2	0 TCGACTAGTCGTTGCGGAGCAGCAATGTACT
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55	0	0 GGTGCTAGGTGTCACGGGTCATGACCCTGT
56	0	0 CCGACTAGGGATGGGTGAACGTTGATTTTT
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0 AGTGCTGGGtag g  
0 TCGACTAGTT long g  
0 CGAACTGGA(long) g  
0 TGAAGTGGATGTTGGGCTCAACTTGGAGCT  
0 TCAACTGGTT long g  
0 TACGCTAGATCGGTGCGGGTTTGAAGCTT  
0 ATTACTCGATGTGTGCGATACATGGCACGC  
0 TCAACTAGTAGTCGGATCTTAATAGATTGCG  
4 ATCACTTGATtag f  
0 TCAACTGGTTGTTGGGAGGGTCTCTTCTCAG  
0 AGTGCTGGATGTCGGGAAGCCTATCTTTTCC  
0 TCGACTAGTCGTTTCAAGAGCAGCAATGCACT  
0 TCAACTGGTT long f  
0 GGTACTAGGtag o  
0 AGTACTAGGtag f  
0 CCGATTAGGGATGAGTGAACGTTGCATTAT  
0 CCGACCAGGGATATGAGTTGTTAGGAATAT  
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0 TCAACTGGTCGTTGGGAGGGTTTCTTCTCAG  
0 GGTACTAGGlong g  
0 AGAACTAGCCGTTCCGGTCCCGTATGGGATT  
0 ATAAGTCGTT long f  
0 AGCACTAGACGCTGGGTGGGTGACCGTCCG  
0 GGCAGTGGtag o  
0 CGAACTGGAtag g  
0 TCACTAGACTGATGCGGTTTTGACGCCGT  
0 TCAACTGGTTGTTGGGAGGGTTTCTTCAAGT  
2 CCGACTCGGATTCAGATGATTCAAAAAGTT  
0 AATGCTAGCCGTTGGCCAGCTTGCTGGTCA  
0 AGAACTGGGTAGTGGTCCGGGCATGGGAT  
2 CGTGTTGGAC tag f  
0 AATACTAGGTGTTGGATACATTTGTATCCAG  
0 TCAACTGGTT tag f  
0 ATGACTCGATGTTGGCGATACAGCCAGCGT  
0 GATACTAGGtag c  
0 CTAAGTCGTT long g  
0 TCTACTAGTT(long) f  
0 GGCAGTGGlong f



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4	0	0 CCAACCAAAGATAAGGGTGGGAAAAACAA/
5	0	0 TCTACTAGTT(long f
6	0	0 TGCATTTGGTGTTGGGCCGATTAGGTTCAG
7	0	0 AATGCCAGAC(long f
8	0	0 TCAACTAGTTGTTCCGGTGAGGAGATTCATT
9	0	0 AGTGCTAGCTGTTGGGGGGTTACCTCTCAG
10	0	0 CTAACTCGAT(long g
11	0	0 TCAACTAGTTGTTCCGGTGTGGAGACTCATT
12	0	1 TCAACTAGATGTTGGGAGGGTTAAACCTTT
13	2	0 CCGACTCGGATTCAGATGAATAAAGTTCAT
14	0	2 TGTGCTAGATGTCGGGGTTTTAAACTTCGG
15	0	0 GATGCTAGATGTTGGTAATTTCCGGTTATCA
16	2	0 TGCACTAGGT(tag p
17	2	0 TACACCAGACTGGTGCGGTTTTGACGCCGT/
18	0	0 CCGACTAGG(long o
19	0	0 TCAACCGTTGTTGGGAGGGTTTCTTCTCAC
20	0	0 CTTACTCGACGTCCGGCCCCCTGCGGTCGTG
21	0	0 TCAACTAGGTGTTGGGAGGGTCAAACCTTT
22	0	0 TCAACTAGTTGTCGGATCTTAATAGATTGGT
23	0	2 CCAACCAGGGATCGAGGACAGTCCCATGGT
24	4	0 TGCGCTTGGTGTTGGGCCGATTAGGTTCAG
25	2	0 TCCACTAGATTGTGGCACTTTTAACGGTGTC
26	0	0 TCAACTAGGT(tag f
27	0	0 ATGACTTGGTGTGTCGGGTTTTAATTCCCG
28	0	0 CCGACTCGGTTTCAGATGAATCAAAAAGTTC/
29	0	0 AATGTAAAAAAAAAAAAATAATTTTTATTTTA
30	0	0 GAAGCTAGC(long g
31	0	0 CTAACGATGGACGCGGGGAATCAGAAAGA/
32	0	0 CCGACCCGGATTCAGATGAATCAAAAAGTT
33	0	0 ATTACTCGCTGCTAGATGGCAACGTTTAGTC
34	0	0 AGCACTGGG(long f
35	0	0 TCAACTAGAT(long g
36	0	1 CCGACCAGGGATCGAGGACAGTCCCATGGT
37	2	0 ATCACTAGATTTTGGTCGTATAGTCAGAGTC
38	0	0 GATACTAGCTGTTGGGAGTAATTTCCGGTGG
39	0	0 TCAACTAGCTGTTCCGGTGAGGAGACTCATT
40	3	1 GATACCAGCTGTTGGGAGTAATTTCAGTGG
41	3	0 ATCACTCGATGTTGGCGATACACAGCCAGC
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4 0 TCAACTAGGTGCTGGGTGGGTAAAACCATT  
5 0 2 GATACTTGTCGTTGGAGGTATTGACCCCTTC  
6 0 0 GATACTAGCTGTTGGAGGAACTTCGGTGG  
7  
8 4 0 CCGACTAAGGATCGGCAGAAGTCATTTTTG/  
9 4 0 CGAACTAGCT tag g  
10 0 2 TGCACTTGGTGTGGGCGGATTAGGTTGAG  
11 0 0 TCGACTAGGGATCGGTGGACGTTGCATAGC  
12 0 0 AGTACTAGATATCGGGATTTATTTTCGGTGTG  
13 0 0 CCAGCTAGGGATATGTGGACGTTTGTGTTGA/  
14 0 0 GGTACTAGCT tag f  
15 0 0 GATACTTGTTGGAGGTATTGACCCCTTCAGT  
16 0 0 CTTACTCGACGTACGGCCCTGGTGGCTGTG/  
17 0 0 GATACTAAATGCTGTCAAAAACAGTGTTGA/  
18 0 0 TCAACTAGTTGTTCTGTGAGGAGACTCATTC  
19 0 0 CTTACTCGACGTCCGGCCCCTGTGGTCGTG/  
20 0 0 GGCCTAGGTGTGGGGAGCATTTCACGTTTC  
21 0 0 TATACTTGGTGTAATCGGACTCAACCCCGAT  
22 0 0 TTGACTAGGT long f  
23 0 0 CTGACTTGGT tag o  
24 0 0 CCGACTTGGGATTGGAGGCATGCACTTTCC/  
25 0 0 CCAACTAGGAATATGTGGACGTTTGTGTTGA/  
26 0 0 CCGACTAAGGATCGGCAAAGGTCATTATTG/  
27 0 0 TCATCTAGGTGTTGGGAGGGTTAAACCTTT/  
28 0 0 ATGACTTGATGTTGGCGATATACAGCCAGC/  
29 0 0 AACACTGGAGAAAGGGGGCTTCGGCCTTCT  
30 0 0 GATACTTGTTGTTGGAGATATTGACCCCTTC  
31 0 2 TCAACAGGTGTTGGGAGGGTTAAACCTTT/  
32 2 0 ATGACTCGAT tag g  
33 0 2 TACACTAGACTGGTGTGGTTTTGACGCCGT/  
34 0 0 ATTACTCGAC long g  
35 0 0 TCAACTAGTTGTCGGGTCTTATTAGGCTTGG  
36 0 0 GATGCTAGCCGTCGGTCAGCTTGCTGATCG/  
37 2 3 TCAACTAGGTGTTGGGAGGGTTAAACCTTC  
38 0 0 GGCCTAGCTTGGGGTCTCCTGTGTGATCC/  
39 0 0 TGTACTTGATGTACCTAGGCTCAACCCTGGC  
40 0 0 TCAACTAGGGATATGTGGACGTTTGTGTTGA/  
41 0 0 CCGACTGGAGTGGAGGAGTCACAATTCATA  
42 0 0 GGTACCAGGTTGTGGACTTGCATGGGTTCA

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4	0	0 CCGACTTAGGATTGGAGGCGTGCAC TTTCC
5	2	2 TCAACTAGTTGTTGGGTCTTAATAGACTTGG
6	0	0 CCGACCAGGGATATGAGTTGTTAAGATTAC
7		
8	0	0 ATAACTAGCT long f
9	0	0 TCAACTAGGTGTTGGGTGGGTATAACCATT
10		
11	0	0 CCGACCGGGGATGGGGAGAGGTAATACTT
12	2	2 CCGACTCGGATTCATGAATCAAAAAGTTCA
13	2	2 CCGACCAGGGATATGAGTAGGTTATTTCAT
14		
15	0	0 TCAACTGGTTGTTGGGAGGGTTTCTTCAC
16	0	0 CCGACTAGG long c
17	0	0 AATACTAGGT tag g
18		
19	0	0 CCGACTGTAGATTAGAAGACGTTAATCAAG
20	0	0 CCGACTAGCAATCCGCCGGCGTGGTTTCGA
21		
22	0	0 CCGACCGGGGATGGGAGAGGTAATACCTT
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24	0	0 ATTACTCGTTGCTGGGAGGTAATTTTCAGT
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26	0	0 CCGACTAGGGATATGTGGACGTTTGTGTA
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28	0	0 CCAACTAGGGATATGTGGACGTATGTTGA
29	0	0 CCGACTAGGGATTGGGGAGTCATCAAGCTC
30		
31	0	0 AGCACTAGG tag p
32	0	0 CGCACTAGACCA GTGCGGTTTTGACGCCGT
33	0	0 TATGCTAGACCGGTGTGGTTTTGACGCCGT
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35	0	0 TATACTAGGTGTAGCTGGACTCAACCCCA
36	0	0 TTTACTAGTGTTGCGGGTATTTATTTATCTG
37		
38	0	0 TTTACTTGCTGTTGGGGGCAACCTAAGTAG
39	0	0 GATGCTAGCC long g
40	0	0 CCGACTAGCGATCCGCCGGCGTGGTTTTGA
41		
42	0	0 CGAACTGGATGTTGGGCTCAACTTGGGGCT
43	0	7 CCGACTCGATTCAGATGAATCAAAAAGTTCA
44		
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46	0	0 CTTACTCGACGTACGGTCCTGGCGGCTGTG
47		
48	0	0 GATACTTGTTGTTGGAGGTATTAACCCCTT
49	0	0 TCAACTGGTTGTTGGGAGGGTTTCTTCTCA
50	0	4 TTTACTTGCTGTTCCGGTCTTCGGATTGAGTG
51		
52	0	4 GATACTAGCTGTTGGAGGAACTTCAGTAG
53	0	0 CATATTTGAGGTGGGGGATTTCGACCCCTT
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56	0	0 ATCTCTCGGTTTTTCGGAGTATCGACCCTCTG
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4 0 0 TCGACTAGCTGTTGGAATCCTTGAGATTTTA  
5 0 0 CCGACTTGGGGTTGGAGGCGTGCACTTTCC  
6 0 0 TCTACTAGTT(long f  
7 0 0 TCAACTAGGAGTTGGGTGGGTAAAACCATT  
8 0 0 ATTACTCGACATACGCAATACACAGTGTGTG  
9 0 0 ATTACTAGGT long p  
10 0 0 CGAACTGATGTTGGGCTCAACTTGGAGCTC  
11 0 0 TCGACTGGTTGTTGGGAGGGTTTCTTCTCAC  
12 0 0 CGCACTAGACCGGTGCGGTTTTGACGCCGT  
13 0 0 AGTGCTAGACGTTGGGGTTATAAACTTCAG  
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15 0 0 GATACTAGCTGTTGGGGTAATTTCACTGG  
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25 0 0 ACAACTAGAC tag o  
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31 0 0 AGTGCTCGTC long o  
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33 0 0 CGCACTAGACCGGTGTGGTTTTGACGCCGT  
34 0 0 AGAACTGGACGTTGGGAGGGATTGCGCTCT  
35 0 0 AGAACTAGGCGTTGGAAGGTATTACCTTCT  
36 0 0 AATACTAGGTGTTGGATGCATTAGCATCCA  
37 0 0 CCAACTAGGGAGATGTGGACGTTTGTGTTGA  
38 2 2 CCGACTCAGGATTGGCAGACGTCCTTACCG  
39 0 0 TACGTTGGCT long g  
40 0 0 ATTACTTGATGTTGGCGATACACAGCCAGC  
41 0 0 TCAACTAGTC tag g  
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5	0	0 GATACTAGGTGTTGGAGAGATTCAAATCAT
6	0	0 CCGACTTGGGATTAGAGGCGTGCACCTTCCG
7	0	0 ATGACCCGATGTTGGCGATACACAGCCAGC
8	0	0 ATGACTCGATGTTGGCGTTACACAGCCAGC
9	0	0 ATGACTTGGGGTGTCTGGGTTTTAAGTCCCG
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11	0	0 ATCACTCGATGTTGGCGATACGCAGCCAGC
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16	0	0 TTCTCTCGCTtag p
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18	0	0 ATTACTAGATGCTGGCAAGTTGTTGTCAGTC
19	0	0 CCGACCAGGGATATGAGTTGTTAGGAATAT
20	0	0 CCGACTAGGGATCGGTCCACGTTATTCTCTG
21	0	0 GATACTTGGTGTGTGGGGTATTTAGTCCCCA
22	0	0 ATTGCTAGTTlong g
23	2	0 CCGACCAGGGATATGAGTTGTATATTTCAA
24	3	0 TCGACTAAGGATGATAAAATATTAATGA
25	0	2 ATCACTAGATTTTGGCTGTATGGTCAGAGTC
26	0	2 ATGACTTGGTGTGTCTGGGTTTTAAGTCCCG
27	0	0 TCAACTAGTTGTCGGACCTTAATAGATTTGG
28	0	0 TCAACTAGTTGTCGGGTCTGTTAAGGATTTG
29	3	0 CTAACGATGGACGCGGGAAATCAGAACATC
30	0	0 TCAACTAGTTGTTCCGGTGAGGAGGCTCATT
31	2	0 ATTACTCGATtag f
32	2	2 TCAGCTAGTTtag g
33	0	0 TCGACTGGTTlong f
34	0	0 ATGACTTGGTGCGTCTGGGTTTTAAGTCCCG
35	0	0 TCAACTAGTTGTCGGATCTTATAGATTTGGT
36	0	0 TACTACTAGATTGGTGCGGTTTTGACGCCGT
37	0	0 TACTACTAGACTGGTGCGGTTTGACGCCGT
38	0	0 AGCACTGGA1long f
39	0	0 AGAACTAGGTGTCGTGGGGGTTGACCCCCG
40	0	0 AGCACTAGCTtag g
41	0	0 CGCACTTGGTCTGGAGCGGTTTGACTCCGTT
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8 0 0 CGCACTGGATCGGTGCGGGTTTGACCCCGT  
9 0 0 TGCACTCGGTGTTGGGCCGATTAGGTTTCAG  
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38 3 2 ATGGTTGGATGTTGGCGATACACCGTCAGC  
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41 0 0 TCGACTGAAGATCAGTTAAAGTCTATTTAA  
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26	0	0 TCGACTAGCGATCCGCCGGCGTGTTTCGAT
27	0	0 CCGACCAGGGATATGAGTTGTTATGGTTAT
28	0	0 GATACTTGTTGTTGGAGGTATTGACCCCTTT
29	0	0 GGTACTAGG1 long g
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32	0	0 AGCACTAGACGTCGGGCGGTGACCGTCCGC
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34	0	0 AGCACCAGACGCTGGTGGGGTGACCTGCCG
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2 0 CTAACGATGGACGCGGGGAATCAGAACAT(

2 0 GATACTAGCTGTTGGGAGAAATTTCACTGG

2 0 CCGACCAGTGATCGAGGACAGTCCCATGGT

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0 0 CCGACTAGCGATCCGCCGGCGTGTTCCGA

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0 0 CACGTTTGGT long f

0 0 GATACTAGGTtag g

0 0 TCGACTAGGTGTTCCGGGAAGGAGACTTCTC



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41	0	0 ATTACTCGACATACGCGATACACAGTGTGC
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0 TATGCTAGACCGGTGCGGTTTTGACGCCAT/  
0 GCGCTAGG<sup>-</sup> long g  
0 TCAACTGGTTGTTAGGAGGGTTTCTTCTCAG  
0 GGTGCTGGATGTCGGGGGCTTGCCCTTCGG  
0 TCAACTGGTT tag f  
0 TCAACTAGTTGTCGGGTCCTATTGGGCTTGC  
0 TCGACTAGGGATGAGTGAACGTTGCATTAT/  
0 TCAACTGGATGTTGGGAGGGTTTCTTCTCAC  
0 CCAACTAGGGATATGTGGACGTTTGTGAAG  
0 AGCACTGGG1 long f  
0 GATACTAGGC long o  
0 TCAACTGGTT tag f  
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0 CCGACTAGGC long f  
0 TCAACTGTTGTTGGGAGGGTTTCTTCTCAGT  
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0 CCGACTAGGC tag g  
0 CCGACTGGGGATGAGTGAACGTTGCATTAT  
0 CCGACTTGGGATTGGAGGCGTGCATTATCC  
0 CCAACTGGGGATATGTGGACGTTTGTGTTGA/  
0 TCAACTGGTTGTTGGGTCAACTGACTCAGT/  
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0 0 TCAACTAGTTGTTCCGGTGAGGAGACACATT/  
0 0 CGAACTGGA1 long g  
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53	0	0 ATAAGT long g
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56	0	0 TCAACTGGTT tag f
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0 CTAACTCGTT tag g  
0 CCGACAAGG(long g  
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2 AGCACTGGACGTCGGGTGGGTGACCGTCCC  
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0 AATGCTAGATGTTGGCGAGCATGCTCGTCA  
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0 TGCACTTGGTGTTTGGCCGATTAGGTTTCAGT  
0 AATACTCGATtag f  
0 ATGGCTCGATtag f  
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0 GATACTAGCTlong g  
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28	0	0 GGTGCTAGATGTTGGGAAGCTTGCTTTTCG
29	0	0 CCGACTCGGATTCAGATGAATATTAAGTTCA
30	0	0 TCGACTAGGTGTTGCGGAAGGAGACTTCTT
31	0	0 AGAACTAGGTGTCGTAGGTGTTGACCCCCG
32	0	0 TCGACCAAGGATAAGAGGTCGTAATTATCT
33	0	0 TTCACTAGTGTTGCGGGTATATATTTATCTG
34	0	0 GAAACTCGACATCAGCGATACACTGTTGGT
35	0	0 TATACTAGAAGTAGGAGGGCTCAACCCCCC
36	0	0 CCGACTGTAGATTAGAAGACGTTAATTAAG
37	0	0 TACACTAAAC tag f
38	0	0 CCGACTAGGC long f
39	0	0 CGAACTGGATGTTGGGCTCAACTTGAGCTC
40	0	0 ATTACTCGACATACGCGATACACTGTGTGTC
41	0	0 GGTGCTCGGTGTCGGGGGTATCGACCCCTC
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0 GATACTTGTTGTTGGAGGTTTGACCCCTTCA  
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0 AGCACTGGAC long g  
0 ATTACTCGTTGCTGGGAGGAACTTTCACTC  
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0 CCAACTAGGGATATGTGGACGTCTGTTTGA/  
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0 CCGACTAGGGATCGGTGGACATTGCATAGC  
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0 CCGACCAAGC tag p  
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0 TCAACTAGGTGTTGGGAGGGTTAAACCTT  
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0 AATGCTTGGT long o  
0 GGTACTTGGTGTTGGTGGTATTGACCCCATC  
0 GATACTAGGCGTATCGGGTATCGACGCCTG  
0 TCGCTAGGTGTAGGAGGTGTCGACCCCTT  
0 CTTACTCGACATACGGCCCTGGCGGCTGTG/  
0 TGGACTTGGC tag f  
0 TCGACTAGCCGTTCCGAGCAGCAATGCACT/  
0 GGTACTAGGCGTCGGGGGAGCGACCCCTC  
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0 ATTACTCGACGTGTGCGATACACGGCACGC/  
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0 AGTGCTAGATGTCGGGGGGAAACCTTCGGT



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8	0	0 ATTACTCGTTTTTGGGGTTTATGATTCAGAG
9	0	0 AGAACTAGG1long g
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11	0	0 TCAACTAGCTtag g
12	0	0 TCAACTAGGTGGGGAGGGTTAAACCTTTTA
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20	0	0 TAAACTCGACATTAGCGCTATACTGTTAGTG
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22	0	0 AATGCCAGCC long g
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24	0	0 CCAACTAGGT long f
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7 0 CTGACCAAGGATAAGAGGTCGTAATTATCT  
8 0 CACGTTTGCTGTAAGAGGAATCGATTCCTTT  
9 0 TCAACTAGGTGTTGGGAGGGTTAAACCTTA  
10 0 TCAACTGGTT long g  
11 0 TCAACTAGGTGTAAAACCATTTAGTACCGG/  
12 0 CCAACTAGGGATATGTGGACGTTTCGTTTGA/  
13 0 AGGACTAGGTGATGGATGAGTTAAACTCAT  
14 0 TCAACTAGGT long f  
15 0 CCGACCAGGGATTAGGAGACGTTAAATTTT,  
16 0 TTTACTTGCTGTTTGGCCTTTGGGTTGAGCG  
17 0 ATTACTCGATGTGTGCGATACACTGTACGTC  
18 0 TCAACAAGTTGTCGGATCTTAATAGATTTGC  
19 0 CCGACTCGGGATCGGTGAGCGTGATTTTTTT  
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21 0 CCGACTAGGGATCGGTGGATGTTTTATTGA/  
22 0 GATACTCGAC tag g  
23 0 GATACTTGTTGTTGAAGGTATTGACCCCTTC  
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25 0 TCAACTAGTTGTCGGATCTATAGATTTGGTA  
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34 0 ATTACTCGCTGCTAGAAGGCAACTTTTAGTC  
35 0 AATGCCAGCCGTTGGGGAGCTTGCTCTTTA/  
36 0 ATGACTCGATGTTGGCGATGTACAGCCAGC  
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40 0 TTTACTTGCTGTTTGGTTTTTCGGACTGAGTG  
41 0 CCGACCGGGCATGGGGAGAGGTAATACCTT  
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6	0	0 TGTGCTAGATGTTGGGCGGCCTAGCCGTT(
7	0	0 CCGACTCGGATTCAGATGAATATTAAAGTT(
8	0	0 CTGACTTGGTGTCGCAGGTTTTAAGTCCTGC
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38	0	0 TCAACTAGGGTTTGGGAGGGTTAAACCTTT
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15 2 0 TGCACTTAGTGTTGGGCCGATTAGGTTCAGT  
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5	0	0 AGGACTGGG` long g
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8	0	0 AATGCCAGTC long f
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0 AGTACTAGGTGTAGGCGGAGTGAAATCTGT  
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0 CCGACTAGTGATCCGCCGGCGTGGTTTCGA  
0 TACGTTGAGTTAGAGCAGCTCTGACGCCGT  
0 CGCACTAGACCGGTGCGGTTTCGACGCCGT  
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0 GATACTAGGCGTATCGGGTATCGACCTCTG  
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0 CACACTAGGTCTTAGTGGATTCGACCCCACT  
0 TATGCTAGACCGGTGCAGTTTTGACGCCGT  
0 CCAACTAGGGATATGTGGACGTTTGTAA  
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0 AATACTAGGCGTAGGTAGAGTCAAATCTTT  
0 CTAACCTCGTTTTTGGGGCGTAGGTTTCAGAC  
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0 TGAGCTTGGCGTTGGTGGGTAAACTCCAT  
0 AGTACTCGACATACGCGATACACAGTGTGT  
0 GATACTTGTGTTGGAGGTATTGACCCCTTC  
0 GGTACTAGGTAGCGGCCTGTCATGGGGTCC  
0 CCGACTAGG long g  
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0 GGTACTGGGTAGGGGGCTCGCCGATGGGC  
0 GCGACCGAGATTCAGGAAATGCCAAGATGC  
0 GGTGCTAGGTGTCGCGGGTTTTGATCCCTG  
0 GGGACTGGG tag g  
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6	0	0 CATACTTGGT long o
7	0	0 TCAACTGGTTATTGGGAGGGTTTCTTCTCAG
8	0	0 GCGACTGAGATTCAGGAAATGCCCAAGATC
9	0	0 CCGACTAGGGATGAGTGAACGTTGCGTTAT
10	0	0 CTTACTCGACGTACGGCCCTGGCGGCTGTAC
11	0	0 CGAACTGGATGTTGGTCACAACTCGGAGAT
12	0	0 AGAACTACGTGTCGTGGGTGTTGACCCCCG
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17	0	0 CCGACTCGGATTCATATGAATCAAAAAGTT
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23	0	0 AATGCTTGGTGTCTGGAGTTTTAAATCTCTG
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0 0 CCGGTTAGG long g  
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0 0 ATTACTCGATGTGCGCGATACACGGCACGC  
0 0 AGTGCTAGAT long g  
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0 0 GATGCTAGCC tag o  
0 0 CCGACTCGGA long f  
0 0 ATCACTAGATTTTGGCCGTATGGTCAGAGTC  
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0 0 CGAACTGGA long f  
0 0 CCGACTAGGGATCGGTGGATGTTGCATAGC  
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0 0 CATGCTGGCTGTCGGAGTTATTCACCCCTTC  
0 0 CCGACTTGGTGTTCGGTTTTAAGTCCGGC  
0 0 TCAACTGGTT long g  
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9	0	0 TCAACTAGTTGTCGGACCTTTGGGTTTGGTA
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11	0	0 AGTGCTAGCT long g
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13	0	0 GGCAGTAGGtag g
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0 GATACTAAGTGTGTCGGGTTACCGCCGGT  
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10	0	0 TCGACTAGCC tag g
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13	0	0 TCAACTAGATGTCGGATCTTAATAGATTTGC
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9	0	0 AATACTAGCTGTTGGAGGAACTTCAGTGG
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20	0	0 TCGACTAGTC long g
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24	0	0 TGTGCTTGTC tag f
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32	0	0 AGAGCTAGCC tag f
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39	0	0 AAGACTCGATGTTGGCGATACACAGCCAGC
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41	0	0 TCAACTAGTTGTGGGATCTTAATAGATTTG
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0 CTTACTCGTTGTTAGGCTTTCGGGCTGAGTG  
0 CTAACGATGGACGCGGGGAATCAGAACATT  
0 AGCACTAGACGTCAGGTGGGTGACCGTCCG  
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0 TATGTTGAGTTAGAGCGGCTCTGACGCCGT  
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0 ATGACTTGATGTGTCGGGTTTTAAGTCCCGC  
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0 TCAACTAGTTGTCGGATCTAAATAGATTTGC  
0 TGTGCTAGAC tag f  
0 ATTACTCGATGTTGGTGATACACGGCCAGC  
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0 AGCTAGACGTCGGGCGGGTGACCGTCCGG  
0 AGAGCTAGATGTCGGCACGCATGCGTGTCC  
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0 ATCACTAGATTTTGGCCGTATAGTCAGAGTT  
0 ATGACTCGATGTTGGAGATACACAGCCAGC  
0 CCGACTCAGGATGGGCAGTCCGTTGTTCCG  
0 ATCACTCGCT long f  
0 GATGCTAGACGTTGGCGAGCATGCTCGTCA  
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0 ATGACTCGATGTTGGCGATACACAGCAGCG  
0 CCGACTAGG long c  
0 AATGCTAGACGTTGGCGAGCATGTTTCGTCA  
0 AGTACTAGATAGTGGACTTTCATGGGTTCA  
0 ATCACTGGATTTTGGCCGTATGGTCAGAGT  
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0 TACACTAGACTGGTGCGGTTTTGAGGCCGT

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6	0	0 TATGCTTGGTGTTGGGTCGCAAGACTCAGT/
7	0	0 TTTACTTGCTGTTTGGCTTTTCGGGTTGAGTG
8	0	0 ATAACTAGCT long g
9	0	0 AGATCTAGGTGTCGTGGGTGTTGACCCCCG
10	0	0 CTTACTCGTTGTTTGGCTTTTCGGGCTGAATG
11	0	0 ATTACTCGATGTGTGCGATTACGGCACGCC
12	0	0 CTGACTTGGTGTCCTCAAGTTTTAAATCTTGG
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21	0	0 GGCAGTGGGCGAGGGGACTCGCCGATGGGT
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34	0	0 TCAACTAGTTGTTCCGGTGAGGAGACGCATT/
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0 TTAACTAGTTGTCGGATCTGTTTAAGGATTT  
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0	2	CCAACCAGGTTTCATCTGGGGACTTTTATGA
0	2	CCGACCAGGGATATGAGGTAAAAAAGTA
0	2	TCAACTAGCTGTTTGAAACATTAGATTTTGA
0	2	CCGACCAGGGATCGAGGACAGTCCCACAAC
0	2	CCGGAGCTAACGCGTTAAGTCAGCCGCCTG
0	2	TCGACCAGACGTCGGGGGTGTCAACCCCTC
0	2	ATGGCTTGGTGTGTCGGGTTTTAAGTCCCG
0	0	TCAACTGGTAGTTGGGTCTTAATTGACTCAG
0	0	TCAACTGGTTGCTGTGTCTTAAGTACTCAG
0	0	GATAATTGTTGTTGGAGGTATTGACCCCTTC
0	0	TCAACTAGGTGTTGGGTGGGTAAAACCATA
0	0	GATACTTGTTCTTGGAGGTATTGACCCCTTC
0	0	GATACTAGTTGTTGGAGGTATTGACCCCTTC
0	0	TCAACTAGGTGTTTGGAGGGTTAAACCTTTT
0	0	GATACTTGTTGTTGGATGTATTGACCCCTTC
0	0	GATACTTGTTGTTGGAGGTATTGTCCCTTC
0	0	GATACTTGTTGTTGGAGGTATTGACACCTTC
0	0	GATACTTATTGTTGGAGGTATTGACCCCTTC
0	0	TCAACTAGTTlongg
0	0	CCGACTTGGGATTGGAGGCGTCACTTTAC
0	0	CGAACTGGATGTTGGGCTCAACTTGGAACT
0	0	GATACTAGCTGTTGGGAGCAAATTCAGTGG
0	0	CGAGCTGGATGTTGGGCTCAACTTGGAGCT
0	0	TCAACTAGGTGATGGGAGGGTTAAACCTTT
0	0	GATACTTGTTGTTGTAGGTATTGACCCCTTC
0	0	CCGACCTGGGATTGGAGGCGTCACTTTCC
0	0	TCAACTAGGTGTTGGGAGGGTTAAACCTTT
0	0	TCAACTAGGTGTTGGGTGGGTAAAACCTATT
0	0	TCAACTGGTTGGGGGTCTTAAGTACTCAG
0	0	TCAACTGGTTGTTGGGTCTTAATTGACTAAG
0	0	CCAACCTAGGGATATGTGGGCGTTTGTGTA
0	0	CGAACTGGATGTTGGTCTCAACTCGGTGAT
0	0	CGCACTAGACCGGTGCAGTTTTTGACGCCGT
0	0	TCAACAGGTTGTTGGGAGGGTTTCTTCTCAG
0	0	CGCACCAGACCGGTGCGTTTTTGACGCCGT
0	0	ATTACTCGATGCTGGGAGGTAACCTTTCAGT
0	0	CCAACCAGGGATATGTGGACGTTTGTGTA
0	0	CGAACTGGAtagf

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4	0	0 CCGACTTGGGATTGGTGGCGTGCAC TTTCC
5	0	0 CCAACTGGTT tag f
6	0	0 TCAACTAGTTGTTCCGGTGCGGAGACTCATTC
7	0	0 CGCACTAGACCGGTGCGGTTTTGACACCGT,
8	0	0 CGGACTTGGGATTGGAGGCGTGCAC TTTCC
9	0	0 TCAACTAGGTGTTGGGTGGGCAAAACCATT
10	0	0 TCAACTAGGTGTTGGGAGGGTTAATCCTTTT
11	0	0 CCGCCTTGGGATTGGAGGCGTGCAC TTTCC
12	0	0 GTTACTTGTTGTTGGAGGTATTGACCCCTTC
13	0	0 TCAACTAGGTGTTGGGTGGGTAAAACCTTT
14	0	0 TCAACTGGGTGTTGGGTGGGTAAAACCATT
15	0	0 GATTCTTGTTGTTGGAGGTATTGACCCCTTC
16	0	0 TCAACTAGGTGTTGGGTAGGTAAAACCATT
17	0	0 CCGACTTGGGATTGGAGGCGTGCAC TTTCC
18	0	0 CCGACTTGGGATTGGAGGCCTGCAC TTTCC
19	0	0 TCAACTGGTTGTTGGGAGAGTTTCTTCTCAG
20	0	0 CCGACTTGGGATTGAAGGCGTGCAC TTTCC
21	0	0 ATTGCTCGTTGCTGGGAGGTAACTTTCAGTC
22	0	0 CCGACTTGGGATTGGAGGCGTGCAATTTCC
23	0	0 ATTACTCGACATACGCGATACACGGTGTGT
24	0	0 TCAACTAGGTGTTGGGTGTGTAAAACCATT
25	0	0 CCGACTTGGGATCGGAGGCGTGCAC TTTCC
26	0	0 CGAACTGGATGTTGGGCTCAACTTGGAGCT
27	0	0 CCGACTTGGGATTGGAGGCGTGCAC TTTCA
28	0	0 TCAACTGGTTGTTGGGAGTGTTTCTTCTCAG
29	0	0 TCAACTGGTTGTTGGGAGGGTTTCTTATCAG
30	0	0 TCAACTAGTTGTTCCGGTGAGGAGACTCGTT
31	0	0 TCAACTAGGTGTTGGGTGGGTAAAACCATT,
32	0	0 TCAACTGGTTGTTGGGAGGGTTTCTTCTGAC
33	0	0 TCGACTAGGTGTTCCGGAAGGAGACTTCTG
34	0	0 TCAAGTGGTTGTTGGGAGGGTTTCTTCTCAG
35	0	0 ATTACTCGTTACTGGGAGGTAACTTTCAGTC
36	0	0 CCGACTAGCGATCCGCCGGCGTGGGTTCGA
37	0	0 GCGACTTGGGATTGGAGGCGTGCAC TTTCC
38	0	0 CCGACTAGGGATCGGTCCACGTTACTTTTTG
39	0	0 TCAACTAGGTGTTGGGAGGGTTAAACCTTT
40	0	0 CGAACTGGATGTTGGTCTCAACTCGGAGAT
41	0	0 CCAACTAGGCATATGTGGACGTTTGTTGA/
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0 0 CGAGCTGGATGTTGGTCTCAACTCGGAGAT  
0 0 CGAACTGGATGTTGGCCTCAACTCGGAGAT  
0 0 CCAACTAGGGATGAGTGAACGTTGCATTAT  
0 0 CCGACTAGGGATCGGTCCACGTTTTTTTTTG  
0 0 TCAGCTGGTTGTTGGGAGGGTTTCTTCTCAG  
0 0 CAAACTGGATGTTGGTCTCAACTCGGAGAT  
0 0 CTAACTCGTTTTTGGGGTGTAAAGTTTCAGAG  
0 0 CCGTCTTGGGATTGGAGGCGTGCACCTTTCC  
0 0 TCAACTAGTTGTTTCGATGAGGAGACTCATT  
0 0 TCAACTGGTTGTTTGGAGGGTTTCTTCTCAG  
0 0 TCGACTAGGTGTTTCGGGAAGGAGTCTTCTT  
0 0 CGAATTGGATGTTGGTCTCAACTCGGAGAT  
0 0 TCAACTGGTTGTTGGCAGGGTTTCTTCTCAG  
0 0 CGAACTGGA1tag g  
0 0 CTAACTCGTTTTTGGGGCGTAAGTTTCTGAG  
0 0 CCGACTTGGGATTGGAGGCGTGAACCTTTCC  
0 0 CCGACTTGGGATTGGAGACGTGCACCTTTCC  
0 0 CCGACTAGGGATCGGTCCACGTTATTTTTTG  
0 0 CCGACTAGGGATCGGTCCACGTTATTTTTCC  
0 0 CGAACTGGATGTTGGGCTCAACTTTGAGCT  
0 0 CTAATTCGTTTTTGGGGCGTAAGTTTCAGAG  
0 0 TCAACTGGTT long g  
0 0 CCGACTTGGGATTGGAGGCTTGCACCTTTCC  
0 0 CTAACTCGTTTTTGGGGCGTAAGTTTCAGAG  
0 0 CCGACTTGGGATCGGTCCACGTTATTTTTTG  
0 0 CGAACTGGATGTTGGTGTCAACTCGGAGAT  
0 0 TCAACTAGTTGTTTCGGTGAGGAGACTCACT  
0 0 CGAACTGGATGTTGGTCTCAACTCTGAGAT  
0 0 CGAACTGGATGTTGGTCTCAACTCGGAAAT  
0 0 CCGACTAGAGATCGGTCCACGTTATTTTTTG  
0 0 CCGACTCGGGATTGGAGGCGTGCACCTTTCC  
0 0 CCGACTTGGGATTTGAGGCGTGCACCTTTCC  
0 0 TCTACTAGTTATCGGGTCTTAATTGACTTGG  
0 0 CGAACTGGATGTTGGGCTCAACTTGGTGCT  
0 0 CCGACTTGGGATTGGAGGCGTGCACCTTTCC  
0 0 TCAACTGGTTCTTGGGAGGGTTTCTTCTCAG  
0 0 GATACTAGCTGTTGGGAGTAACTTCAGTGG  
0 0 CCGACCAGGGATCGAGGACTGTCCCATGGT



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4	0	0 CCGACTCGGATTCAGATGAATCAAAAAGTT(
5	0	0 GATACTAGCTGTTGGTGGAAACTTCAGTGG
6	0	0 GATACTAGCTGTTGGAGGAAATTTTCAGTGG
7		
8	0	0 GATACTAGCTGTTGGAGGAAACTTCATTGG(
9	0	0 TCAACTAGTTGTCGGATCTTAATAGATTTGG
10	0	0 GATACTAGATGTTGGAGGAAACTTCAGTGG
11	0	0 CCGACCAGGGTTCGAGGACAGTCCCATGGT
12	0	0 CCGACCAGGGATCGAGGACAATCCCATGGT
13	0	0 CCGACTCGGATTCAGATGAATCAAAAATTC
14	0	0 GATACTAGCTGTTGGGAGTAATTTTCAGTAG(
15	0	0 CCGACCAGGGATCGAGGACAGTCCCACGGT
16	0	0 AATACTTGGTGTAAGTGGACTCAACCCTAGT
17	0	0 GATACTAGCTGTAGGAGGAAACTTCAGTGG
18	0	0 ATTACTCGATGTTGGCGATATACAGCCAGC(
19	0	0 ATGACTCGATGTTGGCGATACACACCCAGC(
20	0	0 CCGACTCGGATTCAGATGAATCAAAAAGTT(
21	0	0 TACACTAGACTGGTGCGGTTTTTAACGCCGT/
22	0	0 ATGACTCAATGTTGGCGATACACAGCCAGC(
23	0	0 AGTGCTAGAC tag o
24	0	0 ATTACTCGATGTTGGCGATACACAGCTAGC(
25	0	0 CCCACTCGGATTCAGATGAATCAAAAAGTT(
26	0	0 ATTACTCGCTGCTGGATGGCAACGTTTAGTC
27	0	0 CCGACTCGGATTCAGATGAATCAAAAACTTC
28	0	0 TCAACTAGTTATCGGATCTTAATAGATTTGG
29	0	0 CCGACTCGGATTCAGATGAATCAAAAATTT(
30	0	0 AATGCTAGACGTTGGCGAGCATGCTCGTCG
31	0	0 ATTACCCGATGTTGGCGATACACAGCCAGC(
32	0	0 ATTACTCGACGTTGGCGATACACAGCCAGC(
33	0	0 TCAACTAGTTGTCGGATCTTAATAGATTTGG
34	0	0 ATGACTCGATGTTGGCGATACGCAGCCAGC
35	0	0 ATTACTCGATGTGTGCGATACACGGCACAC(
36	0	0 ATGACTCGAT tag g
37	0	0 CCGACCAGGGATCGAGGGCAGTCCCATGGT
38	0	0 AATGCTAGACGTTGGTGAGCATGCTCGTCA(
39	0	0 TACATTAGACTGGTGCGGTTTTTGACGCCGT/
40	0	0 TCGACTAGTCGTTCCGAGCAGCCATGCACT(
41	0	0 ATTACTCACTGCTAGATGGCAACGTTTAGTC
42	0	0 TACACTAGACTGGTGCGGTTTTTGACGCCGA/
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4 0 0 TACTAGACTGGTGCGGTTTTGACGCCAT/  
5 0 0 TATACTTGTGTAAGTGGACTCAACCCTAGT  
6 0 0 CCGACCAGGGATCGAGGACAGTCCCATTGT  
7 0 0 CCGACAAGGGATCGAGGACAGTCCCATGGT  
8 0 0 CCGACTCGGATTCACATGAATCAAAAAGTT  
9 0 0 CCGACCAGGGATCGAGGACAGTGGCATGGT  
10 0 0 ATGACTCGATGTTGGCGATACACAGCCAGC  
11 0 0 CACTAGACTGGTGCGGTTTTGACGCCGT/  
12 0 0 TGCACTTGGTGTTGGGCCGATTAGGTTCA  
13 0 0 CCGACCAGGGATCGAGAACAGTCCCATGGT  
14 0 0 GATGCTAGCTGTTGGGAGTAATTTCAAGTGG  
15 0 0 GATACTAGCTGTTGGAGGGAAGTTCAAGTGG  
16 0 0 CCGACCTGGGATCGAGGACAGTCCCATGGT  
17 0 0 ATGACTTGGTGTTGGCGGTTTTAAGTCCCA  
18 0 0 TACTAGGCTGGTGCGGTTTTGACGCCGT/  
19 0 0 CTACGATGGACGCGGGGAATCAGAACATC  
20 0 0 TATGCTTGGTGTAAGTGGACTCAACCCTAGT  
21 0 0 TACGCTAGACTGGTGCGGTTTTGACGCCGT/  
22 0 0 AATACTCGCTGCTAGATGGCAACGTTTAGTC  
23 1 0 CCGACCAGGGATCGAGGACAGTCCCATGGT  
24 1 0 TGCACTTGGTGTTGGGCCGATTAGCTTCAGT  
25 1 0 TGCACTTGGTATTGGGCCGATTAGGTTCA  
26 0 0 CCGTCCAGGGATCGAGGACAGTCCCATGGT  
27 0 0 TACTAGACTGGTGCGATTTTGACGCCGT/  
28 0 0 TCGACTAGTAGTTCGGAGCAGCAATGCACT  
29 0 0 ATTACTCGATGTTGGCGATACACAGCCAGC  
30 0 0 TGCACTTGGTGTTGGGCCGATTAGGTTCA  
31 0 0 ATGACTCGATGTTGGCGATACACAGCCAGC  
32 0 0 TTGACTCGATGTTGGCGATACACAGCCAGC  
33 0 0 CCGACCAGGGATCGAGGACAGTCCCATGAT  
34 0 0 TCAACTAGGTGTTGGGAGGGTTAAACCTTT  
35 0 0 TCGACTAGTCGTTTCGGAGCAGCAATGCACT/  
36 0 0 TCGACTAGTCGTTTCGGAGCAGCAATGCACT/  
37 0 1 GTTACTAGCTGTTGGGAGTAATTTCAAGTGG  
38 0 1 TATTCTTGGTGTAAGTGGACTCAACCCTAGT  
39 0 1 TCAACTAGGTGTTGGGAGTGTTAAACCTTT  
40 0 1 GATACTAGCTGTTGGAGGAACTTCAGAGG  
41 0 1 TATACTTGGTGTAAGTGGACACAACCCTAGT  
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4	0	1 GGTACTAGCTGTTGGAGGAACTTCAGTGG
5	0	1 GATACTAGCTGTTGGAGCAAACCTTCAGTGG
6	0	1 CCGACTAGGGATCGAGGACAGTCCCATGGT
7	0	1 GATACTAGCTGTTGGGAGTAAATTCAGTGG
8	0	1 ATTACTCGGTGCTAGCGATATACGGCTAGT
9	0	1 GATACTAGCTGTTGGAAGAACTTCAGTGG
10	0	1 TGCACTTGGTGTGGGCCGATTAGGTTCAG,
11	0	
12	0	1 GATACTAGCTGTCTGGGAGTAATTTTCAGTGG
13	0	
14	373563	463918
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For Peer Review

taxon_data	long	long_total	long_this	support	confidence
g	GTAGTCCACG	18	18	2271	0.99647732
g	GTAGTCCACG	12	12	244	0.9795082
g	CTAGTCTTAA	12	12	29	0.89655172
g	GTAGTCCACG	12	12	42	1
g	GTAGTCCACG	12	12	535	0.97570093
GCC	CTAGTCTTAA	8	8		
g	GTAGTCCACG	10	10	713	0.99298738
g	GTAGTCTTAA	12	12	3	1
g	GTAGTCCACG	12	12	207	0.98067633
g	GTAGTCTATG	11	11	10	1
g	GTAGTCCACG	12	12	3	1
g	GTAGTCCACG	12	12	300	0.99
g	GTAGTCCACG	12	12	564	0.94858156
g	GTAGTCCACA	10	10	2	1
AGA	GTAGTCTCAA	10	10		
g	GTAGTCCACG	12	12	4	1
CTA	GTAGTCCACG	8	8		
g				24	0.91666667
g	GTAGTCCACG	12	12	32	1
f	GTAGTCCGCA	7	6	2	1
f	GTAGTCCACA	12	12	4	1
ATC	GTAGTCCACG	10	10		
CGA	GTAGTCTCAA	7	7		
g	GTAGTCCACG	12	12	589	0.99151104
GAG	GTAGTCCACG	11	11		
g	GTAGTCCACG	9	9	9	1
o	GTAGTCCTAG	12	12	2	1
GG	GTAGTCCACG	12	12		
p	CTAGTTCTGA	6	6	3	1
g	GTAGTCTTAA	8	8	17	1
f	GTAGTCCACA	12	12	10	1
GGC	GTAGTCCGCA	11	11		
g	GTAGTCCACG	12	12	37	1
CACA	GTAGTCCCAG	7	7		
g				91	0.96703297
g	GTAGTCCACG	12	12	176	1
f	GTAGTCCACA	12	12	4	1

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4	ATC	GTAGTCCACG	6	6		
5	f	GTAGTCCACG	12	12	59	0.94915254
6	TAAC	GTAGTCCTAA	8	8		
7	TGA	GTAGTCCAAA	12	12		
8						
9	g				5	1
10	gAC	GTAGTCCACG	6	6		
11	o	GTAGTCCACG	12	12	5	1
12	CGT	GTAGTCCACG	11	11		
13						
14	g	GTAGTCCACG	5	5	25	1
15	g	CTAGTCTTAA	6	6	36	1
16	g	GTAGTCCACG	12	12	86	1
17	g	GTAGTCCACG	12	12	12	1
18	f	GTAGTCCACA	6	6	2	1
19	ATC	GTAGTCCACG	12	12		
20	f	GTAGTCCACG	8	8	15	1
21	g	GTAGTCCACG	12	12	246	0.99593496
22	g				10	1
23	g	GTAGTCCACG	12	12	2	1
24	g	GTAGTCCACG	6	6	3395	0.99145803
25	f	GTAGTCCGCA	12	12	6	1
26	f				25	1
27	f	GTAGTCCACG	12	12	5	0.8
28	CA	GTAGTCCTAG	12	12		
29	TGA	GTAGTCTCAA	12	12		
30	GGG	GTAGTCCTAG	12	12		
31	TTT	GTAGTCCCAG	6	6		
32	ATG	GTAGTCTTAA	12	12		
33	g	GTAGTCCACG	12	12	24	1
34	gCC	GTAGTCCACG	9	9		
35	ACT	GTAGTCTTGA	12	12		
36	GG	GTAGTCCTAG	12	12		
37	c	GTAGTCTCAA	12	12	4	1
38	g				7000	0.95485714
39	TTG	GTAGTCCCAG	7	7		
40	TAG	GTAGTCCACG	12	12		
41	g	GTAGTCCACG	8	8	116	0.99137931
42	g	GTAGTCCACG	12	12	68	0.97058824
43	TCG					
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f	GTAGTCCGCA	6	6	8	1
ATC	GTAGTCCACG	12	12		
o	GTAGTCCTGG	12	12	26	1
g	GTAGTCCACG	12	12	3	1
o	GTAGTCCACG	12	12	11	0.90909091
g				8	1
o	GTAGTCCACG	9	9	30	0.96666667
GC	GTAGTCCACG	7	7		
GGG	GTAGTCCTAG	6	6		
TTT	GTAGTCCCAG	7	7		
p	GTAGTCTTAA	12	12	4	1
AATT	GTAGTCCCAG	6	6		
g				57	1
GG	GTAGTCCACG	6	6		
CGC	GTAGTCCACG	12	12		
g				547	0.99268739
CA	GTAGTCCACA	6	6		
f	GTAGTCCACG	12	12	8	1
ATA	GTAGTCTTAA	12	12		
g				49	1
g	GTAGTCCACG	6	6	96	1
GCT	GTAGTCCACG	6	6		
AG	GTAGTCCACG	7	7		
g	GTAGTCCACG	12	12	110	1
g	GTAGTCCACG	12	12	126	0.93650794
g	GTAGTCCACG	9	9	4199	0.87639914
g	GTAGTCCACG	12	12	6	1
GTG	GTAGTCCATG	7	7		
GC	GTAGTCCACG	9	9		
ATGA	GTAGTCTTAA	6	6		
g	GTAGTCCACG	12	12	896	1
g				11	1
ATAC	GTAGTCCCAG	6	6		
g	GTAGTCCACG	8	8	6	1
f	GTAGTCCACG	12	12	2	1
g	GTAGTCCACG	8	8	5	1
ATC	GTAGTCCCAG	6	6		
g	GTAGTCCACG	9	9	63	0.98412698

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4	CCA	GTAGTCCACA	6	6		
5	g				599	0.99165275
6	f	GTAGTCCACG	12	12	16	0.9375
7						
8	g	GTAGTCCACG	6	6	21	0.80952381
9	g	GTAGTCCACA	6	6	76	0.98684211
10						
11	c				7	1
12	CGG	GTAGTCCACG	6	6		
13	icGG	GTAGTCCACG	12	12		
14						
15	GGT	GTAGTCCTAG	12	12		
16	TGC	GTAGTCCTAG	6	6		
17						
18	f	GTAGTCCACG	6	6	2	1
19	TAT					
20						
21	g	GTAGTCCACG	12	12	564	0.99468085
22	AGAA	GTAGTCCCAG	6	6		
23	igCT	GTAGTCCCAA	11	11		
24						
25	f	GTAGTCCACG	11	11	13	0.92307692
26	f	GTAGTCCACG	6	6	8	1
27						
28	TCC	GTAGTCTTAA	6	6		
29	f				15	1
30	p	GTAGTCCATG	7	7	2	1
31	iac	GTAGTCCACG	6	6		
32						
33	g				755	0.99337748
34	o	GTAGTCCACG	6	6	3	1
35						
36	TA	GTAGTCCACG	12	12		
37	f	GTAGTCCACG	12	12	5	1
38						
39	f	GTAGTCCACG	6	6	41	0.92682927
40	ATC	GTAGTCCACG	6	6		
41						
42	g	GTAGTCCTGG	7	7	38	1
43	g	GTAGTCCACG	12	12	29	1
44						
45	p	CTAGTTCAAA	12	12	3	1
46	o				49	0.95918367
47	AAA					
48						
49	f	GTAGTCCACG	6	6	2	1
50	g	GTAGTCCACG	6	6	4	1
51	GTG	GTAGTCCACG	8	8		
52						
53	CCG	GTAGTCCTAG	6	6		
54	CTC	GTAGTCCAAC	6	6		
55						
56	GT	GTAGTCCACG	6	6		
57						
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3						
4	f	GTAGTCCACG	12	12	3	1
5	g	GTAGTCCACG	12	12	115	1
6	o	GTAGTCCCAG	6	6	2	1
7						
8	GTC	GTAGTCCACA	9	9		
9	f	GTAGTCCACG	9	9	3	1
10	f	GTAGTCCACG	6	6	2	1
11						
12	g				32	1
13	CTG	GTAGTCCACG	7	7		
14	f	GTAGTCCGCA	6	6	3	1
15						
16	f	GTAGTCCACG	12	12	11	1
17	f	GTAGTCCACA	6	6	2	1
18						
19	g	GTAGTCCACG	6	6	59	0.98305085
20	TCG	GTAGTCCACG	6	6		
21						
22	g				1184	0.80152027
23	c				20	1
24						
25	g	GTAGTCCACG	12	12	1199	0.96747289
26	CTAT	GTAGTCTTAA	12	12		
27						
28	GAG	GTAGTCCACG	6	6		
29	f	GTAGTCCACG	12	12	20	1
30	CTG	GTAGTCCACG	6	6		
31	f	GTAGTCCACG	12	12	4	1
32	f	GTAGTCCACA	12	12	2	1
33						
34	f				111	0.99099099
35						
36	o	GTAGTCCACG	6	6	34	0.97058824
37	AAT	GTAGTCTTAA	6	6		
38						
39	ATC					
40	o	GTAGTCCTAG	6	6	8	1
41						
42	GGT	GTAGTCCTAG	12	12		
43	o	GTAGTCCACG	12	12	3	1
44	g	GTAGTCCACG	12	12	2	1
45	o	GTAGTCCACG	12	12	2	1
46						
47	CTG	GTAGTCCACG	9	9		
48						
49	g				13	1
50	g				73	1
51	TC	GTAGTCCACG	6	6		
52						
53	g	GTAGTCCACG	7	7	4	1
54	g	GTAGTCCACG	6	6	2	1
55						
56	TG	GTAGTCCTG	6	6		
57						
58						
59						
60						



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2						
3						
4	GGC	GTAGTCCACG	8	8		
5	g	GTAGTCCACG	12	12	225	1
6	ATG	GTAGTCTTAA	12	12		
7						
8	GGG	GTAGTCCTAG	6	6		
9	c	GTAGTCCTAG	12	12	9	1
10	g	GTAGTCCACG	12	12	633	0.99842022
11	f	GTAGTCCACG	6	6	3	1
12						
13	g	GTAGTCCACG	9	9	784	0.99617347
14						
15	g	GTAGTCCACG	11	11	15	1
16	CGC	GTAGTCCACA	6	6		
17						
18	GG	GTAGTCCACG	11	11		
19	p	GTAGTCCTAG	6	6	2	1
20						
21	f	GTAGTCCACG	6	6	14	1
22	g	GTAGTCCACG	12	12	23	0.91304348
23	TT	GTAGTCCACA	6	6		
24						
25	g	GTAGTCCACG	11	11	3	1
26	g	GTAGTCCGCA	12	12	11	1
27						
28	f	GTAGTCCACG	11	11	5	0.8
29	CTG	GTAGTCCACG	12	12		
30						
31	g	GTAGTCCACG	7	6	47	1
32	g	GTAGTCCACG	6	6	11	1
33	GCC	GTAGTCCACG	6	6		
34						
35	g	GTAGTCCACA	6	6	4	1
36	CA	GTAGTCCTAG	12	12		
37						
38	o	GTAGTCCACG	6	6	3	1
39	g	GTAGTCCACG	12	12	20	0.9
40	GTT	GTAGTCCATG	6	6		
41						
42	CT	GTAGTCCTAG	6	6		
43	CAG	GTAGTCCATG	6	6		
44						
45	GGT	GTAGTCCTAG	6	6		
46	CCT	GTAGTCCACA	6	6		
47	GTG	GTAGTCCACG	6	6		
48						
49	g	GTAGTCCACG	11	11	19	1
50	g	GTAGTCCACG	6	6	104	0.97115385
51						
52	g	GTAGTCCACG	12	12	19	1
53	g	GTAGTCCACG	12	12	3385	0.88094535
54	f	GTAGTCCACG	6	6	44	0.95454545
55						
56	f	GTAGTCCACG	6	6	2	1
57						
58						
59						
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CGG	GTAGTCCACG	6	6		
TA	GTAGTCCACG	11	11		
GTG	GTAGTCCACG	6	6		
f	GTAGTCCACG	6	6	64	0.890625
g	GTAGTCCACG	6	6	37	1
AC	GTAGTCCACG	6	6		
c				27	1
g	GTAGTCCACG	6	6	261	0.97318008
AG	GTAGTCCACG	12	12		
f	GTAGTCCACG	12	12	5	0.8
g	GTAGTCCACG	6	6	38	1
c	GTAGTCCTGG	6	6	20	1
g	GTAGTCCACG	6	6	3	1
g				86	1
TT	GTAGTCTACA	6	6		
ATC	GTAGTCCACG	6	6		
AAAA	GTAGTCCCAG	6	6		
f	GTAGTCCACG	6	6	8	1
o	GTAGTCCTAG	6	6	8	1
g	GTAGTCCACG	6	6	29	1
TAA					
g	GTAGTCCACG	6	6	3	1
GC	GTAGTCCACG	7	7		
g	GTAGTCCACG	12	12	294	0.9829932
f	GTAGTCCACG	6	6	4	1
ACG	GTAGTCTTAA	6	6		
TA	GTAGTCCACG	12	12		
CCA					
f	GTAGTCCACG	6	6	7	1
g	GTAGTCCACA	7	6	41	0.97560976
g	GTAGTCCACG	12	12	35	0.94285714
g	GTAGTCCACG	12	12	3	1
TGA	GTAGTCTTAT	12	12		
f	GTAGTCCACG	6	6	20	1
g	GTAGTCCACG	6	6	15	1
g				159	1
GGT	GTAGTCCACG	11	11		
c	GTAGTCCTAG	6	6	13	1

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4	g	GTAGTCCACG	6	6	2	1
5	gTA	GTAGTCCACG	6	6		
6	TCG	GTAGTCCACG	12	12		
7						
8	f	GTAGTCCACG	6	6	234	0.96153846
9	GGC	GTAGTCCACA	12	12		
10						
11	gTA	GTAGTCCACG	12	12		
12	g	GTAGTCTTAA	11	11	44	1
13	ACC	GTAGTCCACG	12	12		
14						
15	TT	GTAGTCTATT	6	6		
16	CGG	GTAGTCCACG	12	12		
17						
18	.GG	GTAGTCCAAC	6	6		
19	TCC	GTAGTCCACG	7	7		
20						
21	CCG	GTAGTCCACG	6	6		
22	iTA	GTAGTCCACG	6	6		
23						
24	c				15	1
25	ATT	GTAGTCCACG	6	6		
26	g	GTAGTCCACG	6	6	3	1
27						
28	g				174	0.92528736
29	f	GTAGTCCACG	10	10	2	1
30	GGTG	GTAGTCCACG	6	6		
31						
32	c	GTAGTCCTAG	6	6	5	1
33	f	GTAGTCCACG	6	6	3	1
34						
35	g	GTAGTCCACG	6	6	3	1
36	o	GTAGTCCACG	6	6	3	1
37	iGC	GTAGTCCACG	12	12		
38						
39	f	GTAGTCCACG	12	12	4	1
40	f	GTAGTCCACG	11	11	38	1
41						
42	g				74	1
43	g	GTAGTCCATG	7	6	156	0.98717949
44	TGG	GTAGTCCACA	6	6		
45						
46	f				16	0.8125
47	f	GTAGTCCACG	10	10	4	1
48						
49	g	GTAGTCTTAA	6	6	8	1
50	g	GTAGTCCACG	11	11	51	0.98039216
51						
52	gAC	GTAGTCCAAA	6	6		
53	o	GTAGTCCACG	6	6	2	1
54	ATT	GTAGTCCACG	12	12		
55						
56	c	GTAGTCCTAG	6	6	375	0.99733333
57						
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59						
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3							
4	TAT						
5	TAT	GTAGTCTTAA	7	7			
6	CCG	GTAGTCCACG	12	12			
7							
8	ATC	GTAGTCCACG	12	12			
9	g	GTAATCCTAG	6	6	3		1
10	f	GTAGTCCAAC	11	11	4		1
11							
12	g	GTAGTCCACG	6	6	6		1
13	f				8		1
14							
15	TGG	GTAGTCCACG	6	6			
16	g	GTAGTCCACG	6	6	9		1
17							
18	GGT	GTAGTCCTAG	6	6			
19	g	GTAGTCCACG	12	12	452	0.80309735	
20	ATC	GTAGTCCACG	12	12			
21							
22	CTG						
23							
24	TAT						
25	g	GTAGTCCACG	6	6	5		1
26	g	GTAGTCCACG	5	5	211	0.94312796	
27							
28	TCA	GTAGTCCTAA	6	6			
29	g	GTAGTCCACG	12	12	3		1
30	f	GTAGTCCACG	11	11	25		1
31							
32	f	GTAGTCCACG	6	6	27	0.96296296	
33	f	GTAGTCCACG	6	6	2		1
34							
35	TAG	GTAGTCCACG	12	12			
36	f	GTAGTCCACG	10	10	2		1
37	ACT	GTAGTCCACG	6	6			
38							
39	g	GTAGTCCACG	6	6	56	0.96428571	
40	f	GTAGTCCACG	6	6	3		1
41							
42	g	GTAGTCCACG	12	12	820	0.9402439	
43	ATC	GTAGTCCACG	10	10			
44							
45	g				288		1
46	ATA	GTAGTCCACG	12	12			
47							
48	o	GTAGTCCACG	7	7	17		1
49	f	GTAGTCCACG	12	12	9		1
50	GTG	GTAGTCCACG	5	5			
51							
52	g	GTAGTCCACG	7	7	349	0.99426934	
53	f	GTAGTCCACG	6	6	19		1
54							
55	g	GTAGTCCATG	9	9	155	0.9483871	
56	c	GTAGTCCTAG	6	6	3		1
57							
58							
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4	f	GTAGTCCACG	6	6	14	1
5	g				1378	0.99492017
6	f	GTAGTCCACG	11	11	3	1
7	f	GTAGTCCACG	6	6	13	1
8						
9	AGT	GTAGTCCACG	12	12		
10	f	GTAGTCCACG	12	12	3	1
11						
12	ATG	GTAGTCCATG	6	6		
13	T CCT	GTAGTCCTAG	6	6		
14						
15	g	GTAGTCCACG	12	12	6	1
16	GTG	GTAGTCCACG	6	6		
17						
18	g	GTAGTCTCTA	12	12	8	1
19	o	GTAGTCCACG	12	12	3	1
20						
21	o	GTAGTCCACG	6	6	82	0.96341463
22	f	GTAGTCCACG	6	6	3	1
23	g	GTAGTCCACG	5	5	5	1
24						
25	g	GTAGTCCACG	6	6	315	0.98095238
26	GGTG	GTAGTCCACG	7	7		
27						
28	f	GTAGTCCACG	6	6	4	1
29	GC	GTAGTCCACG	6	6		
30						
31	g	GTAGTCCACG	12	12	83	1
32	GGG	GTAGTCTCAA	6	6		
33	ATGA	GTAGTCTCTA	6	6		
34						
35	CCG	GTAGTCCACG	7	7		
36	f	GTAGTCCGCA	12	12	4	1
37	AGT	GTAGTCCACA	6	6		
38						
39	g	GTAGTCCACG	6	6	53	1
40	ATTC	GTAGTCCATG	6	6		
41						
42	GTG	GTAGTCCACG	6	6		
43	f	GTAGTCCACG	6	6	7	1
44						
45	g	GTAGTCCACG	6	6	6	1
46	TA	GTAGTCCACG	6	6		
47	GTG	GTAGTCCACG	6	6		
48						
49	GTG	GTAGTCCACA	6	6		
50	TCA	CTAGTCTTAA	6	6		
51						
52	GTG	GTAGTCCACG	6	6		
53	GG	GTAGTCCACG	11	11		
54						
55	g	GTAGTCCACG	12	12	12190	0.9973749
56	TAC	GTAGTCCATG	6	6		
57						
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59						
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3						
4	iTG	GTAGTCCACG	6	6		
5	g	GTAGTCCACG	12	12	7	0.85714286
6	gGTG	GTAGTCCACG	6	6		
7						
8	CCA	GTAGTCCACA	6	6		
9	f	GTAGTCCATG	6	6	2	1
10	f	GTAGTCCTGG	6	6	5	1
11						
12	TCC	GTAGTCCTAG	12	12		
13	o	GTAGTCCACG	6	6	125	0.96
14	f	GTAGTCCATG	7	7	5	1
15						
16	iTC	GTAGTCCACG	6	6		
17						
18	g	GTAGTCCTGG	6	6	16	1
19	c	GTAGTCCACG	6	6	3	1
20						
21	GG	GTAATCCTAG	6	6		
22	o				22	0.95454545
23	GG	GTAGTCCACG	12	12		
24	f	GTAGTCCACG	12	12	3	1
25						
26	CTG	GTAGTCCACG	12	12		
27	c	GTATTCCTGG	12	12	33	0.90909091
28	g	GTAGTCCACG	11	11	3	1
29	g	GTAGTCCACG	12	12	180	0.98888889
30	p	GTAGTCCACG	6	6	16	0.875
31	ATT	CTAGTCTTAA	6	6		
32	f	GTAGTCCACG	6	6	69	0.91304348
33	GTG	GTAGTCCATG	6	6		
34	AG	GTAGTCCACG	6	6		
35	TGG	GTAGTCCACG	6	6		
36	AG	GTAGTCCACG	10	10		
37	ATGA	GTAGTCTTAA	6	6		
38	f	GTAGTCCACG	6	6	43	0.90697674
39	g	GTAGTCCACG	12	12	7	1
40	g	GTAGTCCACG	6	6	2	1
41	GT	GTAGTCCACG	7	7		
42	iTA	GTAGTCCACG	6	6		
43	g	GTAGTCCACA	6	6	310	0.99354839
44	gTC	GTAATCCACG	6	6		
45	GGT	GTAGTCCACG	6	6		
46	p	GTAGTCCACG	6	6	28	0.96428571
47	gGTG	GTAGTCCACG	6	6		
48						
49						
50						
51						
52						
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58						
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1						
2						
3						
4	o	GTAGTCCACG	6	6	2	1
5	f	GTAGTCCACG	12	12	4	1
6	CGG	GTAGTCCACG	6	6		
7						
8	iGG	GTAGTCCTAG	6	6		
9						
10	g	GTAGTCCACG	12	12	2	1
11	o	GTAGTCCATG	7	7	2	1
12	c	GTAGTCCACG	12	12	3	1
13	g	GTAGTCCACG	12	12	23	0.95652174
14						
15	TCT	GTAGTCCACG	8	8		
16	GG	GTAGTCCACG	12	12		
17						
18	f	GTAGTCCACG	6	6	10	1
19	g	GTAGTCCACG	6	6	886	0.996614
20						
21	g	GTAGTCCTAG	12	12	3	1
22	AA	GTAGTCTTAA	6	6		
23						
24	CTG	GTAATCCACG	12	12		
25	ATC	GTAGTCCACG	8	8		
26	o	GTAGTCCTGG	6	6	14	1
27	f	GTAGTCCACG	7	7	2	1
28						
29	g	GTAGTCCACG	6	6	196	1
30	TTTC	GTAATCCTAG	6	6		
31						
32	f	GTAGTCCACG	6	6	16	1
33	g	GTAGTCCACA	10	10	2	1
34						
35	CGG	GTAGTCCACG	12	12		
36	c	GTAGTCCACG	12	12	21	1
37	GAC	GTAGTCCGCA	11	11		
38						
39	p	GTAGTCCACG	6	6	3	1
40	o	GTAGTCCACG	6	6	73	0.91780822
41						
42	g	GTAGTCCACG	6	6	106	0.94339623
43	AAG	GTAGTCTTAA	6	6		
44						
45	TAT					
46	g	GTAGTCCACG	6	6	6924	0.99581167
47	f	GTAGTCCACG	6	6	2	1
48						
49	f	GTAGTCCTGG	8	8	9	0.88888889
50	GCC	GTAGTCCATG	6	6		
51	GG	GTAGTCCACG	6	6		
52						
53	GT	GTAGTCCACG	6	6		
54	ATC	GTAGTCCACG	7	7		
55						
56	g	GTAGTCCACG	6	6	2	1
57						
58						
59						
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2						
3						
4	GG	GTAGTCCACG	5	5		
5	f	GTAGTCCACG	7	7	56	1
6	TAT					
7	TAT					
8						
9	c	GTAGTCCTGG	6	6	8	1
10	o	GTAGTCCACG	8	8	10	0.9
11						
12	CAG	GTAGTCCACG	6	6		
13	g	GTAGTCCACG	10	10	248	0.99193548
14	GTT	GTAGTCCACA	6	6		
15	GG	GTAGTCCACG	6	6		
16						
17	TAT					
18						
19	g	GTAGTCCACG	7	7	159	0.97484277
20	g	GTAGTCCACG	9	9	3	1
21	g	GTAGTCCACG	7	7	8	0.875
22						
23	TTT	GTAGTCCTAG	11	11		
24	g	GTAGTCCACG	7	6	12	0.91666667
25	g	GTAGTCTTAA	6	6	13	1
26	g	GTAGTCCACG	6	6	20	0.95
27	p	GTAGTCCACG	6	6	2	1
28	f	GTAGTCCACG	6	6	3	1
29						
30	GTT	GTAGTCCACG	7	7		
31	g	GTAGTCCACG	6	6	1566	0.9559387
32	g	GTAGTCCACG	12	12	4	1
33	f	GTAGTCCACG	6	6	3	1
34	p				5	0.8
35	o	GTAGTCCACG	10	10	16	1
36	AG	GTAGTCCGCA	6	6		
37	GTG	GTAGTCCACG	6	6		
38	TA	GTAGTCCACG	6	6		
39	TA	GTAGTCCACG	6	6		
40	TA	GTAGTCCACG	6	6		
41	TA	GTAGTCCACG	6	6		
42	GG	GTAGTCCACA	6	6		
43	AC	GTAGTCTTAA	5	5		
44	p	GTAGTCCATG	6	6	13	1
45	TAA	GTAGTCCTAA	12	12		
46	f	GTAGTCCACG	12	12	8	1
47	g	GTAGTCTTAA	5	5	11	1
48	TCCC	GTAGTCCTAG	11	11		
49						
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51						
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2						
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4	g	GTAGTCCACG	8	8	893	0.96976484
5	.TCT	GTAGTCCTAG	6	6		
6	g	GTAGTCCACG	6	6	6	1
7	f	GTAGTCCACG	6	6	7	1
8						
9	CCG	GTAGTCCACG	6	6		
10	iTA	GTAGTCCACG	6	6		
11						
12	o	GTAGTCCACG	6	6	9	0.88888889
13	g	GTAGTCCACG	7	7	37	1
14						
15	g				7	1
16	.TTA	GTAGTCTTAA	6	6		
17	f	GTAGTCCACA	6	6	2	1
18						
19	TAG	GTAGTCCACG	6	6		
20	f	GTAGTCCACG	6	6	14	1
21	f	GTAGTCCACG	6	6	2	1
22						
23	TAG	GTAGTCCACA	4	4		
24	.CA	GTAGTCCATG	6	6		
25						
26	g	GTAGTCTCTA	8	8	23	1
27	.CGG	GTAGTCCATG	6	6		
28						
29	c	GTAGTCCTAG	12	12	15	1
30	g	GTAGTCCACG	6	6	441	0.98185941
31	g	GTAGTCCACG	6	6	5	0.8
32	g	GTAGTCCATG	5	5	6	1
33						
34	.CCC	GTAATCCTAG	6	6		
35						
36	TCG					
37	.TTA	GTAGTCTTAA	6	6		
38	f	GTAGTCCACG	6	6	4	1
39						
40	GAG					
41	g				3	1
42	f	GTAGTCCACG	12	12	25	1
43						
44	.GGG	GTAGTCCTAG	6	6		
45	ACG	GTAGTCCTAG	12	12		
46						
47	ATT					
48	AGT	GTAGTCCACG	12	12		
49	TAT	GTAGTCTTAA	6	6		
50	g	GTAGTCCACG	6	6	4	1
51	CG	GTAGTCCACG	6	6		
52						
53	c	GTAGTCCTAG	6	6	25	1
54	g	GTAGTCCACG	6	6	6	1
55						
56						
57						
58						
59						
60						

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2							
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4	g	GTAGTCCACG	6	6	37		1
5	f				4		1
6	g	GTAGTCCACG	12	12	6		1
7	GT	GTAGTCCACG	6	6			
8	CGG	GTAGTCCACG	6	6			
9	g	GTAGTCCTGG	12	12	44		1
10	TT	GTAGTCCACG	5	5			
11	g	GTAGTCCACG	6	6	2		1
12	f	GTAGTCCACG	6	6	2		1
13	ACG	GTAGTCTTAA	6	6			
14	f	GTAGTCCACG	6	6	12		1
15	f				17		1
16	AGT	GTAGTCCACG	11	11			
17	ATC	GTAGTCCACG	6	6			
18	g				6		1
19	CCG	GTAGTCCACG	6	6			
20	g	GTAGTCCACG	6	6	5		1
21	g				7		1
22	CGG	GTAGTCCACG	7	7			
23	g	GTAGTCCACG	6	6	17		1
24	o	GTAGTCCTAG	6	6	3		1
25	AA	GTAGTCCACG	6	6			
26	GAA	GTAGTCCTAA	6	6			
27	GTG	GTAGTCCACG	6	6			
28	CTG	GTAGTCCTTG	7	7			
29	GTG	GTAGTCCACG	6	6			
30	CTG						
31	GG	GTAGTCCACG	7	7			
32	CTGG	GTAGTCCACG	6	6			
33	CTG						
34	ACC	GTAGTCTTAA	5	5			
35	f	GTAGTCCACG	10	10	6		1
36	g	GTAGTCCACG	6	6	62	0.91935484	
37	TTG	GTAGTCCACG	6	6			
38	g	GTAGTCCACG	7	7	397	0.94710327	
39	CCG	GTAGTCCTAG	6	6			
40	f				7		1
41	g	GTAGTCCACG	6	6	73	0.98630137	
42							
43							
44							
45							
46							
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48							
49							
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54							
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1						
2						
3						
4	g	GTAGTCCATG	6	6	6	1
5	GC	GTAGTCCACG	10	10		
6	g	GTAGTCCACG	7	6	5361	0.99981347
7						
8	TAG					
9	TA	GTAGTCCACG	11	11		
10						
11	g	GTAGTCCACG	6	6	2	1
12	g	GTAGTCCTTG	8	8	2	1
13						
14	TTA					
15	TA	GTAGTCCACG	6	6		
16						
17	g	GTAGTCCACG	9	9	2144	0.99113806
18	g	GTAGTCCACG	11	11	2	1
19	c	GTAGTCCTAG	6	6	3	1
20						
21	CCG	GTAGTCCACG	6	6		
22	g	GTAGTCCACG	11	11	122	1
23						
24	p				3	1
25	CGG	GTAGTCCCTA	6	6		
26	c	GTAGTCCACG	12	12	2	1
27						
28	p	GTAATCCTAG	6	6	6	1
29	f	GTAGTCCACG	7	7	8	1
30	o	GTAGTCCACG	10	10	33	1
31						
32	TGAG	GTAGTCTCAA	6	6		
33	TC	GTAGTCCACG	12	12		
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35	TC	GTAGTCCTAG	6	6		
36	GC	GTAGTCCACG	9	9		
37	f	GTAGTCCACG	10	10	2	1
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39	TAT	GTAGTCTTAA	5	5		
40	CGC	GTAGTCCACG	6	6		
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42	g	GTAGTCCACG	12	12	6960	0.99813218
43	GAC	GTAGTCGCAA	5	5		
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45	g	GTAGTCCACG	6	6	62	0.98387097
46	g	GTAGTCCACG	6	6	6	1
47	f	GTAGTCCTAG	10	10	47	1
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49	GGC	GTAGTCCACG	5	5		
50	g	GTAGTCCACG	10	10	5	1
51	CTG	GTAGTCCACG	6	6		
52						
53	g	GTAGTCCACG	9	9	2	1
54	g	GTAGTCCACG	12	12	10	1
55	f	GTAGTCCACG	6	6	3	1
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3	GGT					
5	g	GTAGTCCATG	6	6	13	1
6	g	GTAGTCCACG	6	6	47	1
8	g	GTAGTCCACA	5	5	8	1
9	TAG	GTAGTCCACG	6	6		
11	TGT	GTAGTCCACG	6	6		
12	g	GTAGTCCACG	6	6	5	0.8
14	o	GTAGTCCACA	6	6	6	1
15	GGT	GTAGTCCACG	6	6		
16	CGGG	GTAGTCCACG	6	6		
18	CGC	GTAGTCCACG	6	6		
19	g	GTAGTCCACG	6	6	22	0.86363636
20	CTG	GTAGTCCTTG	6	6		
22	GTG	GTAGTCCACG	6	6		
23	ACT	GTAGTCCTGG	7	7		
25	GG	GTAGTCCTAG	7	7		
26	TCA	GTAGTCCTAA	6	6		
28	f	GTAGTCCACG	5	5	2	1
29	g	GTAGTCCACA	6	6	5	1
30	g	GTAGTCCTGG	12	12	21	1
32	g	GTAGTCCTAA	7	6	53	1
33	TCC	GTAGTCCACG	6	6		
34	o	GTAGTCCACG	6	6	6	1
36	c	GTAGTCCTAG	6	6	6	1
37	TAG	GTAGTCCACG	12	12		
39	g				36	1
40	CGG	GTAGTCCACG	6	6		
42	g	GTAGTCCACG	6	6	3	1
43	g	GTAGTCCACG	12	12	55	0.92727273
45	CGAG	GTAGTCCACG	6	6		
46	CAG					
47	TA	GTAGTCCACG	8	8		
49	g	GTAGTCCTGG	6	6	2	1
50	f	GTAGTCCTAG	7	7	2	1
52	CG	GTAGTCCACG	6	6		
53	f	GTAGTCCTGG	7	7	142	0.98591549
54	GA	GTAGTCCACG	9	9		
56	ATC	GTAGTCCACG	6	6		

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4	5TC	GTAGTCCATG	6	6		
5	g	GTAGTCCACG	6	6	2	1
6	g	GTAATCCTAG	12	12	2	1
7	p	CTAGTTCCAA	6	6	12	1
8	CAT	CTAGTCTTAA	6	6		
9	CCG	GTAGTCCACG	10	10		
10	CGA	GTAGTCTCAA	6	6		
11	GGG	GTAGTCCTGG	6	6		
12	GGC	GTAGTCCGCA	6	6		
13	f	GTAGTCCACG	6	6	3	1
14	ATC	GTAGTCCACG	9	9		
15	5TCG	GTAGTCCACG	10	9		
16	GCGCT	GTAGTCTCGA	6	6		
17	CTG					
18	g	GTAGTCCACG	5	5	78	0.98717949
19	TA	GTAGTCCACG	6	6		
20	TCC	GTAGTCCTAG	10	10		
21	GG	GTAGTCCACG	6	6		
22	AA	GTAGTCCACG	6	6		
23	CTG	GTAGTCCTTG	7	7		
24	CTG					
25	CGG	GTAGTCCTGG	12	12		
26	f				20	1
27	CGG	GTAGTCCACG	6	6		
28	c	GTAGTCTACG	12	12	2	1
29	f				2	1
30	GAA	GTAGTCCTAA	10	10		
31	g	GTAGTCCCAA	5	5	44	1
32	g	GTAGTCCTAG	6	6	5	0.8
33	g	GTAGTCCACG	7	7	117	0.97435897
34	f	GTAGTCCACG	7	7	2	1
35	CAG	GTAGTCCACG	6	6		
36	CAT	CTAGTCTTAA	7	7		
37	GAA					
38	g	GTAGTCCACG	6	6	26	0.92307692
39	f	GTAGTCCACG	6	6	51	0.98039216
40	g				12	1
41	AC					
42						
43						
44						
45						
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4	g	GTAGTCTTGG	6	6	3	1
5	GCC	GTAGTCCACG	6	6		
6	AG	GTAGTCCACG	5	5		
7						
8	.CC					
9	GC	GTAGTCCACG	6	6		
10	GTA	GTAGTCCACG	10	10		
11	CGG	GTAGTCCACG	6	6		
12						
13	.CGG	GTAGTCCATG	7	7		
14						
15	g	CTAGTCTTAA	6	6	4	1
16	GTG	GTAGTCTTAA	6	6		
17						
18	TAT	GTAGTCTTAA	6	6		
19	AGT	GTAGTCCACG	12	12		
20	CAT	CTAGTCTTAA	6	6		
21						
22	CTG	GTAGTCCTAG	8	8		
23	f	GTAGTCCATG	6	6	4	1
24						
25	ACC	GTAGTCCACG	7	7		
26	c	GTAGTCCACG	6	6	6	1
27	TTG	GTAGTCCTAG	5	5		
28	AT	GTAGTCTTAA	6	6		
29	AG	GTAGTCCACG	6	6		
30						
31	TAT					
32						
33	ATC	GTAGTCCACG	6	6		
34	f				2	1
35						
36	g				553	0.99638336
37	g	GTAGTCCACG	6	6	28	0.89285714
38	c	GTAGTCTCAA	5	5	4	1
39						
40	GGT	GTAGTCCACG	6	6		
41	GCG	GTAGTCCACG	6	6		
42						
43	g	GTAGTCCACG	6	6	38	1
44	g	GTAGTCCACG	6	6	19	1
45	c	GTAGTCCACG	7	7	3	1
46						
47	g	GTAGTCCACG	9	9	73	1
48	CAT	CTAGTCTTAA	6	6		
49						
50	ACT	GTAGTCTTAA	5	5		
51	g	GTAGTCCACG	5	5	5	1
52	TT	GTAGTCCACG	3	3		
53						
54	TAT					
55						
56	o	GTAGTCCACG	6	6	8	0.875
57						
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59						
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4	f	GTAGTCCACG	10	10	6	0.83333333
5	f	GTAATCCTAG	6	6	6	1
6	f	GTAGTCCACG	4	4	4	1
7						
8	GGG	GTAGTCCATG	6	6		
9	g	GTAGTCTTAA	4	4	40	1
10	g	GTAGTCCACG	6	6	194	0.9742268
11	g	GTAGTCCACG	6	6	2	1
12	g	GTAGTCCACG	6	6	2	1
13	g	GTAGTCCACG	6	6	3	1
14	g	GTAGTCCACG	6	6	3	1
15	g	GTAGTCCACG	6	6	3	1
16	g	GTAGTCCTGG	7	7	4	1
17						
18	g				3859	0.99559471
19	g				46	0.97826087
20	AGT	GTAGTCCACG	11	11		
21	AGT	GTAGTCCACG	10	10		
22	CCG	GTAGTCCTAG	6	6		
23	o	GTAGTCTTAA	5	5	3	1
24	TAG					
25	g	GTAGTCCACG	5	5	7	1
26	TGC	GTAGTCCACA	4	4		
27	g	GTAGTCTCAA	6	6	53	1
28	ATT	GTAGTCCACG	6	6		
29	f	GTAGTCCATG	10	10	4	1
30	TA	GTAGTCCACG	6	6		
31	c	GTAGTCCACG	6	6	2	1
32	GAG	GTAGTCCACG	6	6		
33	CAT	CTAGTCTTAA	7	7		
34	TAG	GTAGTCCACG	11	11		
35	CAC	GTAGTCCTAG	6	6		
36	TT					
37	TTT	GTAGTCCACG	6	6		
38	g	GTAGTCTTAA	6	6	3	1
39	AG	GTAGTCTACG	6	6		
40	g	GTAGTCCACG	6	6	30	1
41	AC	GTAGTCCACG	6	6		
42	CAG	GTAGTCCTGG	9	9		
43	f				5	1
44	CG	GTAGTCCACG	6	6		
45	CTG	GTAGTCCTCG	10	10		
46						
47						
48						
49						
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51						
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c				34	0.97058824
f	GTAGTCCGCA	6	5	28	1
\CG	GTAGTCCACG	6	6		
f	GTAGTCCACG	10	10	4	1
g	GTAGTCCACG	9	8	2	1
\GTA	GTAGTCCACG	12	12		
GTG	GTAGTCCATG	6	6		
CGG	GTAGTCCACG	4	4		
CT	GTAGTCCACG	6	6		
TAT	CTAGTCTTAA	6	6		
g	GTAGTCCACG	6	6	6	1
g	GTAGTCCACG	7	7	4	1
g	GTAGTCCACG	7	7	2	1
TT					
\CTC	GTAGTCCTAG	11	11		
g	GTAGTCCACA	6	6	140	0.98571429
\AG	GTAGTCCACG	10	10		
GTG	GTAGTCCACG	6	6		
g	GTAGTCCTAG	7	7	12	1
c	GTAGTCCTGG	6	6	7	0.85714286
p	GTAGTCCACG	6	6	2	1
g	GTAGTCCACG	6	6	2	1
g	GTAGTCCACG	6	6	5	1
f	GTAGTCCACG	6	6	12	0.83333333
TAG	GTAGTCCACG	9	9		
o	GTAGTCCATG	6	6	4	1
TG	GTAGTCCTTG	9	9		
g	GTAGTCCACG	8	8	220	1
\AT	CTAGTCTTAA	6	6		
\CT					
.CTT	GTAGTCCTAG	6	6		
g	GTAGTCCACG	6	6	3	1
g	GTAGTCCTGG	8	8	11	1
f	GTAGTCCACG	6	6	9	1
ATG					
g	GTAGTCCACG	6	6	2	1
GGG	GTAGTCCACG	6	6		
f	GTAGTCCACG	6	6	2	1



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3						
4	TAG	GTAGTCCACG	12	12		
5	ATT	GTAGTCCACG	6	6		
6	p				6	1
7						
8	TT	GTAGTCTATT	6	6		
9	TGG	GTAGTCCACG	4	4		
10	GCT	GTAGTCCACG	8	8		
11						
12	g	GTAGTCCTAG	12	11	12	1
13	g	GTAGTCCTGG	6	6	4	1
14	g	GTAGTCCACG	5	5	327	0.9969419
15						
16	ATA	GTAGTCCACG	5	5		
17	GTG	GTAGTCCACG	5	5		
18	GTG	GTAGTCCACG	5	5		
19	GTG	GTAGTCCTAG	5	5		
20	GGT	GTAGTCCACG	6	6		
21						
22	CAG	GTAGTCCTGG	7	7		
23	g	GTAGTCTTAA	2	2	8	1
24						
25	CTG	GTAGTCCACG	10	10		
26	g	GTAGTCCACG	6	6	3	1
27	TGG	GTAGTCCACG	6	6		
28						
29	ATG					
30	g				2	1
31	f	GTAGTCCACG	6	6	8	1
32						
33	g				12	1
34	f	GTAGTCCACG	6	6	4	1
35						
36	CCG	GTAGTCCACG	6	6		
37	g	GTAGTCCACG	3	3	135	1
38	CTG	GTAGTCCACG	4	4		
39	ATC	GTAGTCCACG	6	6		
40						
41	g	GTAGTCCACG	5	5	2	1
42	TGG	GTAGTCCGCC	5	5		
43	g	GTAGTCCACG	4	4	6	0.83333333
44	TGT	GTAGTCCACG	6	6		
45	TAT	GTAGTCTTAA	6	6		
46						
47	g				2	1
48	g	GTAGTCCACG	6	6	24	1
49	o	GTAGTCCACG	7	7	14	1
50						
51	g	GTAGTCCACG	4	4	33	1
52	TAT	GTAGTCTTAA	6	6		
53	AG	GTAGTCCATA	6	5		
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4	GGC	GTAGTCCACG	7	6		
5	ACG	GTAGTCTCAA	4	4		
6	GG	GTAGTCCACG	5	5		
7						
8	GCT					
9	f	GTAGTCCACG	6	6	2	1
10						
11	g	CTAGTCTTAA	3	3	17	1
12	g	GTAGTCCACG	6	6	2	1
13	AGC	GTAGTCCACG	6	6		
14						
15	GG	GTAGTCCACG	6	6		
16	g	GTAGTCCACG	4	4	91	0.98901099
17						
18	TCC	GTAGTCCACG	6	6		
19	TA	GTAGTCCACG	5	5		
20						
21	g	GTAGTCCACG	6	6	191	0.97905759
22	g	GTAGTCCACG	5	5	4	1
23	TAAC	GTAGTCCTAA	6	6		
24						
25	g	GTAGTCCTAG	6	6	2	1
26	CGG	GTAGTCCACG	4	4		
27	GGT	GTAGTCCACG	6	6		
28	TA	GTAGTCCACG	6	6		
29						
30	c				25	1
31						
32	CCG	GTAGTCCACG	8	8		
33	g	GTAATCCTAG	6	6	4	1
34	AG	GTAGTCCACA	5	5		
35						
36	g	GTAGTCCACG	5	5	2	1
37	p	CTAGTTCAAA	7	7	71	1
38						
39	g				184	0.99456522
40	f	GTAGTCCACG	6	6	5	1
41						
42	CTA	GTAGTCCACG	6	6		
43	AG	GTAGTCCACG	6	6		
44	GGA	GTAGTCTTAA	5	5		
45						
46	g				6	1
47	CGC	GTAGTCCACG	6	6		
48	f	GTAGTCCGCA	6	6	3	1
49						
50	GT	GTAGTCCACG	5	5		
51						
52	AG					
53	TTG					
54						
55	o				37	1
56	f	GTAGTCCGCA	5	5	4	1
57						
58						
59						
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4	GTG						
5	CGT	GTAGTCCACG	6	6			
6	GCC	GTAGTCCATA	6	6			
7	TAG	GTAGTCCACG	9	9			
8	TAT	GTAGTCTTAA	6	6			
9	TAG	GTAGTCCACG	10	10			
10	g	GTAGTCCTAG	6	6	2		1
11	AGT	GTAGTCCACG	5	5			
12	TAT						
13	GTG	GTAGTCCATG	7	7			
14	ACT	GTAGTCTCAA	5	5			
15	o	GTAGTCCTGG	5	5	3		1
16	TAT	GTAGTCCTGG	5	5			
17	g	CTAGTCTCAA	6	6	679	0.99410898	
18	g	GTAGTCTTAA	4	4	6		1
19	g				9		1
20	g	GTAGTCTTAA	4	4	63	0.98412698	
21	g	GTAGTCCACG	5	5	217	0.80184332	
22	GTG	GTAATCCCCA	4	4			
23	CCT						
24	o	GTAGTCCTAG	6	6	4		1
25	g	GTAGTCCACG	5	5	5		1
26	g	GTAGTCTCAA	6	6	4		1
27	TAG	GTAGTCCACG	8	8			
28	g	GTAGTCTTAA	5	5	37	0.86486486	
29	TGA	GTAGTCTCTT	8	8			
30	CTG	GTAGTCCTTG	9	9			
31	CGG	GTAGTCCATG	5	5			
32	g	GTAGTCCACG	6	6	8		1
33	TCC	GTAGTCCTAG	6	6			
34	GCG	GTAGTCCACG	5	5			
35	ATA	GTAGTCCACG	5	5			
36	g	GTAGTCCACG	8	8	3		1
37	f	GTAGTCTTAA	5	5	233		1
38	g				48	0.95833333	
39	g				9		1
40	TAG	GTAGTCCACG	5	5			
41	g	GTAGTCCACG	6	6	4		1
42							
43							
44							
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48							
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f	GTAGTCCACG	7	6	2	1
TTG					
g	GTAGTCCACG	4	4	2	1
f	GTAGTCCACG	6	6	8	1
f	GTAGTCCACG	7	7	3	1
CCG					
AA	GTAGTCCACG	5	5		
TA	GTAGTCCACG	5	5		
AAA	GTAGTCTTAA	7	7		
GTG	GTAGTCCACG	6	6		
TCG	GTAGTCCACG	6	6		
o	GTAGTCCACG	5	5	13	0.92307692
f				2	1
g	GTAGTCCTGG	6	6	3	1
GT	GTAGTCCATG	6	6		
g	GTAGTCCACC	6	6	368	0.99728261
TCG	GTAGTCCACG	5	5		
o	GTAGTCCACG	5	5	2	1
o	GTAGTCCTAG	4	4	3	1
CGAC					
ATT	GTAGTCCACG	6	6		
g	GTAGTCCACG	5	5	3	1
GTG	GTAGTCCTAG	6	6		
o	GTAGTCCACG	6	6	46	0.93478261
CAT	CTAGTCTTAA	5	5		
CTCC					
GTG	GTAGTCCACG	5	5		
g	GTAGTCCACG	4	4	575	0.99304348
GTG	GTAGTCCATG	5	5		
CAT	CTAGTCTTAA	4	4		
g				227	0.99559471
CGCC	GTAGTCCACG	7	7		
CGG	GTAGTCCCTA	8	8		
TG	GTAGTCCACG	6	6		
CCG	GTAGTCCACG	4	4		
ACC	GTAGTCTCGA	7	7		
g	GTAGTCCACG	5	5	3	1
o	GTAGTCCACG	5	5	2	1

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4	GGC	GTAGTCCACA	5	5		
5	f	GTAGTCCACG	6	6	6	0.83333333
6	g	GTAGTCCACG	4	4	2	1
7	iTA	GTAGTCCACG	5	5		
8						
9	g	GTAGTCCACG	6	6	4	1
10	TAAC	GTAGTCCTAA	4	4		
11						
12	ICT	GTAGTCTTAA	5	5		
13						
14	ATG					
15	ATG					
16						
17	g				278	1
18	g	GTAGTCCACG	7	7	2	1
19	o	GTAGTCCTAG	5	5	7	1
20						
21	f	GTAGTCCACG	5	5	138	0.96376812
22	GTG	GTAGTCCACG	8	8		
23	g	GTAGTCCACG	4	4	110	0.99090909
24						
25	GTG	GTAGTCCACG	6	6		
26						
27	o				423	0.99763593
28	g	GTAGTCCACG	6	6	9	0.88888889
29	f	GTAGTCCACG	4	4	2	1
30						
31	TG					
32	AGT	GTAGTCCACG	6	6		
33	iTA	GTAGTCCACG	4	4		
34						
35	CTG	GTAGTCCTTG	5	5		
36	IGC	GTAGTCCACG	6	6		
37	iTA	GTAGTCCACG	5	5		
38						
39	AGC	GTAGTCCACG	5	5		
40	g	GTAGTCCACG	5	5	5	1
41						
42	g				10	1
43	IGC	GTAGTCCACA	5	5		
44	CAT	CTAGTCTTAA	5	5		
45						
46	CGG	GTAGTCCACG	6	6		
47						
48	g	GTAGTCCACG	4	4	3636	0.99779978
49	f	GTAGTCCACG	5	5	74	1
50	g	GTAATCCTAG	7	7	13	1
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52	TAG	GTAGTCCACG	5	5		
53	AT					
54						
55	g	GTAGTCCACG	9	9	2	1
56	g				2475	0.99313131
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g	GTAGTCCACG	5	5	10	1
ATAT	GTAGTCTTAA	6	6		
p	GTAGTCCACG	6	6	2	1
GAG	GTAGTCCACG	4	4		
f	GTAGTCCACG	4	4	3	1
TCGG	GTAGTCCATG	6	6		
GCG	GTAGTCCACA	3	3		
CTCT					
g	GTAGTCCTGG	5	5	2	1
CAG					
CAG	GTAGTCCTAG	5	5		
g	GTAGTCCTGG	4	4	4	1
AGT	GTAGTCCACG	7	7		
o				3	1
o	GTAGTCCTAG	5	5	12	1
TAG	GTAGTCCACG	9	9		
CAG	GTAGTCCGCA	8	8		
CAG	GTAGTCCGCA	6	6		
TG	GTAGTCCTTG	7	7		
GTG	GTAGTCCACG	5	5		
CAT	CTAGTCTTAA	5	5		
GTG					
g	GTAGTCCACG	5	5	2	1
GAC	GTAGTCCACG	4	4		
GC	GTAGTCCACG	6	6		
AAG					
f	GTAGTCCACG	6	6	3	1
g	GTAGTCCACG	6	6	5	1
CAG	GTAGTCCACG	6	6		
g				23	1
GGTG	GTAGTCCACG	5	5		
TAG	GTAGTCCACG	7	7		
g	GTAGTCCACG	7	7	2	1
g	GTAGTCCACG	5	5	5	1
GCT	GTAGTCCACG	7	7		
f	GTAGTCCATG	7	7	2	1
GC	GTAGTCTATG	5	5		
CGG	GTAGTCCACG	6	6		

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4	g	GTAGTCCACG	6	6	7	0.85714286	
5	p	GTAGTCCACG	5	5	2		1
6	p	GTAGTCTTAA	4	4	2		1
7	gTC	GTAGTCCACG	5	5			
8	A	GTAGTCTGAA	5	5			
9	TTC	GTAGTCCTAG	4	4			
10	TCGT	GTAGTCCACG	6	6			
11	g				11		1
12	TGT	GTAGTCCACG	5	5			
13	GGC	GTAGTCTCAA	3	3			
14	GGG	GTAGTCCATG	5	5			
15	ACT	GTAGTCTTAA	4	4			
16	g	GTAGTCTCAA	3	3	120	0.98333333	
17	CAA	CTAGTCTTAA	5	5			
18	ACA	GTAGTCCTAG	5	5			
19	GCC	CTAGTCTTAA	5	5			
20	AGT	GTAGTCCATG	5	5			
21	CTG	GTAGTCCTGG	6	6			
22	TA	GTAGTCCACG	5	5			
23	AA	GTAGTCCACG	6	6			
24	TAG	GTAGTCCACG	7	7			
25	g	GTAGTCCACG	4	4	4		1
26	g	GTAGTCCACG	1	1	14		1
27	f	GTAGTCCACG	5	5	9		1
28	f	GTAGTCCACG	5	5	2		1
29	gTA	GTAGTCCACG	6	6			
30	g	GTAGTCCTTG	5	5	2		1
31	GTG	GTAGTCCACA	4	4			
32	g	GTAGTCCATG	7	7	10659	0.99924946	
33	GC						
34	CAT	CTAGTCTTAA	5	5			
35	gCT	GTAGTCTTAA	4	4			
36	AGT	GTAGTCCACG	7	7			
37	g	GTAGTCCACG	6	6	26		1
38	f	GTAGTCCACG	6	6	36	0.97222222	
39	TCC						
40	g				131	0.81679389	
41	AGT	GTAGTCCACG	6	6			
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4	f				3	1
6	GGT	GTAGTCCACG	5	5		
8	f	GTAGTCCACA	5	5	15	1
9	g	GTAGTCCCGA	5	5	2	1
11	g	GTAGTCCACG	6	6	2	1
12	g	GTAGTCCTAG	9	9	4	1
13	CAT	CTAGTCTTAA	6	6		
15	5AC					
16	CAG					
18	CAT	CTAGTCTTAA	6	6		
19	GCGGC	GTAGTCTCGA	5	5		
20	CAG	GTAGTCCATG	6	6		
22	c	GTAGTCCACG	5	5	13	1
23	g	GTAGTCCACG	4	4	14	1
25	TGT	GTAGTCCACG	6	6		
26	5TA	GTAGTCCACG	5	5		
27	GTG	GTAGTCCACG	3	3		
29	GCT	GTAGTCCACG	4	4		
30	5TG	GTAGTCCACG	4	4		
32	CAT	CTAGTCTTAA	6	6		
33	o	GTAGTCCACG	6	6	20	1
34	5GA	GTAGTCCACG	4	4		
36	5TA	GTAGTCCACG	6	6		
37	g	GTAGTCCACG	5	5	2	1
38	g	GTAGTCCACG	5	5	4	1
40	5CG	GTAGTCCACG	5	5		
42	5GG	GTAGTCCATG	4	4		
43	CAT	CTAGTCTTAA	4	4		
44	5GG	GTAGTCCTAG	5	5		
46	5AG					
47	f	GTAGTCCACG	5	5	4	1
48	f	GTAGTCCACG	6	6	24	0.91666667
50	TTC	GTAGTCCACG	5	5		
52	5AG	GTAGTCCACG	4	4		
53	5GTG					
54	5TG	GTAGTCCTTG	5	5		
56	5AG	GTAGTCCACG	8	8		



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4	AG	GTAGTCCACG	4	4			
5	CTG	GTAGTCCACG	5	5			
6	GTG	GTAGTCCACG	4	4			
7	CAT	CTAGTCTTAA	4	4			
8	CAC	GTAGTCCTGG	6	6			
9	f	GTAGTCCACA	5	5	9		1
10	GA	GTAGTTTTAA	4	4			
11	o	GTAGTCCACG	5	5	2		1
12	g	GTAGTCCTGG	4	4	3		1
13	ATC	GTAGTCCACG	7	7			
14	p	GTAGTCCTGG	5	5	2		1
15	TGG	GTAGTCCACG	4	4			
16	f	GTAGTCCACG	4	4	2		1
17	g	GTAGTCCACG	7	7	44	0.86363636	
18	o	GTAGTCCACG	4	4	4		1
19	CCG						
20	g				2		1
21	CGG	GTAGTCCACG	4	4			
22	ATG	GTAGTCTTAA	4	4			
23	AGT	GTAGTCCACG	6	6			
24	IAA	GTAGTCCACG	4	4			
25	g				24860	0.9928399	
26	g	GTAGTCCACG	6	6	2		1
27	TGT	GTAGTCCACG	6	6			
28	TA	GTAGTCCACG	4	4			
29	g	GTAGTCCACG	4	4	24		1
30	CAG	GTAGTCCACG	6	6			
31	GCC	CTAGTCTTAA	4	4			
32	f				7		1
33	ICGG	GTAGTCCATG	4	4			
34	AA	GTAGTCCACG	6	6			
35	TTC	GTAGTCCACG	5	5			
36	TA	GTAGTCCACG	5	5			
37	f	GTAGTCCACG	7	7	3		1
38	ITC						
39	TG						
40	CGG	GTAGTCCTGG	5	5			
41	GCC	CTAGTCTTAA	6	6			
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4	g	GTAGTCCACG	5	5	2	1
5	GG	GTAGTCCACG	4	4		
6	ACT	GTAGTCTTGA	4	4		
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8	GGC					
9	g	GTAGTCCTGG	4	4	12	1
10	GGC					
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12	g	GTAGTCCACG	4	4	3	1
13	f	GTAGTCCACG	4	4	11	1
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15	GGT	GTAGTCCACG	4	4		
16	c	GTAGTCCTAG	6	6	6	1
17	g	GTAGTCTTGG	4	4	5	1
18	AA	GTAGTCCACG	5	5		
19	CTT	GTAGTCCACG	6	6		
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21	AGA	GTAGTCTCAA	5	5		
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23	g	GTAGTCCTGG	5	5	6	1
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25	g				7	1
26	CGG					
27						
28	GTG	GTAGTCTTAA	4	4		
29	TAG	GTAGTCCACG	6	6		
30						
31	o	GTAGTCCACG	5	5	5	1
32	TAG					
33	GAT	GTAGTCTCAA	5	5		
34						
35	GGT	GTAGTCCACG	4	4		
36	GTG	GTAGTCCACG	4	4		
37	GG					
38						
39	CAT	CTAGTCTTAA	4	4		
40	TGG	GTAGTCCACG	5	5		
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42	TA	GTAGTCCACG	5	5		
43	g	GTAGTCCACG	3	3	2	1
44	TA	GTAGTCCACG	4	4		
45						
46	TGT	GTAGTCCACG	3	3		
47						
48	g				2	1
49	TCTC	GTAGTCCTGG	5	5		
50	ACT	GTAGTCTTAA	1	1		
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52	TA	GTAGTCCACG	4	4		
53	ATT	GTAGTCTCAA	3	3		
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55	CGC	GTAGTCCTGG	6	6		
56	g	GTAGTCCACG	2	2	17	1
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4	CCT	CTAGTCTTAA	5	5		
5	g	GTAGTCCACG	3	3	99	0.84848485
6	TTT	CTAGTCTTAA	6	6		
7	TAG	GTAGTCCACG	6	6		
8	GCC	CTAGTCTTAA	5	5		
9						
10	g				404	0.88861386
11	f	GTAGTCCACG	4	4	2	1
12	CAT	CTAGTCTTAA	4	4		
13						
14	g				3	1
15	TGC	GTAGTCCACA	4	4		
16	ATG					
17						
18	TGC	GTAGTCTATG	4	4		
19	ATG					
20						
21	CAT	CTAGTCTTAA	6	6		
22						
23	g	GTAGTCCACG	5	5	15	1
24	f	GTAGTCCACG	5	5	2	1
25	TTG	GTAGTCCACG	5	5		
26	g	GTAGTCCTAG	5	5	9	1
27	TGCC	GTAGTCCATG	5	5		
28	TA	GTAGTCCACG	5	5		
29	g	GTAGTCCACG	4	4	68	1
30	g	GTAGTCTTAA	2	2	4	1
31	g	GTAGTCCACG	6	6	27	1
32	TAG					
33	TAG	GTAGTCCACG	7	7		
34	g	GTAGTCCACG	4	4	12	1
35	o				3	1
36	CTG	GTAGTCCTGG	6	6		
37	TCCC	GTAGTCCTGG	8	8		
38	CAG	GTAGTCCATG	5	5		
39	g				1819	0.99780099
40	CCT	CTAGTCTTAA	4	4		
41	TGA	GTAGTCTTAA	6	6		
42	g	GTAGTCCACG	5	5	72	0.97222222
43	CAG	GTAGTCCACG	5	5		
44	g				54	1
45	TAG	GTAGTCCACG	6	6		
46	GCC	CTAGTCTTAA	5	5		
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GCC	CTAGTCTTAA	4	4		
f				2	1
AGTA	GTAGTCCACG	5	5		
GTG	GTAGTCCACG	6	5		
CTG					
AGC					
ATA	GTAGTCCACG	5	5		
CAT	CTAGTCTTAA	3	3		
GGTG					
g	GTAGTCTTAA	5	5	33	0.87878788
f	GTAGTCCATG	4	4	13	1
GC	GTAGTCTATG	4	4		
AGA	GTAGTCTCAA	5	5		
TGT	GTAGTCCACG	5	5		
TAG	GTAGTCCACG	5	5		
AC					
g	GTAGTCCACG	3	3	50	1
ATC	GTAGTCCACG	4	4		
g				35	0.8
p	GTAGTCCACG	4	4	2	1
AA	GTAGTCCACG	6	6		
GCC	CTAGTCTTAA	4	4		
f				30	1
CAT	CTAGTCTTAA	2	2		
GAG	GTAGTCCACG	6	6		
GG					
g				300	0.96333333
g	GTAGTCCACG	6	6	2	1
g	GTAGTCCACG	5	5	88	0.93181818
AG	GTAGTCCACG	3	3		
GC	GTAGTCTCAA	5	5		
f				196	0.98469388
GTG	GTAGTCCACG	4	4		
CAG	GTAGTCCACG	6	6		
CCG	GTAGTCCACG	4	4		
o				11	1
ATC	GTAGTCCACG	4	4		
TG	GTAGTCCACG	4	4		

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4	g	GTAGTCCACG	4	4	23	1
5	p	GTAGTCCACG	6	6	5	1
6	TTT	GTAGTCCACG	4	4		
7	TAG	GTAGTCCACG	6	6		
8						
9	g	GTAGTCCACG	4	4	5	1
10	CTCG	GTAGTCCACG	4	4		
11						
12	CCG					
13						
14	g				2	1
15	g	GTAGTCCACG	4	4	3	1
16						
17	g				13	1
18	TAG	GTAGTCCACG	2	2		
19	TTC	GTAGTCCACG	5	4		
20						
21	f				3	1
22	ATA	GTAGTCCACG	5	5		
23						
24	GAG					
25	CTC	GTAGTCCACG	4	4		
26	g	GTAGTCCACG	2	2	2	1
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28	TAG					
29	TAT	GTAGTCCACG	3	3		
30	TCT	GTAGTCTTGA	3	3		
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32	GGC	GTAGTCCGCA	3	3		
33						
34	f				7	1
35	CCG	GTAGTCCTGG	2	2		
36	TAG	GTAGTCCACG	6	6		
37	CAT	CTAGTCTTAA	4	4		
38						
39	g	GTAGTCTCTT	3	3	32	0.96875
40	f	GTAGTCCACG	4	4	2	1
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42	g				7	1
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44	g				2	1
45	TG					
46	TTT	GTAGTCCACG	3	3		
47						
48	f				12	1
49	CAT	CTAGTCTTAA	3	3		
50	f	GTAGTCCACG	7	7	2	1
51	AC	GTAGTCCACG	5	5		
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53	g				65	1
54	GTC	GTAGTCCACG	2	2		
55	TC	GTAGTCCACG	5	5		
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4	g				6		1
5	CAT	CTAGTCTTAA	4	4			
6	g	GTAGTCCACG	3	3	9		1
7							
8	g				21	0.9047619	
9	ATGA	GTAGTCTTAA	5	5			
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11	g	GTAGTCCACG	3	3	3		1
12	CT	GTAGTCCACG	2	2			
13	GAC	GTAGTCCACG	3	3			
14							
15	g				27	0.88888889	
16	TACC	GTAGTCCACG	3	3			
17	TTG	GTAGTCCTAG	3	3			
18							
19	AG	GTAGTCCACG	4	4			
20							
21	CAT	CTAGTCTTAA	4	4			
22	GGG	GTAGTCCACG	5	5			
23	TA	GTAGTCCACG	5	5			
24							
25	AGT						
26	ACC	GTAGTCTTAA	4	4			
27	GCT						
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29	GTG	GTAGTCCACA	3	3			
30	CGC	GTAGTCCACG	4	4			
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32	GG	GTAGTCCACG	3	3			
33	TA	GTAGTCCACG	4	4			
34	CAG	GTAGTCCACG	4	4			
35							
36	GAGA						
37	c	GTAGTCCTAG	5	5	2		1
38							
39	GGT						
40	f				3		1
41							
42	AG	GTAGTCCACG	2	2			
43	g	GTAGTCCTGG	4	4	5		1
44	TA	GTAGTCCACG	4	4			
45							
46	AC						
47	ACC	GTAGTCTTAA	4	4			
48							
49	g				8		1
50	AGA	GTAGTCTTAA	3	3			
51	GCT	GTAGTCTTAA	5	5			
52							
53	g				261	0.98467433	
54	f	GTAGTCCACG	3	3	2		1
55							
56	f	GTAGTCCATG	4	4	3		1
57							
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4	ACC	GTAGTCTTAA	3	3		
5	p				4	1
6	iGC					
7	TA					
8						
9	AA					
10	f	GTAGTCCACG	3	3	2	1
11	GAG	GTAGTCCACG	4	4		
12	CCG	GTAGTCCTAG	3	3		
13	iGG					
14	GCC	CTAGTCTTAA	3	3		
15	GAG	GTAGTCCACG	5	5		
16	g				6	1
17	TA	GTAGTCCACG	3	3		
18	TAT					
19	GTG	GTAGTCCACG	5	5		
20	p	GTAGTCCTAG	4	4	8	0.875
21	GAG	GTAGTCCACG	4	4		
22	GTC	GTAGTCCACA	3	3		
23	GCC	GTAGTCCGCA	4	4		
24	f	GTAGTCCTAG	3	3	4	1
25	GTC					
26	GGT					
27	g	GTAGTCCACG	2	2	2	1
28	f				7	1
29	TAAC	GTAGTCCTAA	3	3		
30	TG	GTAGTCTACA	4	4		
31	CGG	GTAGTCCACG	4	4		
32	iTA	GTAGTCCACG	3	3		
33	GCT	CTAGTCTTAA	4	4		
34	GAG	GTAGTCCACG	5	5		
35	TGG	GTAGTCCACG	4	4		
36	g	GTAGTCCACG	4	4	2	1
37	AG					
38	TAG	GTAGTCCACG	6	6		
39	CAG	GTAGTCCACG	6	6		
40	GT	GTAGTCCACG	4	4		
41	GAG					
42	AG					
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AG	GTAGTCCACG	3	3		
TAG	GTAGTCCACG	3	3		
GGG	GTAGTCCACG	5	5		
ACT					
GTG					
ACG					
AGAG					
CTG	GTAGTCCACG	3	3		
g	CTAGTCTTAA	3	3	17	1
ATC					
f				29	0.93103448
CTG	GTAGTCCACG	3	3		
GTG	GTAGTCCACG	5	4		
ATC					
CTG	GTAGTCCTTG	4	4		
GGT	GTAGTCCACG	3	3		
GCC	CTAGTCTTAA	3	3		
AT					
TTG	GTAGTCTTGA	4	4		
g	GTAGTCTTAA	1	1	2	1
f				2	1
TAG	GTAGTCCACG	7	7		
TT	GTAGTCCACG	1	1		
g	GTAGTCCACG	2	2	64	1
TA	GTAGTCCACG	2	2		
g				59	0.81355932
g	GTAGTCCACG	3	3	3	1
g	GTAGTCCTAG	3	3	14	1
CAT	CTAGTCTTAA	3	3		
AG	GTAGTCCACG	3	3		
g	GTAGTCCACG	2	2	2	1
CTG	GTAGTCCACG	5	4		
GC					
AC	GTAGTCTTAA	2	2		
TAG	GTAGTCCACG	5	5		
TGT					
GG	GTAGTCCACG	5	5		
CTG	GTAGTCCACG	4	4		



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4	AG					
5	CGG	GTAGTCCACG	4	4		
6	TAG	GTAGTCCACG	5	5		
7						
8	g	GTAGTCCACG	4	4	14	1
9	AGA	GTAGTCTCAA	3	3		
10	f				2	1
11						
12	ATC	GTAGTCCACG	4	4		
13	ACT	GTAGTCTTAA	1	1		
14						
15	f				4	1
16	CTG					
17	CTG	GTAGTCCACG	3	3		
18						
19	AG					
20	AGT					
21						
22	f	GTAGTCCACA	4	4	10	1
23	g	GTAGTCTTAA	4	4	7	1
24	p	GTAGTCCACG	3	3	6	1
25						
26	g				130	0.99230769
27	CTG	GTAGTCCTAG	4	4		
28	CTGT	GTAGTCCACG	4	4		
29						
30	GATT					
31						
32	g	GTAGTCCACG	3	3	93	0.8172043
33	g	GTAGTCCATG	2	2	7	1
34	CACT					
35						
36	f				4	1
37	AGA	GTAGTCTCAA	3	3		
38	CTG	GTAGTCCATG	3	3		
39	TGA	GTAGTCTTAA	4	4		
40	f	GTAGTCCACG	3	3	6	1
41						
42	GTC	GTAGTCCACA	5	5		
43						
44	TAG					
45	CTA					
46						
47	c	GTAGTCCACG	3	3	2	1
48	TAG					
49						
50	g	GTAGTCCACG	3	3	20	1
51	TAA	GTAGTCCACG	3	3		
52						
53	g	GTAGTCTCAA	2	2	10	1
54	TAA	GTAGTCTTGA	3	3		
55						
56	f	GTAGTCCTAG	3	3	3	1
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4	AG						
5	GAG	GTAGTCCACG	5	5			
6	g	GTAGTCCACG	6	6	5	1	
7	g	GTAGTCCACG	3	3	2	1	
8	g	GTAGTCCACG	3	3	2	1	
9	AG	GTAGTCCACG	4	4			
10	g	GTAGTCCACG	2	2	4	1	
11	o	GTAGTCCACG	3	3	18	1	
12	g	GTAGTCCACG	3	3	47	1	
13	g	GTAGTCCACG	3	3	23	0.95652174	
14	g	GTAGTCCACG	3	3			
15	CAT	CTAGTCTTAA	3	3			
16	GAG						
17	CCG						
18	c				81	0.95061728	
19	f	GTAGTCCTGG	3	3	20	0.9	
20	g	GTAATCCTAG	3	3	3	1	
21	f				15	1	
22	g				4	1	
23	GT						
24	TA	GTAGTCCACG	3	3			
25	CAT	CTAGTCTTAA	4	4			
26	AA	GTAGTCCACG	4	4			
27	g	GTAGTCCACG	2	2	97	0.91752577	
28	GAG						
29	GTG						
30	g	GTAGTCCACG	2	2	109689	0.88585911	
31	c	GTAGTCCACG	2	2	21	1	
32	CAC	CTAGTCTTAA	2	2			
33	CAG						
34	GG						
35	TGA						
36	GCC	CTAGTCTTAA	3	3			
37	CGG	GTAGTCCTAG	2	2			
38	TA	GTAGTCCACG	3	3			
39	AG	GTAGTCCACG	2	2			
40	TG	GTAGTCCACG	3	3			
41	GTG	GTAGTCCTAG	2	2			
42	CTAG						
43	g				6	1	
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5	p	GTAGTCTTAA	3	3	18	0.94444444
6	o	GTAGTCCTGG	3	3	1493	0.98861353
7						
8	CT	GTAGTCCACG	3	3		
9	GTG	GTAGTCCACG	3	3		
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11	TAG	GTAGTCCACG	3	3		
12	g				72	0.94444444
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14	g				21	1
15	TATA					
16						
17	g				10	1
18	GAG	GTAGTCCACG	4	4		
19	GAG	GTAGTCCACG	4	4		
20						
21	f	GTAGTCCACG	4	4	26	1
22	AA	GTAGTCCACG	3	3		
23						
24	f				2	1
25	TGA	GTAGTCCACG	1	1		
26	AG	GTAGTCCACG	2	2		
27	TAG	GTAGTCCACG	4	4		
28						
29	f				7	1
30	GTA					
31						
32	AG	GTAGTCCACG	2	2		
33	TT	GTAGTCCACG	2	2		
34						
35	CT	CTAGTCTTAA	4	4		
36	AG					
37						
38	AG					
39	AG	GTAGTCCACG	2	2		
40	AT					
41						
42	AC	GTAGTCTTAA	1	1		
43	TGC	GTAGTCTATG	5	5		
44	GTC	GTAGTCCACA	4	4		
45						
46	CT	GTAGTCCACG	2	2		
47	AGC	GTAGTCTTAA	3	3		
48						
49	CAT	CTAGTCTTAA	3	3		
50	GTG	GTAGTCCACG	3	3		
51						
52	CAT					
53	TTG	GTAGTCCCAG	3	3		
54	TAT	GTAGTCTTAA	3	3		
55						
56	g	GTAGTCTCAA	2	2	2	1
57						
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4	AAG					
5	TAG	GTAGTCCACG	4	4		
6	TGG	GTAGTCCACG	3	3		
7						
8	CTG	GTAGTCCATG	4	4		
9	GTC					
10						
11	GTG	GTAGTCCACG	3	3		
12	GCC	GTAGTCTATG	3	3		
13	f	GTAGTCCACG	3	3	16	1
14						
15	GCC	CTAGTCTTAA	3	3		
16	TAG	GTAGTCCACG	5	5		
17						
18	g	GTAGTCCACG	4	4	14	1
19	TTG	GTAGTCCACG	4	4		
20	CAT	CTAGTCTTAA	5	5		
21						
22	CGT					
23	TCG	GTAGTCCTAG	3	3		
24						
25	o	GTAGTCCACG	3	3	62	1
26	f	GTAGTCCACG	4	4	24	1
27						
28	TAG					
29	TAT					
30	GTG	GTAGTCCTAG	5	5		
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32	GAG					
33	GCC	CTAGTCTTAA	3	3		
34	GTG	GTAGTCCACG	3	3		
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36	GTGC	GTAGTCCACG	3	3		
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38	g				2	1
39	ATC	GTAGTCCACG	3	3		
40	g	GTAGTCCACG	3	3	3	1
41	TGC	GTAGTCTATG	4	4		
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43	GGA					
44	TG					
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46	TCTG					
47	f				7	1
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49	g	GTAGTCCACG	3	3	46	1
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51	g				157	0.97452229
52	CTAA	GTAGTCTCTA	2	2		
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54	g				3899	0.98281611
55	g	GTAGTCCACG	3	3	2	1
56	GTC	GTAGTCCACA	3	3		
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4	CAT	CTAGTCTTAA	3	3		
5	GTC					
6	ATC	GTAGTCCACG	2	2		
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8	CGG					
9	ACG					
10	AC					
11	T	GTAGTCCACG	2	2		
12	GT	GTAGTCCACG	2	2		
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14	k	GTAGTCTTAA	2	2	4	1
15	CGT	GTAGTCCACG	2	2		
16	AC	GTAGTCTTAA	2	2		
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18	g				498	0.98995984
19	ACT	GTAGTCTTAA	3	3		
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21	g	GTAGTCCACG	3	3	2	1
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23	g	GTAGTCCACG	4	4	3	1
24	f	GTAGTCCACG	3	3	16	0.9375
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26	GTC	GTAGTCCACG	5	5		
27	TAG	GTAGTCCACG	4	4		
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29	GTG					
30	ACC	GTAGTCTTGA	1	1		
31	ATC	GTAGTCCACG	2	2		
32	GTG	GTAGTCCACG	2	2		
33	AGT	GTAGTCCACG	3	3		
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36	g				7	1
37	GTG					
38	AGT	GTAGTCCACG	3	3		
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40	g				29	1
41	ACC	CTAGTCTTAA	3	3		
42	CAT	CTAGTCTTAA	3	3		
43	TCG	GTAGTCCTAG	2	2		
44	GT					
45	CAT	CTAGTCTTAA	5	5		
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47	g	GTAGTCCACG	2	2	2	1
48	CCG	GTAGTCCTAG	4	4		
49	GG	GTAGTCCACG	2	2		
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51	AG					
52	GTC					
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CAT	CTAGTCTTAA	3	3		
GGT	GTAGTCCACG	3	3		
ACC					
TTT	GTAGTCCACG	2	2		
AGT	GTAGTCCACG	2	2		
TAC					
CAT	CTAGTCTTAA	2	2		
GGC	GTAGTCCACG	2	2		
ATT	CTAGTCTTAA	3	3		
g	GTAGTCCTAG	3	3	5	1
TCC	GTAGTCCTAG	3	3		
g	GTAGTCCACG	2	2	40	0.85
TGA	GTAGTCTCAA	3	3		
g	GTAGTCCACG	2	2	24	1
AGT	GTAGTCCACG	1	1		
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GAC	GTAGTCTCAA	2	2		
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CGA	GTAGTCTCAA	2	2		
GTC					
TAG	GTAGTCCACG	3	3		
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GACA	GTAGTCTTAA	3	3		
CGA	GTAGTCCACG	3	3		

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4	GTC	GTAGTCCACA	4	4		
5	TTCC	GTAGTCCTGG	2	2		
6	g				5	1
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10	p	GTAGTCCACG	2	2	2	1
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12	CAG					
13	TTT	GTATTTGCTG	2	2		
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15	TGA					
16	f	GTAGTCCACG	3	3	3	1
17	f	GTAGTCCACG	2	2	5	1
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19	AC	GTAGTCCACG	4	4		
20	TAG	GTAGTCCACG	4	4		
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22	TAG					
23	GGT					
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25	g	GTAGTCCACG	1	1	2	1
26	CTG	GTAGTCCTGG	3	3		
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28	TAA					
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32	GTC	GTAGTCCACA	2	2		
33	AG					
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36	CAA					
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47	CAG					
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49	g	GTAGTCCACG	3	3	23	0.95652174
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53	ACT					
54	TAGA	GTAGTCCATA	2	2		
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56	TA	GTAGTCCACG	2	2		
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ATC					
TCG	GTAGTCCTAG	2	2		
GCC	CTAGTCTTAA	3	3		
GCC	CTAGTCTTAA	2	2		
GCG	GTAGTCCTAG	3	3		
CTT	GTAGTCCTAG	2	2		
TAA	GTAGTCCTAA	2	2		
f	GTAGTCCGCA	2	2	2	1
TAG	GTAGTCCACG	2	2		
CAG	GTAGTCCACG	3	3		
CTG					
TAG	GTAGTCCACG	2	2		
GAG	GTAGTCCACG	4	4		
g	CTAGTCTCAA	2	2	11	1
GTC	GTAGTCCACA	2	2		
ATT	CTAGTCTTAA	3	3		
CTG	GTAGTCCTGG	2	2		
TAA					
CGA	GTAGTCTCAA	2	2		
AGA	GTAGTCTCAA	2	2		
ATC	GTAGTCCACG	2	2		
ATC	GTAGTCCACG	3	3		
CG					
GTC	GTAGTCCACA	1	1		
TCT	GTAGTCTTAA	1	1		
g	GTAGTCCACG	1	1	9	0.88888889
CCA	GTAGTCCACA	2	2		
CGT	CTAGTCTTAA	4	4		
GCC	CTAGTCTTAA	2	2		
g	GTAGTCCATG	2	2	25	1
TGT					
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GAG	GTAGTCCACG	3	3		
GGT	GTAGTCCACG	1	1		
ACG	GTAGTCTCAA	1	1		



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4	g				81	1
5	g	GTAGTCCACG	3	3	2	1
6	g	GTAGTCCACG	2	2	30	0.93333333
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8	CAG	GTAGTCCACG	2	2		
9	g	GTAGTCCACG	2	2	9	0.88888889
10	ATC	GTAGTCCACG	2	2		
11	GTC	GTAGTCCACA	3	3		
12	TA	GTAGTCCACG	2	2		
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14	f	GTAGTCCACA	3	3	2	1
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16	TA					
17	GT	GTAGTCCACG	1	1		
18	GAG	GTAGTCCACG	4	4		
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20	g	GTAGTCCACG	3	3	4	1
21	o	GTAGTCCACG	2	2	2	1
22						
23	f				6	1
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25	CGA	GTAGTCTCAA	2	2		
26	GCG					
27	TGC	GTAGTCTATG	3	3		
28						
29	TA					
30	g	GTAGTCCACG	2	2	2579	0.99961225
31	GAG	GTAGTCCACG	2	2		
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33	f	GTAGTCCACG	2	2	6	1
34	GTG	GTAGTCCACG	2	2		
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36	o				61	0.95081967
37	g				2	1
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40	AC	GTAGTCCACG	2	2		
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42	AT	CTAGTCTTAA	3	3		
43	GTG	GTAGTCCACG	2	2		
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45	ACT					
46	f				2	1
47	TG	GTAGTCCACG	2	2		
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49	f				2	1
50	CCA					
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52	c				1962	0.99745158
53	g	GTAGTCCACG	2	2	7028	1
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55	g	GTAGTCCACG	2	2	39	1
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4	AAAG						
5	g	GTAGTCCACG	2	2	5	1	
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8	g	GTAGTCCACG	2	2	112	0.96428571	
9	gAG	GTAGTCCACG	3	3			
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11	TGG						
12	g	GTAGTCCACG	3	3	2	1	
13	gAG	GTAGTCCACG	3	3			
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15	TAG	GTAGTCCACG	3	3			
16							
17	TG						
18	TGT	GTAGTCCACG	3	3			
19	gTG						
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21	p				132	0.97727273	
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23	g	GTAGTCTTAA	1	1	213	0.99061033	
24	gTA	GTAGTCCACG	1	1			
25	gGT	GTAGTCCACG	1	1			
26	GT	GTAGTCCACG	1	1			
27	TAG	GTAGTCCACG	3	3			
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29	AA						
30	TGA						
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32	TGC	GTAGTCTATG	2	2			
33	AT	GTAGTCCTGG	2	2			
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35	g	GTAGTCCACG	4	4	131	0.99236641	
36	gCG	GTAGTCCTAG	1	1			
37	ATT	CTAGTCTTAA	2	2			
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39	TT	GTAGTCTATT	2	2			
40	g	GTAGTCCACG	2	2	3	1	
41	ATCA	GTAGTCCCAG	2	2			
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43	CAT	CTAGTCTTAA	2	2			
44	gGT	GTAGTCCGCA	2	2			
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46	f	GTAGTCCTAG	2	2	2	1	
47	g	GTAGTCCACG	2	2	4	1	
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49	TAA	GTAGTCTTAA	3	3			
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51	CTA						
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53	gAG						
54	CTA						
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56	GTT	GTAGTCCACA	2	2			
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6		ICTA	GTAGTCCACG	3	3	
7		ACT	GTAGTCTTAA	2	2	
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9		g			5	1
10		TGT	GTAGTCTATG	3	3	
11		ATG	GTAGTCTTAA	1	1	
12		AGC	GTAGTCCACG	1	1	
13		AGA	GTAGTCTCAA	2	2	
14		f	GTAGTCCTGG	2	2	6
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16		GA	GTAGTCCACG	1	1	
17		CGT	GTAGTCCACG	1	1	
18		AGC	GTAGTCCTAA	1	1	
19		AG	GTAGTCCACG	3	3	
20		GT	GTAGTCCACG	2	2	
21		TCC	GTAGTCCACG	2	2	
22		TG	GTAGTCCTTG	2	2	
23		f	GTAGTCCTAG	2	2	7
24						1
25		o			19	1
26		GCC	CTAGTCTTAA	2	2	
27		AGA	GTAGTCTCAA	2	2	
28		ACA	GTAGTCTTAA	2	2	
29		AG	GTAGTCCACG	2	2	
30		GTC				
31		TTC				
32		AG	GTAGTCCACG	2	2	
33		AGT	GTAGTCCACG	2	2	
34		g			3	1
35		ATC	GTAGTCCACG	3	3	
36		g	GTAGTCCACG	2	2	2
37		ITA				1
38		GTG	GTAGTCCACG	2	2	
39		TAG	GTAGTCCACG	3	3	
40		CAG				
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42		AGA	GTAGTCTCAA	2	2	
43		CTC	GTAGTCTTTA	2	2	
44		CAG	GTAGTCCTGG	2	2	
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5	ATG					
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7	g	GTAGTCCACG	1	1	84	0.96428571
8	TAG	GTAGTCCACG	1	1		
9	TAA	GTAGTCTTAA	1	1		
10	TTT	CTAGTCTTAA	3	3		
11	TAG	GTAGTCTTGA	3	3		
12	ATA	GTAGTCCACG	2	2		
13	g	GTAGTCTCAA	2	2	63	1
14	g				4	1
15	GAA					
16	TGA					
17	TACC	GTAGTCTTAA	2	2		
18	TAC					
19	CCG	GTAGTCCCGC	1	1		
20	AGA	GTAGTCTCAA	1	1		
21	AGA	GTAGTCTCAA	1	1		
22	TCCC	GTAGTCTTAA	1	1		
23	c				8	0.875
24	ATC	GTAGTCCACG	2	2		
25	ATC	GTAGTCCACG	2	2		
26	TTG	GTAGTCTTGA	2	2		
27	CA	GTAGTCTTAG	2	2		
28	TGA					
29	g	GTAGTCCACG	2	2	2	1
30	TGA					
31	CAG					
32	ATT	CTAGTCTTAA	1	1		
33	TGC	GTAGTCTCAA	1	1		
34	CGT	GTAGTCCACG	2	2		
35	AG	GTAGTCCACG	2	2		
36	TCA	GTAGTCCACG	4	4		
37	GC					
38	CTA	GTAGTCCACG	2	2		
39	CCG	GTAGTCTTGA	2	2		
40	TCA					
41	AG					

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5	GCC	CTAGTCTTAA	2	2		
6	g	GTAGTCCACG	2	2	5	1
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8	gTC	GTAGTCCACG	1	1		
9	p	GTAGTCCTAG	1	1	6	1
10	AGT	GTAGTCCACG	1	1		
11	gTA					
12	ATT	GTAGTCCACG	2	2		
13	TGT	GTAGTCCACG	2	2		
14	TA	GTAGTCCACG	2	2		
15	CTA					
16	GG					
17	ATC	GTAGTCCACG	3	3		
18	CA	GTAGTCCTAG	2	2		
19	GCC	CTAGTCTTAA	2	2		
20	CTG	GTAGTCCACG	2	2		
21	TAG					
22	GGTG	GTAGTCCACG	2	2		
23	.CGA	GTAGTCTCAA	2	2		
24	AC					
25	o				15	1
26	ATC	GTAGTCCACA	2	2		
27	A					
28	TGC	GTAGTCTATG	3	3		
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30	gTC	GTAGTCCACG	2	2		
31	o	GTAGTCCACG	2	2	5	1
32	GAG					
33	ATC	GTAGTCCACG	2	2		
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36	gTG	GTAGTCCACG	2	2		
37	AGA	GTAGTCTCAA	2	2		
38	ACT	GTAGTCTTGA	3	3		
39	g	GTAGTCCACA	1	1	18	1
40	gTC					
41	g	GTAGTCCACG	1	1	23	0.95652174
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4	CAT	CTAGTCTTAA	1	1			
5	TCA	GTAGTCCTCG	1	1			
6	GCC	CTAGTCTTAA	2	2			
7	GTC	GTAGTCCACA	2	2			
8	GTC	GTAGTCCACA	2	2			
9	GTC	GTAGTCCACA	2	2			
10	GCG	GTAGTCCTAG	2	2			
11	GTG	GTAGTCCACG	2	2			
12	GTC	GTAGTCCACA	2	2			
13	ATA						
14	GGT	GTAGTCCTAG	2	2			
15	CTG	GTAGTCCACG	1	1			
16	CAT	CTAGTCTTAA	2	2			
17	p	GTAGTCCACG	1	1	2		1
18	ATT	CTAGTCTTAA	1	1			
19	TTT	GTAGTCCACG	1	1			
20	ATG	GTAGTCTTAA	1	1			
21	AC	GTAGTCTTAA	1	1			
22	ACG	GTAGTCCTAG	1	1			
23	g	GTAGTCCACG	1	1	798		1
24	TA	GTAGTCTTGA	2	2			
25	TTT	GTAGTCTCAA	2	2			
26	CA						
27	GTG	GTAGTCCTAG	2	2			
28	TA	GTAGTCCACG	2	2			
29	GT						
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31	GAG	GTAGTCCACG	2	2			
32	f				2		1
33	g				2		1
34	f	GTAGTCCACG	2	2	11	0.90909091	
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36	AA	GTAGTCCACG	2	2			
37	ATC	GTAGTCCACG	3	3			
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39	f	GTAGTCCTAG	2	2	27		1
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22	TTA	GTAGTCCACG	3	3		
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34	TGC	GTAGTCTATG	2	2		
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44	3AC					
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7	GAG	GTAGTCCACG	1	1		
8	g	GTAGTCCACG	1	1	7	1
9	CAT	CTAGTCTTAA	1	1		
10	CAG	GTAATCCTAG	1	1		
11	AC	CTAGTTCTAA	1	1		
12	CGCT	GTAGTCCTGG	1	1		
13	GTC	GTAGTCCACG	1	1		
14	AG	GTAGTCCACG	2	2		
15	TGT	GTAGTCCACG	2	2		
16	GCC	CTAGTCTTAA	2	2		
17	AG	GTAGTCCACG	2	2		
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19	ATA	GTAGTCCACG	2	2		
20	GCC	CTAGTCTTAA	1	1		
21	AG	GTAGTCCACG	1	1		
22	TG	GTAGTCCTTG	1	1		
23	ATC	GTAGTCCACG	1	1		
24	AG	GTAGTCCACG	1	1		
25	g	GTAGTCCACG	1	1	23	0.86956522
26	TGA	CTAGTTCTGA	1	1		
27	ATG	GTAGTCTTAA	1	1		
28	CA	GTAGTCCACG	1	1		
29	g	GTAGTCCTGG	1	1	2	1
30	TGT					
31	CA	GTAGTCCACG	2	2		
32	TGT	GTAGTCCACG	2	2		
33	GTC	GTAGTCCACG	2	2		
34	GTG					
35	g	GTAGTCCACG	2	2	194	1
36	CAT	CTAGTCTTAA	2	2		
37	TAA	GTAGTCCACG	2	2		
38	GT	GTAGTCCGCA	2	2		
39	AG	GTAGTCCACG	2	2		
40	ATA	GTAGTCCACG	2	2		
41	CAT	CTAGTCTTAA	2	2		
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6	ATA	GTAGTCCACG	2	2		
7	GAG	GTAGTCCACG	2	2		
8	GAG	GTAGTCCACG	2	2		
9	GAG	GTAGTCCACG	2	2		
10	CCG	GTAGTCCTAG	2	2		
11	GAG	GTAGTCCACG	2	2		
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13	CAAA					
14	CTA					
15	TGA					
16	TGA	GTAGTCTTAA	2	2		
17	g	GTAGTCCTAG	1	1	10	1
18	ATC	GTAGTCCACA	1	1		
19	ATC	GTAGTCCACA	1	1		
20	ATC	GTAGTCCACA	2	2		
21	ATC	GTAGTCCACA				
22	ATC	GTAGTCCACA				
23	ATC	GTAGTCTTAA	2	2		
24	GCC	CTAGTCTTAA	2	2		
25	ATC	GTAGTCCACG	1	1		
26	ATC	GTAGTCCACG	1	1		
27	ATC	GTAGTCCTAA	1	1		
28	ATC	GTAGTCCTAA	1	1		
29	TGT	GTAGTCCAAA	1	1		
30	ATC	GTAGTCCACG	1	1		
31	ATC	GTAGTCCACG				
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34	ATC	GTAGTCCACG				
35	ATC	GTAGTCCACG	1	1		
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37	ATC	GTAGTCCACG	1	1		
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45	ATC	GTAGTCCACG	2	2		
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47	ATC	GTAGTCCACG	1	1		
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53	ATC	GTAGTCCACG	1	1	4	1
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55	ATC	GTAGTCCACG	1	1		
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f	GTAGTCCACG	1	1	2	1
CGT	GTAGTCCTAG	1	1		
CCCC	GTAGTCCTGG	1	1		
GTC	GTAGTCCACA	1	1		
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GTT	GTAGTCCACG	1	1		
CAT	CTAGTCTTAA	1	1		
CAG	GTAGTCCACG	1	1		
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ATT	GTAGTCTCAA	1	1		
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GAG	GTAGTCCACG	1	1		
GAG	GTAGTCCACG	1	1		
GGT	GTAGTCCTAG	1	1		
GTC	GTAGTCCACA	1	1		
TGC	GTAGTCCTGG	1	1		
CA					
CAG	GTAGTCCACG	2	2		
GAG	GTAGTCCACG	2	2		
GAG	GTAGTCCACG	3	3		
TGG	GTAGTCCACG	2	2		
GCG					
GAG					
TTA	GTAGTCTTGA	2	2		
GAG					
GTC					
TGA	GTAGTCTTAA	1	1		
GCG	GTAGTCCTAG	1	1		
GC	GTAGTCCGCA	1	1		
GTC	GTAGTCCACG	1	1		
CCCG					
GAC	GTAGTCTCAA	1	1		
GAC					
g	GTAGTCCATG	1	1	481	0.997921
TCCC	GTAGTCCTGG	1	1		
GTT	GTAGTCCACG	1	1		
GTC					

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6	iTA	GTAGTCCACG	1	1		
7	iTGT	GTAGTCCACG	1	1		
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9	g	GTAGTCCACG	1	1	2	1
10	TA	GTAGTCCACG	1	1		
11	CGA	GTAGTCTCAA	1	1		
12	TA	GTAGTCCACG	1	1		
13	ACT	GTAGTCTCAA	1	1		
14	f	GTAGTCCTAG	1	1	2	1
15	o	GTAGTCCTAG	1	1	2	1
16	g	GTAGTCCACG	1	1	3	1
17	TGA	GTAGTCTTAA	1	1		
18	g	GTAGTCTTAA	1	1	39	1
19	AA	GTAGTCCACG	1	1		
20	TAAC	GTAGTCCTAA	1	1		
21	GGT	GTAGTCCACG	2	2		
22	ATT	CTAGTCTTAA	2	2		
23	CG					
24	g	GTAGTCTTAA	2	2	4	1
25	CGA	GTAGTCTCAA	2	2		
26	GCC	CTAGTCTTAA	2	2		
27	AGA					
28	AC	GTAGTCCACG	2	2		
29	ATG					
30	TTT					
31	TA	GTAGTCCACG	3	3		
32	ATC	GTAGTCCACG	2	2		
33	ATA	GTAGTCTTAA	2	2		
34	TCA					
35	TGC	GTAGTCTATG	2	2		
36	GTC	CTAGTCTTAA	2	2		
37	CAG	GTAGTCCACG	2	2		
38	GAG	GTAGTCCACG	2	2		
39	g	GTAGTCCACG	2	2	2	1
40	GTC	GTAGTCCACA	2	2		
41	ATC	GTAGTCCACG	2	2		
42	TGA	GTAGTCTTAA	2	2		
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5	GAG	GTAGTCCACG	2	2		
6	f	GTAGTCCACG	2	2	2	1
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8	TG	GTAGTCCTTG	2	2		
9	g	GTAGTCCACG	2	2	40	0.925
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11	g				88	1
12	CGG	GTAGTCCACG	2	2		
13	TGA	GTAGTCTCAA	2	2		
14	TA	GTAGTCCTTG	2	2		
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16	GAG					
17	TAG					
18						
19	TTG					
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21	TA	GTAGTCCACG	2	2		
22	GCC	CTAGTCTTAA	2	2		
23	GCC	CTAGTCTTAA	2	2		
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25	ATGA	GTAGTCTTAA	3	3		
26	ATC	GTAGTCCACG	2	2		
27	g	GTAGTCCACG	2	2	3	1
28	GT	GTAGTCCACG	2	2		
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30	AC	GTAGTCTTAA	1	1		
31	AC	GTAGTCCACG	1	1		
32						
33	CAG	GTAGTCCACG	1	1		
34	AC					
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36	c	GTAGTCCACG	1	1	3	1
37	g	GTAGTCCACG	1	1	11	1
38	g	GTAGTCCACG	1	1	6800	0.99602941
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42	CAG	GTAGTCCACG	1	1		
43	CT	GTAGTCTTAA	1	1		
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45	g	GTAGTCCACG	1	1	156	0.98076923
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47	AC	GTAGTCTTAA	1	1		
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49	AC	GTAGTCTTAA	1	1		
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51	GCG	GTAGTCCACG	1	1		
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53	g	GTAGTCCACG	1	1	2	1
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56	g	GTAGTCCACG	1	1	4	1
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5	TT					
6	GAC	GTAGTCCACG	1	1		
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8	o				140	0.96428571
9	CAG	GTAGTCCACG	1	1		
10	AT	GTAGTCTTAA	1	1		
11	GG	GTAGTCCACG	1	1		
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13	GAC					
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15	GGT	GTAGTCCACG	1	1		
16	g	GTAGTCCACG	1	1	3	1
17	GTG	GTAGTCCACG	1	1		
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19	GAG	GTAGTCCACG	1	1		
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21	g				70	0.9
22	g	GTAGTCCACG	1	1	107	0.97196262
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24	GTG					
25	CGA	GTAGTCTCAA	1	1		
26	ATC	GTAGTCCACG	1	1		
27						
28	AC	GTAGTCTTAA	1	1		
29	ACT	GTAGTCCACG	1	1		
30						
31	g	GTAGTCCACG	1	1	4	1
32	g				10	0.8
33	g	GTAGTCTTAA	1	1	3	1
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35	ACCC	GTAGTCCTAA	1	1		
36	ATA					
37	ATC	GTAGTCCACG	3	3		
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39	GAG					
40	GCT	GTAGTCCGCA	2	2		
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42	GAG	GTAGTCCACG	2	2		
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45	TG	GTAGTCCTTG	2	2		
46	ATA	GTAGTCCACG	2	2		
47	GCG	GTAGTCCTAG	2	2		
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49	TGCC	GTAGTCCCAG	2	2		
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51	CTA					
52	ATT	GTAGTCCACG	2	2		
53	TGC	GTAGTCTATG	2	2		
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55	TT					
56	ACA					
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6	CAA	GTAGTCCACA	2	2			
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8	g	GTAGTCCACG	2	2	9		1
9	GTG	GTAGTCCACG	2	2			
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11	GTC						
12	TGC	GTAGTCTATG	2	2			
13	TAG	GTAGTCCACG	2	2			
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15	CTA						
16	TG						
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18	CAT	CTAGTCTTAA	2	2			
19	GCG	GTAGTCCTAG	2	2			
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21	TA						
22	GAG						
23	f	GTAGTCCACG	2	2	2		1
24	GCG	GTAGTCCTAG	1	1			
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26	GG	GTAATCCTAG	1	1			
27							
28	g	GTAGTCCACG	1	1	2939	0.98775094	
29	GC	GTAGTCCGCA	1	1			
30	GTC	GTAGTCCACA	1	1			
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32	TTA						
33	TG						
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35	TGA	GTAGTCTCAA	1	1			
36	GTC	GTAGTCCACA	1	1			
37	TGA	GTAGTCTCAA	1	1			
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39	GCG	GTAGTCCACG	1	1			
40	AC	GTAGTCCACG	1	1			
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42	A						
43	g	GTAGTCCACG	1	1	70		0.9
44	ATT	CTAGTCTTAA	1	1			
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46	CTT	CTAGTCTTAA	1	1			
47	GG	GTAGTCCACG	1	1			
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49	GAG	GTAGTCCACG	2	2			
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51	TA						
52	TG						
53	CTA						
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55	GTC	GTAGTCCACA	2	2			
56	CAT	CTAGTCTTAA	2	2			
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5	iTA	GTAGTCCACG	2	2		
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7	GTC	GTAGTCCACA	2	2		
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10	GAG	GTAGTCCACG	2	2		
11	iGTG	GTAGTCCACG	2	2		
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13	AGTA					
14	iGTG					
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16	g				5	1
17	GGG	GTAGTCCACG	2	2		
18	TTG					
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21	TCG	GTAGTCCTTG	2	2		
22	iTA	GTAGTCCACG	2	2		
23						
24	c	GTAGTCCACG	1	1	2	1
25	AGT	GTAGTCCACG	1	1		
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27	TG					
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29	CTA					
30	GTG	GTAGTCCACA	1	1		
31	TCG	GTAGTCTATG	1	1		
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33	g	GTAGTCCACG	1	1	125	1
34	f	GTAGTCCACA	1	1	2	1
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36	GGT	GTAGTCCACG	1	1		
37	g	GTAGTCCACG	1	1	10	1
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39	iTA					
40	ATC	GTAGTCCACG	1	1		
41	TTG					
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43	iGC	GTAGTCCGCA	1	1		
44	GTC	GTAGTCCACA	1	1		
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46	CGG	GTAGTCCACG	1	1		
47	TAG					
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49	CCT	GTAGTCCACG	1	1		
50	TGC	GTAGTCTATG	2	2		
51	CTC	GTAGTCCACG	2	2		
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56	GTG	GTAGTCCACA	1	1		
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5	TAG	GTAGTCCACG	1	1			
6	AGC	GTAGTCTTAA	1	1			
7	TGC	GTAGTCTATG	1	1			
8	ATT	GTAGTCCACG	1	1			
9	GAT	GTAGTCTCAA	1	1			
10	GTC	GTAGTCCACA	1	1			
11	TCT	GTAGTCTTAA	1	1			
12	GTC	GTAGTCCACA	1	1			
13	TTT	GTAGTCCCAG	1	1			
14	GTC	GTAGTCCACA	1	1			
15	CTG	GTAGTCCACG	1	1			
16	TA	GTAGTCCACG	1	1			
17	AATT						
18	CGA	GTAGTCTTAA	1	1			
19	TGC	GTAGTCTATG	2	2			
20	TGC	GTAGTCTATG	2	2			
21	TGC						
22	CAT	CTAGTCTTAA	2	2			
23	TGC	GTAGTCTATG	2	2			
24	ATC	GTAGTCCACG	2	2			
25	TGC						
26	TGA						
27	CTG						
28	GTG	GTAGTCCACG	1	1			
29	ATT	CTAGTCTTAA	1	1			
30	GGG	GTAGTCCACG	1	1			
31	CGG	GTAGTCCACG	1	1			
32	TGA	GTAGTCCAAA	1	1			
33	CA	GTAGTCCTAG	1	1			
34	GTC						
35	CTG	GTAGTCCATG	1	1			
36	GGA						
37	f	GTAGTCTTGG	1	1	3	1	
38	g	GTAGTCTTAA	1	1	17	1	
39	AGT	GTAGTCCACG	1	1			
40	CTG						
41	CGG	GTAGTCCATG	1	1			
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4	.GT	GTAGTCCACG	1	1		
5	GCC	CTAGTCTTAA	1	1		
6	ATGA	GTAGTCTTAA	1	1		
7	CTC	GTAGTCCACG	1	1		
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9	g	GTAATCCTAG	1	1	4	1
10	GAC	GTAGTCCGCA	1	1		
11	GTAT	GTAGTCTTAA	1	1		
12	CGC	GTAGTCCACG	1	1		
13	AGA	GTAGTCTCAA	1	1		
14	GG	GTAGTCCACG	1	1		
15	CAG	GTAGTCCACG	1	1		
16	GTG	GTAGTCCACG	1	1		
17	CTAG	GTAGTCCACG	1	1		
18	CGG	GTAATCCTAG	1	1		
19	ATG	GTAGTCTTAA	1	1		
20	ATTA					
21	ATG	GTAGTCTTAA	1	1		
22	TTGA					
23	GTG	GTAGTCCACG	1	1		
24	p	GTAGTCTTAA	1	1	3	1
25	CTC	GTAGTCTTAA	1	1		
26	TTA	GTAGTCCACG	1	1		
27	GTG	GTAGTCCACG	1	1		
28	ATC	GTAGTCCACG	1	1		
29	o	GTAGTCCTAG	1	1	5	1
30	CAG	GTAGTCCACG	1	1		
31	ATG	GTAGTCCTGG	1	1		
32	CTG	GTAGTCCACG	1	1		
33	CGT	GTAGTCCACG	1	1		
34	f	GTAGTCTTAG	1	1	9	1
35	GAG	GTAGTCCACG	1	1		
36	CGGT	GTAGTCCACG	1	1		
37	CA	GTAGTCCACG	1	1		
38	AGT	GTAGTCCACG	1	1		
39	GGT	GTAGTCCTAG	1	1		
40	GTC	GTAGTCCACA	1	1		
41	TAG					
42	TATC	GTAGTCCACG	1	1		
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4	CAA						
5	ATG	GTAGTCTTAA	1	1			
6	TA	GTAGTCCACG	1	1			
7	AG	GTAGTCCACG	1	1			
8	AC	GTAGTCCACG	1	1			
9	g	GTAGTCCTGG	1	1	4		1
10	AT						
11	g	GTAGTCCACG	1	1	2		1
12	GTG	GTAGTCCACG	1	1			
13	AC	GTAGTCCACG	1	1			
14	AC	GTAGTCTTAA	1	1			
15	TA	GTAGTCCACG	1	1			
16	g				2		1
17	AGT	GTAGTCCACG	1	1			
18	AGA	GTAGTCTCAA	1	1			
19	TC						
20	TC	GTAGTCCACG	1	1			
21	f	GTAGTCCACG	1	1	13		1
22	g	GTAGTCCACG	1	1	11	0.81818182	
23	TC	GTAGTCCACG	1	1			
24	g	GTAGTCCACG	1	1	202	0.99009901	
25	TCT	GTAGTCCATG	1	1			
26	TA	GTAGTCCACG	1	1			
27	CGA	GTAGTCTCAA	1	1			
28	AC						
29	ACT	GTAGTCCTGG	1	1			
30	CCG	GTAGTCCACG	1	1			
31	GT	GTAGTCCACG	1	1			
32	GTG	GTAGTCCACG	1	1			
33	ATC	GTAGTCCACG	1	1			
34	AAT	GTAGTCCTAA	1	1			
35	AG	GTAGTCCACG	1	1			
36	AGA	GTAGTCTCAA	1	1			
37	AC	GTAGTCCACG	1	1			
38	TGAC	GTAGTTCAAA	1	1			
39	TA	GTAGTCCTAG	1	1			
40	GTT	GTAGTCCATG	1	1			
41	TA	GTAGTCCACG	1	1			
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4	GG	GTAGTCCACG	1	1		
5	CTA	GTAGTCCACG	1	1		
6	CTC					
7	TGA					
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9	TG	GTAGTCCTGG	1	1		
10	GTG	GTAGTCCACG	1	1		
11						
12	g	GTAGTCCACG	1	1	2	1
13	AGC	GTAGTCCACG	1	1		
14	AGA	GTAGTCTCAA	1	1		
15	TTG	GTAGTCCACG	1	1		
16	f	GTAGTCCACG	1	1	27	0.96296296
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18	ATA	GTAGTCTTAA	1	1		
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20	GT	GTAGTCCACG	1	1		
21	CTC	GTAGTCCACG	1	1		
22	CTA					
23	CTG	GTAGTCCTAA	1	1		
24	TGA	CTAGTTCTGA	1	1		
25	CGC	GTAGTCTTAA	1	1		
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27	g				2	1
28	AG	GTAGTCCACG	1	1		
29	CAG	GTAGTCCACG	1	1		
30	AC					
31	CTA					
32	ATG	GTAGTCTTAA	1	1		
33	GAC	GTAGTCTCAA	1	1		
34	TGA	CTAGTTCTGA	1	1		
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36	GTG	GTAGTCCACG	1	1		
37	CTG	GTAGTCCTGG	1	1		
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39	GC	GTAGTCCGCA	1	1		
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41	GTC	GTAGTCCACA	1	1		
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43	CC	CTAGTTCTGA	1	1		
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45	GC	GTAGTCCACG	1	1		
46	AAC	GTAGTCCTAA	1	1		
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4	CTG						
5	CCG	GTAGTCCACG	1	1			
6	AGT	GTAGTCCACG	1	1			
7	CAC	CTAGTCTTAA	1	1			
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9	GGG						
10	GTC	GTAGTCCACA	1	1			
11	CAG	GTAATCCTAG	1	1			
12	AC	GTAGTCCACG	1	1			
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17	AG	GTAGTCCACG	1	1			
18	TCG	GTAGTCCTAG	1	1			
19	TAAC	GTAGTCCTAA	1	1			
20	CAG	GTAGTCCACG	1	1			
21	GTG	GTAGTCCACG	1	1			
22	TG						
23	TGA	CTAGTTCTGA	1	1			
24	AGA	GTAGTCTCAA	1	1			
25	ATA	GTAGTCCACG	1	1			
26	GGT	GTAGTCCACG	1	1			
27	CCG	GTAGTCCACG	1	1			
28	AG	GTAGTCCTAG	1	1			
29	TCGG						
30	g	GTAGTCCACG	1	1	3		1
31	GGG	GTAGTCCTAG	1	1			
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33	GTC						
34	CGT	GTAGTCCACA	1	1			
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37	CA	GTAGTCCTAG	1	1			
38	AC	GTAGTCCACG	1	1			
39	GTC	GTAGTCCACA	1	1			
40	g	GTAGTCTTAA	1	1	46	0.86956522	
41	TAG	GTAGTCCACG	1	1			
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43	CTG	GTAGTCCACG	1	1			
44	TG	GTAGTCCTG	1	1			
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3	f	GTAGTCCGCC	1	1	2	1	
4							
5	iCTA						
6	f				5	1	
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8	GC	GTAGTCCACA	1	1			
9	ATC						
10	TGC	GTAGTCTATG	2	2			
11	GAG	GTAGTCCACG	2	2			
12	GAG	GTAGTCCACG	2	2			
13	GAG	GTAGTCCACG	2	2			
14	GAG	GTAGTCCACG	2	2			
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16	CTA						
17	iCTA						
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19	TGC	GTAGTCTATG	2	2			
20	TTC	GTAGTCCACG	1	1			
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22	g	GTAGTCCACG	1	1	3	1	
23	GTC	GTAGTCCACA	1	1			
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26	iTT	GTAGTCTACG	1	1			
27	iAC	GTAGTCCGCA	1	1			
28							
29	TAT						
30	GAG	GTAGTCCACG	1	1			
31	TG	GTAGTCCACG	1	1			
32							
33	o	GTA	1	1	170	0.94117647	
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36	AGA	GTAGTCTCAA	1	1			
37	TA	GTAGTCCACG	1	1			
38	ATGA	GTAGTCTTAA	1	1			
39	AGA	GTAGTCTCAA	1	1			
40							
41	ACA						
42							
43	GT	GTAGTCCACG	1	1			
44	TC	GTAGTCCACG	1	1			
45							
46	o				13	0.92307692	
47	GA	GTAGTCCACG	1	1			
48	ATG	GTAGTCTTAA	1	1			
49	iTA	GTAGTCCACG	1	1			
50	iTA						
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52	GC	GTAGTCCACG	1	1			
53	GTC	GTAGTCCACG	1	1			
54	ATC	GTAGTCCACG	1	1			
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56							
57							
58							
59							
60							

3	GCC	GTAGTCCATG	1	1		
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5	g	GTAGTCCTGG	1	1	2	1
6	GAG	GTAGTCCACG	1	1		
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8	CGC	GTAGTCCTGG	1	1		
9	g	GTAGTCCACG	1	1	826	0.98910412
10	ATA	GTAGTCCACG	1	1		
11	GAC	GTAGTCTTAA	1	1		
12	AGA	GTAGTCTCAA	1	1		
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14	GAA	GTAGTCCACG	1	1		
15	TGAC	GTAGTCTTAA	1	1		
16	ACG	GTAGTCTTAA	1	1		
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18	TGA					
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20	GGG	GTAGTCTCAA	1	1		
21	GAC	GTAGTCTTAA	1	1		
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23	ATGA	GTAGTCTTAA	1	1		
24	CAG	GTAGTCCACG	1	1		
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26	CAG	GTAGTCCACG	1	1		
27	CCG	GTAGTCCTAG	1	1		
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29	TAG					
30	CGA	GTAGTCTCAA	1	1		
31	ATC	GTAGTCCACG	1	1		
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33	GC	GTAGTCCACG	1	1		
34	g	GTAGTCCACG	1	1	2	1
35	TCG	GTAGTCCACG	1	1		
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37	g				4	1
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39	GAG					
40	TCG	GTAGTCCACG	1	1		
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43	GTG	GTAGTCTTAA	1	1		
44	CCA	GTAGTCCTAG	1	1		
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46	TAG					
47	AAG					
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49	GTG	GTAGTCTACA	1	1		
50	ATC	GTAGTCCACG	1	1		
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53	GAA	GTAGTCCTAA	1	1		
54	GGT	GTAGTCCACG	1	1		
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56	TCG	GTAGTCCACG	1	1		
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5	TAT	GTAGTCTTAA	1	1		
6	AGA					
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8	AGA	GTAGTCTCAA	1	1		
9	CGA	GTAGTCTCAA	1	1		
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11	GAG	GTAGTCCACG	1	1		
12	ATG					
13	GG	GTAGTCCTAG	1	1		
14	GTC	GTAGTCCACA	1	1		
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16	TAAC	GTAGTCCTAA	1	1		
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18	AGA	GTAGTCTCAA	1	1		
19	AGT	GTAATCCTAG	1	1		
20	TA	GTAGTCCACG	1	1		
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22	CAG	GTAGTCCACG	1	1		
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24	AGA	GTAGTCTCAA	1	1		
25	GACG	GTAGTCTTAA	1	1		
26	GAC					
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28	g	GTAGTCCACG	1	1	2	1
29	TAAC	GTAGTCCTAA	1	1		
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35	CGA	GTAGTCTCAA	1	1		
36	TGA	GTAGTCTCAA	1	1		
37	GAG					
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39	GTG	GTAGTCCTTG	1	1		
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42	GGC	GTAGTCCACG	1	1		
43	AGA					
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46	AGT	GTAGTCCACG	1	1		
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48	GTC	GTAGTCCACA	1	1		
49	AC	GTAGTCCACG	1	1		
50	AC	GTAGTCCACG	1	1		
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52	ITC					
53	GGT	GTAGTCCACG	1	1		
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56	CGC					
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6	AGG	GTAGTCCACG	1	1		
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8	g	GTAGTCCACG	1	1	12	1
9	CGG	GTAGTCCTAG	1	1		
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11	GCC	GTAGTCCACG	1	1		
12	AT	CTAGTCTTAA	1	1		
13	CAG	GTAGTCCACG	1	1		
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15	GG	GTAGTCCTAG	1	1		
16	TCG	GTAGTCTACG	1	1		
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18	GTG					
19	TAG	GTAGTCCACG	1	1		
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21	f	GTAGTCCTAG	1	1	3	1
22	TAG	GTAGTCCACG	1	1		
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24	CCT	CTAGTCTTAA	1	1		
25	ATC	GTAGTCCACG	1	1		
26	AG	GTAGTCCACG	1	1		
27	TA	GTAGTCCACG	1	1		
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29	CGA	GTAGTCTCAA	1	1		
30	GAC	GTAGTCTCAA	1	1		
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51	AT	CTAGTCTTAA	1	1		
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5	CGA	GTAGTCTCAA	1	1		
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11	ATC	GTAGTCCACG	1	1		
12	AGA	GTAGTCTCAA	1	1		
13	TCC	GTAGTCCACG	1	1		
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15	ITA	GTAGTCCACG	1	1		
16	ITG	GTAGTCCACG	1	1		
17	AG	GTAGTCCACG	1	1		
18	GCC	CTAGTCTTAA	1	1		
19	GAA					
20	GG	GTAGTCCACG	1	1		
21	g	GTAGTCCACG	1	1	25	0.88
22	f	GTAGTCCACG	1	1	5	0.8
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24	CCCG	GTAGTCCTAG	1	1		
25	ITC	GTAGTCCACG	1	1		
26	ATG	GTAGTCTTAA	1	1		
27	GTC	GTAGTCCACA	1	1		
28	ITA	GTAGTCCACG	1	1		
29	GCT	GTAGTCCACA	1	1		
30	TCG	GTAGTCCACG	1	1		
31	f	GTAGTCCACG	1	1	2	1
32	CAG					
33	CGC	GTAGTCCACG	1	1		
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35	TGA	GTAGTCCAAA	1	1		
36	GCG					
37	AGT					
38	GG	GTAGTCCAAC	1	1		
39	AG					
40	GCC	CTAGTCTTAA	2	2		
41	GTC	GTAGTCCACG	2	2		
42	AG	GTAGTCCACG	2	2		
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5	TG	GTAGTCCTTG	2	2	
6	CTA				
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8	AGCC	GTAGTCCATG	1	1	
9	GTC	GTAGTCCACA	1	1	
10	TAG	GTAGTCCACG	1	1	
11	TGA	GTAGTCTCGA	1	1	
12	CAA	GTAGTCTCAA	1	1	
13	CTG	GTAGTCCTTG	1	1	
14	TAAC	GTAGTCCTAA	1	1	
15	g	GTAGTCCACG	1	1	322 0.99068323
16	CCGG				
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18	CTGC	GTAGTCCACG	1	1	
19	ATC	GTAGTCCACG	1	1	
20	GGT				
21	TGA	GTAGTCCAAA	1	1	
22	GG	GTAGTCCTAG	1	1	
23	AGT	GTAGTCCACG	1	1	
24	TAT	GTAGTCTTAA	1	1	
25	CGA	GTAGTCTCAA	1	1	
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27	CAT	CTAGTCTTAA	1	1	
28	CGT	GTAGTCCACG	1	1	
29	TAAT	GTAGTCCTAA	1	1	
30	TA	GTAGTCCACG	1	1	
31	TCG	GTAGTCCACG	1	1	
32	TA				
33	g	GTAGTCTTAA	1	1	41 0.82926829
34	GTC	GTAGTCCACA	1	1	
35	AC	GTAGTCCGCA	1	1	
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37	TAG	GTAGTCCACG	1	1	
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39	TGA				
40	AGA	GTAGTCTCAA	1	1	
41	GTC	GTAGTCCACG	1	1	
42	GGA	GTAGTCTCAA	1	1	
43	TGA				
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6	ATA						
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9	CA	GTAGTCCTAG	1	1			
10	CTG						
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12	CGG	GTAGTCCACG	1	1			
13	TGA						
14							
15	TCG						
16	ATC	GTAGTCCACG	1	1			
17	GGC	GTAGTCCGCA	1	1			
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21	GGT	GTAGTCCACG	1	1			
22	TAG	GTAGTCCATG	1	1			
23							
24	ATC	GTAGTCCACG	1	1			
25	AGA	GTAGTCTCAA	1	1			
26	ACC						
27							
28	CTG	GTAGTCCACG	1	1			
29	GAC	GTAGTCCACG	1	1			
30	GCC	CTAGTCTTAA	1	1			
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32	CAG	GTAATCCTAG	1	1			
33	GTC						
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35	GG	GTAGTCCACG	1	1			
36	CTG	GTAGTCCTGG	1	1			
37	g	GTAGTCCTAT	1	1	2		1
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39	CA	GTAGTCCTAG	1	1			
40	TG	GTAGTCTACA	1	1			
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43	ATC						
44	CGA	GTAGTCTCAA	1	1			
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47	TCCC	GTAGTCCTGG	1	1			
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49	GCTT	GTAGTCCCAA	1	1			
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52	g	GTAGTCCTGG	1	1	22	0.95454545	
53	CGA	GTAGTCTCAA	1	1			
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56	GTG	GTAGTCCACG	1	1			
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GCC	CTAGTCTTAA	1	1		
o	GTAGTCCACG	1	1	2	1
iTA	GTAGTCCACG	1	1		
iGCT	GTAGTCCCAA	1	1		
CGA	GTAGTCTCAA	1	1		
CGT	GTAGTCCACG	1	1		
CAG	GTAGTCCACG	1	1		
CGG	GTAGTCCACG	1	1		
.TCC	GTAGTCCACG	1	1		
ATG	GTAGTCCTGG	1	1		
CGG	GTAGTCCACG	1	1		
CAG	GTAGTCCACG	1	1		
CAT	CTAGTCTTAA	1	1		
TAG	GTAGTCTCAA	1	1		
CAG	GTAGTCCACG	1	1		
GTC	GTAGTCCACA	1	1		
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GG					
TA	GTAGTCCACG	1	1		
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TCG					
GAG	GTAGTCCACG	1	1		
\AG					
iTA					
GGG	GTAGTCCACG	2	2		
AG	GTAGTCCACG	2	2		

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6	g	GTAGTCTTAA	1	1	14	1
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8	GTC	GTAGTCCACA	1	1		
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10	GTC	GTAGTCCACA	1	1		
11	GTC	GTAGTCCACA	1	1		
12	TGC	GTAGTCTATG	1	1		
13	GTC					
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15	g	GTAGTCCACG	1	1	7	1
16	GCG	GTAGTCCTAG	1	1		
17	GCG	GTAGTCCACG	1	1		
18	GCG	GTAGTCCACG	1	1		
19	g	GTAGTCCACG	1	1	38	1
20	g	CTAGTCTTAA	1	1	6	1
21	GGA	GTAGTCCACA	1	1		
22	GGA	GTAGTCCACA	1	1		
23	ACG	GTAGTCCACG	1	1		
24	ACG	GTAGTCCACG	1	1		
25	TAG	GTAGTCCACG	2	2		
26	CTGA	GTAGTCTTAA	2	2		
27	TAG	GTAGTCCACG	1	1		
28	TAG	GTAGTCCACG	1	1		
29	GGA	GTAGTCTCAA	1	1		
30	ATA	GTAGTCCACG	1	1		
31	ATC	GTAGTCCACA	1	1		
32	ATC	GTAGTCCACA	1	1		
33	f	GTAGTCCACG	1	1	16	1
34	ATG	GTAGTCTTAA	1	1		
35	ATG	GTAGTCTTAA	1	1		
36	AGAG	GTAGTCCTAA	1	1		
37	GG					
38	GGT	GTAGTCCTAG	1	1		
39	GGT	GTAGTCCTAG	1	1		
40	g	GTAGTCCACG	1	1	54	0.90740741
41	GGT	GTAGTCCTAG	1	1		
42	GGT	GTAGTCCTAG	1	1		
43	ATA					
44	GTC	GTAGTCCACA	1	1		
45	ATC	GTAGTCTTAA	1	1		
46	ATC	GTAGTCTTAA	1	1		
47	ATG	GTAGTCTTAA	1	1		
48	ATC	GTAGTCCACG	1	1		
49	ATC	GTAGTCCACG	1	1		
50	CAG	GTAGTCCACG	1	1		
51	CACC	GTAGTCCTAG	1	1		
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53	AT	CTAGTCTTAA	1	1		
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55	AT	CTAGTCTTAA	1	1		
56	CTC	GTAGTCCATG	1	1		
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CGG	GTAGTCCACG	1	1		
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GTC	GTAGTCCACG	1	1		
ATAT					
GAG	GTAGTCCACG	1	1		
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TGA	GTAGTCCAAA	1	1		
g	GTAGTCCACG	1	1	269	0.97769517
AGT	GTAGTCCACG	1	1		
g	GTAGTCCACG	1	1	2	1
AC	GTAGTCTTAA	1	1		
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AC	GTAGTCCACG	1	1		
g	GTAGTCCACG	1	1	556	0.98561151
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TA	GTAGTCCACG	1	1		
GAG	GTAGTCCACG	1	1		
TA	GTAGTCCACG	1	1		
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TGA	GTAGTCCAAA	1	1		
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GTG	GTAGTCCACG	1	1		
g	GTAGTCCACA	1	1	8	1
GTG	GTAGTCCTAG	1	1		
GGG	GTAGTCCTAG	1	1		
ATC	GTAGTCCACG	1	1		
GTC	GTAGTCCACA	1	1		
CA					
CGT	GTAGTCCCAG	1	1		
AC	GTAGTCTTAA	1	1		
ATG	GTAGTCTTAA	1	1		
CAG	GTAGTCCACG	1	1		
GTC	GTAGTCCACG	1	1		
AC	GTAGTCCACG	1	1		
ACT	GTAGTCCACG	1	1		
GTC	GTAGTCCACG	1	1		

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4	TGA				
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6	GCC	GTAGTCCACG	1	1	
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8	g				45 1
9	CAT	CTAGTCTTAA	1	1	
10	AC	GTAGTCTTAA	1	1	
11					
12	TGC	GTAGTCCACG	1	1	
13	TT	GTAGTCCACG	1	1	
14					
15	AGA	GTAGTCTCAA	1	1	
16	CAG	GTAGTCCACG	1	1	
17	AG	GTAGTCCACG	1	1	
18					
19	GG	GTAGTCCACG	1	1	
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21	TC				
22	AG	GTAGTCCACG	1	1	
23	GCC	GTAGTCCACG	1	1	
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25	TA				
26	ATC	GTAGTCCACG	1	1	
27	GG	GTAGTCCTAG	1	1	
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29	AG	GTAGTCCACG	1	1	
30	AC	GTAGTCTTAA	1	1	
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32	GAG	GTAGTCCACG	1	1	
33	CCC	GTAGTCCTAG	1	1	
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37	GAG	GTAGTCCACG	1	1	
38					
39	ATC	GTAGTCCACG	1	1	
40	CGA	GTAGTCTCAA	1	1	
41					
42	TG	GTAGTCCACG	1	1	
43	GAC	GTAGTCTCAA	1	1	
44	CGA	GTAGTCTCAA	1	1	
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47	TGT	GTAGTCCACG	1	1	
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49	CT	GTAGTCCTAG	1	1	
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52	CAG				
53	GAG	GTAGTCCACG	1	1	
54	GTC	GTAGTCCACA	1	1	
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56	ATC	GTAGTCCACG	1	1	
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ACC	GTAGTCCACG	1	1		
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GTC					
AC	GTAGTCTTAA	1	1		
AA					
ATG	GTAGTCTTAA	1	1		
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TTT	CTAGTCTTAA	1	1		
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TA	GTAGTCCACG	1	1		
GCC	GTAGTCCATG	1	1		
GAC	GTAGTCTCAA	1	1		
ACT	GTAGTCCTAG	1	1		
AC	GTAGTCTTAA	1	1		
TCC	GTAGTCCACG	1	1		
GGG	GTAGTCCAAC	1	1		
GA					
g	GTAGTCCACA	1	1	2	1
CAC	GTAGTCCACG	1	1		
g	GTAGTCCACG	1	1	3	1
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CAT	GTAATCCTAG	1	1		
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GGT	GTAGTCCACG	1	1		
ATGA	GTAGTCTTAA	1	1		
CTCT	GTAGTCCTAG	1	1		
CCG	GTAGTCCACA	1	1		
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TTC	GTAGTCCTGG	1	1		
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AGT	GTAGTCCACG	1	1		
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CGC	GTAGTCCACG	1	1		
ATC	GTAGTCCACG	1	1		



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6	ATA	GTAGTCCACG	1	1		
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13	ATG	GTAGTCTCAA	1	1		
14	CAG	GTAATCCTAG	1	1		
15	TGA					
16	TGA					
17	ATC	GTAGTCCACG	1	1		
18	ATT	GTAGTCCACG	1	1		
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21	ATC	GTAGTCCGCA	1	1		
22	ATG	GTAGTCCACG	2	2		
23	ATG	GTAGTCCACG	2	2		
24	ATG	GTAGTCCACG	2	2		
25	ATC	GTAGTCCACG	2	2		
26	ATG	GTAGTCTTAA	2	2		
27	ATG	GTAGTCCACG	2	2		
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46	ATC	GTAGTCCACG	1	1		
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56	ATG	GTAGTCTTAA	1	1		
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5	TTG	GTAGTCCCAG	1	1			
6	GTC	GTAGTCCACG	1	1			
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8	ATC	GTAGTCCACG	1	1			
9	TAG	GTAGTCCACG	1	1			
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12	GTG	GTAGTCCACG	1	1			
13	ACT	GTAGTCTTGA	1	1			
14	TC	GTAGTCCACG	1	1			
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16	g	GTAGTCCTAG	1	1	3		1
17	GG	GTAATCCTAG	1	1			
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19	CACA						
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21	TG						
22	CCC	GTAGTCCAAG	1	1			
23	TG	GTAGTCCTTG	1	1			
24	TTG	CTAGTCTTAA	1	1			
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26	CTG						
27	TA						
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33	GTG	GTAGTCCACG	1	1			
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35	GTC	GTAGTCCACG	1	1
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8	TCC	GTAGTCTTAA	1	1	
9	TG	GTAGTCCTTG	1	1	
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34	GTG	GTAGTCCACG	1	1	
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36	GA	CTAGTTCAAA	1	1	
37	TGA	GTAGTCTCAA	1	1	
38	g	GTAGTCCACG	1	1	36 1
39	TGA	GTAGTCTCAA	1	1	
40	TGA	GTAGTCTCAA	1	1	
41	TTT				

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4	AGT	GTAGTCTTAA	1	1		
5	TTTA					
6	GT					
7	GT					
8	GT					
9	GGG	GTAGTCCTAG	1	1		
10	TGG	GTAGTCCACG	1	1		
11	GGG	GTAGTCCTAG	1	1		
12	GT	GTAGTCCACG	1	1		
13	TA	GTAGTCCACG	1	1		
14	TA	GTAGTCCACG	1	1		
15	AG					
16	AG					
17	AG	GTAGTCCACG	1	1		
18	AG	GTAGTCCACG	1	1		
19	AG	GTAGTCCACG	1	1		
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22	AG	GTAGTCCACG	1	1		
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24	AG					
25	AG					
26	AG	GTAGTCCACG	1	1		
27	AG	GTAGTCCACG	1	1		
28	g	GTAGTCCACG	1	1	3	1
29	GCC	CTAGTCTTAA	1	1		
30	CAG					
31	CTA					
32	CAG	GTAGTCCACG	1	1		
33	TAG	GTAGTCCACG	1	1		
34	AG	GTAGTCCACG	1	1		
35	GCC	CTAGTCTTAA	1	1		
36	TAC	GTAGTCCACG	1	1		
37	TAG	GTAGTCCACG	1	1		
38	TAA	GTAGTCCACG	1	1		
39	TA	GTAGTCCACG	1	1		
40	AGA					
41	CAG	GTAGTCCACG	1	1		
42	ATC	GTAGTCCACG	1	1		
43	TA	GTAGTCCACG	1	1		
44	ATC	GTAGTCCACG	1	1		
45	TAC					
46	AGA	GTAGTCTCAA	1	1		
47	g	GTAGTCCACG	1	1	16	1
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3	GCC	CTAGTCTTAA	1	1		
4					2	1
5	g					
6	GAG	GTAGTCCACG	1	1		
7	ATC	GTAGTCCACG	1	1		
8	GCC	CTAGTCTTAA	1	1		
9	TAG					
10	GAG	GTAGTCCACG	1	1		
11	GCC	CTAGTCTTAA	1	1		
12	AG	GTAGTCCACG	1	1		
13	GAG	GTAGTCCACG	1	1		
14	TAG	GTAGTCCACG	1	1		
15	AG	GTAGTCCACG	1	1		
16	TAG	GTAGTCCACG	1	1		
17	AG	GTAGTCCACG	1	1		
18	TAG	GTAGTCCACG	1	1		
19	TCC	CTAGTCTTAA	1	1		
20	GCC	CTAGTCTTAA	1	1		
21	ATA	GTAGTCCACG	1	1		
22	GCC	CTAGTCTTAA	1	1		
23	GAC	GTAGTCCGCA	1	1		
24	GCC	CTAGTCTTAA	1	1		
25	GTC					
26	GAG	GTAGTCCACG	1	1		
27	GCC	CTAGTCTTAA	1	1		
28	CGG	GTAGTCCACG	1	1		
29	GCC	CTAGTCTTAA	1	1		
30	ATA	GTAGTCCACG	1	1		
31	ATA					
32	GAG	GTAATCCACG	1	1		
33	AAG	GTAGTCCACG	1	1		
34	ATA	GTAGTCCACG	1	1		
35	GAG					
36	ATA					
37	GAC	GTAGTCCGCA	1	1		
38	TTGA	CTAGTTCTGA	1	1		
39	GCC	CTAGTCTTAA	1	1		
40	GAC	GTAGTCTTAA	1	1		
41	TAA	GTAGTCCACG	1	1		
42	TAG	GTAGTCCACG	1	1		
43	AGA	GTAGTCTCAA	1	1		



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4	CAG	GTAGTCCACG	1	1		
5	CAG					
6	CGA	GTAGTCTCAA	1	1		
7	AC	GTAGTCTTAA	1	1		
8	ATA	GTAGTCCACG	1	1		
9	CAG	GTAGTCCACG	1	1		
10	AC	GTAGTCCACG	1	1		
11	ATC	GTAGTCCACG	1	1		
12	ACC	CTAGTCTTAA	1	1		
13	ATG	GTAGTCCACG	1	1		
14	ATA	GTAGTCCACG	1	1		
15	ATG					
16	CAG					
17	ATA	GTAGTCCACG	1	1		
18	ATG					
19	CAG					
20	ATA	GTAGTCCACG	1	1		
21	G	GTAGTCCACG	1	1	2	1
22	ATC					
23	ACC	CTAGTCTTAA	1	1		
24	ACC					
25	ATC	GTAGTCTTAA	1	1		
26	ATC	GTAGTCTTAA	1	1		
27	ATC	GTAGTCTTAA	1	1		
28	CAG	GTAGTCCACG	1	1		
29	ATC	GTAGTCCACG	1	1		
30	G	GTAGTCCACG	1	1	2	1
31	ACC	CTAGTCTTAA	1	1		
32	ATC	GTAGTCCACG	1	1		
33	AC	GTAGTCTTAA	1	1		
34	CAG	GTAGTCCACG	1	1		
35	ATG	GTAGTCCACG	1	1		
36	CAG	GTAGTCCACG	1	1		
37	CAG					
38	AC	GTAGTCTTAA	1	1		
39	GCC	CTAGTCTTAA	1	1		
40	GCC	CTAGTCTTAA	1	1		
41	TA	GTAGTCCACG	1	1		
42	CAG	GTAGTCCACG	1	1		
43	GCC	CTAGTCTTAA	1	1		
44	CTA	GTAGTCCACG	1	1		
45	TGA	GTAGTCTTAA	1	1		
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4	CAG						
5	CTA	GTAGTCCACG	1	1			
6	CTA						
7	CTA	GTAGTCCACG	1	1			
8	CTA						
9	ICA						
10	ICTA	GTAGTCCACG	1	1			
11	TGA	GTAGTCTTAA	1	1			
12	TGA	GTAGTCTTAA	1	1			
13	TGA	GTAGTCTTAA	1	1			
14	CAT	CTAGTCTTAA	1	1			
15	CAT						
16	CTA						
17	TTGA	GTAGTCTTAA	1	1			
18	TTG	GTAGTCCTTG	1	1			
19	TTG						
20	ICTA						
21	GTC	GTAGTCCACA	1	1			
22	GTC	GTAGTCCACA	1	1			
23	GTC	GTAGTCCACA	1	1			
24	GAT	CTAGTCTTAA	1	1			
25	GAT	CTAGTCTTAA	1	1			
26	ATC	GTAGTCCACG	1	1			
27	GTC	GTAGTCCACA	1	1			
28	GTC	GTAGTCCACA	1	1			
29	f	GTAGTCCACG	1	1	4		1
30	GTC						
31	GTC						
32	CAT	CTAGTCTTAA	1	1			
33	GGC	GTAGTCCGCA	1	1			
34	GGC	GTAGTCCGCA	1	1			
35	CAT	CTAGTCTTAA	1	1			
36	TA						
37	CAT	CTAGTCTTAA	1	1			
38	CAT	CTAGTCTTAA	1	1			
39	GTG	GTAGTCCACG	1	1			
40	GTC	GTAGTCCACA	1	1			
41	GTC	GTAGTCCACA	1	1			
42	GTC	GTAGTCCACA	1	1			
43	IAA	GTAGTCCACG	1	1			
44	IAA	GTAGTCCACG	1	1			
45	GTC	GTAGTCCACA	1	1			
46	GTC	GTAGTCCACA	1	1			
47	GTC	GTAGTCCACA	1	1			
48	g	GTAGTCCACA	1	1	5		0.8
49	TTGA	GTAGTCTTAA	1	1			
50	GTG	GTAGTCCACG	1	1			
51	GTG	GTAGTCCACG	1	1			
52	ATC	GTAGTCCACG	1	1			
53	GAG	GTAGTCCACG	1	1			
54	GGC	GTAGTCCGCA	1	1			
55	GGC	GTAGTCCGCA	1	1			
56	ATC	GTAGTCCACG	1	1			
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4	ATC	GTAGTCCACG	1	1
5	TG	GTAGTCCTTG	1	1
6	TGA	GTAGTCTTAA	1	1
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8	CTAT	CTAGTCTTAA	1	1
9	TTGA	GTAGTCTTAA	1	1
10	GTT	GTAGTCCACA	1	1
11	ATC	GTAGTCCACG	1	1
12	TAC	GTAGTCTATG	1	1
13	TGA	GTAGTCTTAA	1	1
14	CTA	GTAGTCCACG	1	1
15	ICTA			
16	TGA			
17	GGC	GTAGTCCTAG	1	1
18	ATC	GTAGTCCACG	1	1
19	CTATA			
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21	ATC	GTAGTCCACG	1	1
22	GGC	GTAGTCCGCA	1	1
23	TTGG	GTAGTCTTAA	1	1
24	TGC	GTAGTCTATG	1	1
25	TGC	GTAGTCTATG	1	1
26	TGA			
27	ATC			
28	GAG	GTAGTCCACG	1	1
29	GTT	GTAGTCCACA	1	1
30	TGA	GTAGTCTATG	1	1
31	GAC	GTAGTCCACA	1	1
32	GTC	GTAGTCCACA	1	1
33	TGA	GTAGTCTTAA	1	1
34	TTG	GTAGTCCACG	1	1
35	AAG	GTAGTCCACG	1	1
36	GTG	GTAGTCCACG	1	1
37	CTA	GTAGTCCACG	1	1
38	TG	GTAGTCCTTG	1	1
39	TAG	GTAGTCCACG	1	1
40	ICTA	GTAGTCCACG	1	1
41	TTG			
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CTA	GTAGTCCACG	1	1
CTA	GTAGTCCACG	1	1
TGA	GTAGTCTTAA	1	1
CTA			
GCC			
CTA	GTAGTCCACG	1	1
AGC	GTAGTCTATT	1	1
CTA	GTAGTCCACG	1	1

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5	Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
6	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac
7	Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymeno	Carchesium
8						
9	Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
10						
11	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Zoogloea
12						
13	Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
14						
15	Eukaryota	Gracilipodida			Filamoeba	
16	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
17						
18	Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Spirochaetac	Spirochaeta
19	Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona	Nitrosomonas
20						
21	Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Thermomona
22	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Thauera
23	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagace	Chryseolinea
24						
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26	Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
27						
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29	Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydi	Candidatus Pr
30	Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria	Flavobacteriu
31						
32	Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17	
33	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
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37	Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae	
38						
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40	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	Blvii28 waste
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42	Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
43						
44	Eukaryota	Metazoa				
45						
46	Eukaryota	Basidiomycot	Tremellomyc	Tremellales	Trichosporon	Trichosporon
47	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
48						
49						
50	Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
51						
52						
53	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
54	Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
55						
56	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
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Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Ornatilinea
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales		
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	Elizabethkingia
Eukaryota	Ciliophora	Intramacronucleus	Conthreop	Oligohymenophorea	
Bacteria	Bacteroidetes	Sphingobacteriales	Sphingobacteriales	Chitinophagaceae	
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Candidatus Clostridia
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	NS9 marine group	
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	
Bacteria	Bacteroidetes	Sphingobacteriales	Sphingobacteriales	Chitinophagaceae	
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae	Nitrosomonas
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	
Bacteria	Bacteroidetes	Sphingobacteriales	Sphingobacteriales	env.OPS 17	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	Elev-16S-1166	
Bacteria	Verrucomicrobia	Opitutae	Opitutales	Opitutaceae	Opitutus
Eukaryota	Cercozoa	Novel Clade	Gran-3		
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadales	Aquabacterium
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriales	Flavobacterium
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Hyphomonadales	Woodsholea

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4	Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
5		
6	Bacteria	Cyanobacteri Melainabacte Obscuribacterales
7		
8	Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomona Nitrosomonas
9	Bacteria	Acidobacteria Acidobacteria Subgroup 3
10		
11	Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonac Candidatus Cc
12	Bacteria	Proteobacteri Betaproteobacteria
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18	Eukaryota	LKM74
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20	Bacteria	Proteobacteri Deltaproteob Myxococcales Haliangiaceae Haliangium
21		
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24	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
25		
26		
27	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
28		
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30	Eukaryota	Basidiomycot Tremellomyc Tremellales
31		
32	Bacteria	Proteobacteri Gammaprote Pseudomona Pseudomona Pseudomonas
33		
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36	Bacteria	Proteobacteri Alphaproteob Rhizobiales Bosea
37	Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Denitratisoma
38		
39	Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonac Stenotrophon
40	Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonad Comamonas
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46	Bacteria	Proteobacteri Alphaproteob Rhodobacter Rhodobacteraceae
47	Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonac Candidatus Cc
48		
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50	Bacteria	Proteobacteri Alphaproteob Caulobacteria Caulobacteria Brevundimon
51	Bacteria	Bacteroidetes Flavobacterii Flavobacteria NS9 marine group
52		
53	Bacteria	Proteobacteri Alphaproteob Rhodospirilla Rhodospirilla Defluviicoccus
54		
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56	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
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Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas Aquimonas
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae Geothrix
Bacteria	Verrucomicro	OPB35 soil group		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	CCU22
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	JG37-AG-20
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	OC31			
Bacteria	Proteobacteri	Alphaproteob	Caulobacteria	Caulobacteraceae
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	Elev-16S-1166
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomonadaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Gemmata
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga Ferruginibacte
Eukaryota	Metazoa			
Bacteria	Acidobacteria	Holophagae	Subgroup 7	
Bacteria	Chlorobi	Ignavibacteri	Ignavibacteri	BSV26
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona Nitrosomonas



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4	Bacteria	Proteobacteri Alphaproteob Rhodospirillal I-10
5	Bacteria	Proteobacteri Alphaproteob Sphingomonadales
6	Bacteria	Elusimicrobia Elusimicrobia MVP-88
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9	Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae
10	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
11	Bacteria	Proteobacteri Deltaproteob Bdellovibrion Bdellovibrion Bdellovibrio
12		
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14	Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
15	Bacteria	Gemmatimon Gemmatimon Gemmatimon Gemmatimonadaceae
16	Bacteria	Bacteroidetes Flavobacteri Flavobacteria NS9 marine group
17	Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
18		
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21	Bacteria	Actinobacteri Actinobacteri Micrococcales
22	Bacteria	Planctomycet OM190
23	Bacteria	Proteobacteri Alphaproteob Sphingomona Sphingomonadaceae
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29	Bacteria	Gemmatimon Gemmatimon Gemmatimon Gemmatimonadaceae
30		
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32	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
33	Bacteria	Chlorobi Chlorobia Chlorobiales OPB56
34	Bacteria	Proteobacteri Alphaproteob Rhizobiales
35	Bacteria	Acidobacteria Acidobacteria Subgroup 3
36		
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40	Bacteria	Acidobacteria Acidobacteria Subgroup 17
41		
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43	Bacteria	Acidobacteria Acidobacteria Subgroup 3
44	Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomona Nitrosomonas
45	Bacteria	Acidobacteria Acidobacteria Subgroup 3
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48	Bacteria	Verrucomicro Verrucomicro Verrucomicro Verrucomicro Prostheco
49	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
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53	Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirilla Defluviicoccus
54	Bacteria	Planctomycet Phycisphaera Phycisphaera Phycisphaera SM1A02
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Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae
Bacteria	Planctomycet	BD7-11		
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobacteri
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae
Bacteria	Chloroflexi			
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	NS9 marine group
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Xanthobacter
Bacteria				Acidocella
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Leptospiraceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteraceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillal
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillal
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	WCHB1-69
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae

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Bacteria	Proteobacteri	Betaproteoba	Hydrogenoph	Hydrogenophilaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Bacteroidetes			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteraceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Devosia
Bacteria	Verrucomicro	OPB35	soil group	
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria Cloacibacteriu
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae Opitutus
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderiac Chitinimonas
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria Flavobacteriu
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrobiaceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagace; Holophaga
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Cryomorphac Crocinitomix
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirillaceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona; Nitrosomonas
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Verrucomicro	OPB35	soil group	

Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Eukaryota	Ochrophyta	Chrysophyceae	Chromulinales		
Bacteria	Verrucomicro	OPB35	soil group		
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas	Plasticicumula
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Sulfuritalea
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	NS9	marine group
Bacteria	Planctomycet	OM190			
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	JG35-K1-AG5	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Thauera
Bacteria	Proteobacteri	Alphaproteob	DB1-14		
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12	marine group
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteriaceae	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12	marine group
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Eukaryota	Ochrophyta	Diatomea	Bacillariophyt	Bacillariophyc	Pinnularia
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Devosia
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales		
Bacteria	Cyanobacteri	Chloroplast			

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Schlesneria
Bacteria					
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	B79	
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteri	Mesorhizobiu
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Phaselicystid	Phaselicystis
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas	Pseudoxantho
Bacteria	Proteobacteria		Rhizobiales	Hyphomicrob	Rhodoplanes
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	F0723	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Nitrosomonadaceae	
Bacteria					
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteri	Mesorhizobiu
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	KD3-93	
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Chryseobacte
Bacteria	Chlorobi	Chlorobia	Chlorobiales	SJA-28	
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteri	Leucobacter
Bacteria	Acidobacteria	Subgroup 22			

Bacteria	Proteobacteri	Betaproteoba	Neisseriales	Neisseriaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Alcaligenaceae
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriu
Eukaryota	Tubulinea	Arcellinida	Echinamoebida	Echinamoeba
Bacteria	Chloroflexi	Thermomicro	JG30-KF-CM45	
Bacteria	Actinobacteri	Actinobacteri	PeM15	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Sphingobacte Nubsella
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriu
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Hyphomonad Hirschia
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Defluviicoccus
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae

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Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera	Brevundimon
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12 marine group	
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	DEV007	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Bacteroidetes	BD2-2			
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10	
Bacteria	Chloroflexi	Ardenticatenia			
Bacteria	Chloroflexi	Chloroflexia	Chloroflexale	Roseiflexacea	Roseiflexus
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Chloroflexi				
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	MNG7	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Sandaracinaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobactera	Roseomonas
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla	Ferrovibrio
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Nocardioidaci	Nocardioides
Bacteria	Armatimonadetes				

Bacteria	Proteobacteri Alphaproteob DB1-14
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Proteobacteri Betaproteoba Rhodocyclale: Rhodocyclace Candidatus Ac
Bacteria	Proteobacteri Deltaproteob Myxococcales
Bacteria	Proteobacteria
Bacteria	Proteobacteri Alphaproteob Caulobacteral Hyphomonad Woodsholea
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria NS9 marine group
Bacteria	Proteobacteri Gammaprote Xanthomonas Xanthomonadaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pirellula
Bacteria	Acidobacteria Acidobacteria Subgroup 4
Bacteria	Proteobacteri Alphaproteob Rickettsiales mitochondria
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteria Flavobacteriu
Bacteria	Gemmatimon Gemmatimon Gemmatimon Gemmatimonadaceae
Eukaryota	Euglenozoa Kinetoplastea Metakinetopl Neobodonida Neobodo
Bacteria	
Bacteria	Armatimonadetes
Bacteria	Proteobacteri Betaproteoba SC-I-84
Bacteria	Proteobacteri Deltaproteob Myxococcales Polyangiaceae Sorangium
Bacteria	Proteobacteri Betaproteoba Burkholderial Burkholderiaceae
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 4 DS-100
Bacteria	Proteobacteri Deltaproteob Myxococcales Polyangiaceae Byssovorax



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Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Verrucomicro OPB35 soil group
Bacteria	Proteobacteri Gammaprote Xanthomonadales
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Reyranelia
Bacteria	Proteobacteri Gammaprote Xanthomonas Xanthomonas Pseudoxantho
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae Runella
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadace Rhizobacter
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadace Sphaerotilus
Eukaryota	Ascomycota Saccharomyc Saccharomycetales
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Armatimonadetes
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Proteobacteri Betaproteoba Burkholderial Oxalobacteria Massilia
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirilla Dongia
Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae
Bacteria	Candidate division BRC1
Bacteria	Proteobacteri Betaproteoba SC-I-84
Bacteria	Candidate division BRC1
Bacteria	Proteobacteri Deltaproteob Myxococcales mle1-27
Eukaryota	Ascomycota Sordariomycete Microascales Microascaceae

Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Brucellaceae	Ochrobactrun
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Nannocystace	Nannocystis
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Bacteria	Proteobacteri	Betaproteoba	SC-I-84		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Pedomicrobiu
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona	Nitrosomonas
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Spirochaetaceae	
Bacteria	Acidobacteria	Holophagae	Subgroup 10	ABS-19	
Bacteria	Proteobacteri	Betaproteoba	Methylophila	Methylophilaceae	
Eukaryota	Tubulinea	Arcellinida	Echinamoebida	Vermamoeba	
Bacteria	Chloroflexi	KD4-96			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Acidovorax
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
Bacteria	Proteobacteri	Betaproteoba	Hydrogenoph	Hydrogenophilaceae	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Phaselicystida	Phaselicystis
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	I-10	
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas	Xanthomonas
Bacteria	Verrucomicro	OPB35 soil group			
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangi	Tetrasphaera

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Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Azospira
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla( Defluviicoccus
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	AKIW659
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillal Candidatus Al
Bacteria	Actinobacteri	Actinobacteri	Kineosporiale	Kineosporiace Kineosporia
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales I Candidatus Ca
Bacteria	Acidobacteria	Acidobacteria	Subgroup 17	
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	NS9 marine group
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad( Hydrogenoph
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteraceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae

Bacteria	Actinobacteri	Actinobacteri	Micrococcales
Bacteria	Proteobacteri	Gammaprote	Pseudomonadales
Bacteria	Proteobacteri	Alphaproteob	Caulobacteri
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales
			Simkaniaceae
			Candidatus Fr
Bacteria	Proteobacteri	Betaproteoba	Burkholderial
Bacteria	Proteobacteri	Deltaproteob	Myxococcales
Bacteria			Sandaracinaci
			Sandaracinus
			Planctomycet OM190
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales
Bacteria			Hyphomicrob
			Hyphomicrobi
			Chloroflexi
Bacteria	Chloroflexi	TK10	
Bacteria	Chloroflexi		
Bacteria	Actinobacteri	Actinobacteria	
Bacteria	Chloroflexi	Thermomicro	JG30-KF-CM45
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales
			SM2D12
Bacteria	Proteobacteri	Gammaprote	Pseudomona
			Pseudomona
			Pseudomonas
Bacteria	Proteobacteri	Gammaprote	Chromatiales
Bacteria	Proteobacteri	Deltaproteob	Myxococcales
Bacteria			Haliangiaceae
			Haliangium
			Planctomycet
			Planctomycet
			Planctomycet
			Planctomycetaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale
			Rhodocyclace
			Sulfuritalea
Bacteria	Actinobacteri	Acidimicrobi	Acidimicrobia
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales
			Hyphomicrobiaceae

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Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida	Neobodo
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Leptothrix
Bacteria	Proteobacteri	Alphaproteob	DB1-14		
Bacteria	Firmicutes				
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Eukaryota	Ascomycota	Sordariomyce	Hypocreales	Hypocreaceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales		
Bacteria	Planctomycet	OM190			
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellacea	Legionella
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Dokdonella
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	Verrucomicro	Brevifollis
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	RB41	
Bacteria	Verrucomicro	Spartobacteri	Chthoniobacterales		

Bacteria Proteobacteri Gammaproteo Xanthomonac Xanthomonac Candidatus Cc  
 Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces  
 Eukaryota Metazoa

Bacteria

Bacteria Proteobacteri Alphaproteob Rhizobiales Phyllobacteri Nitratireductc

Bacteria Proteobacteri Deltaproteob Myxococcales 0319-6G20

Bacteria

Bacteria Proteobacteria

Eukaryota Heterolobose Tetramitia Naegleria

Bacteria Cyanobacteri Cyanobacteri SubsectionIII FamilyI Leptolyngbya

Bacteria Proteobacteri Alphaproteob Sphingomona Sphingomonadaceae

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadaceae

Bacteria Bacteroidetes Sphingobacte Sphingobacte Sphingobacteriaceae

Bacteria Gemmatimon Gemmatimon Gemmatimon Gemmatimonadaceae

Bacteria Chlamydiae Chlamydiae Chlamydiales Simkaniaceae Candidatus Rf

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Eukaryota	Intramacronu	Conthreep	Oligohymenophorea		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Proteobacteri	SPOTS	OCT00m83		
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	SM1B06	
Eukaryota	Ascomycota	Sordariomycetes			
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Rhodanobact
Eukaryota	Cercozoa	Novel Clade	Gran-5		
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Chloroflexi	Ardenticatenia			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Actinobacteri	Actinobacteri	Kineosporiale	Kineosporiace	Quadrisphaer
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		

Bacteria	Bacteroidetes	Sphingobacte	Saprospiraceae
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteobacteria	
Eukaryota	Ciliophora	Intramacronu	Conthreep Oligohymeno Tetrahymena
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale Rhodocyclace Methyloversa
Bacteria	Actinobacteri	Actinobacteri	Propionibacte Propionibacte Micropruina
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale Rhodocyclace Azovibrio
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Comamonadaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri	Gammaprote	Pseudomona Pseudomona Pseudomonas
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter Rhodobacter Amaricoccus
Eukaryota	Discosea	Flabellinia	Vannellida
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales Phyllobacteri Mesorhizobiu
Eukaryota		Chlorophyceae	Desmodesmu
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale Anaerolineaceae
Bacteria	Proteobacteria		
Eukaryota	Tubulinea	Euamoebida	Saccamoeba
Bacteria	Proteobacteri	Deltaproteob	Myxococcales Cystobacteria Anaeromyxob
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycetaceae



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Bacteria	Chloroflexi	TK10
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte env.OPS 17
Bacteria	Proteobacteri	Alphaproteob Rhodospirillal Rhodospirillaceae
Bacteria	Proteobacteri	Alphaproteob Rhodospirillal Rhodospirillal Candidatus Al
Bacteria	Proteobacteri	Alphaproteob Rhodospirillal Acetobacteria Stella
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonadaceae
Bacteria	Chloroflexi	Chloroflexia Chloroflexale Roseiflexacea Roseiflexus
Bacteria	Bacteroidetes	Bacteroidia Bacteroidales Porphyromonadaceae
Bacteria	Planctomycet	Planctomycet Planctomycet Planctomycet Pir4 lineage
Bacteria		OPB35 soil group
Bacteria	Armatimonadetes	
Bacteria	Proteobacteri	Deltaproteob Bdellovibrion Bdellovibrion Bdellovibrio
Bacteria	Proteobacteri	Alphaproteob Rhodospirillal Rhodospirilla Defluviicoccus
Bacteria	Proteobacteri	Betaproteoba Burkholderial Alcaligenaceae
Bacteria	Proteobacteri	Deltaproteob Myxococcales
Bacteria	Proteobacteri	Alphaproteob Sphingomonadales
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonadaceae
Bacteria	Planctomycet	Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri	Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob Rhizobiales

Bacteria	Armatimonadetes				
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales		
Eukaryota	Ochrophyta	Diatomea	Bacillariophyt	Bacillariophyceae	
Bacteria					
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydi	Neochlamydia
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteria	Roseomonas
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Sphingobacte	Sphingobacte
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Cytophaga
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae	Shinella
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteria	Acidiphilium
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiaceae	Rickettsia
Bacteria	Proteobacteri	Deltaproteob	GR-WP33-30		
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Novosphingol

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Bacteria	Acidobacteria	Acidobacteria Subgroup 3	PAUC26f
Eukaryota	Ciliophora	Intramacronu Conthreep	Colpodea
Bacteria	Proteobacteri	Betaproteoba Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob Sphingomona	Sphingomonadaceae
Bacteria	Proteobacteri	Betaproteoba Burkholderial	Oxalobacteraceae
Bacteria	Proteobacteri	Betaproteoba Burkholderial	Comamonadaceae
Bacteria	Chloroflexi	Anaerolineae Anaerolineale	Anaerolineac Anaerolinea
Bacteria	Chloroflexi	Ardenticatenia	
Bacteria	Planctomycet	Planctomycet Planctomycet	Planctomycet Schlesneria
Bacteria	Proteobacteri	Betaproteoba Burkholderial	Comamonadaceae
Eukaryota	Metazoa		
Bacteria	Proteobacteri	Betaproteoba Rhodocyclale	Rhodocyclaceae
Bacteria	Chloroflexi	Caldilineae Caldilineales	Caldilineaceae
Bacteria	Proteobacteri	Alphaproteob Rhodobacter	Rhodobacter Amaricoccus
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte	env.OPS 17
Bacteria	Actinobacteri	Thermoleoph Gaiellales	
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte	env.OPS 17

Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Eukaryota	Phragmoplast	Embryophyta			
Eukaryota	Ochrophyta	Chrysophyceae	Ochromonadales	Paraphysom	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Defluviicoccus
Eukaryota	Ascomycota	Saccharomyc	Saccharomyc	Incertae Sedi	Candida
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae	
Bacteria	Elusimicrobia	Elusimicrobia	Lineage IIc		
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales	Candidatus Or
Eukaryota	Cercozoa	Cercomonadidae			Eocercomona
Eukaryota	Ochrophyta	Diatomea	Bacillariophyt	Bacillariophyc	Nitzschia
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas	Candidatus Cc
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacte	Meganema
Eukaryota	Ascomycota	Saccharomyc	Saccharomycetales		
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas	Dokdonella
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	

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Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Acidobacteria	Holophagae	Subgroup 10	ABS-19
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	PHOS-HE51
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	Verrucomicro Prosthecobac
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteriæ Microbacteriu
Bacteria	Proteobacteri	Gammaprote	NKB5	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Eukaryota	Ascomycota	Sordariomycetes		
Bacteria	Proteobacteri	Gammaprote	Methylococcæ	Methylococcæ Methylosarcir
Bacteria	Proteobacteri	Betaproteoba	TRA3-20	

Bacteria	Proteobacteria	Rhizobiales
Bacteria	Proteobacteria	Alphaproteobacteria Rhodospirillales Rhodospirillaceae Defluviicoccus
Bacteria	Proteobacteria	Alphaproteobacteria Rhizobiales Rhizobiales In Bauldia
Bacteria	Actinobacteria	Actinobacteria Micrococcales Microbacteriaceae
Bacteria	Proteobacteria	Betaproteobacteria Rhodocyclales Rhodocyclaceae
Bacteria	Elusimicrobia	Elusimicrobia Lineage IIb
Bacteria	Proteobacteria	Gammaproteobacteria Xanthomonadales Xanthomonadales Incertae Sedis
Bacteria	Proteobacteria	Alphaproteobacteria Rhizobiales Bradyrhizobium Bosea
Bacteria	Acidobacteria	Acidobacteria Subgroup 6
Bacteria	Actinobacteria	Acidimicrobiales Acidimicrobiaceae Acidimicrobiales Incertae Sedis
Bacteria	Proteobacteria	
Bacteria	Proteobacteria	Betaproteobacteria Rhodocyclales Rhodocyclaceae Candidatus Acidithiobacillus
Bacteria	Proteobacteria	Gammaproteobacteria Xanthomonadales Xanthomonadales Candidatus Acidithiobacillus
Bacteria	Proteobacteria	Gammaproteobacteria Aeromonadales Aeromonadales Aeromonas
Bacteria	Firmicutes	
Bacteria	Planctomycetes	Planctomycetes Planctomycetes Planctomycetes Schlesneria
Bacteria	Proteobacteria	Betaproteobacteria Rhodocyclales Rhodocyclaceae Candidatus Acidithiobacillus
Bacteria	Firmicutes	Clostridia Clostridiales Peptostreptococcales Incertae Sedis

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Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Candidate division	BRC1			
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Actinobacteria				
Bacteria	Acidobacteria	Acidobacteria	Subgroup 17		
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Cloacibacteriu
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla	Ferrovibrio
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteria	Roseomonas
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae	

Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonadaceae
Bacteria	TM6			
Eukaryota	LKM15			
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonadaceae
Eukaryota	Chlorophyceae			
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangi
Bacteria	Proteobacteri	Gammaprote	Pseudomonadales	Tetrasphaera
Bacteria	Actinobacteri	Thermoleoph	Solirubrobact	480-2
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae
Bacteria	Proteobacteri	Gammaprote	Pseudomonas	Moraxellaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylorosul
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149
Bacteria	Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae
				Chlorobium



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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Spirochaetaceae
Eukaryota	Tubulinea	Arcellinida	Arcellina	Arcella
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae Blvii28 waste\
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Pirellula
Bacteria	Bacteroidetes			
Bacteria	Actinobacteri	Acidimicrobii	Acidimicrobia	Acidimicrobia Candidatus M
Bacteria	Proteobacteri	Betaproteoba	TRA3-20	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera SM1A02
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae

Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Chloroflexi Thermomicro JG30-KF-CM45
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Gemmata
Bacteria	NPL-UPA2
Bacteria	Proteobacteri Alphaproteob Rhizobiales
Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Propionivibric
Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	Chlamydiae Chlamydiae Chlamydiales Parachlamydi Candidatus Pr
Bacteria	Proteobacteri Gammaprote Enterobacteri Enterobacteriaceae
Bacteria	Proteobacteri Alphaproteob Rhodospirilla Rhodospirilla Inquilinus
Bacteria	Proteobacteri Alphaproteob Sphingomona Sphingomonadaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 3 SJA-149
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae

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Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Actinobacteri Actinobacteri Propionibacte Propionibacte Propionificell;
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Planctomycet BD7-11
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pirellula
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pir4 lineage
Bacteria	Proteobacteri Betaproteoba B1-7BS
Bacteria	Proteobacteri Deltaproteob Myxococcales; Haliangiaceae Haliangium
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonada Comamonas
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteria Chryseobacte

Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Comamonas
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Hydrogenoph
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Proteobacteri	Gammaprote	Pseudomonas	Pseudomonas	Pseudomonas
Eukaryota	Basidiomycot	Wallemiomyc	Geminibasidi	Geminibasidi	Geminibasidi
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiales	In Nordella
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Acetobacteria	Roseomonas
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteria	Microbacteriu
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Tropicimonas
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	

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Bacteria	Chlorobi	Chlorobia	Chlorobiales	SJA-28
Eukaryota	Basidiomycot	Tremellomyc	Tremellales	Trichosporon
Bacteria	Actinobacteri	Actinobacteria		Trichosporon
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangiaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga
Bacteria	Candidate division	OD1	Taibaiella	
Bacteria	Bacteroidetes			
Eukaryota	Discosea	Longamoebia	Centramoebida	Acanthamoeb
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonas
Bacteria	Bacteroidetes		Burkholderiaceae	
Bacteria	Bacteroidetes			
Bacteria	Acidobacteria	Acidobacteria	Subgroup 17	

Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrion
Bacteria	Chloroflexi				
Bacteria	Proteobacteri	Gammaprote	Methylococcc	Methylococcc	Methylocaldu
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagace	Holophaga
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Gammaprote	Legionellales	Coxiellaceae	Coxiella
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad	Comamonas
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17	
Eukaryota	Basidiomycot	Microbotryon	Sporidiobolal	Incertae Sedi	Rhodotorula
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Sphingomona
Bacteria	Verrucomicro	Opitutae	Opitiales	Opitutaceae	Opitutus
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymeno	Vorticella

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Eukaryota	Gracilipodida	Filamoeba
Bacteria	Actinobacteri Actinobacteri Frankiales	Nakamurellac Nakamurella
Bacteria	Proteobacteri Betaproteoba Burkholderial	Burkholderiac Lautropia
Bacteria	Proteobacteri Betaproteoba Burkholderial	Comamonadac Comamonas
Bacteria	Proteobacteri Alphaproteob Rhizobiales	Hyphomicrob Devosia
Bacteria	Planctomycet Pla4 lineage	
Bacteria	Proteobacteri Deltaproteob Myxococcales	Nannocystaceae
Bacteria	Planctomycet Planctomycet Planctomycet	Planctomyces
Bacteria	Proteobacteri Betaproteoba Burkholderial	Comamonadac Comamonas
Bacteria	Proteobacteri Betaproteoba Burkholderial	Comamonadaceae
Bacteria	Bacteroidetes Sphingobacte	Sphingobacte Chitinophagaceae
Bacteria	Chloroflexi Anaerolineae	Anaerolineale Anaerolineaceae

Eukaryota Metazoa

Bacteria Proteobacteri Alphaproteob Rhizobiales Hyphomicrobiaceae

Bacteria Proteobacteri Alphaproteob Rhodospirillales Rhodospirillales Candidatus Al

Bacteria Candidate division WS3

Bacteria Planctomycetes Planctomycetes Planctomycetes Planctomycetaceae

Bacteria Proteobacteri Betaproteob Burkholderiales Comamonadaceae

Bacteria Proteobacteri Betaproteob Nitrosomonas Nitrosomonadaceae

Bacteria Verrucomicro Opitutae Opitutaes Opitutaceae Opitutus



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Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymenophorea
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrobiaceae
Eukaryota	Ochrophyta	Chrysophyce	Chromulinales	Spumella
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	cvE6
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacte
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellacea Legionella
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Pirellula
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae

Bacteria	Proteobacteri Deltaproteob Bdellovibrion; Bdellovibrion; Bdellovibrio
Bacteria	Acidobacteria Acidobacteria Subgroup 4 Elev-16S-573
Bacteria	Proteobacteri Deltaproteob Myxococcales mle1-27
Bacteria	Spirochaetae Spirochaetes Spirochaetale Spirochaetaceae
Eukaryota	Basidiomycot Tremellomyc Tremellales Tremellaceae Cryptococcus
Bacteria	SHA-109
Bacteria	Proteobacteri Gammaprote Enterobacteri Enterobacteriaceae
Bacteria	Proteobacteri Alphaproteob Sphingomona Sphingomonadaceae
Bacteria	Fibrobacteres Fibrobacteria Fibrobactera Fibrobacterac possible genu
Bacteria	Actinobacteri Thermoleoph Solirubrobact 480-2
Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomonadaceae
Bacteria	Planctomycet OM190
Bacteria	Bacteroidetes Flavobacteri; Flavobacteria Flavobacteria Chryseobacte
Eukaryota	Cercozoa Glissomonadida Amb-18S-112
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycetaceae

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Bacteria	Proteobacteri	Alphaproteob	Caulobacteria	Caulobacteria	Brevundimon
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Sandaracinac	Sandaracinus
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Thauera
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Hyphomicrob
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromon	Paludibacter
Bacteria	Bacteroidetes	BD2-2			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae	
Eukaryota	Tubulinea	Euamoebida			BOLA868
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia	Afipia
Bacteria	Firmicutes	Bacilli	Bacillales	Staphylococc	Staphylococc
Bacteria	Bacteroidetes				
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Defluviicoccus

Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrobiaceae
Eukaryota	LKM11			
Bacteria	Acidobacteria	Acidobacteria	Subgroup 6	
Bacteria	Proteobacteri	Gammaproteob	Xanthomonas	Xanthomonas Lysobacter
Bacteria	Proteobacteri	Gammaproteob	Xanthomonas	Xanthomonas Arenimonas
Bacteria	Bacteroidetes	Sphingobacteri	Sphingobacteri	Chitinophagales Ferruginibacter
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae
Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae
Eukaryota	Cercozoa	Incertae Sedis		Gymnophrys

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	JG35-K1-AG5
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona
Bacteria	Proteobacteri	Gamma	Xanthomonadales	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacteriaceae
Bacteria	Proteobacteri	Gamma	Xanthomonas	Xanthomonas
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonas
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera

## Eukaryota

Bacteria Proteobacteri Betaproteoba Hydrogenoph Hydrogenoph Thiobacillus

Bacteria Proteobacteri Alphaproteob Rhizobiales Hyphomicrob Ancalomicrob

Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Zoogloea

Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclaceae

Bacteria Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Candidatus Al

Bacteria Bacteroidetes Sphingobacte Sphingobacte Saprospirace Haliscomenok

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonade Aquabacteriu

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria	Chryseobacte
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Solimonadace	Solimonas
Bacteria	Bacteroidetes	VC2.1	Bac22		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiales	In Nordella
Bacteria	Cyanobacteri	Cyanobacteri	SubsectionIII	FamilyI	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiales	In Rhizomicrobiu

Bacteria Actinobacteri Actinobacteri Propionibacte Propionibacte Marinilutecoc

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonade Acidovorax

Bacteria TM6

Bacteria Chlorobi Chlorobia Chlorobiales SJA-28

Bacteria Actinobacteri Actinobacteri Propionibacte Propionibacteriaceae

Bacteria Proteobacteri Betaproteoba Burkholderial Oxalobactera Janthinobacte

Bacteria Proteobacteri Gammaprote Thiotrichales Thiotrichacea Thiothrix



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Bacteria      Bacteroidetes    Cytophagia      Cytophagales    Cytophagaceae

Eukaryota                      Trebouxiophyceae                      Auxenochlorella

Bacteria      Proteobacteria    Gammaproteobacteria    Legionellales    Legionellaceae    Legionella

Bacteria      Proteobacteria    Gammaproteobacteria    Pseudomonadales    Moraxellaceae    Perleucidinibacter

Bacteria	Deinococcus-Deinococci	Thermales	Thermaceae	Meiothermus
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Deltaproteob	GR-WP33-30	
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Actinobacteri	Actinobacteri	Corynebacter	Mycobacteria
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	PHOS-HE51
Bacteria	Proteobacteri	Deltaproteob	GR-WP33-30	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Cyanobacteri	Chloroplast		
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria
Bacteria	Proteobacteri	Betaproteoba	Methylophila	Methylophilaceae
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae

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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteraceae
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
				Lewinella
Bacteria	Candidate division	BRC1		
Eukaryota	Ascomycota	Eurotiomycet	Chaetothyriales	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteri
				Mesorhizobiu
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Deltaproteob	Desulfobacte	Desulfobulba
				Desulfobulbu

Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Runella
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Adhaeribacter
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga	Chitinophaga

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Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomonadaceae	
Eukaryota		Chlorophyceae			
Bacteria	Firmicutes	Clostridia	Clostridiales	Family XII	Acidaminobac
Bacteria	Chloroflexi				
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiales	In Nordella

Bacteria Proteobacteri Betaproteoba Burkholderial Oxalobacteraceae

Bacteria Chloroflexi

Bacteria Proteobacteri Gammaprote Xanthomonadales

Bacteria Proteobacteri Deltaproteob Sh765B-TzT-29

Bacteria Deinococcus- Deinococci Deinococcale: Deinococcace Deinococcus

Bacteria Proteobacteri Betaproteoba Rhodocyclale: Rhodocyclace Thauera

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Bacteria	Candidate division OD1
Bacteria	Proteobacteri Alphaproteob Caulobactera Caulobactera Brevundimon
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Zoogloea
Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomonadaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycetaceae
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces

Bacteria Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Blvii28 waste\



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Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga	Chitinophaga
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Sphingobacte	Sphingobacte
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Bacteroidetes				

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Isosphaera

Bacteria Verrucomicro Spartobacteri Chthoniobact FukuN18 freshwater group  
Bacteria Chthonomon; Chthonomon; Chthonomon; Chthonomon;

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Bacteria      Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae

Archaea      Euryarchaeot Methanomicr Methanomicrobiales

For Peer Review

Bacteria      Actinobacteri Actinobacteri Micrococcales

Bacteria Actinobacteri Actinobacteri Frankiales Nakamurella

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadaceae

Bacteria Planctomycet Planctomycet Planctomycet Planctomycetaceae

Bacteria Cyanobacteri Melainabacte Obscuribacterales

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadaceae

Eukaryota Ascomycota Eurotiomycet Eurotiales Trichocomaceae

Eukaryota Basidiomycot Tremellomyc Tremellales Trichosporon Trichosporon

Bacteria Proteobacteri Gammaprote Xanthomonac Xanthomonac Thermomona

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Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadales	Sphingomonadaceae
Bacteria	Spirochaetae	Spirochaetes	Spirochaetales	Leptospiraceae	Leptospira
Bacteria	Proteobacteria	Gamma	Legionellales	Coxiellaceae	Aquicella
Bacteria	Bacteroidetes	vadinHA17			
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	
Bacteria	Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Burkholderiales	Cupriavidus
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadales	Sphingomonadales
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	

Bacteria	Acidobacteria	Acidobacteria Subgroup 3
Bacteria	Proteobacteria	Betaproteobacteria Burkholderiales Comamonadaceae
Bacteria	Bacteroidetes	Sphingobacteriales Sphingobacteriaceae
Bacteria	Bacteroidetes	Flavobacteriales Flavobacteriaceae Chryseobacteriaceae
Bacteria	Actinobacteria	Actinobacteriales Propionibacteriales Propionibacteriaceae
Bacteria	Bacteroidetes	Flavobacteriales Flavobacteriaceae Chryseobacteriaceae
Eukaryota	Ochrophyta	Diatomea Bacillariophyta Bacillariophyceae Placconeis

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Rhodoplanes
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Novispirillum
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae	Rhizobium
Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae	1

Bacteria Actinobacteri Acidimicrobii Acidimicrobia Acidimicrobia Candidatus M

Bacteria Proteobacteri TA18

Bacteria Bacteroidetes Sphingobacte Sphingobacte Sphingobacteriaceae

Bacteria Bacteroidetes Cytophagia Cytophagales Cytophagaceae

Bacteria Bacteroidetes Flavobacterii Flavobacteria Flavobacteria Flavobacteriu



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For Peer Review

Archaea	Euryarchaeot	Halobacteria	Halobacterial	Deep Sea Hydrothermal Ver
Eukaryota	Ascomycota	Sordariomycete	Sordariales	Coniochaetaceae

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces

Eukaryota Schizoplasmodiida

Bacteria Acidobacteria Acidobacteria Subgroup 4

Bacteria Chloroflexi Anaerolineae Anaerolineae Anaerolineaceae

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Alcaligenacea	Achromobacti
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Stenotrophon
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia	Afipia
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona	Nitrosomonas
Eukaryota	Basidiomycot	Agaricomycet	Polyporales		

Bacteria	Proteobacteri Deltaproteob Myxococcales 0319-6G20
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillaceae
Bacteria	Proteobacteri Betaproteoba Burkholderial Oxalobacteraceae
Bacteria	Actinobacteri Acidimicrobii Acidimicrobiales
Bacteria	Proteobacteri Betaproteoba SC-I-84

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Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Gemmata

Bacteria Proteobacteri Alphaproteob Rhodobacter Rhodobacteraceae

Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Thauera

Bacteria Actinobacteri Actinobacteria

Bacteria Proteobacteria Gammaproteobacteria Xanthomonas Xanthomonas Thermomonas



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Bacteria

Bacteria      Firmicutes      Bacilli      Lactobacillale   Enterococcac   Enterococcus

Bacteria      Chlorobi      Ignavibacteriæ   Ignavibacteriæ   BSV26

Bacteria Proteobacteri Alphaproteob Sphingomona Sphingomona Sphingomona

Bacteria Proteobacteri Alphaproteob Rhizobiales Hyphomicrob Pedomicrobiu

Bacteria Proteobacteri Betaproteoba Rhodocyclale Rhodocyclaceae

Bacteria Proteobacteri Alphaproteob Rickettsiales SM2D12

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Bacteria      Proteobacteri   Alphaproteob   Sphingomona   Sphingomona   Sphingobium

Eukaryota      Ascomycota   Eurotiomycet   Eurotiales      Trichocomace   Talaromyces

Eukaryota Ciliophora Intramacronu Litostomatea Haptoria Amphileptus

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Isosphaera

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Bacteria      Acidobacteria Acidobacteria Subgroup 3

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19 Bacteria Proteobacteri Alphaproteob Rhizobiales  
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33 Bacteria Proteobacteri Gammaprote Xanthomonac Xanthomonadaceae  
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40 Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadæ Lampropedia  
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Bacteria	Firmicutes	Bacilli	Lactobacillales	Streptococcales	Lactococcus
Bacteria	Actinobacteria	Actinobacteria	Propionibacteres	Propionibacteres	Micropruina
Bacteria	Firmicutes	Erysipelotrichi	Erysipelotrichi	Erysipelotrichi	Turicibacter
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Haliangiaceae	Haliangium
Bacteria	Bacteroidetes				

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Chitinophaga

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Bacteria	Proteobacteri	Gammaprote	Pseudomona	Pseudomona	Pseudomonas
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	Ohtaekwangia
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteraceae	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Cryomorphac	Crocinitomix

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Bacteria	Cyanobacteri	Cyanobacteri	SubsectionIII	FamilyI	Leptolyngbya
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae	Rhizobium
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Hyphomicrob

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Bacteria Proteobacteria Deltaproteob Bdellovibrion Bdellovibrion Bdellovibrio

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Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Thauera
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirillaceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Nitrosomonadaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	F0723	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga	Flavitalea

Bacteria Proteobacteria Alphaproteobacteria Rhodospirillales DA111

Bacteria Bacteroidetes Sphingobacteriales Sphingobacteriales ST-12K33

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Bacteria      Proteobacteri Alphaproteob Sphingomona Sphingomona Sphingopyxis

Bacteria      Verrucomicro Verrucomicro Verrucomicro Verrucomicrobiaceae

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Bacteria Proteobacteria Betaproteobacteria Burkholderiales Comamonadaceae Aquabacterium



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Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Betaproteoba	Hydrogenoph	Hydrogenophilaceae
Bacteria	Proteobacteri	Gammaprote	Thiotrichales	Thiotrichacea
				Methylohalon
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	KD3-93

Bacteria Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae

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Bacteria Cyanobacteri Cyanobacteri SubsectionIII FamilyI

Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Flavisolibacte

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Bacteria	Proteobacteri	Deltaproteob	Desulfobacte	Desulfobulba	Desulfobulbu
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	WCHB1-69	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Magnetospiril

Bacteria Proteobacteria Alphaproteobacteria Rhodobacteriales Rhodobacteraceae

Bacteria Chloroflexi Anaerolineae Anaerolineales Anaerolineaceae

Bacteria Bacteroidetes Flavobacteriia Flavobacteria Flavobacteriu

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Bacteria      Proteobacteri   Betaproteoba   Burkholderial   Comamonadaceae

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Bacteria Proteobacteria Gammaproteobacteria Xanthomonas Xanthomonas Rhodanobacter

Bacteria Proteobacteria Betaproteobacteria Burkholderia Comamonada Pelomonas

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Bacteria      Proteobacteri   Alphaproteob   Rhodospirillales

Bacteria      Bacteroidetes   Sphingobacte   Sphingobacte   Sphingobacte   Sphingobacte

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GTGTGCAGGTTCTCTTTGAGCACCAAACCATC	0	8
GTGTTCAAGGCTCCCTTGCGGGCACTCCCGAATC	14509	1545
CTAGACCAATCAAGAAAGAACTCTCAATCTGTC	17	309
CCCATAGAATCAAGAAAGGACCGTCAACCTGTC	2500	3072
CTCATGGAATCAAGAAAGAGCTATCAATCTGTC	9969	4296
GTGTCCAGGCTCTCTTTGAGCACTCCTAAATC	2025	8811
CCCATCCGATCCTCTGAAGGGCCTTCTCGTCTG	0	0
CCCACCGAATCAAGAAAGAGCTCTCAATCTGTC	5813	2621
GTGCATGTTCCACCCTTGCGGGTGTGGCTCTGC	150	305
CCCATTTAATCAAGAAAGGGCTATCAACCTGTC	10	94
GTGCTTGTTCCACCCGAAGGGCGTGGCCTCTCT	3866	1922
GTGTCCAGGCTCCCTTTGCGGGCACGAATCCATC	2395	2743
GTGTACAGACCCTTGCGGGCTAAACTATCTCTA	0	0
GTGTCCAGGCTCTCTTTGAGCACCAAGCCATC	1222	876
GTGTACCGACCCTTGCGGGCGACGACATTTCTG	28	2
GTGTTCCGGCTCTCTTTGAGCACTCCCAAATC	847	666
CCCATAGAATCAAGAAAGAGCTATCAATCTGTC	2712	2988
GTGTTCTGGTTCCCGAAGGCACTCCTCGATCTC	823	1483
TGTTTCGAGTCTCCGGTTTCCCTTCGACGACTC	3	0
GAGCACGCTGGTATTGCTACCTCGTCAGGCTTT	507	790
GTGTTCTGGCTCCCGAAGGCACCCTCGCCTCTC	791	390
GTGCTGGTTCCGGTCTTGCGACTGTGGCTCTAC	703	1109
GTGCAGCAGCCCCGAAGGGAAATACCATCTCTG	0	0
CCCATAGAATCAAGAAAGAGCTCTCAATCTGTC	632	299
GTGTTCAAGTTCTCTTGCGAGCACTCCCGAATC	490	391
GAGCACGCTGGTATTGCTACCTCGTTAGGCTTT	684	928
TGTAAACTGTCTTGCGAAAGACTAGTTTCCTAA	0	0
TCCAATAAATCGAGAAAGGTCTTTAACCTGTCA	694	777
GTGTTCAAGTTCTCTTGCGAGCACTCCAGATC	430	453
CTCAATAAATCAAGAAAGATCTTCAATCTGTCA	738	539
GTGTCCAGGCTCCCTTTGCGGGACCAAGCCATC	573	597
GTGTTCAAGTTCTCTTGCGAGCACTCCCAAATC	51	136
AGTTTCGTGTCCTTGCGGAAAGCTCCCTTTCAG	624	577
GTGTCTTAATTCCCTTTGCGGGCACTTTTGCATC	593	413
CCCACAGAATCAAGAAAGGCCTTAAGCCTGTCA	0	0
GTCTCGGGGCTCCTTTGCGCACCCCCATCTCT	31	65
AGTTTCGTGCCCTTGCGGGAAGTCTCCTTTCAG	0	0

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4	GTGCAAGTTTCACTCCGAAGAGCAACTTTCTGA	364	570
5	GTCTCGGGGCTCCTTGCGGCACCTCCCATCTCT	83	106
6	GTGTTCCGATTCCCGAAGGCACTCCCGCATCTC	405	1137
7	GTGTTGCAGCTCCCTTTCGGGCACTTCCTCATC	122	74
8	TTCAGGGGATCGAGAAAGAACTCAATCTGTC	0	0
9	GTGACCGTTGTACCCTTGCGGGCCTACATCTAC	266	648
10	TCCACAAAATCAAGAAAGAGCTTTCAATCTGTC	12	10
11	TACTGGCAGTGTATTGCTACAAAGTGAGCTTTC	579	296
12	CCCACAGAAATTAAGAAAGAGCTATCAATCTGT	460	310
13	GTGTTCAAATTCTCTTTCGAGCACGATTCCATC	429	278
14	CGCATAGTGTCCCGAAGGAAGATCGGCTTTCAC	391	258
15	GTGTACGTTCCACCCAGAGGGTGTGGCTCCTCT	370	499
16	GTCTCGGGGTTCTTGCGGCACTGCCCATCTCT	0	0
17	GTGCAAGCTCCCTTGCGGGTCGTTACCTTTCA	35	36
18	GTCTCTGGATTCCCTTGCGGGCACGCCGACTTT	364	291
19	CCCATAGAATCAAGAAAGAGCTCTCAAATCTGT	452	81
20	CCCATAAAATCAAGAAAGAGCTCTCAATCTGTC	7	9
21	GTTCAGGCTCCCTTGCGGGTCGGTCACCTTTCG	183	247
22	GTGTACGTTCCACTCAGAATGAGTGTCAATTAC	0	0
23	GTGTGGACGCCAGCCGAAGTGAAGGACCTCATC	0	0
24	GTGTCCTGGCTCCCGAAGGCACCCCCGCCTCTC	195	440
25	GTGTTCCGGCTCCCTTTCGGGCACACCCAAATC	289	306
26	GTGTACGTTCCACCCAGAATGGGTGTCAATCAC	10	739
27	TGTAATCTGTGTATTGCTACAAAACCCCTTTC	338	330
28	GTGTGCAGGTTCTCTTTCGAGCACTCCCAGATC	46	1029
29	GAGCACGCTGGTATTGCTACCTCGTAAGGCTTT	168	314
30	TGCTCCTTGTTCTTGCGAAACGATCCATCTCTG	0	0
31	TGCAGGCAGGAACTGGTTACCCAGATCATCCTA	319	273
32	GTGCAGGTCACACCCGAAGGTAATCAGCCAGCT	80	66
33	TACTGCCTGTATATTGCTATAAAGACCCCTTTC	331	127
34	TCTCACTCGCTCCCCGAAGGGCACCAAGACATT	0	0
35	TGCAGGCAGGAGCCGGTTACCCGGATCATCCTA	254	247
36	AGTTTCGTGTCCTTGCGGAAGGCTCCCTTTCAG	0	0
37	GTGTCCAGGTTCCCTTTCGGGCACGAATCCATC	254	244
38	CCCATAGAATCAAGAAAGATCTTCAATCTGTCA	195	341
39	TGCTCTTTGTCCTTGCGGAAAAACCATCTCTG	38	29
40	TTCAAGGGATCGAGAAAGAACTCAATCTGTC	0	0
41	GTGTCCAGGCTCCCTTGCGGGCACCTCTCGTT	126	200
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4	TGCATCCGGCCCCGAAGGGCGATCAGCTTTCAC	0	0
5	GTTTAAACTCCCTTGCGGGTCGATCCAATTTCT	0	0
6	AGTTTCGGGTCATTGCTGACTAACTCCTTTCAG	234	164
7	GTCTCTGGATTCCCTTGCGGGCACATCAGCTTT	23	33
8	CGCACCCGGCCCCGAAGGGCTGTACAGTTTCCC	0	0
9	GTGTGGCGTCCGGCCGAACCGACTCCCCGCTCT	188	272
10	AGTTTCGTGTCCTTGCGGAAAGCTTCCTTTCAG	14	21
11	GTGTTGCAGCTCCCTTTCGGGCACTTTCTCATC	216	137
12	CTCTAGGAATTATGAAAGAACAATCAACCTGTC	0	0
13	GTGTCTTAATTCCCTTTCGGGCACTTTTACATT	20	8
14	GTGCACGTTCCGGTCTTGCGACTGTGGCCCCAC	0	0
15	TGCAGGCAGGAGCTGGTTACCCAGATCGTTCTA	85	218
16	TATCACGCGTATATTGCTATAAAACCAGCTTTC	146	116
17	GTCTCTGGATTCCCTTGCGGGCACGTCGACTTT	0	0
18	GTGTCCAGGCTCTCTTTCGAGCACGAATCCATC	203	195
19	GTCTGCGCTCTCCGAAGAGTCGTTCCCCTTTCA	148	196
20	GTGTTCCGATTCCCTTTCGGGCACCCCCACCTC	105	246
21	GTAATATTAAATTAATAAAAAATAATAAAAAATTT	0	0
22	TGCTCCATGTCCTTGCGGAAGAGTCCATCTCTG	186	187
23	GTCTTTGGGCTCCTTGCGGCACCCCCATATCTC	107	227
24	CCCATGGAATCAAGAAAGAGCTATCAATCTGTC	2	243
25	TGCTCCTTGTTCTTGCGAAAAAATCCATCTCTG	15	16
26	TACTGGCAGTGTATTGCTACAAAGAGAGCTTTC	115	116
27	GTGCAGGTCACACCCGAAGGTAATCAGCCGACT	127	177
28	GTGACCGCTCCCCGAAGGGTCGTTCCGCTTTCA	155	145
29	GTGCAAGCTTCCCGAAGGATCGTTCCGCTTTTCG	83	117
30	AACCACAGGTTCCCCGAAGGGCACCCCGAACTT	116	217
31	TGAAAAATGTCCGAAGAAAAGTCTATTTCTAAA	76	545
32	GTGCAAACTCTCCTTGCGGAGTCGTCACCCCTT	6	0
33	GTGCATGTTCCGGTCTTGCGACTGTGGCTCTAC	89	107
34	TACGATCTGTGTATTGCTACAAAATGAGCTTTC	62	61
35	GTGTCCAGGCTCCCTTTCGGGCACCTCCACCTC	85	218
36	CCCATAGAATCAAGAAAGATCCTTTTAATCTGT	98	155
37	GTGTTGCAGTTCTCTTTCGAGCACTTTCTCATC	100	127
38	GTGTGGACGCCAGCCGAAGTGAAGAACGGGATC	4	9
39	TGAAAAATGTCCGAAGAAGGATCTATTTCTAAA	0	0
40	CGCACCCGGCCCCGAAGGGCTGCACAGTTTCCC	0	0
41	GTCTTCAGGTCCCCTTGCGGGGTACTCGGCTGT	84	202
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GTGCACGGA CTCCGAAGAGGGGCCGATGTTTCC	84	151
GTGTCTTAATTCCCTTTCGGGCACTTCTACATC	147	145
GTGCACCAGTCCCGAAGGAAAGGACCCTTTCAG	174	124
CCCACCTAATCAAGAAAGAGCTCTCAATCTGTC	31	23
GTGCAGCAGTCCCGAAGGAAAGACGCCTTTCAG	0	0
GTGCAAGCTCCCTTGCGGGTCGTTACCTTTCG	17	7
GTGCAGGCTCCCGAAGGGTCGTTCCACTTTCG	65	226
GTGTCTCAATTCCCTTTCGGGCACCTCTGCATC	196	153
GTGTTCTAGCCAGCCGAAGTGAAGGAAGTCATC	125	95
TGCTTCGCGTCCCGAAGGAAACCCGGCTTTCAC	102	137
ATACTGCAGTCCCTTGCGGGAAGTCCCTGTTTC	123	109
CCCATTTAATCATGAAAGAGCTATCAATCTGTC	0	33
GTGTTCAAGATTCTCTTTCGAGCACGATTTCATC	114	103
GTACCAAGTCCCCTCTTGCGAGGTTCCCTGAGG	64	151
GCTAAGAAATTAAGTATCAAAAAAAGGAAAAA	13	20
CCCACAGAATCAAGAAAGAGCTCTCAATCTGTC	68	84
CGACCAACAACCGGCTTTACGGTTTCGCCCCCT	29	189
TGAGAGCCGTCCGAAGAAAGGCCTGTTTCCAAG	0	0
GTGTTCCGGCCAGCCGAAGTGAAGAAAGGCATC	62	48
GTGATAGTCCAGCCGAAGTGAAGAAAGGCATC	0	0
TGTAAAGTGTCCGAAGAAAAAAGTGTTCAGT	0	0
TGTAAAGGTCTTTGCAGACTGTATACTTTCAT	0	0
GTGTCCCGGTTCTCTTTCGAGCACTCCCGCATC	92	60
TGTTTCTCGCTCCGAAGAGAAGACACCTTTCAG	0	0
GTGCACGTTCCAGTCTTTCGACCGTCATTCTG	0	0
GTGCACGTTCCGCCCTTGCGGGTGTGGCTTCCC	0	0
TCTCACTCGTTCCCCGAAAGGCACCCCGGCATC	102	100
GTACAAGACCCCTTGCGGGTAAACGACTTTCAT	130	87
GTGATGGCTCGCCGAAGCGTCGTTCCCCTTTCG	0	0
GCTGCCATATCAAGAAAGTGTATCAAGCTGTC	92	135
GTGCAGGCTCCCGAAGGGTCGTTCCGCTTTCG	34	84
GTGCACGTTCCACTCTTGCGAGCGTGGCTCCTG	71	129
GTGTGGGATCCGGCCGAACCGACAGAAATAATC	0	0
GTGCACGTTCCACCCTTGCGGGTGTGGCTCGAC	0	0
GTGTCCACGTCCCGAAGGGAAGAAATCCATCT	2	3
GTGTCCAGGTTCCCTTTCGGGCACCAAGCCATC	56	73
TATCCCGCGTGTATTGCTACAAGGGTAGCTTTC	61	117
TGCAGGCAGGAGCTGGTTACCCAGATCGCTCTA	74	98



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4	AAGTAGCAGCCCCTTGCGGGGAAGGGCACTTTC	67	78
5	GTACAGGCTTCCGAAGATCGTTCCGCTTTCGCT	40	92
6	GTGTGCAGGTTCTCTTTCGAGCACTTCCAAATC	21	237
7	GTGTTGCGGTTCCCGAAGGCACCAATCCATCTC	0	0
8	AGTTTCGTGCCCTTGCGGGAAGCTCCCTTTCAG	0	0
9	CTATATGGGTCCCGAAGGAAACTCTATCTCTA	54	47
10	CGCATAGTGTCCCGAAGGAAGATTGGCTTTCAC	4	59
11	GTGCACGTTCCATTCTTGCGATTGTCATCGATG	2	0
12	ACCACACAATCAAGAAAGGGCTATTAACCTGTC	0	0
13	GTGTTCTGATTCCCGAAGGCACTCCCGCATCTC	0	2
14	GTGTCTCGGTTCTCTTTCGAGCACCTCCGCATC	55	94
15	GTGACCGGACTCCGAAGAGGGGCCAGGGTTTCC	34	35
16	CGACTCCGGTCCCTTGCGGGAAGGCGATGTTTC	76	88
17	GTGTTGCAGCTCCCTTTCGGACACTTCCTCATC	55	23
18	ATACTGCAGTCCCTTGCGGGAAATCCCTGTTTC	84	54
19	GTGCTCAAATTCCCTTTCAGGCACACTTCCATC	61	75
20	GTGTGGAAGCCAGCCGAAGTGAAGAACCCGATC	0	2
21	CGCACGCCGTCCGAAGAAGAGGATGTTTCCACC	4	0
22	GTGTTACGGTTCTCTTTCGAGCACCAAGCCATC	103	34
23	GTGTTCCGATTCCCGAAGGCACTCTCGCATCTC	0	191
24	AAGTGGCAGCCCCTTGCGGGGAAGGGAAGTTC	28	76
25	GTGTTCAAGCTCCCTTGCGGGCACTCCCAAATC	25	15
26	CGACTCTACTCCCTTGCGGGATAACGATGTTTC	38	48
27	GTCTCACGGTTCCCGAAGGCACCAATCCATCTC	4	11
28	TGTAACCTGTGTATTGCTACAAAGACCCCTTTC	29	59
29	GTGTGGCGTCCAGCCGAAGTGAAGAGACCATCT	58	33
30	GTGTCACGGTTCCCGAAGGCACCAATCCATCTC	37	27
31	GTTACGTTGTACCCTTGCGGGCCTCATAGATG	0	0
32	GTGCACGTTCCGGTCTTGCGACTGTGGCTCTAC	68	92
33	GTGCAGCCGCCTTTCGGAAGGTGCATCTCTGCA	0	0
34	CTCATAGAATCAAGAAAGAGCTATCGATCTGTC	57	31
35	GTGTCCTAGTCCCCGAAGGGAAAGCCACGTCTC	5	0
36	GTGCACGTTCCGACCCCGAAGGGCTGTCATTCT	55	78
37	GTGTTCCGGCTCCCTTTCGGGCACTCCCAAATC	69	66
38	TGCTTTGTGTCCCGTAGGAAAATACCGTTTCCG	0	0
39	GTAACGGCTCCCGAAGGTCGGTCCCCTTTCGGT	2	0
40	GTGTGGACGCCAGCCGAAGTGAAGGACCCCGTC	0	0
41	TGTTTTGGACCAGTAACCTGGCTGTTGGCATT	31	30
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4	GTGCCTGTTCCGGTCTTGCGACTGTGGCCCCAC	64	59
5	GTGTTCAGGCTCTCTTGCGAGCACTCCCAAATC	0	0
6	GTCTTTGGGCTCCTTGCGGCACCCCCACATCTC	42	48
7	AAGTGACAGCTCCTTGCGGAGAGGGCGGCTTTC	51	60
8	GTGCACGTTGTACCCTTGCGGGCCTGGCCGATG	52	50
9	GTGTAGGCTCCCCGAAGGGTCGTTCTGCTTTCG	38	72
10	GTGCTTGTTCCACCCAGAGGGTGTGGCCTCTCT	44	41
11	TACGATCTGTGTATTGCTACAAAAGAGCTTTC	0	0
12	GTGTTCCAGCCAGCCGAAGTGAAGGAAGCGATC	7	4
13	GTCTTACCGTTCCCTTGCGGGCACCCCAGCTTT	50	45
14	TACTACCCGTATATTGCTATAAAATACCCTTTC	28	42
15	CCCACAGAATCGTGAAAGAGCTCTCAGTCTGTC	0	0
16	GTGAATGAGCTCCGAAGAGGGGCCCCCTGTTTCC	18	11
17	GTGTTCTGGCTCCCGAAGGCACCCTCGGCTCTC	2	0
18	GTGCTCCACCCTCGAAGGCCAACCGGTTTCCCG	23	38
19	GTATATCGGCTGCAAGCAGCTGCAGTATCTCTA	0	0
20	GTATTGGACCCCTTGCGGGTAATCCTCTTTC	50	58
21	TACTGGCGGTGTATTGCTACACTATGAGCTTTC	51	41
22	GTGTGGTATCCAGCCGAAGTGAAGGACCATCT	0	0
23	TACTACCTGTATATTGCTATAAGAACCCTTTC	22	57
24	GTGTTGTATCCAGCCGAAGTGAAGGAACCATCT	5	7
25	AACTACAGGTTCTCCGAAGAGCACCCCGACCTT	9	11
26	GTGCACGTTGTACTCTTGCGAGCCTCATTGACG	47	37
27	TACTGGCAGTGTATTGCTACAAAGATCCCTTTC	0	0
28	TGAAAGACGTCCGAAGAAATATCTGTTTCCAAA	47	13
29	CGACTCCCGTCCCTTGCGGGAAACCCATATTTTC	43	55
30	GTATAAGCTCCCGAAGGTCGTTCCCCTTTTCGGT	0	0
31	GTGTCCAGGCTCTCTTTCGAGCACTCCCAAATC	21	71
32	GTGTTCAGGCTCCCTTGCGGGCACTCCCGAATA	32	2
33	GTACAGGCTCCCTTGCGGGTCGGTCACCTTTCG	19	0
34	GTGTGCAGGTTCTCTTTCGAGCACCCCCAGATC	2	153
35	GTGTTGCAGCTCCCTTTCGGGCACTTCCACATC	21	28
36	GTGTTCTGGTTCTCTTTCGAGCACTTTCACATC	35	32
37	GTGCTTGTTCCACCCAGAGGGTGTGGCTCCTCT	32	42
38	GTGTGCAGGTTCTCTTTCGAGCACTCCCAAATC	10	147
39	GTGACCGAGCTCCGAAGAGCTTTCAGGTTTCC	38	56
40	ATACTACCGTCCCTTGCGGGAACTCTACTTTC	72	24
41	GTCTCCTTGTGTATTGCTACAAAGCCCTATTTTC	0	0
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4	GTCACCGGTCCAGCCGAAGGAATCCATC	13	31
5	GTGTCTTAATTCCTTTGCGGCACTCTTACATC	0	0
6	GTGCACGTTCCGGCCTTGCGGCTGTGGCACCAG	22	32
7	GTGTGGGATCCGGCCGAACCGACAAAAACGATC	0	0
8	GTCTCCGGTCCAGCCGAAGGAAGAACTCCGTC	29	61
9	GTGTCACGTTCCCGAAGGCACTCCTCTATCTC	32	51
10	GGATCATGGTTCTCTTGCGAGCACCCCAAACCTT	15	38
11	GTGTTTCAGATTCTCTTCGAGCACGATTCCATC	38	29
12	GTGCGGACTCCGGCCGAACCGAAGGGACCGTCT	35	48
13	TGTAAATTGTCCGAAGAAAAATCTGTTTCCAAA	30	37
14	AAGTGGCGGCTCCTTGCGGAGAGAGAGGCTTTC	21	47
15	AACTATAGGTTCTCCGAAGAGCACCCCAAACCTT	17	69
16	TGTATGGAGCTCTTGCGAGCGTTCCTTTTCAG	45	18
17	GTTTGTACTCTACAAAAGGTCATAATTCAAAAA	0	0
18	GTGTTCCCGTTCCCTTTGCGGCACCCCGGATC	41	40
19	GTCTCGGGGTTCCCTTGCGGCACCTCCCATCTCT	0	0
20	AACCGTAGATTCTCCGAAGAGCACCCCGATACT	53	16
21	CGACTCGACTCCCTTGCGGGATAGCAATGTTTC	31	38
22	CCCACAGAATCACGAAAGAGCTCTCAGTCTGTC	0	0
23	GTGCACGTTCCACTCTTGCGAGCGTGGCCCTAC	48	18
24	GTCTTTGGGCGGACTTGTTGGTGGGGGACTCCT	14	50
25	GTCACGGCTCCTTGCGGTCCCTCACCTTTTCGGC	0	3
26	GTGTATTGGTTCTCTTGCGAGCACTCCCAAATC	0	0
27	GTCTTCAGGCCTGCCTTGTTGAGCAGGGGGCCTA	12	49
28	GAACAAAGTTTTTATATCCAAAAAATATAATGG	12	0
29	GTATAGGCTCCCGAAGGTCGTTCCCTTTTCGGT	0	0
30	GTGTCCCTGTCCCCGAAGGGAAAACCGGATCTC	11	28
31	CGACTCCCGTCTCTTGCGAGAAGGCCATATTC	12	29
32	GTTTCATGTTGTACCCTTGCGGGCCTCACAAATG	23	32
33	GTACAGCTTGCCGACTTGACGGCTCGTTCCCCT	15	51
34	TGTATGAAGCCCTTGCGGGCGATCACCTTTCAG	5	2
35	GCATCGGCTCCCCGAAGGGTCGTTCCGCTTTC	7	16
36	GTGCAGATGCCCCGAAGGGAGATACCATCTCTG	0	0
37	GTGACTGTTCCACCCTTGCGGGTGTGGCCCCTC	8	22
38	CGACTGGACCCCTTGCGGAGTAACGATATTC	43	29
39	AGTTTCGTGTCTTGCGGAAAAATCCCTTTCAG	26	63
40	GTCATTGTCCAGCCGAAGGAAGGAAAGTGTC	0	0
41	GAACAAAGTTTTTTTAACCAAAAAACATAATGG	75	6
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4	GTCACCGGTCCAGCCGAACTGAAGGATTCCATC	0	0
5	GTGTCCAGATTCCCTTTTCGGGCACCCCCACCTC	0	0
6	TCCTACCTCCCCGAAGGGAAACCTCATCTCTG	34	24
7	TGTAACCTGTGTATTGCTACAAAGCCCCCTTTC	5	37
8	GTAATGGCTCCCCGAAGGGTCGTTCCGCTTTCG	6	10
9	GTGTGGACGCCAGCCGAACTGAAGGACCCGATC	0	0
10	GTGTTCCCAGCTCCGAAGAGAAGGTCTCATCTC	0	0
11	GTGCTCAAATTCCTTTTCAGGCACACCCCTATT	0	0
12	CGCACGTTGTCCGAAGAAGATCACGTTTCCGCG	0	2
13	GTGCTTGTTTCACCCCGAAGGGTAGCTACGCTG	26	36
14	GTGTCCTGGCTCTCTTTCGAGCACTCCCGCATC	35	13
15	GTGTCCAGGCTCCCTTTTCGGGCACCAATCCATC	21	18
16	GTGCAAGCTTCACTCCGAAGAGCAGACCTCTAA	0	0
17	GCACAGGATTTCTCTTGCGAGTTGGCCGACGTT	0	0
18	GTTTTGGGGCCCAAAGGACCTGACATCTCTGC	33	25
19	GTCTCGGGGCTCCTCGCGGCACCCCCCATCTCT	0	0
20	CACCACAAGTTCTCTTGCGAGCACTCCACGTT	3	4
21	GTGTGTGACCCAGCCGAACTGAAGGAATCCATC	0	0
22	GTCAAAGCTCCCCGAAGGGTCGTTCCACTTTTCG	14	25
23	GTGAACAGCCCTTACGGACCCGACATCTCTGCC	11	24
24	ATATAGCGGCCCCGAAGGCGACCCTGTCTCCAGG	0	0
25	TACAAAATGTATATTGCTATAAAATGAGCTTTC	35	28
26	GTATCAGCGCTCCTCTCGGCACTCCCCAATCTC	41	20
27	CGCATAGTGCCCCGAAGGGAGATCGGCTTTCAC	0	0
28	GTGCAAGCTGGTATTGCTACCTCGTCTCCCTTT	26	22
29	CTGCAGCAGTTCTTGCGAAAAACGACATCTCTG	23	24
30	CGACTCCGGTCCCTTGCGGGAAGTCCCTGTTTC	22	23
31	GTGTCCTGGTTCTCTTTCGAGCACCTCCGCATC	22	29
32	GTTTTGGGGCCCTTGCGGACCTGACATCTCTGC	28	20
33	GTGTTCCGGCTCCCTTTTCGGGCACCCCCAGCTC	0	11
34	GCTAGGAAATTAAGTATCAAAAAAAAAAGAAAAA	19	37
35	GTGCAGGCTCTCTTGCGAGTCGTTCCGCTTTCG	13	26
36	GTGCACGTTGTACCTTGCGGCCTCACCGACGTT	10	19
37	CCTGTAAAATCAAGAAAGAACTTCAATCTGTCA	0	2
38	GTGTATACGTTCCAAACGGCACTTTCTTCTTTC	0	0
39	GTCTTGTCGTTCCCGAAGGCACTCCCGCATCTC	24	30
40	GTGCAAAGGTTCCCCGAAGGGCACTCCAACCTT	8	21
41	CTGCAGCAGTTCTTGCGAAAAGGCACATCTCTG	15	59
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4	GTGTGCAGGTCACCGAAGTGAAGAGATCCGTCT	0	0
5	GTATCCGGTCCAACATAAATGAAGGTCTCCATCT	0	0
6	GTGCTCCGGCCCCCTTGCGGGAAGAAAGGCATCT	6	46
7			
8	GTGTTCCAATTCCCTTTCGGGCACCCCCAACTT	19	16
9	GTGTTCCGGCTCCCTTTCGGGCACCCCCAACTC	15	30
10			
11	ATTCTGGCTTAGGGCTGAACCTATCGTTCCCCT	0	0
12	GTAAGGACGCTCTTGCGAGCCATTCCCGTTTCC	0	0
13	GTGCACGTTGTACCCGAAGGCCTGGCTCCTGTT	8	6
14			
15	GTCTTAGCGTTCCCGAAGGCACCAATCCATCTC	10	18
16	TGCACGCGACTGGTTGCCAGCTATAACATCTC	16	16
17			
18	GTGCTTGTTCCACCCGAAGGGCGTGGCTCTACT	12	37
19	GTGTTCTGGCTCTCTTTCGAGCACTCCCAAATC	22	32
20	CGATGGCGGCCTCCGAAGAGGAGACGATATTTC	10	36
21			
22	GTGACTGTTCCACTCTTGCGAGCGTTACTCCTG	26	24
23	GTGCACCAGCCCCGAAGGGAAGACTCCTTTCAG	13	17
24	GTGCACGTTCCGGCCTTGCGGCTGTGGCTCCAG	15	13
25			
26	CTCATGGAATCAAGAAAGAGCTATCGATCTGTC	33	18
27			
28	GTGCTCCTCCCACCCGAAGTGAAGGAATGCCTT	0	0
29	TTAAGTCAATCAAGAAAGAGCTATCAATCTGTC	7	30
30	GTGTGCGATCCAGCCGAAGTGAAGGAACCATCT	18	18
31			
32	TGCAACCAGTCCCGAAGGACGATCAGCTTTCAC	0	0
33	GTGTTCAGGCTCCCTTACGGGCACTCCCGAATC	5	0
34	GCAAGGAAATCAGCCATAAAAGAAAAAATAATA	0	0
35			
36	GTGTTCCGGTTCCCTTTCGGGCACCCCCAGCTC	4	26
37	CGTAGCCAGTCCGAAGAAGATCTGCTTTCACAG	0	0
38			
39	GTGTGCAGGTTCCCTTTCGGGCACAATCCCATC	25	24
40	TGAGAACCGTCCGAAGAAAGGTCTGTTTCCAGA	0	0
41			
42	GTATACCGACCTTGCGGGGCACCCATCTCTGGA	0	0
43	GTGTTCCAGTTCCCTTTCGGGCACACCTCAATC	0	0
44	GTCTTGTCGCTCCCGAAGGCACTCCCGCATCTC	0	0
45			
46	CCCACAAAATCAAGAAAGAGCTCTCAATCTGTC	3	39
47	ATGTACCGGTCTATTGCTAGAAATTCGCTTTC	0	0
48			
49	GTGTGCAGGTTCTCTTTCGAGCACGAATCCATC	0	3
50	GTCTTAGATCCGGATTGCTCCGAAAGTACATTT	0	0
51	AGTTTCGTGTCATTGCTGAAAGGTGGCTTTCAC	10	7
52			
53	CCACTCCGGTCCCCGAAGGGAGGACCTCATCTC	19	27
54	CTGCATCAGTTCTTGCGAAAAACGACATCTCTG	24	26
55			
56	GTGCACGTTCCACCCGAAGGCGTCATTGACCTT	13	16
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GTGTGGCGTCCAGCCGAACTGAAGGAATCCATC	37	21
GTGTGAAAGCCAGCCGAACTGAAGGACCTCATC	0	0
GTGTCCCGGCTCCCTTTGCGGGCACCCACCTC	12	28
GTTCAAGCTCCCGAAGGTCGTTCCGCTTTGCT	33	15
GTGTTCCAGTTCCCTTTGCGGGCACTCCCAGATC	14	13
ATCGAAATCAATTAACCTAAAAAATATCTAAGT	25	22
GTGTTGAGTTCCCGAAGGCACCAATCCATCTC	8	62
GTGCACCGGTCCCTTGCGGGAAAGACGCCTTTC	14	8
GTGTCCCGTCCGGCCGAACCGAAGACCCCGGTC	14	40
GTCCTGGTCCAGCCGAACTGAAGGAAAAGATC	2	0
GTGTTCAGGCTCTCTTTGAGCACCTTCGCATC	18	27
GTGCAAGAGCTCCCTTGCGGGCACCCAGCTT	8	4
GTGTGGGGGCCAGCCGAACTGAAGGGTCAGATT	0	0
CCCACATTATCAAGAAAGCTCTTCACTCTGTCA	9	12
GTATAGGCTCCCTTGCGGGTCGTTCCCTTTG	0	0
GTATTTTCATATAAAATTTGAAAATCATAGAAA	26	8
GTGTTCAGGTTCTCTTTGAGCACTCCAACGTC	0	0
CCCATAGAATCAAGAAAGAGCTCTCAACCTGTC	0	0
TGTAAATTGTCCGAAGAAATATCTGTTTCCAAA	26	19
TACCGGCGACGTATTGCTACGCTATGAGCTTTC	0	0
TACTGGCAGTGTATTGCTACAAAGATGGCTTTC	19	11
GTGTGCAGGTTCTCTTTCAAGCACCAAACCATC	0	0
CGCAAATTGTCCGAAGAACGACTGATTTCTCAA	13	6
ACCAATAAATCAAGAAAGAACTTTAATCTGTCA	2	0
CGACTCAAGTCCCTTGCGGGAAAACCGTGTTTC	18	30
GTGCTAGCTCCCCGAAGGGTCGTTCCGCTTTG	10	22
GTCTTCTGGTCTACCTTGTTGGGTAGAGGGCCCT	0	0
GTGTGTAGGCTCCCTTGCGGGCACCTCTAGTT	10	28
TGTATGGTGTCTTGCGGGCGATCACCTTTCAG	4	15
GTGCTGGTTCCACCTTGCGGCGTCAGCTCCCTT	0	0
GTGTTGAGGTTCCCTTTGCGGGCACCGCCACCTC	13	13
AGTTTTGTGTCTTGCGAAAGCCACCTTTCGGCA	21	14
GTGCGGGCGTTACCTTGCGGTACTGACCGATCT	12	13
TGCTTTGTGTTCTATTGCTAGACCTACAGGCTT	0	0
GTCTTTGTGCTTCTTGTTGGAAGGGAGCCACTTT	7	34
CGACTCTAGTCCCTTGCGGGAAGGCCATGTTTC	2	0
CTGCACGAGTCCCGAAGGAAGACCTCATCTCTG	14	9
TGTTTCGGGTCCGTTGCCCGGACGGACGCTGT	19	9

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4	CTGCAAGCTCCCTTGCGGGTCGTTCCCCTTTCA	0	0
5	TGTTTCGTGTCCCGAAGGAAGAACGGCTTTCAC	0	6
6	GTGTTATGGCTCTCTTTCGAGCACTCCCAAATC	22	24
7	GTGTTCTAGCCAGCCGAAGTGAAGGAAGCGATC	16	18
8	GTGCATGTTCCACCCGAAGGCGTGGCTCTGCTT	0	0
9	GTAGGTAAATAAATAATATAACAATGTCACAAT	0	0
10	GTGTCCAGGCTCCCGAAGGCACCCTCGCCTCTC	14	19
11	GTCTCACCATTCCCTTGCGGGCAGTCGACTTT	22	12
12	AGTTTCGTGCCCCGAAGGGCGCATCCATCTCTG	0	2
13	GTGACTGTTCCACCCTTGCGGGCGTAGCCCCAC	3	17
14	GTGTGCAGGTCACCGAAGTGAAGGATCCCGTCT	7	22
15	GATTATATGTTATTTAATTAATTACTAAAATTA	0	0
16	GTGCAAACCTCCCCTTGCGGGGTCGTCACCCTTT	12	22
17	GTGTGCAGGTTCTCTTTCGAGCACCAACCATCT	0	0
18	GTCTCCGCGCCCCGAAGGGACTCTAGATCTCTC	0	0
19	GTGTTCCGGTTCTCTTGCGAGCACTGCCAAATC	0	0
20	GACTCAAATAATTATAAAAATGCAAGCTATTCC	0	0
21	GTCTCGGGGCTCCTTGCGGCACCCTCCATCTCT	11	11
22	GTGCTGGCTCCCCGAAGGGTCGTTCCGCTTTTCG	10	25
23	GTGCTCCTCCCACCCGAAGTGAAGGATTCTTTT	22	8
24	GTGTCCTGGCTCTCTTGCGAGCACCCAACTT	11	34
25	GTGCACGTTCCGACCCCGAAGGGCTGTCCCCCT	18	23
26	GTGTACAGGTTCTCTTTCGAGCACCAAACCATC	0	0
27	TTTATATACACTCAGTTCTATTGTTCAATAAAT	0	0
28	GTGGAGCACCTCGAAGGCGACGGCCTTTCAGC	9	20
29	CCCAAAGAATCAAGAAAGAGCGCTCAATCTGTC	10	0
30	GTGCATGTTCCACCCAGAGGGGCGTGGCCCTG	6	10
31	GTCCTGGCTCCCTTGCGGGTCGTCGGGCTTTCA	11	15
32	GTGTGGGAGCCAGCCGAAGTGAAGGATCCGATC	0	0
33	TGTTTTGGGTTTGATTACTCAAACCTATCACTAT	25	8
34	GTGCACGTTCCACCCGAAGGGTGTGGCTCCTGT	0	0
35	CGCACCCGGCCCCGAAGGGCTGACACCTTTCGG	0	0
36	GTATGCAGGTTCTCTTTCGAGCACCAAACCATC	0	0
37	GTCCGCGCTCTCCGAAGAGTCGTTCCCCTTTTCG	6	16
38	GTCTCGGGGCTCCTTTCGGCACCACTCATCTCT	10	17
39	CCCAACGAATCATGAAAGAGCTATCAATCTGTC	25	7
40	GTGTTCCAGCTCCCTTTCGGGCACTCCCAAATC	0	0
41	TACTGGCAGTGTATTGCTACACTATAAGCTTTC	16	17
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4	GTGAATCTGCCCTTGCGGGAAGGGGTATCTCTA	4	17
5	TGCCACTTGCCCCGAAGGGAAGGCACCTTTTCGG	15	2
6	GTGATCGCTGCCCCGAAGGCTCGTTCCCCTTTTCG	13	18
7	TTCAAACAATCATGAAAGATCTTTGAATTCTGT	23	14
8	GTGTGGTGTCCAGCCGAAGTGAAGAGTCCCGTC	0	0
9	GTATAGAAGTGTCCAAAGAGTCCTGCATCTCTG	0	0
10	GTGCAAAGCGGGTATTGCTACCCTATCCGGCTT	10	22
11	TGCTTTGTGTCCCGAAGGAAACCCGGCTTTTCAC	16	12
12	GTGTGGCGTCCAGCCGAAGTCCCAGGTC	8	18
13	GTGATGGTCCACCCGAAGTGACGACAAGCTTTC	0	0
14	GTGTCCAGTCCAATAAATGAAGAAAGCCATCT	0	0
15	GTGACTGTTCCACTCTTGCGAGCGTCATTCTCTG	6	12
16	GTGTTAGCCTTCGATTGGATACGATCGGGAGAA	0	0
17	GTGTTGCAGCTCTCTTCGAGCACTTTCTCATC	12	13
18	TGTATACTGTCTCTTGCGAGCCAATCACCTTTC	10	6
19	AGTTTCGTGTCTTGCGGTCTGACCTGTTTCCA	10	8
20	GTGTTTAGATTTCCTTTCGGACACAATTTTCATC	2	2
21	GTCTCAGAGCTCCTCGCGGCACCCTCCATCTCT	10	7
22	GTGCAGACTCCCCTTGCGGGGTCGTCACCCTTT	2	0
23	GTGTCCCGGCTCTCTTCGAGCACTCCCGCATC	12	11
24	GTGTGGTAGCCAGCCGAAGTGAAGAGCCAGTC	0	0
25	GTGATCGTTCCACCCGAAGGCGTCATCCCCCTT	6	13
26	GTACGGGGACCTGTTGCCAGGCTGCGACATCTC	0	0
27	GAATGCCGGCTCCCTTGCGGGCACCCCGATATT	0	35
28	GTCAGTATCCAGCCGAAGTGAAGGGATCCATC	0	0
29	ATACAGGCAACCGACTTAACGGTTTCATTCGACT	3	11
30	CCCAAACAATCAAGAAAGAGCTATCAATCTGTC	25	10
31	GTGCAAGAGTTCCCGAAGGCACCCCGCCCTTTC	5	9
32	GTGCATGTTCCACCCGAAGGCGTGGCCCTGCTT	0	14
33	GTGCAAAGCGGGTATTGCTACCCTATCCGCCTT	6	10
34	AGTTTCGTGTCTTGCGGAAAGACCCCTTTCAG	20	7
35	GTGTCCACGCCCCTTGCGGGGAGGAACTCATCT	9	12
36	GTGCAAGCTGGTATTGCTACCTCGTCAGACTTT	15	11
37	GTGTCTTAATTCCCTTTCGGGCACTTTTACATC	5	8
38	GTGATCAGGTCCCTTGCGGGACACCGACGTTTC	4	13
39	GTCACCGGTCCAGCCGAAGTGAAGGTATCCATC	19	8
40	GTGCTCTACCGGCCGAACCGAAGTAGTTTGTG	0	0
41	GTGCACGCTCCCCGAAGGGTCGTTCCGCTTTCG	0	2
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4	GTGTGCAGGTTCTCTTTGAGCACCAAACCATA	0	0
5	TGTATAGAGCCCCGAAGGGCGATCAGCTTTCAC	10	0
6	GCTATCGGATCAAGAAAGCGCTATCAAGCTGTC	14	10
7	GTGTCCACGCCCCTTGCGGGGAGGAACCCATCT	9	7
8	TGCAATCGGTCTCCGAAGAGAAAGCCACCTTTC	17	5
9	GTGCACGTTGTACCTTGCGGCCTCGCCGACGTT	8	8
10	GTGTTACGTTCCCGAAGGCACAATCTCATCTC	0	0
11	GTGTCCAGGTTCTCTTTGAGCACCAAGCCATC	12	10
12	GCATAAAGTAAGCTATATTATAACATGTGTATA	6	11
13	GTATAGGCTCCCTTGCGGGTCGTTCCCCTTCA	12	13
14	GTGCGCAGGTTCTCTTTGAGCACCAAACCATC	0	0
15	GTGTTACGGCTCCCTTTGCGGCACCCTCACATC	3	13
16	AGTTTTGTGCCCCGAAGGGAAGCCACCTTTCGG	14	11
17	CGACACCGACCCTTGCGGGCTTGACATCTCTG	8	8
18	CTGTAGCAGTTCTTGCGAAAAGGCACATCTCTG	9	9
19	GTGTCCTGGTCCCCGAAGGGAAACTGCATCTC	6	24
20	AGTTTCGTGCTCCGAAGAGAATCCTGCTTTCAC	0	0
21	GTCTCTCTGTAGTATTGCTACTAAAGTCGTATT	13	5
22	GTGCTCGCTCCTCCCTTGCGGGAGGTCGTCACC	0	0
23	GTGCACGTTCCACCCTTGCGGGTGTCATCCCTG	6	9
24	GTATACCGACCTTGCGGGGAGAACATTTCTGAA	5	8
25	CTGCAGAATTCCTGACGGGAAGCCCGACTTTC	0	0
26	GTGCACGTTCCACCCGAAAGCGTCAGTGACCTT	13	3
27	GTGGAGCACCTCGAAGGCGACCGGCTTTCACC	6	7
28	GAGCAGGATGGTATTGCTACCTCGTTAGGCTTT	5	16
29	GTCTCTCTGTTGTATTGCTACAAAAGCCGTATC	0	0
30	GTGTTGAGGCTCCGAAGAGCTTGGTCCATCTC	11	16
31	TCTCACTGATTCCCCGAAGGGCACTCTCGCTTT	0	16
32	GTGCACGTTCCAACCTTGCGGCTGTGGCTCTAC	3	10
33	AGTTTCGTGTCATTGCTGAAGAGTGGCTTTCAC	8	8
34	GTGTTCCAGCCAGCCGAAGTGAAGACCTCCATC	6	9
35	GTGTGCAGATTCTCTTTGAGCACCAAACCATC	0	0
36	AACCACAAGTTCTCCGAAGAGCACCCCCACCTT	0	7
37	GTGCACGAGTCCCGAAGGACGCTACCATCTCTG	0	0
38	TGCAGGCAGGAGCCGATTACTCGGATCACACTA	14	10
39	AGTTTCGGGTCATTGCTGACTGACTTCTTTCAA	9	0
40	GTGCACGCTCTCCGAAGAGTCGTTCCGCTTTCG	0	2
41	GTGTTCCGGTTCCCTTTGCGGCACAGCCACCTT	0	22
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AGTTTTGTGCTCCGAAGAGAAGACCGCTTTCAC	13	9
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GTGTGCAGGTTCTCTTTTGAACACCAAACCATC	0	0
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GTGTTACGGCTCTCTTTGAGCACCAAGCCATC	0	0
ATGTGCAGGTTCTCTTTGAGCACCAAACCATC	0	0
GTGCACGTTCCGGCCTTGCGGCTGTGGCTTCCC	0	0
GTCTGCGCTCTCCGAAGAGTCGTTCCCCTTTG	6	9
GTGTCCCGATTCCCTTTGCGGCACCCCAGCTC	10	14
GTGCACGCTCCCTTGCGGGTCATCCTGGTTTCC	0	8
GTCTTTGGGTCTTCCTTGTGGGAAGAGGAGCTG	0	0
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GTCTCCAGGTTCCCGAAGGCACTCCCGCATCGC	10	6
GTGTTGTATCCAGCCGAAGTAAAGGACCGTCT	0	0
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GTAACCGCTCCCCGAAGGGTCGTTCCGCTTTG	4	9
GTGCACGTTCCACCCGAAGGCGTCATCGACCTT	5	8
CTGCACGAGTTCTTGCGAAAAGGCACATCTCTG	2	3
CGATGGCGGCTCCCGAAGGAGAGACGACCTTTC	4	8
GTGATAGCTTCCGGATTGGATACCGTTCGTTCC	5	11
GTGCAACAGGCCCCTTGCGGGGAAAGCCCATCT	9	5
GATATAATAACAGTAATAATTATTTTTTCAAAT	0	18
CGACTCCCGTCCCTTGCGGGAAACCTCTGTTTC	7	13
CGATAGCACTCCCGAAGGACACAGCCTTTCAGC	0	0
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TGCTTTGTGTCCTTTGCAGGCCTACATGCTTTC	0	0
GTGTTACGGCTCTCTTTGAGCACTAAGCCATC	0	0
GTGCGAGCTTCCCTTGCGGGATCGTCAGGCTTT	9	5
TGCACTCGGCTTGGTTTTACCCAAGAGATCCCC	11	6
GTGTGCAAGCTCTCTTTGAGCACTCCCAGATC	0	0
TGCTCTTTGTTCTTGCGAAAAATCCATCTCTG	0	0
CGGCTGGTTCCTGACTTTACAGGTCGTTCCCTC	2	10
GTGTGGGACCCAGCCGAAGTAAAGGACATCATC	0	0
CCCATCAAATCATGAAAGAGCTATCAATCTGTC	19	5
GTGTCTTGTTCCCTTTTTTCAAAAAGGCACCT	0	0
CCCATAGAATCAAGAAAGAGCTCTCGATCTGTC	16	0
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4	GTC	0	0
5	GTCTCCAGGTCTCCGAAGAGAAAACCTACTTTC	3	0
6	TCTCACCAGCTTCCCGAAGGACACCCCCACATC	6	3
7	TCTCACTCGCTCCCCGAAAGGCACCAAGGCATC	0	0
8	GTGGAAGTTTCACACCGAAGTGCAGCCTTCTGA	9	11
9	CCATCCGATCCTCTGAAGGGCCTTCTCGTCTGT	0	0
10	GTGTGGGAGCCAGCCGAAGTGAAGGGTCGCGTC	0	0
11	CCCACTGAATCAAGAAAGAGCTTTCAATCTGTC	6	6
12	GTGCACGGTCCAGCCAACTGAAGAAAAGCATT	0	8
13	GTGTTGCAGTTCCTTTTCGGGCACTTTCTCATC	3	4
14	GTCTCTCTGTCTCTTGCGAGCCTACAATATCTC	0	0
15	GTTGAGGCTCCCGAAGGTCTGGTCCGCTTTTCGCT	0	0
16	GTGTGCAGGTTCCCTTTTCGGGCACAATCTCATC	12	7
17	CTACACGGTGTCCGAAGACAGCCCCACTTTTCAT	0	0
18	GTACACAATCATTAACTTAACATAATAAGCTGA	0	0
19	TGAAAGACGTCCGAAGAAAAAACTGTTTCCAGT	7	16
20	GTGCAGGAGGTCCCTTGCGGGAAACGACCATCT	0	0
21	GTGCTGGAAGTCCGAAGAGGGGCTCACGTTTCC	6	4
22	GTGTTACGTTTCTCTTTTCGAGCACTCCCACCTC	7	9
23	GTGTTACGGCTCTCTTTTCGAGCACTCCTCTATC	3	16
24	GTGCAAAGGCTCCCCGAAGGGCACCCCACTTT	2	4
25	GTGCTGGTTACACCCTTGCGGGCAATTTGCCAC	4	8
26	GTCACCGCGCCTCCGAAGAGGACTGCCATCTC	0	0
27	GTGTACGTTCCATTCTTGCGATTGTCATTGATG	0	0
28	GCTGCCAAATCAAGAAAGTGCTATCAAGCTGTC	3	29
29	GTGCAGGCTTCACTCCGAAGAGCAGACCTCCGA	5	9
30	CTGCAGGCAACCGGCTTAACGGTTCATTTGACT	0	0
31	GTGTGCAGGTTCTCTTTTCGAGGACCAAACCATC	0	0
32	GTGTTCTCGCCAGCCGAAGTGAAGAAAGTCATC	6	9
33	GTGCACGTTCCACCCAAAGGGCGTGGCTCCTCT	5	8
34	GTAATGGCTCCCCGAAGGGTCGTTCCGCTTTCA	2	5
35	TACTGGCAGTGTATTGCTACAAAATGAGCTTTC	6	3
36	TACTGGCGGTATATTGCTATAAAGAGAGCTTTC	13	7
37	GTGCACGTTCCGGTCTTGCGACTGTGGCTCTCC	3	6
38	GTCTTCACGTCTTCCTTTTGGGAAGAGGGCACCC	5	4
39	GTGTGGGAGCCAGCCGAAGTGAAGGACCTGATC	0	0
40	GCACAGGTTCCACCTTGCGGCGTCGCCGACGTT	0	0
41	GTGTCCTGGCTCCCTTGCGGGCACGCCGCTTT	2	5
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GTGCACCGGTCTCTTGCGAGAAGGACACCTTTC	7	3
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GTGGCACACCCTCGAAGGCGACCCACTTTCGTG	0	0
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AACCACAAGTTCTCCGAAGAGCACCCCCGCCTT	0	6
GTGTTCTGGCTCTCTTTCGAGCACTCTCACATC	0	0
CCCATAGAATCAAGAAAGAGCTCTCAGTCTGTC	0	0
GTATCCAAGCCAGCCGAAGTGAAGAAATCCATC	0	0
GTGTTCCCGCCAGCCGAAGTGAAGGATTCCATC	0	0
GTGTTGTATCCAGCCGAAGTGAAGGATCCATCT	26	2
TGCAGACAGGAGCCGGTTACCCGGATCATCTCA	5	3
CGACTCCTGTCTCTTGCGAGAAGGCGATATTTT	6	8
GTGTCCCGGTTCCCTTTCGGGCACCAAACCATC	0	0
GTACTAGCTCTCTTGCGAGTCGTTCCCTTTTCG	0	0
GTGTATGCTGATATTGCTATCTCGTCAGACTTT	4	8
CGACTCCCGTCCCTTGCGGGAAATCCATGTTTC	7	9
TGCATCGTGCCCCGAAGGGCGCTTCACCTTTCA	3	7
GTGTTCCAGTTCTCTTTCGAGCACTCCCAAATC	5	3
GTACAAGCTCCCGAAGGTCTGTTCCCTTTTCAGT	0	0
GTGCACGTTCCACCCGAAGGCGTCAATGACCTT	5	4
GGGGCGAGTTTTATTAATATTATTAATTTGTTC	0	0
GTGTTCCGACCTATTGCTAGGAGGAGTCCATCT	5	5
GTCTTCTGGTCTCCTTGTGGGAGAGGGCCCACT	5	6
GTGTGGGAGCCAGCCGAAGTGAAGGATCACATC	0	9
TTGTCTATCTCATACTAATTCTCTAATAGACTC	9	4
GTGTGGCGTCCGGCCGAACCGACTCCCAGATCT	5	6
GTGCGGAGTCCGGCCGAACCGAAGGGACCGTCT	5	10
GTGCATGTTCCACCCTTGCGGGTGTGGCCGAAC	2	5
TCTCACTAGCTCCCCGAAGGGCAAATCTCCATC	4	12
GTGCAGGTTCCACCCGAAGGCGTGGCTCTACTT	3	5
GTAATAGCTCCCCTTGCGGGACACCGGCTTTCA	0	0
GTGTGGAGGTTCTCTTTCGAGCACCAAACCATC	0	0
AGTTTCGTGTCATTGCTGAAGGGATCCTTTCAG	5	0
GTGTGTAGGTCCCCGAAGGGAAGAAAGGCATCT	4	10
GCTAAGAAATTAATACTATCAAAAAAAGGAAAAAT	0	0
GTGCACGTTTCACCCGAAGGCAGATTACTCAGG	2	2
GTGCACGTTCCACGGCAAGCCGCGTCACCGATG	8	5
GTGTCTGAGTTCCCGAAGGCACCAATCCATCTC	0	14

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4	GTGTGCAGGTTCTCTTCGAGCACCAAACCATCT	0	0
5	GTCTCTCGGTTGTATTGCTACAAAGACTGTATC	0	13
6	CCCATCCGATCCTCTGAAGGGCCTTCTCGTCTA	0	0
7	GTGTATCGGTTCTCTTTCGAGCACCCCCGGATC	5	13
8	GTCTCCAAGTCCCCGAAGGGAAAACCCACTTTC	0	0
9	GTGTGGCGTCCAGCCGAAGTGAAGGAGCAGGTC	5	3
10	GTGTTCTAGCCAGCCGAAGTGAAGGAATCCATC	0	0
11	TGCTTCGTGTCCCTTGCGGGCCTGCCACCTTTC	0	0
12	GTGTTCCGGCCTATTGCTAGGAGGAATCCATT	6	0
13	ATACAGAAGTCCTTTCGGACGATATCATTCTG	6	2
14	GTCTTCCGGTCGTATTGCTACGAAAGCCGTATC	0	10
15	AGTTTCGCGCCCTTGCGGGAAGTCTGCTTTCAC	4	6
16	CCCATAGAATCAAGAAAGAGCTCTCAAATCTGA	10	5
17	GTAAACCGACTCTTGCGAGCTACGACATCTCTG	11	5
18	GTAAAGGCTCCCCGAAGGGTCGCTCAGCTTTCA	4	5
19	AAGTGACAGTCTCTTGCGGAGAGGGTGGCTTTC	3	5
20	GTGCCCAGGTTCTCTTTCGAGCACTCCACATC	5	5
21	GTGCAGGAGGTCCCTTGCGGGAAGCGACCATCT	0	0
22	GTTTTAGGTTCCCCGAAGGGCACTCCCCGATC	0	0
23	GTGTTCAAATTCCCTTTCGGGCACGAATTTATT	0	2
24	GTGTTGCGGTTCCCTTTCGGGCACCCCCGGCTC	0	0
25	GTGTTACGGCTCTCTTTCGAGCACGAAGCCATC	0	0
26	GTTTAGGCTCCCCGAAGGGTCGATCCGCTTTCA	3	3
27	GTGTTTAGATTTCTTTCGGACACAATTCCATC	0	0
28	CCACTACGGCCCCGAAGGGGAAGATGCATCTCTG	0	0
29	GTGTTAGGCTCCCTTGCAAGGCACTCCCGAATC	2	0
30	GTGTTGCGCTCCCGAAGGCACCTTCGACTTTC	0	0
31	CTGCATGTGTCCGAAGAATATGAGCTTTCACCC	0	0
32	GTGCTCCTCCCACCCGAAGTGAAGGACTCCTTT	0	0
33	GTGTCACGGTTCCCGAAGGCACACTCCCATCTC	2	10
34	GTGTGCAGGTTCTCTTTCGAGCACCAACCCATC	0	0
35	GTGTCCAGGTTCCCTTTCGGGCACCGATCCATC	8	5
36	GTGTTAGCGTTCTTGCGGACGTATTCCTTTCG	8	4
37	GTGCGGCCGCCTTTCGGAAGGTACATCTCTGCA	0	10
38	GTCTCCAGGTCCCCGAAGGGGAAGACCTACTTTC	0	0
39	GTGCTAGAAGTTATTTTTTTAACTCAAAGAATA	9	0
40	CGACTGGACCTCCTTGCGGAGTAACCGTGTTTC	4	7
41	GTCACCGATCCAATAAATGAAGGAGTCCTTTT	0	0
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4	GTGTCCTAGCTCCCTTGCGGGCACATCCACGTT	0	0
5	CGACACCAGCCCTTGCGGGCCCCTACATCTCTG	6	5
6	GTGTGGGAGCCAGCCGAAGTGAAGGGTCACGTC	0	2
7	GTGAGTGTGTCTTGCGAACCTCAGGCTTTCACC	3	3
8	GTGTTTCAGGCTCCCTTTCGGGCACCCCTCAATC	2	12
9	TGTTTTGTGTCCTTACGGACTAATTCATCTCTG	2	2
10	GTGCACTTGCCCTTGCGGAGGGTGTATTTCTACA	4	6
11	GTGCACAGACTCCGAAGAGCTATAACATCTCTG	7	0
12	GTCACCTGGTCCAGCCGAAGTGAAGGATACCGTC	0	0
13	GTATTCAGGCTCCCTTGCGGGCACTCCCGAATC	5	0
14	GTGAATCTGCCCTTGCGGGAAGGAATATCTCTA	0	0
15	GTCACCGCGCCTCCGAAGAGGACCATCGATCTC	0	0
16	GTGCACGTTGTACCCTTGCGGGCCTCATTCCTG	2	11
17	GCACTAAGTATTTTATAATTAACGCTCTAATTA	4	3
18	GTAACAAGCTCTTGCGAGAAGACCATTTCTGG	2	5
19	TGAAAATTGTCCGAAGAAAAGCATATCTCTACG	0	0
20	TGCAAGCGGCCATTGCTGGCTGCAAACCTTCAT	0	2
21	GTAAGCTCTCCATTGCTGGACACCGGCTTCA	0	0
22	GCTAGGAAATTAAGTATCAAAAAAAGAAAAAA	8	6
23	GTGAGCAGGTTCTCTTTTCGAGCACCAAACCATC	0	0
24	GTGATCGCGCTCCGAAGAGGGGAACGTGTTTCCA	0	0
25	GTGTGCAGGTTCTCTTCCGAGCACCAAACCATC	0	0
26	GTATAGGGCCCAGCCGAAGTGAAGGAATCCATC	9	2
27	GTGTGGCGTCCAGCCGAAGTGAAGGCTCGAGTT	6	10
28	GTCTCTGGGCTCCTTGCGGCACCCCATATCTC	2	9
29	TGCAGGCAGGAGCCGGTTACCCGGATCGTCCTA	3	6
30	GTGTCTTGTTTCTCTTTCGAGCACTCCCACATC	2	9
31	GTGCATGTTCCACCCAGAGGGTGTGGCTCCTGT	0	0
32	TGCAATCGGTCTCCGAAGAGAAGGCCACCTTTC	5	5
33	GTGCAGGAGCCGGCCGAACCGAAGGTCCATGTT	0	0
34	GTCTCCGGTCCAGCCGAAGTGAAGGATCTCATC	2	10
35	GTAGAAGGTTCCGGAAGTGGATACCGTTGGCCCC	0	3
36	CTCCAAGTGCCCTTGCGGGAAACCACTTTCATG	4	0
37	GTGCACGTTCCACTCTTGCGAGCGTCATGAATG	0	0
38	GTGGTAGCTTCCGGAAGTGGATACCGTTGGGGTA	2	7
39	GTGCACGTTGACTCTTGCGAGCCTCATTCCTG	2	0
40	GTGTCCTGGCTCTCTTTCGAGCACTCCCACATC	3	3
41	GTGTCCAGGTTCTCTTTCGAGCACTCCCACATC	2	0
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4	GTCCCAGTGCCCCGGAGGGAAACCGACTTTTCAC	0	0
5	GTGTCCTGGTTCTCTTTCGAGCACTCCCACATC	7	9
6	GTGCTTGTTCCACTCTTGCGAGTGTGGCTCCAC	4	4
7	TCCACGGAATCGAGAAAGAGCCTTCAGTCCGTC	8	0
8	GTGTGGACGCCAGCCGAAGTGAAGAACCTCATC	0	5
9	GTGTCCACTTTCCCTTTCGGGCACCTAATCCAT	0	0
10	GTTATTAAATACTCTTTCAGTATATTATATATA	0	12
11	GTGTGCAGGTTCTCTTTTGAGCACCAAACCATC	0	0
12	CCCACTTAATCAAGAAAGAGCTATCAATCTGTC	7	6
13	GTGCTCTCTCCGGCCGAACCGAAGGACTCCATC	0	2
14	GTGCTCCACCCTCGAAGGCCTCCCGGTTTCCCG	2	4
15	GTCTCTCTGTTGTATTGCTACAAAGACTGTATC	6	0
16	GTGTTCCGGCTCCCTTTCGGGCACCCCCACCTC	2	9
17	GTCAGTGGTCCAGCCGAAGTGAAGGAAATGATC	2	11
18	GTATACCGACCTTGCGGGGCACCTGTCTCCAGA	0	6
19	GTGCAGGTTCCACCTTGCGGCGTCACCGACGTT	0	0
20	CGCACCCGGCCCCGAAGGGCTGACACCTTTCAG	0	0
21	GTCAGTATCCAGCCGAAGTGAAGGAAACCATC	2	2
22	GTCTCTCGGTTCCCGAAGGCACCAAGTCATCTC	5	0
23	GTGCAAGCTCCCGAAGGTCGTTCCCTTTTCAGT	0	0
24	GTGCCCCGGTTCTCTTTCGAGCACTCCCACATC	2	3
25	GTAACGGCTCCCGAAGGTCGGTCCACTTTTCGTT	0	0
26	GTGTGCAGGTTCTCTCTCGAGCACCAAACCATC	0	0
27	TTGAGAGAATCGAGAAAGAACAAATCAATCTGTC	0	0
28	GTGTGCAAGTTCTCTTTCGAGCACCAAACCATC	0	0
29	GTGTCCAGGTCCCTTGCGGGAAGGAGTCCATCT	0	0
30	TGTAAATTGCTCCGAAGAGAGTTCCAGTTTCCT	0	9
31	TGTATCGAGTCCCGAAGGACGATCCCCTTTCAG	0	2
32	TGCACTCTGTTCTTGCGACCAACGAACTTTCAT	10	4
33	CCCATAGAATCAAGAAAGGACCATCAACCTGTC	0	3
34	GTGCAGATTCCGACTCCGAAGAGCTGTCACCCC	0	2
35	GTAGACAAGCTCTTGCGAGAAGACCATTTCTGA	0	0
36	TGTAACCTGTATATTGCTATAAAGACCCCTTTC	0	4
37	GCATGAGCTAAAAAAAATAATTTAATCTAAAAA	4	2
38	GTGTCCAGGTTCCCGAAGGCACCAATCCATCTC	2	3
39	GTAGGAAACCCTTACGGACCCACCATCTCTGAT	0	5
40	GTGCAAACTCCCCTTGCGGGGTCGTTACCCTTT	0	0
41	GTGTTCCAGTTCCCTTTCGGGCACACCCAAATC	8	0
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GTGTCCCAGTCCCCGAAGGGAAAGCCACATCTC	0	2
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GTGTCCAGGTTCCCTTTTCGGGCACCAATCCATC	4	0
ATGTAACAGTACCGAAGTAAAATACCCTTTCAG	0	0
TGGAATCAGCCCCAAAGGGCGATCACCTTTCAG	0	0
GTGGCGGCTCCCTTGCGGGTCGTCGGGCTTTCA	3	2
GTCAAAGAGTCCCGTGAGGGAAGGAATCCATCT	9	0
CGACTTCAGTCCCTTGCGGGAAATCCATGTTTC	7	0
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GTACAGACTCCCGAAGGTCGTTCCGCTTTCACT	0	4
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CTAGACCAATCAAGAAAGAACTCTCAATCTATC	0	0
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GTATCCGGTCCAGCCGAAGTGAAGACACATCT	0	0
GTCCCACTGCCTATTGCTAGGACTCCCGGATCT	5	0
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GTGTGCAGGTTCTCTTTCGAGCACCAGACCATC	0	0
CGACTCCCGTCCCTTGCGGGAAATCCCTGTTTC	3	8
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GTGTTCAGGCTCCCTTGTTGGGCACTCCCGAATC	3	0
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GTGTTCAGGCTCCCTTGCGGCACTCCCGAATCT	0	0
GTATAAGCTCCCGAAGGTCGTTCCGCTTTCGCT	0	0
GTGCATGTTCCACCCGAAGGTGTCACTTGGCTT	0	4
GTCTTCACGTCTTCCTTGTTGGGAAGAGGGCCCA	0	3
GTATACAGGCCCCGAAAGGCTATACCGTCTCTG	0	0



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4	GTGTAGGTTCCACCCGAAAGCGTCAGCGACCTT	5	2
5	GTGCATGTTCCACCCGAAGGCGTCACTCCGCTT	0	5
6	GTGTACGTTCCATTCTTGCGATTGTCATTCTG	0	4
7			
8	GTGTGCAGGTTCTCTTTGAGCGCCAAACCATC	0	0
9	GTGATTGTTTCACCCGAAGGCAGAGTTATCCCT	3	3
10	GTGCCAGGTTCCGGATTGGATACCGTTCGTTCC	0	4
11	CTATCGGCAACCGACTTTACGGTTCATCGCTAC	0	4
12	ATACTAGCGTCCCTTGCGGGAAGTCCACTTTCA	4	0
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14	GTGCATGTTCCACCCTTGCGGGTGTGGCTCTGA	0	0
15	GTGTCCCGTCCGGCCGAACCGAAAGACCCGGTC	0	4
16	GTGTGGAAGCCAGCCGAAGTGAAGAAAGGCATC	0	0
17	GTGTATCTGCCTATTGCTAGGGGTCCAAACTTT	0	0
18			
19	GTCACCGGTCCAGCCGAAGTGAAGGGATCCATC	3	0
20	GTGTTCCGGTTCCTTTGCGGCACCCCCACCTC	0	2
21			
22	GTCTCTCGGTTCCCGAAGGCACCAATCCATTTC	0	0
23	GTCTCAGAGTTCCCGAAGGCACAACCGCATCTC	2	0
24			
25	GTGCAGCAGTCCCGAAGGAAAGGCGCCTTTCAG	0	0
26	ATACAGAAGTCCTTTCGGACGAAGCCATTCTG	3	2
27	GTCTCGGGGTTCCTCGCGGCACTGCCCATCTCT	3	3
28			
29	GTGGAGCACCTCGAAGGCGACCGGCTTTCGCC	4	3
30	GTGTCCCGATTCCCTTTCGGGCACCCCCACCTC	4	3
31			
32	GTGCACGTTCCGGTCTTGCGACTGTGGCTTCCC	0	0
33	GTGCACCAGCCCCGAAGGGAGGACTCCTTTCAG	0	0
34			
35	TGTTTCGTGTCCCGAAGGAAAAACGGCTTTCAC	0	0
36	GTGCGGGAGCCAGCCGAAGTGAAGGACCCGATC	0	0
37			
38	GTGTCCTCCGTCCCTTGCGGGTCTAGCCTGTTT	8	0
39	GTGCACGCTCCCTTGCGGGTCAACCCCTTTC	4	0
40			
41	GTGTGAGACCCCCGAAGGACCCGACATCTCTGC	2	5
42			
43	TCCATCAAATCAAGAAAGAGCTATCAATCTGTC	0	0
44	GTGTGTGATCCAGCCGAAGTACGGTTACATTT	5	0
45	ACAAACGAATCATGAAAGATCTTTCAGTCTGTC	5	0
46	GTGCACGCTACCCTTGCGGGTTCGTTACGCTTT	0	2
47			
48	GTACGCGTTCCGGACTGGATACCGTTCGTACGT	2	4
49			
50	GTGCTTGTTCCGGTCTTGCGACTGTGGCTCTAC	0	3
51	GTGTGAGTGTTCGGAAGGCACCAATACATTT	0	0
52			
53	ATATAACAGTCCTTGCGGAAGTCTTCATTTCTG	0	0
54	GTGCATGTTCCACCCTTGCGGGTGTACTCCCC	2	4
55	CGACTACAGTCCCCGAAGGGAAAGCCCATGTTT	3	5
56			
57			
58			
59			
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4	GTGTAGAACCCCGAAGGACACCGTATCTCTACG	0	0
5	GTGTGCAGGTTCTCCTTCGAGCACCAAACCATC	0	0
6	GTGTCTTAATTTCTTTTCGAGACTTTTACATC	0	3
7			
8	GTGCTGGGTTCCGGATTGGATAACCGTTCGCTCC	2	0
9	GTGTCCTGGTTCTCTTTCGAGCACTCTCACATC	3	2
10			
11	GTAGTAGGTTCCGGATTGGATAACCGTTCGCACC	2	0
12	GTGTGCGGGTTCTCTTTCGAGCACCAAACCATC	0	0
13	GAGTGCAGGTTCTCTTTCGAGCACCAAACCATC	0	0
14			
15	GTGTGCAGGTTCCCTTTCGAGCACCAAACCATC	0	0
16	GTGCATGTTCCGGCCTTGCGGCTGTGGCCTCCC	0	5
17			
18	GTGTCCAGGCTCTCTTTCGAGCACTCCTAAATA	0	8
19	AGTTTCGTGTCATTGCTGAAGGGTGGCTTTCAC	0	3
20	CTACTAGCATCCGACTTAACGGGTCATTGCACT	0	9
21			
22	GTCTCCAGGTTCCCGAAGGCACTCCCGCATCTC	0	9
23	GTCACGGCTCCTTGCGGTCCGGTCCGGTTTCCCT	4	3
24			
25	GTTATACCCACCCGAAGTGAGAGCTATGTTTC	0	0
26	GTGTTCAAGCTCCCTTGCGGGCACTCCCGAATC	2	0
27			
28	GTGTGGAAGCCAGCCGAAGTGAAGAAGACAATC	4	0
29	GTCTTCGGGGCCAGCCTTGTTGGGCTGGGGGCCTG	2	6
30	CTCCGAGTGTCTTGCGGAAAACCACTTTTCATG	0	0
31			
32	GGTCTGGCGGCCTCGAAGGACTTCTTATTTCTA	0	0
33	GTGTGCAGGTTCTCTTTCGGGCACCAAACCATC	0	0
34			
35	CGACTGGACCCCTTGCGGAGTAATCGTGTTTC	3	3
36	GTGTCAGAGTTCCCGAAGGCACCAATCCATCTC	0	11
37	GTCACCGGTCCAGCCGAAGTGAAGGAAAGAGTC	2	5
38			
39	GTGTTAGCGCGTATTGCTACGCCCAATCGATCT	0	0
40	GTCTCCGCGTCCCGAAGGACCTTCCGCTTTCAC	0	0
41			
42	GTGTGACACCCTCGAAGGCGACCGGCTTTCACC	0	4
43	CGACAGCGGCCCCGAAGGGAAAGTACATCTCTG	0	0
44	GTGTCCAGACTCCCTTTCGGGCACCAAGCCATC	9	0
45			
46	GTACCAAGTCCCCCTTGCGGGGTTCCCTTGCC	0	2
47	GTGTTCAAATTCTCTTTCGAGCACGATTTTCATC	4	0
48			
49	GTGCTAGTTGTTCCCTTGCGGGGCCTACTCTA	0	0
50	GTCTCTGCGTTCCTTTCGGCACACCAGCCTCTC	0	0
51			
52	GTACCAAGTCCCCTCTTGCGAGGTTCCCCTGCG	0	4
53	GTGTGCAGGTTCTCTTTCGAGCATCAAACCATC	0	0
54			
55	GTGCAAAGCGTATGTATTGCTACATACTAACCG	3	2
56	GTCTCTGGATTCCCTTGCGGGCACGCCAACTTT	3	0
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4	CCCACAAAATCAAGAAAGAGCTATCAATCTGTC	3	0
5	TACATTCTGTGTATTGCTACAAAAATCCCTTTC	0	9
6	GTGATCAGGTCCCTTGCGGGACGCCGACGTTTC	0	5
7	GTGTCCAGGTCCCTTGCGGGAAGGAGTCCGTCT	0	0
8	GTGACCGTTGTACCCTTGCGGGCCTACTCCCAC	0	3
9	GTACCCGGTCCAGCCGAAGTGAAGAGGTCGATC	2	2
10	GTGCCCAGGTTCCCGAAGGCACAATCCCATCTC	0	0
11	CTACACGGGTCCCGAAGGAAGACTGTATCTCTA	2	5
12	TGTTTTGGGCCAGTAAACTGGCGATCGGTATTA	2	5
13	TGAAAGACGTCCTTGCGGAAAGAAACCTTTCGG	0	0
14	GTGCACCTCCCACCCGAAGTGAAGGAATCCATT	0	0
15	TCCATAGGATCGAGAAAGAGCTCTCAATCTGTC	0	0
16	GTCTTGCGCTCCTTTCGGAAGTCTGCTTTCAC	0	0
17	GTGTTACGGCTCTCTTTCGAGCACCCCCACCTT	3	2
18	GTGTTCCAGCCAGCCGAAGTGAAGGGTCTCATC	0	0
19	GTGTTCTGGTTCTCTTTCGAGCACTCCCAAATC	0	2
20	TGTTTCGTGTCCCGAAGGAAAGTCTCCTTTCAG	2	2
21	GTCTCCGGTCCAGCCGAAGTGAAGAACCCGGTC	0	3
22	GTGTGCAGGTTCTCTTTCGAGCACCAAACATCT	0	0
23	CGCACGCAGTCCGAAGAAGATCACGTTTCCGCG	0	2
24	GTGTCCAGGCTCCCTTTCGGGCACCCCCACCTC	0	2
25	CTAAACCAATCAAGAAAGAACTCTCAATCTGTC	0	0
26	GTCTATAGGTCTCTTACGAGAAGACCCGATCTC	0	2
27	GTGTCCTGGCTCTCTTTCGAGCACCAAGCCATC	2	0
28	CGATTGCCGTTCCCGAAGGAAACCCGCTATTT	0	0
29	GTGTCCCAGTCCCCGAAGGGAAGAAAGGCATCT	6	4
30	GTGTTCAGACTCCCTTGCGGGCACTCCCGAATC	0	0
31	GTGTTAGCGTCCTTGCGGACGTATTCCCTTTCG	7	2
32	GTGCACGTTCCACCCAGAGGGCGTCATTGACCT	2	2
33	GTGCACGGAAGTCCGAAGAGGGGCTCACGTTTCT	4	0
34	GTGCAAGCTGGTATTGCTACCTCGTCCCCCTTT	0	0
35	CCCACGAAATCAAGAAAGAGCTCTCAATCTGTC	0	0
36	GTGTCCAGGCTCCCTTTCGAGCACCAAGCCATC	0	3
37	GCACTAAGTATCTAATATTTAACTTTATAAATA	0	3
38	GTCTCATGGTTCCTTGCGGCACTCCCACATCTC	0	6
39	GTGAAAAAGCTCCCTTGCGGGCACTCCTCCCTT	0	5
40	GTGCTCCTCCCACCCGAAGTGAAGAACCCCTTT	0	4
41	TGTTTTGAGTCCATTGCTGGAAAATCGGCTTTC	0	2
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5	GTGCAAGAGCTCCCGAAGGCACCCCGCCCTTTC	0	0
6	TGCCAATTGCCCCGAAGGGAAGCCGCCTTTCGG	0	0
7			
8	GTGCATCCGCCTTTCGGAGGGTGTATCTCTACA	0	0
9	GTGTCCAGGTTCCCTTTCGGGCACCCTCACATC	0	3
10			
11	GTGGATGCGCCTTGCGGACCTCAGGCTTTCGCG	0	5
12	GTGCCTGTTCCGGTCTTGCGACTGTGGCCCTAC	0	0
13	GTGCAAGCTCCCGAAGGTCGTTCCCCTTTCGGT	0	0
14			
15	GTGCACGTTCCAGCCGAAGCTGTGGCCCCGCTT	0	0
16	GTGTCCCTTGTCTCTTGCGAGCCTATCCCTATC	0	0
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18	GTGTGACGTCCGGCCGAACCGACTCCCCGCTCT	3	2
19	GTGTTCCGACCTATTGCTAGGAGGATCCCATTTC	0	0
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21	GTCACGGCTCCTTGCGGTTCGGTCCCCTTTCGGT	0	0
22	GTGTCCAGGCTCTCTTTCGAGCACCAAACCATC	0	2
23	GTGTTCAGGCCCCCTTGCGGGCACTCCCGAATC	2	0
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25	GTCTCAATGTTCCCGAAGGCACCAATCTATCTC	0	0
26	GTGCAAAAGCTCCCCGAAGGGCACTCCCGCCTT	0	3
27	GTGTTCCGGTTCCTTTCGGGCACCTCCCGCATC	0	3
28			
29	GAGTTCAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
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31	CTAGACCAATCAAGAAGGAACTCTCAATCTGTC	0	0
32	GTGCACTAGTCCCGAAGGAAAGACACCTTTCAA	0	0
33	GTGTTCAGGCTCCCTTGCGGGGACTCCCGAATC	0	0
34			
35	GTGTTCCGGTTCCTTTCGGGCACCCCCGGCTC	0	0
36	GTGTTCCGGCTCCCTTGCGGGCACTCCCGAATC	0	0
37	GTGCAGGCTCCCGAGGGTCGGTCCCCTTTCGGT	0	0
38			
39	CCCAACCGATCCTCTGAAGGGCCTTCTCGTCTG	0	0
40	GTGCTCTCCCCGGCCGAACCGAAGAACCTGATC	0	0
41			
42	GTGCAGAAGTCCTTGCGGAAAGCACTATCTCTA	2	0
43	GTGTTCAGGCTCCCTTGCGGGCACCCCCGAATC	0	0
44			
45	CCACCGCGGTCCCCGAAGGGAGGACCTCATCTC	3	0
46	GTACAGCGGCCCCGAAGGCGACTACATCTCTGCA	0	3
47	GTGTCCCAGTCCCCGAAGGGAAAACCACATCTC	3	2
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49	GTGCATGTTCCACTCTTGCGAGCGTGGCCCAAC	0	0
50	GTGACCGAGCTCCGAAGAGCTGACCAGGTTTCC	0	0
51			
52	CGCACCCGGCCCCGAAGGGCTGGCACCTTTCAG	0	0
53	GTGCGATAGCCTTTCGGAGGATGCATCTCTGCA	4	2
54	GTGTGCAGGTTCTCTTTCGAGCACCTATGTATT	0	0
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56	GTGAACAGACCCTCGCGGGCTCATGTATCTCTA	0	0
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5	GTCCAACCGTTCTTGCGAACTGCTCACGTTTCC	0	0
6	GTGTTCTGGCTCCCTTGCGGGCACTCCCGAATC	0	0
7			
8	GTGTTAGCGTCCTTGCGGACGCATGCCCTTTCA	3	0
9	GTCTCTGCGCTCCTTTGCAGGCACTCCCACCTT	0	9
10			
11	GTGCTAGCTCCGTATTTCTACGGTCGTCCCCCT	2	0
12	GTCTTACGGTTCCCGAAGGCACTTCCGCATCTC	0	6
13			
14	GTGTAGGCTTCCCGAAGGATCGTTCCGCTTTCG	0	2
15	GTGTTCAAGGCTCCCTTGGGGGCACTCCCGAATC	0	0
16	GTGACAGTCTCCGGACTIONGATACCGGCCCCCG	3	4
17	GTCATACTGCTGTATTGCTACAGAAACTIONGATT	5	0
18	GTCTCTGGATTCCCTTACGGGCACGCCGACTTT	3	0
19			
20	CCCATAGAATCAAGAAAGGACCGTCAACCTATC	0	0
21			
22	CCCATAGAATCAAGAAAAGACCGTCAACCTGTC	0	0
23			
24	CCCATGGAATCAAGAAAGGACCGTCAACCTGTC	0	0
25	AACCACAGATTCCCCGAAGGGCACCTCATCTT	0	0
26	GTGTTCTCGCCAGCCGACTIONGAAGGAAACCATC	0	0
27			
28	GTGCAGGTTCCACCCGAAGGCGTGGCTCTGCTT	3	6
29	GTGTTACGGTTCTCTTTCGAGCACTCCTCTATC	0	2
30	GTGTCCCGACCTATTGCTAGGAGGAATCCATCT	2	5
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32	GCTATCGGATCAAGAAAGCGCTATCAACTIONGTC	0	0
33	CGACTCGACTCCCTTGCGGGATAACCATGTTTT	0	2
34	GTGTGTTAGCCAGCCGACTIONGAAGGAAGGCATC	0	0
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36	GTGTTCCGACCTATTGCTAGGAGGAATCCATTT	0	0
37	GTATCCGGTCCAGCCGACTIONGAAGAAATCCATC	0	0
38			
39	GTCTACGGTTCCCGAAGGCACTAAGGCATCTC	0	4
40	GTGCTACACCCTCGAAGGCGGCTCCGATTTCTC	0	4
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42	GTGTTCAAGGCTCCCTCGCGGGCACTCCCGAATC	1	0
43	ATATAGCGGCCCCGAAGGCGCAAACATCTCTGCT	0	0
44	CCCACAGAAATTAAGAAAGAGCTATCAATCTGA	3	2
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46	CTGCAGATGTCCTTGCGGAAGCCGACTTTCGCC	0	0
47	GTCTCTTGGCTCCTTTCGGCACTTCCGCCTCTC	2	0
48			
49	GTCACCGGTCCAGCCGACTIONGAAGGCCCTCTT	0	4
50	GTGTACCGGCCCTTGCGGGCGACGACATTTCTG	0	0
51	AGTTTCGTGTCATTGCTGAAAGACTCCTTTCAG	6	0
52			
53	GTGTAGGCTCTCCGAAGAGTCGTTCCCCTTTCG	0	2
54	GTGTCCAGGCTCTCTTTGAGCACGAATCCATC	0	3
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56	TACTAGCGACGTATTGCTACGCTATAAGCTTTC	0	6
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3			
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5	GTAATATTAAATTAAAAAATAATAAAATTTT	0	0
6	GTGCATGTTCCACCCTTGCGGGCGTCATCCCTG	0	0
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8	GTGTGGACGCCAGCCGAAGTGAAGAACGGAATC	0	0
9	AGTTTCGCGTCATTTCTGAAAGACTCTTTTCGG	2	2
10	CCCACACAATCATGAAAGATCTATTAGTCTGTC	9	0
11			
12	GTGACGACCCCTTGCGGGACTCCCGGCTCGCA	0	2
13	AACTACGAGTTCTCAAAGAGCACCCCGATGTT	0	0
14			
15	GTGTTCCAGCTCCCTTTCGGGCACACCCAAATC	0	0
16	GTGTACGTTCCACCCGAAGGCGTGGCTCTACTT	0	0
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18	GTGTTGCGCTCCTTACGGCACTCCGACCTTTC	0	0
19	TACTGGCGGTGTATTGCTACAAAAACCCCTTTC	0	3
20	CTGGACCAATCAAGAAAGAACTCTCAATCTGTC	0	0
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22	GTGCACGTTCCACCCGAAGGCGTCAGTGACCTT	0	2
23	CCCATAAAATCAAGAAAGAGCTCTCAGTCTGTC	0	3
24			
25	GTGTGCAGGTTCTCTTTCGAGCACAAAACCATC	0	0
26	GTGATTGTTACCCTCTTGCGAGGAATCAATGGG	0	0
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28	GTAAGGCTCCTCCATTGCTGGAGTTCGTTAC	3	0
29	GTGTTCAGGCTCCCTTGCGGGCACTCCCGAACC	0	0
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31	AGTTTCGTGTCCCGAAGGAAAGACCCCTTTCAG	0	2
32	TGTTTCGTGTCCCGAAGGAATGCTCCCTTTCAG	0	0
33	GTGTCCAGACTCTCTTTCGAGCACTCCTAAATC	2	3
34			
35	GTGTATGTTGTACTCAAAGAGCCTCACTGACGT	0	0
36	GTTCACGAGTGTCCAAAGAGTTGACCATTTCTG	0	0
37			
38	GTGTTCCAGCCAGCCGAAGTGAAGAGCTCCATC	5	3
39	TGGAAGCAGCTATTGCTAGCTCATAAGTTTCCC	0	0
40	TGCTTTGTGTCCCTTGCGGGCCTGCATGCTTTC	0	0
41			
42	CTCACTACATTTCTTGCGGCACTCCGATATT	3	0
43	CTCATGGAGTCAAGAAAGAGCTATCAATCTGTC	4	2
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45	GTCTCCGGTCCGGCCGAACCGAAGGTCCGGGTC	0	0
46	GTAGCAGGTTCCGGACTGGTTACCGTTGGCCCC	6	2
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48	GTGTTCAGATTCTCTTTCGAGCACGATCTCATC	0	0
49	TGATACAGGCCCCGAAGGGATATCTGCTTTCAC	0	0
50	CTAGACCAATCAAGGAAGAACTCTCAATCTGTC	0	0
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52	GTGCAGAGACTCTTACGAGAGACGCCGTTTCTG	0	0
53	GTGCAGCAGTCCCGAAGGAAGAGGCCATCTCTG	0	0
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55	GTCTCTGGATTCCCTTACGGGCACGTCGACTTT	0	0
56	CCCATCCAATCCTCTGAAGGGCCTTCTCGTCTG	0	0
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3			
4	GTGCATGTTCCACCCTTGTGGGTGTGGCTCTGC	0	0
5	GTCTTCCTGTTCCGAAGAACGACATACTTTCAT	0	0
6	CCCATCCGATCCTCTGAAAGGCCTTCTCGTCTG	0	0
7			
8	CTCATGGAATCAAGAAGGAGCTATCAATCTGTC	3	0
9	GTGCCAGGTTCCGGACTGGTTACCGTTCGCCCC	0	5
10			
11	ATGTTCAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
12	GTTTAGCAGCCATTGCTGGAAATACTATTTCTA	0	0
13	GTGTTCTAGCCAGCCGAAGTGAAGGAAACCATC	0	4
14			
15	TGCAGACAGGAGCCGGTTACCCGGATCGCCTCA	5	0
16	GCGCATGTTCCACCCTTGCGGGTGTGGCTCTGC	0	0
17			
18	CCCATCCGATCCTCTGAAGGCCTTCTCGTCTGT	0	0
19	GTGTTTAGGCTCCCTTGCGGGCACTCCCGAATC	1	0
20			
21	GTGTGCAGGTTCTTTTCGAGCACCAAACCATC	0	0
22	GTCTCGGGGCTCCTTGCGGCACCATCCATCTCT	0	3
23			
24	CCCATAGAATCAAGAAGGGACCGTCAACCTGTC	0	0
25	GTGCAAAAGCTCCCCGAAGGGCACCCCAACCTT	0	2
26	GTGCTTGTTCACCCAAAGGGCGTGGCCTCTCT	2	0
27			
28	CCCACCAAATCAAGAAAGAGCTCTCAATCTGTC	0	0
29	CCCATAGAATCATGAAAGAGCTCTCAATCTGTC	3	0
30			
31	GTGTTCAGGCTCCCTTGCGGGCGCTCCCGAATC	2	0
32	GTGTCCCGGTTCTCTTTCGAGCACTCCCACATC	3	2
33	GTGTGGTATCCAGCCGAAGTGAAGCCTCATCT	0	0
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35	GTGCAAAGGCCCGAAGGGAGACGCTATTTCTA	0	0
36	AACCACAGATTCTCCGAAGAGCACCCCGAGACT	0	0
37	GTGCATGCTCCCCGAAGGGTCCATCAGCTTTCA	0	4
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39	GTGCAAACTAATTACTCAAAAAGAGTATTTAAA	0	0
40	CCCCTAAATCAAGAAAGAGCTCTTAATCTGTC	2	0
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42	GTGAAGACCCGGCCGAACCGAAAAAGTAGATCT	5	0
43	GTGTTCCAGCCAGCCGAAGTGAAGGAAGTCATC	5	0
44	GTGTCCAGGCTCTCTTTCGGGCACGAATCCATC	0	0
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46	GTGCTTGTTCCTCTTGCGAGTAGTCTCCACG	0	0
47	GTCCACCAGCCATAAAGGAGAGTGTATCTCTAC	0	0
48			
49	GTGTGACGTCCAGCCGAAGTGAAGACCGGTCT	0	0
50	CCCACCGAATCAAGGAAGAGCTCTCAATCTGTC	0	0
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52	TGTTTCGTGTCTATTGCTAGAAAGACTCCTTTC	0	0
53	GTGTGATATCCAGCCGAAGTGAAGCCCCATCT	0	0
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55	ACTGGATGTTATGTGCAAATACAATTAATGA	0	0
56	GTGCAGCAGCCCCGAAGGGAAATACCATCTCTA	0	0
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3			
4	GTATTAGAGTTCCTCTCGGCACATCACTATCTC	0	0
5	CCATTTAATCAAGAAAGGGCTATCAACCTGTCA	0	0
6	GTGTTCAAGGCTCCCTTGCGGGCACTCCCGGATC	0	0
7			
8	CTAGACCAATCAAGAAAGTACTCTCAATCTGTC	0	0
9	GTAACCGCTCCCCGAAGGGTCGTTCCGCTTTCA	0	0
10			
11	GTCTATCAGCCTGAAAGGAAGGCGTATCTCTAC	0	0
12	TGAAAATTGTCCGAAGAAGGTTCTATTTCTAAA	0	6
13	GTGTAGGGCCCAAAAGGACACCATATCTCTATG	0	3
14			
15	GTGTGGGAGCCAGCCGAAGGATCAGATT	0	2
16	TGGAATCAGCCCCGAAGGGCGATCACCTTTCAG	4	0
17			
18	GTGTACAGACCCTTGCGGGCTAAACTGTCTCTA	0	0
19	CGCATCGTGCCCCGAAGGGAGATCGGCTTTCAC	0	0
20			
21	GTGTGTGGTCCAGCCGAAGGACGGCTATATCT	0	0
22	GTGAACCGACCCTTGCGGGCGGGGACATTTCTG	0	0
23			
24	GTGTTCAAGGCTCCCTTTCGGGCACCCCCACCTT	0	4
25	GTCACCGCGTCCCCGAAGGGAACCCCAAATCTC	0	4
26	GTGCAAACCGGGTATTGCTACCCTAGCCTGCTT	0	0
27			
28	CTAGACCAATCAAGAATGAACTCTCAATCTGTC	0	0
29	CTAGACCAATCAAAAAAGAACTCTCAATCTGTC	0	0
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31	GTCTCAGAGCTCCCGAAGGCACTCTACGATCTC	0	3
32	GTGTTCAAGGCTCCCTTGCGGGCACTCCTGAATC	1	0
33	GTGTGCAGGTCTCTTTGAGCACCAAACCATC	0	0
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36	GTTACAGCTTCCCGAAGGACCTCATCTTTCAT	0	0
37	GTGCAATAGCTCCCTTGCGGGCACCCCACCGTT	0	0
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39	GTGTGCAGGATCTCTTTGAGCACCAAACCATC	0	0
40	GTGTACAGTCCCGAAGGGCTCCAATATCTCTA	0	0
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42	GTGTGGAAGCCAGCCGAAGTGAAGAGGTCAATC	0	0
43	GTATACCGCCCTTGCGGACCCCATATCTCTATG	3	3
44	GTCTCGGGGCTCCTTGCGGCACTCCCCATCTCT	3	3
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46	CTCATGGAATCAAGAAAAAGCTATCAATCTGTC	3	3
47	GTGCACGTTCCGGTCTTGCGACTGTGGCCCCGC	0	0
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49	GTACGCGTTCCGGACTGGTTACCGTTTGTACGT	0	2
50	GTGTTCAAGTTCTCTTACGAGCACTCCCAAATC	0	0
51	GTCTCCGGTCCAGCCGAAGTGAAGAACCCGCTC	0	0
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53	CCCATAGAATCAAGAAAGAACCGTCAACCTGTC	0	0
54	GTGTGCAGGTTCTCTTTGAGCTCCAAACCATC	0	0
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56	AACCACAGATTCTCCGAAGAGCACCTCATCTT	0	0
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3			
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5	CCCATCCGATCCTCTGAAGGGTCTTCTCGTCTG	0	0
6	GTGTTCCGGTCCCCGAAGGGAACGCCTCATCTC	3	0
7	GTCTTCGTGTTCTTGTGGGAAGGAGCGGCTTT	0	0
8	GTGTGGAAGCCAGCCGAAGTGAAGAGACCAATC	0	0
9	TACAGACTGTGTATTGCTACAAAACCTCTTTC	0	3
10	GTCTTTGGGTCTCTTGTGGAGGAGGGCCTGCT	0	3
11	GTGCACGTTCCACTCTTGCGAGCGTCATCTCTG	4	0
12	TACGATCTGTGTATTGCTACAAAACCGGCTTTC	2	0
13	GTGTCCCCGGCTCCGAAGAGAAGAAACCATCTC	0	0
14	GTGTCCAGGTTCCCTTTGAGCACGAATCCATC	0	0
15	CCCACCGAATCAAAAAAGAGCTCTCAATCTGTC	0	0
16	GTGCTCACGTCCCTTGCGGGAAGAACTGCATTTT	0	0
17	GTCTCGGGGCTCCTTGCGGCACTGCTCATCTCT	0	0
18	ATATAACAGTCCTTGCGGAAATAACCATCTCTG	0	0
19	GTTCTAGACCCGGCCGAACCGACGCGACCAATC	0	0
20	GTGCTCCTCCACCCGAAGTGAAGAAGTCCATC	0	0
21	GTGTGTAGGTTCTCTTTGAGCACCAAACCATC	0	0
22	GTGCACGTTCCACCCGAAGGCGTCATAGACCTT	4	0
23	GTGCACGTTGTACCTTGCGGCCTCACTGACGTT	0	0
24	GTCTCCAAGTCCCCGAAGGGAAGAACTACTTTC	0	0
25	AGTTGAAACTGGTAAGGTTTTTCGCGGATCATC	0	0
26	GTGCAGCAGTCCCGAAGGAAGACACTATCTCTA	0	0
27	GTCTCGGGGCTCCTTTGCGCACCCCATCTCTG	0	0
28	TGAGAACCGTCCGAAGAAAGATCTGTTTCCAGA	0	0
29	GTGCAAGCTCCCCGAAGGGTCGATCCACTTTTCG	0	0
30	GTGATCAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
31	CTAGACCAACCAAGAAAGAACTCTCAATCTGTC	0	0
32	CTAGACCAATCAAGAAAGAACTCTCAATCTGCC	0	0
33	GTGTTCAGGCTCCATTGCGGGCACTCCCGAATC	2	0
34	GTGTGCAGGTTCTCTTTGAGCACAAACCATCT	0	0
35	GTGCAACAGGCCCTTGCGGGGAAAACCCATCT	0	0
36	GTCTAGCCGTCCCGAAGGAAAATCCTGGTTTCC	3	0
37	GTCTCACGTTCCCGAAGGCACCCCGCATCTC	0	5
38	GTGTCTGTCCGGCCGAACCGACAGACCCGGTC	0	5
39	GTTACATCCATCTCGAATTTATTTTAAATTCAT	0	2
40	GTCTCACGGCTCCCGAAGGCACTAAGGCATCTC	0	2
41	GTGACACTGTCTTGCGAACCTCAGGCTTTCACC	0	2
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4	GTACTGGGTTCCGGGTTGGATACCGTTCGTTCC	0	2
5	GTGATGGTTACACTCTTGCGAGTAATCGATAGG	0	2
6	GAACCACCGGTCCCCGAAGGGAAGATCCTGTCT	0	2
7	GTCTCCTGGCTCCCCGAAGGGGCACCCACTCC	0	0
8	ATGTCCAGGCTCTCTTTCGAGCACTCCTAAATC	0	4
9	GTGCACGTTCCACCCGAAGGCGTGGCCCGGCTT	0	3
10	GTACAAATTAATAAAATAAACTAATTTAATAATT	0	0
11	GTGTCCGGGCTCCGGGCTGGATACCGTTCGCCCC	0	0
12	GTGTACAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
13	GTGTTCAAGTTCTCTTGCGAGCACTCCCGAATA	0	2
14	TGTTTTGTGCTCTTGCGAGAGAGTACATTTCTG	0	3
15	CTAGACCAATCAAGAAAGAACTCCCAATCTGTC	0	0
16	GTGTTCTCGCCAGCCGAAGGATAACCGTC	0	0
17	CCCATAGAATCAAGAAAGGATCGTCAACCTGTC	0	0
18	GTGCTTGTTCCACTCTTGCGAGTGTCATCACTG	0	0
19	GTCTCTCGATTCTTCTTGCGAAGGCACCCAC	0	0
20	GTGTCCAGGCTCTCTTTCGAGCACCCCTAAATC	0	0
21	GTCTTCCGGTTGTATTGCTACAAAAACGTATC	0	0
22	GTGTTCAAGTTCCCGAAGGCACTTCTACATCTC	0	0
23	GTGTGCAGGTTCTCTTTCGAGCACCGAACCATC	0	0
24	TACTACCTGTATATTGCTATAAAATCCCCTTTC	2	3
25	GTGTCCAGGCTCTCTTTCGAGCACTCCTAAATC	2	3
26	CCCATCCGATCCTCTGAAGGGCCTTCTCGTTTG	0	0
27	TGTAAATTGTCCGAAGAAAAGTCTGTTTCCAAA	0	0
28	GTGTGCAGGTTCTCTTTCGAGCACCAAACCACC	0	0
29	GTGTCTAAATTCCCTTTCGGGCACTTTTGCATC	2	0
30	GTGCTTGTTCCACCCGAAGGACGTGGCCTCTCT	2	0
31	GTGTTCTGGCTCCCGAAGGCAACCTCGCCTCTC	0	0
32	CCCACCGAATCAAGAAGAGCTCTCAATCTGTCA	3	2
33	GTCTCTGCGTTTCTTGCGGCACTCCCAACTCTC	3	2
34	TACCAGCGGTGTATTGCTACAAAGTGAGCTTTC	3	2
35	ATCGCAGGCCCCGAAGGACACCACATCTCTGTG	0	0
36	GTCTCTCGGTTGTATTGCTACAAAACTGTATT	0	0
37	GTGTACAGTCCCCGAAGGGCTCCGATATCTCTA	0	0
38	GTGGACCGGCCTTGCGGCTGCCACGTCTCTGC	0	0
39	GTGCAAATGCCCTTGGTTTCCCAAGAGAGATCC	3	0
40	GTGCAGCAGTCCCTAAGGAAAGGTCCATCTCTG	3	0
41	GTGTGCAGGTTCTCTTTCGAGTACCAAACCATC	0	0
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5	GTGCAGACTTCCCTTGCGGGATCGTCACCCTT	0	0
6	GTGTCTAGGTTCCCTTTCGGGCACCCACATC	0	0
7	GTGTTCCAATTCCCTTTCGGGCACCCCGCATC	0	0
8	GTGTGCAGGCTCTCTTTCGAGCACCAAACCATC	0	0
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10	GTGTACGACCCCGAAGGACACCGTATCTCTACG	0	0
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12	GTGTTCCAGCCAGCCGAAGTGAAGAAAGCCATC	3	0
13	GTTATACCCACCCGAAGTGAAATCTACGTTTC	0	0
14	GTCTCGGGGCTCCTTGCGGCACTGTCCATCTCT	0	0
15	TACTGGCAGTGTATTGCTACAAAAAGAGCTTTC	0	0
16	GTATACGAGTGTCCAAAGAGCTCGGCATCTCTG	0	0
17	CCCACCGAATCAAGAAAGAGCTCTCAATCTGCC	0	0
18	GTATTCCGGCTCTCTTTCGAGCACTCCCAAATC	0	0
19	GTCTCCTCTGTCTCTTGCGAGCCCATCTCTATC	0	0
20	GTGTAAGCTGGTATTGCTACCTCGTCACCCTTT	0	0
21	GTGGCCGGTCCGGGCTGGATACCGTTCGCCCC	0	0
22	GTCACCGCGTCCCCGAAGGGAAGTCAACATCTC	0	2
23	GTGCCCAGATTCCTTGCGGCACTCCCACATCTC	0	0
24	TCGCCGGCTCCCTTGCGGGTCGTCGGGCTTTCA	0	0
25	GTACAGGGGCCTATTGCTAGGCTGCGATATCTC	0	0
26	GTGTTCAGGCTCCCTTGCGGGCACTTCCGAATC	0	0
27	GTCTTTGGGCCGACCTTGTGAGTCAGGGTCCTA	0	0
28	CCCATCCGATCCTCTGAAGGGCCATCGCTCAAC	0	0
29	GTTACAGACGCCTTGCGGCGCTACGATATCGC	0	0
30	GTGCTTGTTCCTCGAAGGGCGTGGCCTCTCT	0	0
31	GTCTCTCGTTCCCTTGCGGGCACCCCTCATC	0	0
32	GTAATAGCTCCCCTTGCGGGACACGAACCTTCA	0	0
33	CCCATCCGATCCTCCGAAGGGCCTTCTCGTCTG	0	0
34	GTGTGCAGGTTCTCTTTCGAGCACCAAACCATT	0	0
35	CCCACCGAATCAAGAAAGAGCTCCCAATCTGTC	2	0
36	TGTTTTGGGCCAGTAACCTGGCTGTTGGCATT	2	0
37	GTGTGCAGGTTCTCTTTCGAGCACCAAAGCCATC	0	0
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39	CAAGACCAATCAAGAAAGAACTCTCAATCTGTC	0	0
40	GTGTGCAGGTTTTCTTTCGAGCACCAAACCATC	0	0
41	CGCACCCGGCCCCGAAGGGCTGTACAGTTTCCA	0	0
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5	GTCTCGGGGCTCCTTGCGGCACTGCCCATCTCT	0	4
6	GTGCTGGTTCCGGACTTGCGACTGTGGCTCTAC	0	4
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8	GTTACATCCATCTCGAATTTATTTTAATTTAT	0	4
9	GTGTCACGGTCCCCGAAGGCACCAATCCATCTC	0	4
10	GTGCCTATTCCGGTCTTGCGACTGTGGCCCCAC	0	4
11	GTTTAGCGCTTGATTGCTACAATTATTACCAT	0	4
12	GTCTTCCGGTTGTATTGCTACAAAAATCGTATC	0	2
13	GTCTTGTCTGTTCCCGAAGGCACCCCTCATCTC	0	2
14	GTGCACGTTCCACCCAAGGGCGTCAATGACCTT	0	2
15	GTGCATGTTCCGACTCCGAAGAGCTGTCATCCC	0	2
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21	GTCTCCACGTTGTATTGCTACAAAAAATACATC	0	0
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23	AACCGCAGGTTCTCCGAAGAGCACCCCCAATTT	0	0
24	GTGCAGCAGTCCCGAAGGAAAGGCCCATTTCTG	2	0
25	GTGTTCAGGCTTCCTTGCGGGCACTCCCGAATC	0	0
26	GAGCACGCTGGCATTGCTACCTCGTCAGGCTTT	0	0
27	GTGCACAGACCTTGCGGGCTAAACTATCTCTA	0	0
28	GTGCAGGTCACACCCGAAGGTAATCAGCCAACT	0	0
29	CTAGACCAATCAAGAAAAAACTCTCAATCTGTC	0	0
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33	GTGATGGTGTCCCGAAGGAAAGGTGTGTTTCCA	0	2
34	GTGCAATTGTCCAAACCGAAGTTTGGAAAGCTA	0	2
35	GTATCCAGGCTCTTTTCGAGCACTCCTAAATC	0	2
36	GTGTCCAGGCTCCCTTTGCGGGCACGAGTCCATC	0	2
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38	GTATAACGGCCCTTGCGGGCGACGACATTTCTG	0	0
39	GTCACCGGTCCAGCCGAAGTGAAGGAAACGATC	0	0
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41	GTGTTCAGGCTCCCTTGCTGGCACTCCCGAATC	0	0
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5	GTGCAAATGTCTAAACCGAAGCTTAGAAAAATA	0	0
6	GTGTACGTTGTACCCGAAGGCCTCATCAATGTT	0	0
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8	GTGTCCAGGCTCCCTTTCTGGGCACCCTCACATC	0	0
9	CCCAAAGAATCAAGAAAGGACCGTCAACCTGTC	0	0
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11	GTGTGGACGCCAGCCGAAGTGAAGAGCCTCATC	0	0
12	GTGTCCCTGGCTCCGAAGAGAAGAAACCATCTC	0	2
13	GGGGATAGTTAAAACAGTTGTATTTTAAATTAT	2	2
14	GTCTCCTGTCCAGCCGAAGTGAAGCTCGATCT	2	2
15	GTGCATGTTCCACTCTTGCGAGCGTGGCCCTGC	2	2
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17	GTGCAGCAGTCCCGAAGGAAAGGCCTATTTCTA	0	2
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20	GTGTTCAGGCTCCCTTGCGAGCACTCCCGAATC	1	0
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23	GTGCTTATTCCACCCGAAGGGCGTGGCCTCTCT	2	0
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25	GTGTTCTAGCCAGCCGAAGTGAAGAATCCATC	2	0
26	GTGTCCAGGCTCCCTTTCTGGGCACAAATCCATC	2	0
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28	TGTTTCAGGTCATTGCTGACTTACTCATCTCTG	2	0
29	GTAGCAGGTTCCGGACTGGATAACCGTTCGTTCC	2	0
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33	GAGTCCAGGCTCTCTTTCTGAGCACTCCTAAATC	0	0
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40	CCCATTATTCAAGAAAGGGCTATCAACCTGTC	0	0
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43	GTGTTCAGGTTCCCTTGCGGGCACTCCCGAATC	0	0
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46	TGTTTCGAGTCTCCAGTTTCCCTTCGACGACTC	0	0
47	GTCACCGGTCCAGCCGAAGTGAAGGTTACCATC	0	0
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50	GTGCTCAGGCTCCCTTGCGGGCACTCCCGAATC	1	0
51	CTCATGGAATCAAGAAAGAACTATCAATCTGTC	3	0
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53	AGTTTTGTGCTCCGAAGAGAAATCCGCTTTCAC	2	0
54	CTCATGGAATCAAGAAAGAGCTATCAATCTATC	2	0
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56	TGTAAGCGGCCCCGAAGGGCTATGAACTTTCAT	0	0
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5	GTGCCCAGATTCCCGAAGGCACAACCTAATCTC	0	0
6	GTGTCACGGTTCCCGAAGGCACCCATCCATCTC	0	0
7	GTGCAGACTCCCCTTGCGGGGTCATCACCCCTT	0	0
8	GTGTCCTGGTTCTCTTTCGAGCACCCCGCATC	0	0
9	AGTTTCGCGCCCCGAAGGGAAGACACCTTTCG	0	0
10	CCCATCCGATCCTCTGAAGGGCCCTCTCGTCTG	0	0
11	GTGTTCAAGGCTCCCTTGCGGGCACTCCCGATTC	0	0
12	CGATAGCACCCCTTGCGGGCAAGGACTTTCATC	0	0
13	CCCATCGAATCAAGAAAGGACCGTCAACCTGTC	0	0
14	CTAGACCAATCAAGAAAGAACTCTCGATCTGTC	0	0
15	GTCTCCAGGTTCCCGAAGGCACTCCCTCATCTC	2	0
16	CCCATAGAATCAAGAAAGGACCGTCAACCTGCC	2	0
17	CCCATAAAATCAAGAAAGAGCTATCAATCTGTC	4	0
18	GTGTAGGCTCCCTTGCGGGCACTCCCGAATCTC	4	0
19	GTGCAGCAGCCCCAAAGGGAATACCATCTCTG	0	0
20	GTGTTCAAGGCTCCCTTGCGGGCACTCCCTAATC	0	0
21	TGCTTCAGGTCTATGGTTTCCCATAGAGAAAAG	0	0
22	TGTTTTGTGTCCCGAAGGAAATTCCGCTTTCAC	0	0
23	GTGCAGCAGCCCCGAATGGAAATACCATCTCTG	0	0
24	CCCATAGAGTCAAGAAAGGACCGTCAACCTGTC	0	0
25	AGTTTCAGGTCAATTGCTGACTGACTTCTTCAA	0	0
26	GTGCATGTTCCACCCTTGCGGGTGGCTCTGCTT	0	0
27	GTGTTCAAGGCTCCTTGCGGGCACTCCCGAATCT	0	0
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29	GTGTGCTGGTTCTCTTTCGAGCACCAAACCATC	0	0
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32	GTGCAACAGCCCCGAAGGGAATACCATCTCTG	0	0
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34	CCTATAGAATCAAGAAAGGACCGTCAACCTGTC	0	0
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37	CCAGACCAATCAAGAAAGAACTCTCAATCTGTC	0	0
38	CTAGACTAATCAAGAAAGAACTCTCAATCTGTC	0	0
39	GTGTTCCGACCTATTGCTAGGAGGAATCCATCT	0	0
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41	GTGCCACACCCTCGAAGGCGACTGGCTTTGACC	0	0
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5	CTAGACCAATCAAGTAAGAACTCTCAATCTGTC	0	0
6	GTTTCATGTTGTACCCTTGCGGGCCTCATCGACG	0	0
7	GTGTGCAGGTTCTCTTTGGAGCACCAAACCATC	0	0
8	TGTGCAGGTTCTCTTTGAGCACCAAACCATCT	0	0
9	GTGTGCAGGTTCTCTTTGAGCACCAAACCGTC	0	0
10	GTGTGGCGTCCGGCCGAACCGACTCCCCGCTTT	0	3
11	GTGCTGGTTCCGGTCTTACGACTGTGGCTCTAC	0	3
12	AACCACAGGTTCCCCGAAGGGAACCCCGAACTT	0	3
13	CCCATAGAATCAAGAAAGAGCTTCAATCTGTCA	0	3
14	GTGTTCCGATTCCCGAAGGCACTCCACATCTC	0	3
15	GTGCTCGGTTCCGGATTGGATACCGTTGCTCC	0	3
16	TCCATAGAATCAAGAAAGAGCTCTCAATCTGTC	0	3
17	GTAACCGGCCCAAAGGGAGGCCACATCTCTGC	0	3
18	GTGCTGGTTACACCCGAAGGCAATCCCTCCACT	0	3
19	GTGCTGGTTCCGGTCTTGCAACTGTGGCTCTAC	0	3
20	GAGCAGGATGGTATTTCTACCTCGTTGGGCTTT	0	3
21	GTGCTCTATGCCCCGAAGGGAAGGCTCCATCTC	0	3
22	GTGCTCTGTTACCTTGCGGCACTCCAGCTTTT	0	3
23	GTGACCATTTGTACCCTTGCGGGCCTACATCTAC	0	3
24	GTGCTGGTTCCGGTCTTGCGAATGTGGCTCTAC	0	3
25	CTAGACCAATCAAGAAAGGACTCTCAATCTGTC	0	0
26	GTGTCCAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
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33	CTCATGGAATCAAGAAAGCGCTATCAATCTGTC	0	0
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36	GTGTCCAGGTTCTCTTTGAGCACGAATCCATC	0	0
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39	AACTACAGGTTCTCCGAAGAGCACCCCGAGATT	0	0
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6	CTACACGGGTCCCGAAGGAAACTGTATCTCTA	0	0
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9	GTCTTCCTGCCACCGAAGTGGCTTCCTCAGTTA	0	0
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12	GTGCAGGTTCCACCTTGCGGCGTCGCCGACGTT	0	0
13	TACAATCTGTGTATTGCTACAAAATGAGCTTTC	0	0
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15	GTGTCCAGGCTCCCTTTCGGGCACGAATCCATA	0	0
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22	GTGTCCAGGCTCCCTTTCGGGCAAGAATCCATC	0	0
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25	GCACTAAGTATTTAATATTTAACTTTATAAATA	0	0
26	GTGTTCCGGCTCTTTTTCGAGCACTCCCAAATC	0	0
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31	GTGTAGCGTCCAGCCGAAGTGAAGGAGCAGGTC	0	0
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46	GTGCTCTATGCCCCGAAGGGAAGGTTCCATCTC	0	0
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5	GTGTTCCGGCTCCCTTTTGGGCACACCCAAATC	0	0
6	GTGTTCCGATTCCCGAAGGCACTCTCGCGTCTC	0	0
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9	GTGTCCCGGCTCTCTTCGAGCACTCCCACATC	0	0
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13	GTGTCCTCCGTCCCTTGCGGGACTAGCCTGTTT	0	0
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16	GTGTCCAAGCTCCCTTTCGGGCACGAATCCATC	0	0
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20	GTGTCCAGGCTCTCTTCGAGCACTCCTAATTC	0	2
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54	GTCTCAGAGTTCCCGAAGGCACCAATCCATCTC	0	0
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11	GAGCATGCTGGTATTGCTACCTCGTCAGGCTTT	0	0
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15	CTAGACCAAACAAGAAAGAACTCTCAATCTGTC	0	0
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17	GTGTCTCCAGTCTCTTGCGAGACTCGCCTGTTT	0	0
18	TGCTCCTTGTCAATTGCTGAAAGACCCGTCTCTG	0	0
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20	GTCTCTAGGTTCCCGAAGGCACTCACTCATCTC	3	0
21	CTCATGGAATCAAGAAAGAGCTATCAATCCGTC	3	0
22	CCCACCGAATCAAGAAGGAGCTCTCAATCTGTC	3	0
23	CCCATAGTATCAAGAAAGAGCTATCAATCTGTC	3	0
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25	TGCAGACAGGAGCCGGTTACCCGGATCGCCCCA	3	0
26	GTACGAGTTCCACCTTGCGGCGTCACCGACGTT	3	0
27	GTCTAAGATCCAGCCGAAGTGAAGGAAACCATC	3	0
28	TGCTCCTTGTCTTGCGGAACGATCCGTCTCTG	3	0
29	CGACTGCGGTCCCTTGCGGGAAGTCCATATTTT	3	0
30	TCACACCCGCCATTGCTGGCCCTCTCATCTCTG	3	0
31	GTGTTAGCAGCCCTTGCGGGAAAGCACGTTTCC	3	0
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34	GTCTCACGATTCCCTTGCGGGCACTTCAGGCGT	0	0
35	CTAGACAAATCAAGAAAGAACTCTCAATCTGTC	0	0
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37	GTCTTCCTGTAGTATTGCTACCTATTCCACATT	0	0
38	CCCATACAATCAAGAAAGAGCTCTCAATCTGTC	0	0
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41	GTGCAGGTTCCACCCGAAGGCGTGGCTCCGCTT	0	0
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7	GTCTCGGGGCTCCTTGCGGCACCCCCATCTCT	0	0
8	GTGTTCAGGCTCCCTTGCGGGCACTCTCGAATC	0	0
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13	GTGTTCAGGTTCTCTGCGAGCACTCCCGAATCT	0	0
14	GTAGTAGGTTCCGGATTGGATAACCGTTCGCCCC	0	0
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25	GTGTACCGACCTTGCGGGTGACGACATTTCTG	0	0
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31	GTGCACGTTGTACCCGAAGGCCTGGCTCCCCTT	0	0
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9	GTGAATACCCGGCCGAACCGAGGCTCTCCATTA	0	0
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13	GTGTGGGATCCGGCTGAACCGACAAAAACGATC	0	0
14	GTCTTCCTGTTCCGAAGAACGACATACTTCCAT	0	0
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9	GTGTCCGGTCCAGCCTAACTGAAGGACAATGTC	0	0
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12	ATGTACCAGTCTATTGCTAGAAATTCGCTTTC	0	0
13	GTGCATGTTCCACCCTTGCGGGTGTGGCTGCTT	0	0
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15	GTTATACCCACCCGAAGTGAGCGTTATGTCTC	0	0
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56	GTATTCCGGCTCCCTTTCGGGCACACCCAAATC	0	0
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13	GTGCTCAAATTCCTTTGAGGCACATCTCCATC	0	0
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10	GTCTCACGGATCCCGAAGGCACCAATCCATCTC	0	0
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4	GTGCAAGCTTCCCAAAGGATCGTTCCGCTTTCG	0	0
5	GTGCACGCTCCGGTCTTGCGACTGTGGCCCCAC	0	0
6	GTCTTGGGGTTCCCTTGCGGCACCGTCCATCTCT	0	0
7	GAGCACGCTGGTATTGCTACCTCGTCAGGCCTT	0	0
8	GTCTAGGAGTCCTTGCGGACGTTTATGTTTCCA	0	0
9	GTCTCTGATTCCCTTGCGGGCACGTCGACTTTT	0	0
10	GTATATCGGCTACAAGCAGCTGCAGTATCTCTA	0	0
11	GTCACCAGGTTCCCGAAGGCACTCCCTCATCTC	0	0
12	CGCACGCAGTCCGAAGAAGATCACGTTTCCGTG	0	0
13	GTGCTAGCTCCGTATTTCTACAGTCGTCCCCCT	0	0
14	GTGTAAAGGCTCCCTTGCGTGCACTCCCGAATC	0	0
15	GTGTACATTCCACCCAGAATGGGTGTTAATCAC	0	0
16	GTA	0	0
17	GTACTCCAGCCAGCCGA	0	0
18	GTGTTCAAGGCTCTCTTGCGGGCACTCCCGAATC	0	0
19	AGTTTCGTGCCTTGCGGGAAGTCTCCTTTCAGA	0	0
20	CCCACAGAAATCAAGAAAGAGCTATCAATCTGT	0	0
21	CCTACAGAATCAAGAAAGGCCTTAAGCCTGTCA	0	0
22	TATTTGAGTCTCCGGTTTCCCTTCGACGACTC	0	0
23	TGCTCTTTGTCCTTGCGGAAAAACCCATCACTG	0	0
24	GTGCAAGTTACACTCCGAAGAGCAACTTTCTGA	0	0
25	ACCACCGAATCAAGAAAGAGCTATCAGTCTGTC	0	0
26	GTGTTCTAGCTCCCGAAGGCACCCTCGCCTCTC	0	0
27	GTACAAGCTCCCGAAGGTCGTTCCCTTTTCAGC	0	0
28	GTGTTCCAGCCAGCCGA	0	0
29	TCTCACTCGCTCCCCGGAGGGCACCAAGACATT	0	0
30	TGTTTCGGGTCTCCGGTTTCCCTTCGACGACTC	0	0
31	CCCATCCGATCTTCTGAAGGGCCTTCTCGTCTG	0	0
32	TGTTTCGAGTCTCCGGTTTCCCTTCGATGACTC	0	0
33	CCCGCAGAATCAAGAAAGGCCTTAAGCCTGTCA	0	0
34	GTGAACCGACTCTTGCGAGCGAGGACATCTCTG	0	0
35	TCTCACTCCCTCCCCGAAGGGCACCAAGACATT	0	0
36	GTGAAGACCCGGCCGAACCGAAGGGCACATCTC	0	0
37	CCCACAGAATCGAGAAAGGCCTTAAGCCTGTCA	0	0
38	CCATAGAATCAAGAAAGGACCGTCAACCTGTCA	0	0
39	CTAGTCCAATCAAGAAAGAACTCTCAATCTGTC	0	0
40	GTGCAGCAGTCCCGAAGGAAAGGTGCCTTTCAG	0	0
41	GTGCAGCAGCCCCGAAGGGAAATACCATCTGGT	0	0
42	CCCATAGAATCAAGAAAGGACCGTCAACCTGTG	0	0
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4	GTTTCAGGCTCCCTTGCGGGCACTCCCGAATCT	0	0
5	GTGTTGCAGCTACCTTTCGGGCACTTCCTCATC	0	0
6	TGTTTCAAGTCTCCGGTTTCCCTTCGACGACTC	0	0
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8	CCCATTTAATCAAGAAAGGGCTATCAACCTATC	0	0
9	CTTGACCAATCAAGAAAGAACTCTCAATCTGTC	0	0
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11	GTATGGGATCCGGCCGAACCGACAGAAATAATC	0	0
12	GCCATACACCCTCGAAGGCTTATCTGGTTTCCC	0	0
13	GTAACGGCTCCCGAAGGTCGGCCCCCTTTCGGT	0	0
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15	AACTGTAGATTCTCCGAAGAGCACCCCGATATT	0	0
16	GGATTACGATTCTCTTGCGAGCACATCAATATT	0	0
17	TACTGGCAGTGAATTGCTACAAAGAGAGCTTTC	0	0
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19	TGTTTCAGGCTCCCTTGCGGGCACTCCCGAATCT	0	0
20	GTGTTTCGCGCCAGCCGAAGTGAAGGAAGCCATC	0	0
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22	GTGTAAGTTTCACTCCGAAGAGCAACTTTCTGA	0	0
23	GTGCATGTTCCATTCTTGCGATTGTCATCGATG	0	0
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25	GTGCTGCAGCCCCGAAGGGAAATACCATCTCTG	0	0
26	GTGCATGTTCCACCCGAAGGCGTGGCCCCGGCTT	0	0
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28	GTCTCGGGGCTCCTTGTTGGCACCTCCCATCTCT	0	0
29	CCCATACAATCAAGAAAGGACCGTCAACCTGTC	0	0
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31	GTGCAGCAGCCCCGAAGAGAAATACCATCTCTG	0	0
32	GCAAGAGATAAAAACTTTATGTTTTTTTCATA	0	0
33	GAGCACGCTGGTATTGCTACCTCGACAGGCTTT	0	0
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35	GTGATCGTTCCAACCTTGCGGCTGTGGCTCTAC	0	0
36	GTGCAGATGCCCCGAGGGGAGATACCATCTCTG	0	0
37	TGCATCCGGCCCCGAAGGGCAATCAGCTTTCAC	0	0
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39	GCCTAAGAGTCTTGCGAGGGCTCCCGTTTCTGG	0	0
40	GTGCACGTTCCGGTCTTACGACTGTGGCCCCAC	0	0
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42	GTACATGTTCCACCCTTGCGGGTGTGGCTCTGC	0	0
43	GTATCTGAGTTCCCTTTCGGGCACCGATCTATC	0	0
44	TGTTTCGAGTCTCCGGTTCCCCTTCGACGACTC	0	0
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46	GTGTGGACGCCAGCCGAAGTGAAGGACCACATC	0	0
47	GTGCTAGTTGTTCCCCTTGCGGGCCTACTCTAC	0	0
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49	GTGTCCACGTCCCCAAAGGGAAGAAATCCATCT	0	0
50	GTGTTTCAGGTTCTCTTGCGAGCACTCCCAAATA	0	0
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52	GTGTCCCGGTCCCCGAAGGGAACCATGGATCTC	0	0
53	GTGTGGAAGCCAGCCGAAGTGAAGAACCTGATC	0	0
54			
55	TGTTTTGTGTCCCTTGCGGGAAGAGTCCATTTC	0	0
56	CCCATTTAATCAAGAAAAGGGCTATCAACCTGT	0	0
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6	GTGTTCCGGCCCTCTTTTCGAGCACTCCCAAATC	0	0
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8	CCCATAGAATCAAGAAAGGTCCGTCAACCTGTC	0	0
9	GTGTGCAGGTTCTCTTTTCGAGCACCAAACCTCT	0	0
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11	GTGTGCAGGTTCTCTTTTCGAGCACCATACCATC	0	0
12	GTGTGCAGGTTCTCTTTTCGAGCACCAAACCATCT	0	0
13	GTGTGCAGGTTCTCTTTTCGAGACCAAACCATCT	0	0
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15	GTGTGCGGTTCTCTTTTCGAGCACCAAACCATCT	0	0
16	GTGTGAGGTTCTCTTTTCGAGCACCAAACCATCT	0	0
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18	CTCATAGAATCAAGAAAGGACCGTCAACCTGTC	0	0
19	GCCATAGAATCAAGAAAGGACCGTCAACCTGTC	0	0
20	CTAGACCAATCAAGAAAGAACTCTCATTCTGTC	0	0
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22	CTAGACCAATCAAGAAAGAACTATCAATCTGTC	0	0
23	GTGTGCAGGTTCTCTTTTCGAGCACCAAATCATC	0	0
24	GTGTGCAGGTTCTCTTTTCGTGCACCAAACCATC	0	0
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26	TGCAGGTTCTCTTTTCGAGCACCAAACCATCTCT	0	0
27	GTGTCCAGGCTCTCTTTTCGAGCACTCATAAATC	0	1
28			
29	GTGACCAGGCTCTCTTTTCGAGCACTCCTAAATC	0	1
30	GTGTCCAGGCTCTCTTTTCGAGCACTCCTAACTC	0	1
31	GTGTCCAGGCTCCCTTTTCGGGCACGAATCGATC	0	1
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33	GTGTGCAGGTCGGAACCTTACCCGACAAGGAATT	0	0
34	GTGTGCAGGTTCACTTTTCGAGCACCAAACCATC	0	0
35			
36	GTGTGCACGCCTCCGAAGAGGACCTGGATCTC	0	0
37	CTCATAGAATCAAGAAAGAGCTATCAATCTGTC	0	0
38	CACACCGAATCAAGAAAGAGCTCTCAATCTGTC	0	0
39	GTGTTTCAGGCTCCCTTGCGGGCACGCCCGAATC	0	0
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41	CTCATGGAATCAAGAAAGAGCTATCAATCTGAC	0	0
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43	CTCATGGAATCAAGAAAGAGCTACCAATCTGTC	0	0
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45	CCCATAGGATCAAGAAAGGACCGTCAACCTGTC	0	0
46	GTGTTTCAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
47	GTGTTTCAGGCTCCCTTGCGGGCACTCCCGAATT	0	0
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49	CCCATAGAATCAAGAAAGGCCGTCAACCTGTC	0	0
50	GCGTTTCAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
51	CTAGACCAATCGAGAAAGAACTCTCAATCTGTC	0	0
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53	GTGTTTCAGGCTCCCTAGCGGGCACTCCCGAATC	0	0
54	GTGTAAAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
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56	CTCATGGAATCAAGAAAGAGCTATCAATCTGTA	1	0
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4	CCCACCGAATCAAGAAAGAGCTATCAATCTGTC	1	0
5	CTCATGGAATCAAGAAAGGGCTATCAATCTGTC	1	0
6	CTCATGGAATCAAGAAAGAGCTAACAATCTGTC	1	0
7	GTGTTCAGGCTCCCTTGCGGGCACTCCCGACTC	1	0
8	CTAGACCAATCAAGAGAGAACTCTCAATCTGTC	0	0
9	GTGTTCAGGCTCCCTTGCGGGCACTCCCCAATC	0	0
10	CTAGACCAATCAAGAAAGAACTCTCAAACCTGTC	0	0
11	CTAGACCAATCAAGAAAGAACTCTCAATCTGTA	0	0
12	CCCATCCGATCCTCTGAAGGGCCTTCTCGTCTC	0	0
13	GTGTTCAGGCTACCTTGCGGGCACTCCCGAATC	0	0
14	GTGTTCAGGCTCCCTTGCGGGCAGTCCCGAATC	0	0
15	GTGTTCAGGCTCCCTTGCGGGCACTCCAGAATC	0	0
16	GTGTTGAGGCTCCCTTGCGGGCACTCCCGAATC	0	0
17	CCCATAGAATCAAGAAAGGACAGTCAACCTGTC	0	0
18	CACATCCGATCCTCTGAAGGGCCTTCTCGTCTG	0	0
19	CTAGACCAATCATGAAAGAACTCTCAATCTGTC	0	0
20	GTGTGCAGGTTCTCTTTGAGCACCAAACATC	0	0
21	GTGTGCAGGTTCTCTTTGAGCACCAAACATC	0	0
22	GTGTGCAGGTTCTCTTTGAGCACCAAACATG	0	0
23	GTGTGCCGGTTCTCTTTGAGCACCAAACATC	0	0
24	GTGTGAAGGTTCTCTTTGAGCACCAAACATC	0	0
25	GTGTGCATGTTCTCTTTGAGCACCAAACATC	0	0
26	GTGTGCAGGTTGTCTTTGAGCACCAAACATC	0	0
27		72764	64006
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Flocs Control 3	Flocs Treated 1	Flocs Treated 2	Flocs Treated 3
3	0	0	0
3437	11789	6506	16243
121	68	268	25
2521	1904	2304	1389
5819	2592	3012	8217
10344	2254	2892	872
2	0	0	2
5302	3490	1724	4451
267	181	164	146
19	21	36	3
2298	2042	1149	2663
2231	1648	1416	1651
0	3	0	0
981	904	597	1026
580	2222	2157	3281
677	1242	856	884
1552	647	576	812
2829	1389	905	1160
4	12	5	11
657	328	459	484
459	403	289	574
1113	830	730	579
0	0	0	0
397	266	277	448
493	361	245	503
935	378	501	724
0	0	0	0
813	536	391	366
515	392	318	314
653	572	430	593
740	523	360	581
69	40	74	32
752	541	325	572
223	150	151	519
0	0	0	0
57	24	36	45
0	0	0	0

556	387	358	286
125	56	39	74
683	140	169	173
190	115	73	120
3	7	8	7
515	372	388	251
6	9	3	14
403	347	283	465
479	363	109	327
466	289	233	374
555	402	248	335
364	318	281	283
0	0	0	0
24	29	30	35
309	223	202	293
289	223	115	419
8	14	10	5
297	324	330	257
0	0	0	0
0	0	0	0
329	224	293	193
376	292	195	262
103	75	471	5
309	173	114	199
357	19	142	2
260	140	179	202
0	0	0	0
245	178	157	274
70	56	46	75
224	227	168	257
0	0	0	0
300	216	140	213
0	0	0	0
244	172	115	188
259	172	182	128
31	16	21	32
0	0	0	0
171	153	177	154



1				
2				
3				
4	0	0	0	0
5	0	0	0	0
6	242	184	95	256
7	50	27	12	16
8				
9	0	0	0	0
10				
11	261	152	126	128
12	23	11	11	5
13	200	157	91	163
14				
15	0	0	0	0
16	15	13	5	15
17				
18	0	0	0	0
19	43	31	38	54
20	319	225	84	148
21				
22	0	0	0	0
23	204	120	101	149
24				
25	244	130	132	123
26	168	117	146	71
27				
28	0	0	0	0
29	161	103	91	147
30	242	143	97	108
31				
32	15	21	440	0
33	18	4	5	9
34				
35	86	73	66	92
36	130	157	113	103
37	192	96	103	154
38				
39	131	84	100	91
40	178	92	102	128
41				
42	226	7	19	0
43	0	0	2	5
44				
45	110	77	77	61
46	63	61	57	42
47	146	122	110	91
48				
49	129	96	172	73
50	158	118	81	112
51				
52	6	13	5	5
53	0	175	265	166
54				
55	0	0	0	0
56	137	125	99	58
57				
58				
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3				
4	147	135	72	101
5	174	82	69	106
6	122	93	61	78
7				
8	87	57	16	43
9	0	0	0	0
10	16	38	17	39
11	152	82	92	52
12	108	56	55	135
13	115	115	88	70
14	141	101	59	115
15	115	54	51	104
16	10	8	25	0
17	150	93	77	88
18	105	126	94	65
19	19	11	16	10
20	55	27	44	63
21	100	84	136	26
22	0	0	0	0
23	113	88	53	85
24	0	0	0	0
25	0	36	26	321
26	0	0	0	0
27	66	112	65	144
28	0	0	0	0
29	0	0	0	0
30	0	0	0	0
31	81	61	67	86
32	78	57	57	99
33	0	0	2	0
34	107	56	54	44
35	93	74	90	59
36	106	52	50	67
37	0	0	0	0
38	0	0	0	0
39	8	5	2	0
40	46	50	29	36
41	113	59	55	34
42	34	48	40	37
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3				
4	102	67	54	53
5	86	52	41	34
6	94	11	55	2
7	0	134	87	128
8	0	0	0	0
9	61	104	54	68
10	13	7	33	3
11	0	0	0	0
12	0	0	0	0
13	0	0	0	0
14	0	0	0	2
15	73	36	44	66
16	51	67	22	18
17	55	51	40	66
18	69	46	26	40
19	61	38	41	72
20	77	47	41	59
21	2	0	0	0
22	7	2	3	3
23	60	65	19	72
24	97	9	44	0
25	75	51	62	30
26	55	40	36	27
27	51	46	39	52
28	13	5	4	2
29	61	46	73	37
30	67	82	46	28
31	112	49	44	28
32	0	0	0	0
33	64	39	25	40
34	0	0	0	0
35	69	45	39	77
36	8	19	4	45
37	58	33	40	46
38	78	28	31	45
39	0	0	0	0
40	0	0	0	0
41	0	0	0	0
42	99	88	17	28
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6	75	47	31	45
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9	59	57	30	36
10	62	30	33	51
11	69	47	39	40
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14				
15	3	4	2	2
16	72	46	32	30
17				
18	45	44	29	31
19	0	0	2	0
20	6	5	7	9
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22	3	6	0	0
23				
24	28	24	35	20
25	0	0	0	0
26	48	33	26	40
27				
28	51	32	36	39
29	2	0	0	0
30	54	47	33	31
31				
32	17	10	3	6
33	13	8	10	10
34				
35	19	22	19	14
36	0	0	0	0
37	13	9	14	22
38				
39	37	34	24	44
40	0	0	0	0
41				
42	75	35	25	4
43	5	22	10	13
44				
45	13	72	46	35
46	50	2	22	0
47	59	36	8	25
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49	43	21	37	53
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5	2	4	0	0
6	46	45	28	22
7	0	0	0	0
8	25	15	32	17
9	57	24	21	15
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11	47	29	18	39
12	45	15	19	37
13	31	26	37	27
14	46	36	20	22
15	47	14	26	20
16	21	30	29	47
17	0	0	0	0
18	27	22	24	37
19	0	0	0	0
20	40	18	15	49
21	44	29	15	28
22	0	0	0	0
23	20	26	24	44
24	33	24	39	9
25	0	2	0	0
26	0	0	0	0
27	37	28	30	13
28	8	3	3	11
29	0	0	0	0
30	22	6	9	11
31	23	18	15	16
32	22	16	21	12
33	32	32	18	21
34	0	2	0	0
35	17	3	9	12
36	0	0	0	0
37	37	27	25	24
38	25	26	14	33
39	31	19	11	20
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41	24	21	6	42
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5	0	0	0	0
6	28	26	24	13
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8	8	11	9	3
9	9	4	7	2
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11	0	0	0	0
12	0	0	0	0
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19	25	15	12	24
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23	46	16	18	15
24	0	0	0	0
25				
26	7	0	4	8
27	0	0	0	0
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29	27	24	19	17
30	27	22	36	12
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33	23	22	15	23
34	33	21	10	25
35	0	0	0	0
36				
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40	28	27	15	25
41	22	24	17	20
42	21	28	19	21
43				
44	6	3	3	10
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46	26	20	15	21
47	33	23	23	15
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49	13	7	17	5
50	0	0	0	0
51	0	0	0	0
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53	28	19	15	19
54	14	11	18	21
55	19	8	22	6
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5	0	0	0	0
6	27	13	22	10
7	35	24	13	23
8	30	19	18	15
9	2	0	0	0
10	0	0	0	0
11	5	8	6	9
12	16	13	9	15
13	13	5	9	9
14	28	15	9	25
15	34	11	18	9
16	18	18	23	14
17	19	25	8	24
18	15	14	13	12
19	32	25	19	14
20	26	6	14	29
21	0	0	0	0
22	25	8	30	14
23	32	27	10	13
24	0	0	0	0
25	0	33	8	32
26	0	0	0	0
27	11	7	7	6
28	0	0	0	0
29	24	12	14	16
30	0	0	0	0
31	0	0	0	0
32	0	0	0	0
33	0	0	0	0
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37	0	0	0	0
38	3	0	0	0
39	0	0	0	0
40	17	12	6	13
41	24	11	14	12
42	21	15	6	18
43	20	10	6	12
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Granules Treated 2	Granules Treated 3	tag	use	taxon_level
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10438	13175	GTGTTCAGGC	long	g
10674	16952	CTAGACCAAT	long	f
8553	7164	CCCATAGAAT	long	g
12	6	CTCATGGAAT	long	o
0	0	GTGTCCAGGC	long	f
3922	4622	CCCATCCGATCCTCTGAAGGGCCTTCTCGTC		
0	0	CCCACCGAAT	long	p
2332	2839	GTGCATGTTCCACCCTTGCGGGTGTGGCTC		
2826	3783	CCCATTTAAT	long	o
0	0	GTGCTTGTTCCACCCGAAGGGCGTGGCCTC		
0	0	GTGTCCAGGCTCCCTTTCGGGCACGAATCC		
1623	1038	GTGTACAGACCCTTGCGGGCTAAACTATCTC		
584	970	GTGTCCAGGC	long	g
21	23	GTGTACCGAC	long	g
586	532	GTGTTCCGGC	long	g
0	0	CCCATAGAAT	tag	k
0	0	GTGTTCTGGT	long	f
1362	1028	TGTTTCGAGTCTCCGGTTTCCCTTCGACGAC		
769	788	GAGCACGCT	tag	g
586	815	GTGTTCTGGC	long	g
270	125	GTGCTGGTTCCGGTCTTGCGACTGTGGCTC		
941	1495	GTGCAGCAGCCCCGAAGGGAAATACCATCT		
463	790	CCCATAGAAT	tag	k
364	429	GTGTTCAGGT	long	g
92	90	GAGCACGCT	long	g
429	1234	TGTAAACTGTCTTGCGAAAGACTAGTTTCCT		
65	77	TCCAATAAATCGAGAAAGGTCTTTAACCTG		
143	125	GTGTTCAGGT	long	g
4	3	CTCAATAAAT	long	c
16	13	GTGTCCAGGC	long	f
433	696	GTGTTCAGGT	long	g
9	11	AGTTTCGTGT	long	f
213	283	GTGTCTTAATTCCCTTTCGGGCACTTTTGCA		
413	510	CCCACAGAATCAAGAAAGGCCTTAAGCCTG		
427	395	GTCTCGGGG	long	g
444	61	AGTTTCGTGCCCTTGCGGGAAGTCTCCTTTC		

51 59 GTGCAAGTTTCACTCCGAAGAGCAACTTTCT  
293 367 GTCTCGGGG(tag) g  
4 4 GTGTTCCGAT long c  
265 359 GTGTTGCAGCTCCCTTTCGGGCACTTCCTCA  
409 382 TTCAGGGGA long o  
10 12 GTGACCGTTGTACCCTTGCGGGCCTACATCT  
402 361 TCCACAAAATCAAGAAAGAGCTTTCAATCTC  
21 26 TACTGGCAGT tag f  
41 68 CCCACAGAAATTAAGAAAGAGCTATCAATC  
45 38 GTGTTCAAAT long g  
0 0 CGCATAGTGTCCCGAAGGAAGATCGGCTTT  
0 0 GTGTACGTTCCACCCAGAGGGTGTGGCTCC  
275 414 GTCTCGGGG long g  
251 459 GTGCAAGCTC tag f  
21 66 GTCTCTGGAT tag o  
35 71 CCCATAGAAT long k  
327 123 CCCATAAAAT tag k  
4 22 GTTCAGGCTC long g  
284 378 GTGTACGTTCCACTCAGAATGAGTGTCAAT  
211 262 GTGTGGACG(long) g  
0 0 GTGTCCTGGC long g  
0 0 GTGTTCCGGC long g  
6 20 GTGTACGTTC long c  
25 39 TGAATCTGT tag f  
0 4 GTGTGCAGG long tag g  
45 43 GAGCACGCTGGTATTGCTACCTCGTAAGGC  
226 115 TGCTCCTTGT tag f  
0 0 TGCAGGCAGGAAGTGGTTACCCAGATCATC  
153 172 GTGCAGGTC/ long c  
3 0 TACTGCCTGTATATTGCTATAAAGACCCCTT  
220 159 TCTCACTCGCTCCCCGAAGGGCACCAAGAC/  
0 0 TGCAGGCAG(tag) o  
223 130 AGTTTCGTGT tag f  
20 25 GTGTCCAGG long c  
0 0 CCCATAGAAT long f  
163 68 TGCTCTTTGT(long) f  
184 137 TTCAAGGGAT long o  
20 57 GTGTCCAGG(long) o

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4	158	320	TGCATCCGGCCCCGAAGGGCGATCAGCTTT
5	167	144	GTTTAAACTCCCTTGCGGGTCGATCCAATTT
6	0	0	AGTTTCGGGT long f
7			
8	185	175	GTCTCTGGATTCCCTTGCGGGCACATCAGCT
9	174	188	CGCACCCGGC long g
10			
11	3	0	GTGTGGCGTC long g
12	155	192	AGTTTCGTGT long f
13	21	42	GTGTTGCAGC long g
14			
15	172	244	CTCTAGGAATTATGAAAGAACAATCAACCT
16	115	192	GTGTCTTAATTCCCTTTCGGGCACTTTTACA
17	153	256	GTGCACGTTCCGGTCTTGCGACTGTGGCCCC
18	76	93	TGCAGGCAGGAGCTGGTTACCCAGATCGTT
19	4	5	TATCACGCGTATATTGCTATAAAACCAGCTT
20			
21	147	261	GTCTCTGGATTCCCTTGCGGGCACGTCGACT
22	6	10	GTGTCCAGGC long g
23			
24	0	0	GTCTGCGCTC long f
25			
26	6	13	GTGTTCCGAT long c
27	161	165	GTAATATTAAATTAAAAAAATAATAAAAA
28	10	8	TGCTCCATGT long f
29	0	0	GTCTTTGGGC long f
30			
31	3	11	CCCATGGAAT tag k
32	101	66	TGCTCCTTGT long f
33	68	35	TACTGGCAGT long g
34			
35	5	8	GTGCAGGTC long c
36	0	0	GTGACCGCTCCCCGAAGGGTCGTTCCGCTT
37			
38	29	33	GTGCAAGCTT tag f
39	0	0	AACCACAGGT tag o
40			
41	0	0	TGAAAAATGT long g
42			
43	93	167	GTGCAAACCTCTCCTTGCGGAGTCGTCACCC
44	38	43	GTGCATGTTC tag g
45			
46	71	55	TACGATCTGT long f
47	0	0	GTGTCCAGGC long c
48			
49	0	0	CCCATAGAATCAAGAAAGATCCTTTTAATCT
50	8	20	GTGTTGCAGT tag g
51			
52	76	122	GTGTGGACGC long f
53	0	0	TGAAAAATGT tag f
54	124	140	CGCACCCGGCCCCGAAGGGCTGCACAGTTT
55			
56	0	0	GTCTTCAGGTCCCCTTGCGGGGTACTCGGC
57			
58			
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3 0 GTGCACGGA(long f  
0 0 GTGTCTTAATTCCCTTTCGGGCACTTCTACA  
9 15 GTGCACCAGT(long g  
73 103 CCCACCTAAT(long p  
90 134 GTGCAGCAGTCCCGAAGGAAAGACGCCTT  
87 118 GTGCAAGCTC(long f  
0 0 GTGCAGGCTC(tag f  
0 0 GTGTCTCAATTCCCTTTCGGGCACCTCTGCA  
4 4 GTGTTCTAGC(long g  
0 0 TGCTTCGCGTCCCGAAGGAAACCCGGCTTT  
15 5 ATACTGCAGT(tag o  
79 80 CCCATTTAAT(long g  
2 0 GTGTTCCAGAT(long c  
0 0 GTACCAAGTC(long g  
79 131 GCTAAGAAATTAAGTATCAAAAAAAGGAA  
44 61 CCCACAGAAT(long g  
0 0 CGACCAACAACCGGCTTTACGGTTCGCCCC  
56 224 TGAGAGCCGTCCGAAGAAAGGCCTGTTTCC  
8 17 GTGTTCCGGC(long g  
102 128 GTGATAGTCCAGCCGAAGTACCGGCTAGT  
37 7 TGTAAGTGT(long g  
70 89 TGTAAGGTCTTTGCAGACTGTATACTTTC  
0 0 GTGTCCCGGT(tag f  
78 45 TGTTTCTCGCTCCGAAGAGAAGACACCTTTC  
60 111 GTGCACGTTCCAGTCTTTCGACCGTCATTCC  
49 60 GTGCACGTTCT(tag g  
0 0 TCTCACTCGT(tag g  
0 0 GTACAAGACC(long f  
76 32 GTGATGGCTCGCCGAAGCGTCGTTCCCCTT  
0 0 GCTGCCATAT(long g  
6 2 GTGCAGGCTC(tag p  
0 0 GTGCACGTTCCACTCTTGCGAGCGTGGCTCC  
56 74 GTGTGGGATCCGGCCGAACCGACAGAAAT/  
61 104 GTGCACGTTCCACCCTTGCGGGTGTGGCTCC  
51 67 GTGTCCACGT(long g  
18 20 GTGTCCAGGT(long c  
0 0 TATCCCGCGT(long f  
16 10 TGCAGGCAGGAGCTGGTTACCCAGATCGCT

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3			
4	0	0	AAGTAGCAGCCCCTTGCGGGGAAGGGCAC
5	6	15	GTACAGGCTT long p
6	0	0	GTGTGCAGGtag g
7	0	0	GTGTTGCGGT long f
8	0	0	GTGTTGCGGT long f
9	90	54	AGTTTCGTGC long f
10	0	0	CTATATGGGT long o
11	41	64	CGCATAGTGTCCCGAAGGAAGATTGGCTTT
12	57	42	GTGCACGTTCCATTCTTGCGATTGTCATCGA
13	23	17	ACCACACAAT long g
14	21	71	GTGTTCTGAT tag g
15	4	6	GTGTCTCGGTTCTCTTTCGAGCACCTCCGCA
16	13	8	GTGACCGGACTCCGAAGAGGGGCCAGGGT
17	0	0	CGACTCCGGTCCCTTGCGGGAAGGCGATGT
18	22	17	GTGTTGAGCTCCCTTTCGGACACTTCCTCA
19	3	3	ATACTGCAGT long o
20	0	0	GTGCTCAAATTCCTTTCAGGCACACTTCCA
21	36	43	GTGTGGAAGtag g
22	36	54	CGCACGCCGTtag f
23	0	0	GTGTTACGGT long f
24	0	0	GTGTTCCGAT long g
25	0	0	AAGTGGCAGCCCCTTGCGGGGAAGGGAAC
26	5	3	GTGTTGAGGCTCCCTTGCGGGCACTCCCAA
27	10	9	CGACTCTACTtag o
28	19	84	GTCTCACGGT long f
29	0	0	TGTAACCTGT tag f
30	0	0	GTGTGGCGTCCAGCCGAAGAGACCA
31	3	0	GTGTCACGGT long f
32	44	54	GTTACGTTGTACCCTTGCGGGCCTCATAGA
33	0	0	GTGCACGTTCCGGTCTTGCGACTGTGGCTC
34	39	105	GTGCAGCCGCCTTTCGGAAGGTGCATCTCT
35	0	0	CTCATAGAATCAAGAAAGAGCTATCGATCT
36	17	12	GTGTCCTAGT long g
37	0	0	GTGCACGTTC long c
38	0	0	GTGTTCCGGC long f
39	34	76	TGCTTTGTGTlong f
40	48	34	GTAACGGCTC long f
41	43	62	GTGTGGACGCCAGCCGAAGGACCCC
42	0	0	TGTTTTGGACCAGTAACCTGGCTGTTGGCA
43			
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0	0	GTGCCTGTTCCGGTCTTGCGACTGTGGCCCC
42	75	GTGTTCCAGGC tag g
0	0	GTCTTTGGGC long f
0	0	AAGTGACAGCTCCTTGCGGAGAGGGCGGC
0	0	GTGCACGTTGTACCCTTGCGGGCCTGGCCG
0	0	GTGTAGGCTCCCCGAAGGGTCGTTCTGCTT
0	0	GTGCTTGTTCCACCCAGAGGGTGTGGCCTC
43	21	TACGATCTGT tag g
43	12	GTGTTCCAGC tag g
0	0	GTCTTACCGTTCCTTGCGGGCACCCAGCT
2	0	TACTACCCGT, long f
35	43	CCCACAGAAT tag k
23	20	GTGAATGAG( tag g
28	40	GTGTTCTGGC tag g
11	10	GTGCTCCACC long o
72	46	GTATATCGGCTGCAAGCAGCTGCAGTATCT
0	0	GTATTGGACCCCTTGCGGGTAATCCTCTTTC
0	0	TACTGGCGGT long f
21	52	GTGTGGTATC long f
0	0	TACTACCTGT, tag f
20	34	GTGTTGTATC long f
23	35	AACTACAGGT long g
8	9	GTGCACGTTGTACTCTTGCGAGCCTCATTGA
27	47	TACTGGCAGT long f
15	14	TGAAAGACG1 tag g
0	0	CGACTCCCGTCCCTTGCGGGAAACCCATATT
33	58	GTATAAGCTC long f
0	0	GTGTCCAGGC long g
31	28	GTGTTCCAGGCTCCCTTGCGGGCACTCCCGA/
2	2	GTACAGGCTC tag f
0	0	GTGTGCAGG1 tag f
7	2	GTGTTGCAGCTCCCTTTCGGGCACTTCCACA
0	0	GTGTTCTGGT long f
0	2	GTGCTTGTTCCACCCAGAGGGTGTGGCTCC
0	0	GTGTGCAGG1 long f
0	0	GTGACCGAG( long f
0	0	ATACTACCGT long p
23	74	GTCTCCTTGCTATTGCTACAAAGCCCTATT



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3		
4	5	16 GTCACCGGTC long f
5	26	38 GTGTCTTAATTCCCTTTCGGGCACTCTTACA
6	0	0 GTGCACGTTCCGGCCTTGCGGCTGTGGCAC
7		
8	31	42 GTGTGGGATCCGGCCGAACCGACAAAAAC
9	0	3 GTCTCCGGTC long g
10	0	0 GTGTCACGGT long g
11		
12	7	7 GGATCATGGTTCTCTTGCGAGCACCCCCAA
13	0	0 GTGTTCAATTCTCTTTCGAGCACGATTCCA
14		
15	0	0 GTGCGGACTC long g
16	0	0 TGTAATTGT long g
17		
18	0	0 AAGTGGCGGCTCCTTGCGGAGAGAGAGGC
19	0	0 AACTATAGGTTCTCCGAAGAGCACCCCCAA
20		
21	0	0 TGTATGGAGCTCTTGCGAGCGTTCCCCTTC
22	24	35 GTTTGTACTCTACAAAAGGTCATAATTCAA
23	0	0 GTGTTCCCGT tag f
24		
25	18	34 GTCTCGGGG long g
26	0	0 AACCGTAGATTCTCCGAAGAGCACCCCGAT
27	0	0 CGACTCGACTCCCTTGCGGGATAGCAATGT
28		
29	19	32 CCCACAGAATCACGAAAGAGCTCTCAGTCT
30	0	0 GTGCACGTT tag g
31		
32	0	0 GTCTTTGGGCCGACTTGTTGGTCGGGGGACT
33	29	30 GTCACGGCTCCTTGCGGTCCCTCACCTTTCG
34		
35	29	10 GTGTATTGGT long g
36	0	0 GTCTTCAGGCCTGCCTTGTGAGCAGGGGGC
37		
38	18	38 GAACAAAGTTTTTATATCCAAAAATATAAT
39	25	40 GTATAGGCTC tag f
40		
41	10	14 GTGTCCCTGT long g
42	7	7 CGACTCCCGTCTCTTGCGAGAAGGCCATAT
43	7	2 GTTCATGTTGTACCCTTGCGGGCCTCACAAA
44		
45	0	0 GTACAGCTTGCCGACTTGACGGCTCGTTCCC
46	25	27 TGTATGAAGCCCTTGCGGGCGATCACCTTTC
47		
48	14	16 GCATCGGCTC long f
49	36	29 GTGCAGATGCCCCGAAGGGAGATACCATCT
50	2	5 GTGACTGTTCCACCCTTGCGGGTGTGGCCCC
51		
52	0	0 CGACTGGACCCCTTGCGGAGTAACGATAT
53	0	0 AGTTTCGTGT long f
54		
55	29	15 GTCACCTTGTC long f
56	0	0 GAACAAAGTTTTTTTAACCAAAAAACATAAT
57		
58		
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8 9 GTCACCGGTC long o  
26 34 GTGTCCAGAT long f  
0 3 TCCTACCTCC tag f  
9 5 TGTAACCTGTGTATTGCTACAAAGCCCCCTT  
23 14 GTAATGGCTCCCCGAAGGGTCGTTCCGCTT  
13 33 GTGTGGACG long g  
14 20 GTGTTCCCAG long f  
16 33 GTGCTCAAATTCCTTTTCAGGCACACCCCTA  
25 32 CGCACGTTGT long p  
0 0 GTGCTTGTTTCACCCCGAAGGGTAGCTACG  
0 0 GTGTCCTGGC long f  
13 5 GTGTCCAGG long g  
19 31 GTGCAAGCTTCACTCCGAAGAGCAGACCTC  
15 27 GCACAGGATTTCTCTTGCGAGTTGGCCGAC  
0 0 GTTTTGGGGC long o  
21 18 GTCTCGGGGCTCCTCGCGGCACCCCCATCT  
16 12 CACCACAAGT long f  
6 11 GTGTGTGACCCAGCCGAAGTGAAGGAATCC  
0 8 GTCAAAGCTCCCCGAAGGGTCGTTCCAATT  
2 0 GTGAACAGC long g  
21 30 ATATAGCGGCCCCGAAGGCGACCCTGTCTCC  
0 0 TACAAAATGTATATTGCTATAAAATGAGCTT  
0 0 GTATCAGCGCTCCTCTCGGCACTCCCCAATC  
20 10 CGCATAGTGCCCCGAAGGGAGATCGGCTTT  
0 0 GTGCAAGCTGGTATTGCTACCTCGTCTCCCT  
0 0 CTGCAGCAGTTCTTGCGAAAAACGACATCTC  
0 0 CGACTCCGGT tag o  
0 0 GTGTCCTGGTTCTTTTCGAGCACCTCCGCA  
0 0 GTTTTGGGGC tag o  
14 26 GTGTTCCGGC long k  
0 0 GCTAGGAAATTAAGTATCAAAAAAAGAA  
0 0 GTGCAGGCTCTCTTGCGAGTCGTTCCGCTTT  
10 10 GTGCACGTTG tag g  
12 27 CCTGTAAATCAAGAAAGAACTTCAATCTGT  
11 5 GTGTATACGT long c  
0 0 GTCTTGTCGT long c  
3 5 GTGCAAAGG long g  
0 0 CTGCAGCAGT long g

1			
2			
3			
4		8	18 GTGTGCAGG1long g
5	26		17 GTATCCGGTCCAACTAAATGAAGGTCTCCA1
6	0		0 GTGCTCCGGC long o
7	0		0 GTGTTCCAATTCCCTTTCGGGCACCCCCAAC
8	0		0 GTGTTCCGGC tag f
9			
10			
11	14		21 ATTCTGGCTT, tag f
12	12		21 GTAAGGACGCTCTTGCGAGCCATTCCC GTT1
13	5		19 GTGCACGTTG long f
14	7		8 GTCTTAGCGT long p
15	7		9 TGCACGCGACTGGTTGCCAGCTATAACAT(
16	0		0 GTGCTTGTTCCACCCGAAGGGCGTGGCTCT,
17	0		0 GTGTTCTGGC long f
18	0		0 CGATGGCGGCCTCCGAAGAGGAGACGATA`
19	0		0 GTGACTGTTC long g
20	0		
21	8		7 GTGCACCAGC long g
22	0		0 GTGCACGTTCCGGCCTTGCGGCTGTGGCTC(
23	0		0 CTCATGGAATCAAGAAAGAGCTATCGATCT(
24	22		25 GTGCTCCTCCCACCCGAAGTGAAGGAATGC
25	0		0 TTAAGTCAATCAAGAAAGAGCTATCAATCTC
26	0		0 GTGTGCGATC long f
27	13		30 TGCAACCAGT long f
28	10		4 GTGTTCAGGCTCCCTTACGGGCACTCCCGA/
29	21		22 GCAAGGAAATCAGCCATAAAAGAAAAAAT/
30	4		18 GTGTTCCGGT tag c
31	18		14 CGTAGCCAGTCCGAAGAAGATCTGCTTTCA(
32	0		0 GTGTGCAGG1long g
33	14		40 TGAGAACCGTCCGAAGAAAGGTCTGTTTCC,
34	10		22 GTATACCGAC long f
35	12		17 GTGTTCCAGTTCCTTTCGGGCACACCTCAA
36	15		36 GTCTTGTCGC long g
37	3		9 CCCACAAAAT tag p
38	15		16 ATGTACCGGTCTATTGCTAGAAATTCGCTT
39	16		8 GTGTGCAGG1long g
40	19		25 GTCTTAGATCCGATTGCTCCGAAAGTACA1
41	3		3 AGTTTCGTGTCAATTGCTGAAAGGTGGCTTTC
42	0		0 CCACTCCGGTCCCCGAAGGGAGGACCTCAT
43	0		0 CTGCATCAGTTCTTGCGAAAAACGACATCTC
44	8		4 GTGCACGTTC tag g
45			
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0 GTGTGGCGTC long f  
10 GTGTGAAAGCCAGCCGAAGGACCTC  
0 GTGTCCCGGC long c  
0 GTTCAAGCTC tag f  
0 GTGTTCCAGTTCCTTTCGGGCACTCCCAGA  
0 ATCGAAATCA long f  
0 GTGTTCGAGT long g  
8 GTGCACCGGTCCCTTGCGGGAAAGACGCCT  
0 GTGTCCCGTCCGGCCGAACCGAAGACCCCG  
10 8 GTCAGTGGTC long o  
0 GTGTTCAGGC long g  
10 20 GTGCAAGAGCTCCCTTGCGGGCACCCCCAG  
11 14 GTGTGGGGCCCCAGCCGAAGGGGTCA  
20 4 CCCACATTATCAAGAAAGCTCTTCACTCTGT  
13 11 GTATAGGCTC long p  
0 9 GTATTTTCATATAAAATTTGAAAATCATAGA  
28 11 GTGTTCAGGT long g  
5 13 CCCATAGAAT long g  
0 0 TGTAAATTGT long g  
16 16 TACCGGCGACGTATTGCTACGCTATGAGCT  
0 0 TACTGGCAGT long f  
0 0 GTGTGCAGGTTCTCTTTCAAGCACCAAACCA  
5 2 CGCAAATTGT tag g  
17 16 ACCAATAAATCAAGAAAGAACTTTAATCTGT  
0 0 CGACTCAAGT tag o  
0 0 GTGCTAGCTC long c  
14 19 GTCTTCTGGTCTACCTTGTTGGGTAGAGGGC  
0 0 GTGTGTAGG long o  
0 0 TGTATGGTGTCTTGCGGCCGATCACCTTTC  
14 9 GTGCTGGTTCACCTTGCGGCGTCAGTCCC  
0 0 GTGTTGAGGTTCCCTTTCGGGCACCGCCAC  
0 0 AGTTTTGTGTCTTGCGAAAGCCACCTTTCGG  
0 0 GTGCGGGCGTTACCTTGCGGTACTGACCGA  
9 13 TGCTTTGTGTTCTATTGCTAGACCTACAGGC  
0 0 GTCTTTGTGCTTCTTGTTGGAAGGGAGCCACT  
2 11 CGACTCTAGTCCCTTGCGGGAAGGCCATGT  
0 0 CTGCACGAGTCCCGAAGGAAGACCTCATCT  
0 0 TGTTCGGGTCCGGTTGCCCGGACGGACGC

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	7	16 CTGCAAGCTCCCTTGCGGGTCGTTCCCCTTT
	8	11 TGTTCGTGTlong f
	0	0 GTGTTATGGC long f
	0	0 GTGTTCTAGC tag g
	12	8 GTGCATGTTC long g
	12	23 GTAGGTAAATAAATAATATAACAATGTCAC/
	0	0 GTGTCCAGGC long g
	0	0 GTCTCACCATTCCCTTGCGGGCACGTCGACT
	6	0 AGTTTCGTGC long g
	0	0 GTGACTGTTCCACCCTTGCGGGCGTAGCCCC
	0	0 GTGTGCAGGtag o
	13	19 GATTATATGTTATTTAATTAATTACTAAAATT
	0	0 GTGCAAACCTCCCCTTGCGGGGTCGTCACCC
	0	0 GTGTGCAGGTTCTCTTTCGAGCACCAACCAT
	13	11 GTCTCCGCGC long g
	0	0 GTGTTCCGGT long f
	12	15 GACTCAAATAATTATAAAAATGCAAGCTATT
	4	5 GTCTCGGGG(long g
	0	0 GTGCTGGCTC tag p
	0	0 GTGCTCCTCCCACCCGAAGTGAAGGATTCC
	0	0 GTGTCCTGGCTCTCTTGCGAGCACACCCAAC
	0	0 GTGCACGTTC long c
	0	0 GTGTACAGGTTCTCTTTCGAGCACCAAACCA
	17	30 TTTATATACACTCAGTTCTATTGTTCAATAAA
	0	0 GTGGAGCAC(long g
	0	13 CCCAAAGAATCAAGAAAGAGCGCTCAATCT
	6	4 GTGCATGTTCCACCCCAGAGGGGGCGTGGCC
	0	0 GTCCTGGCTCCCTTGCGGGTCGTCGGGCTT
	4	11 GTGTGGGAGCCAGCCGAAGTGAAGGATCC
	0	0 TGTTTTGGGTTTGATTACTCAAACCTATCACT/
	13	12 GTGCACGTTCACCCGAAGGGTGTGGCTCC
	12	16 CGCACCCGGCCCCGAAGGGCTGACACCTTT
	0	0 GTATGCAGGTTCTCTTTCGAGCACCAAACCA
	0	0 GTCCGCGCTC long f
	0	0 GTCTCGGGGCTCCTTTCGGGCACCACTCATCT
	0	0 CCAACGAATCATGAAAGAGCTATCAATCTC
	9	7 GTGTTCCAGC tag f
	0	0 TACTGGCAGT long g

0 3 GTGAATCTGC long g  
0 0 TGCCACTTGCCCCGAAGGGAAGGCACCTTT  
0 0 GTGATCGCTG long p  
0 0 TTCAAACAATCATGAAAGATCTTTGAATTCT  
7 9 GTGTGGTGT long f  
2 0 GTATAGAAG tag g  
0 0 GTGCAAAGC long g  
0 0 TGCTTTGTGT tag f  
0 0 GTGTGGCGT tag g  
9 13 GTGATGGTCC long f  
11 9 GTGTCCAGTCCAATAAATGAAGAAAGCCA  
2 2 GTGACTGTTCCACTCTTGCGAGCGTCATTCC  
6 9 GTGTTAGCCTTCGATTGGATACGATCGGGA  
0 0 GTGTTGCAGCTCTCTTTCGAGCACTTTCTCA  
0 0 TGTATACTGT long f  
0 0 AGTTTCGTGT long f  
6 8 GTGTTTAGATTTCTTTCGGACACAATTTCA  
0 0 GTCTCAGAGCTCCTCGCGGCACCCTCCATCT  
13 8 GTGCAGACTCCCCTTGCGGGGTCGTCACCC  
0 0 GTGTCCCGGC long g  
7 16 GTGTGGTAG long f  
0 0 GTGATCGTTC long g  
14 11 GTACGGGGACCTGTTGCCAGGCTGCGACAT  
0 0 GAATGCCGGCTCCCTTGCGGGCACCCCGAT  
11 4 GTCAGTATC long o  
3 6 ATACAGGCA tag f  
0 0 CCCAAACAATCAAGAAAGAGCTATCAATCT  
0 0 GTGCAAGAGTTCCCGAAGGCACCCCGCCCT  
5 0 GTGCATGTTC tag g  
2 0 GTGCAAAGCGGGTATTGCTACCCTATCCGC  
0 0 AGTTTCGTGTCCTTGCGGAAAGACCCCTTTC  
0 0 GTGTCCACGC long g  
0 0 GTGCAAGCTC long c  
5 5 GTGTCTTAAT long g  
2 0 GTGATCAGGTCCCTTGCGGGACACCGACGT  
0 0 GTCACCGGTC long g  
8 7 GTGCTCTACCGGCCGAACCGAAGTAGTTT  
7 9 GTGCACGCTC tag f

1			
2			
3			
4	0	0	GTGTGCAGGTTCTCTTTTCGAGCACCAAACCA
5	0	6	TGTATAGAGCCCCGAAGGGCGATCAGCTTT
6	0	0	GCTATCGGATCAAGAAAGCGCTATCAAGCT
7			
8	0	2	GTGTCCACGCCCCTTGCGGGGAGGAACCCA
9	0	0	TGCAATCGGT long o
10			
11	5	0	GTGCACGTTG tag g
12	4	8	GTGTTACGGT long f
13	0	0	GTGTCCAGGT tag o
14			
15	0	0	GCATAAAGTAAGCTATATTATAACATGTGTA
16	0	0	GTATAGGCTC long p
17			
18	0	0	GTGCGCAGG long g
19	0	0	GTGTTACGGC long o
20			
21	0	0	AGTTTTGTGC long f
22	0	0	CGACACCGACCCTTGCGGGCTTGACATCTC
23	0	0	CTGTAGCAGT long g
24			
25	0	0	GTGTCCTGGT long f
26	6	16	AGTTTCGTGCTCCGAAGAGAATCCTGCTTTC
27			
28	0	0	GTCTCTCTGTAGTATTGCTACTAAAGTCGTA
29	3	11	GTGCTCGCTC tag c
30	2	0	GTGCACGTTCCACCCTTGCGGGTGTCATCCC
31			
32	0	0	GTATACCGAC tag f
33	3	5	CTGCAGAATTCCTGACGGGAAGCCCGACT
34			
35	0	0	GTGCACGTTCCACCCGAAAGCGTCAGTGAC
36	0	0	GTGGAGCACCCCTCGAAGGCGACCGGCTTTC
37			
38	0	0	GAGCAGGAT long g
39	4	13	GTCTCTCTGTTGTATTGCTACAAAAGCCGTA
40	0	0	GTGTTTCGAGC long f
41			
42	0	0	TCTCACTGAT long g
43	0	0	GTGCACGTTCCAACCTTGCGGCTGTGGCTCT
44			
45	0	2	AGTTTCGTGT long o
46	0	0	GTGTTCCAGC tag f
47			
48	0	0	GTGTGCAGATTCTCTTTTCGAGCACCAAACCA
49	0	0	AACCACAAGTTCTCCGAAGAGCACCCCCAC
50	0	13	GTGCACGAG long p
51			
52	0	0	TGCAGGCAG long o
53	0	2	AGTTTCGGGT tag f
54	4	2	GTGCACGCTCTCCGAAGAGTCGTTCCGCTTI
55			
56	0	0	GTGTTCCGGT long o
57			
58			
59			
60			

0 AGTTTTGTGC tag f  
5 GTGTTCCGGC long g  
0 GTGTGCAGGTTCTCTTTCGAACACCAAACCA  
0 GTATACCGCCCTTGCGGACCCTACATCTCTG  
0 GTGCAAGTTTCACCCCGAAGGGCAACCTGG  
4 GTGTTACGGC long f  
0 ATGTGCAGGTTCTCTTTCGAGCACCAAACCA  
4 GTGCACGTTCCGGCCTTGCGGCTGTGGCTT  
0 GTCTGCGCTC long f  
0 GTGTCCCGAT tag g  
0 GTGCACGCTCCCTTGCGGGTCATCCTGGTTT  
7 15 GTCTTTGGGT tag p  
0 GTGTCCAGGT long g  
0 GTCTCCAGGTTCCCGAAGGCACTCCCGCATC  
3 5 GTGTTGTATCCAGCCGAACTGAAAGGACCG  
0 0 GTCTTCTGGTCATCCTTGTTGGGATGAGGGC  
3 0 GTAACCGCTC tag f  
0 0 GTGCACGTTC tag g  
6 7 CTGCACGAGTTCTTGCGAAAAGGCACATCTC  
0 0 CGATGGCGG tag f  
0 0 GTGATAGCTT tag g  
0 0 GTGCAACAG tag k  
0 0 GATATAATAACAGTAATAATTATTTTTTCAA  
0 0 CGACTCCCGTCCCTTGCGGGAAACCTCTGTT  
10 6 CGATAGCACTCCCGAAGGACACAGCCTTTC  
7 8 GTCTCTCGGT tag c  
3 3 TGCTTTGTGT long f  
3 16 GTGTTACGGC long f  
0 0 GTGCGAGCTTCCCTTGCGGGATCGTCAGGC  
0 0 TGCACTCGGCTTGTTTTACCCAAGAGATCC  
8 11 GTGTGCAAG long g  
2 5 TGCTCTTTGT long f  
0 0 CGGCTGGTTCCTGACTTTACAGGTCGTTCCC  
6 9 GTGTGGGACCCAGCCGAACTGAAGGACATC  
0 0 CCCATCAAAT tag o  
5 2 GTGTCTTGGTTCCTTTTTTACAAAAGGCAC  
0 0 CCCATAGAAT tag o  
0 0 TGTTTTGGGTTTGATTACTCAAAGTGCATT



1		
2		
3		
4	4	2 GTCACTGATC tag c
5	2	3 GTCTCCAGGTCTCCGAAGAGAAAACCTACT
6	0	0 TCTCACCAGCTTCCCGAAGGACACCCCCACA
7		
8	6	2 TCTCACTCGCTCCCCGAAAGGCACCAAGGC
9	0	0 GTGGAAGTTTCACACCGAAGTGCAGCCTTC
10		
11	4	9 CCATCCGATCCTCTGAAGGGCCTTCTCGTCT
12	5	9 GTGTGGGAGCCAGCCGAACTGAAGGGTCG
13	0	0 CCCACTGAAT long g
14		
15	0	0 GTGCACGGTCCAGCCAAACTGAAGAAAAGC
16	7	4 GTGTTGCAGTTCCTTTCTGGGCACTTTCTCA
17		
18	8	7 GTCTCTCTGTCTCTTGCGAGCCTACAATATC
19	6	5 GTTGAGGCTC long f
20	0	0 GTGTGCAGG long g
21		
22	2	2 CTACACGGTG long p
23		
24	10	6 GTACACAATCATTAACATAATAAGCT
25	0	0 TGAAAGACG tag g
26	2	5 GTGCAGGAGGTCCCTTGCGGGAAACGACC
27	0	0 GTGCTGGAA tag f
28	0	0 GTGTTACGGT tag g
29		
30	0	0 GTGTTACGGC tag g
31		
32	0	6 GTGCAAAGG long g
33	0	0 GTGCTGGTTACACCCTTGCGGGCAATTTGCC
34		
35	6	0 GTCACCGCG long f
36	8	5 GTGTACGTTCCATTCTTGCGATTGTCATTGA
37	0	0 GCTGCCAAATCAAGAAAGTGCTATCAAGCT
38		
39	0	0 GTGCAGGCTTCACTCCGAAGAGCAGACCTC
40	7	9 CTGCAGGCA long f
41	0	0 GTGTGCAGGTTCTCTTTGAGGACCAAACC
42		
43	0	0 GTGTTCTCGCCAGCCGAACTGAAGAAAGTC
44		
45	0	2 GTGCACGTTCCACCCAAAGGGCGTGGCTCC
46	5	0 GTAATGGCTC tag f
47	0	0 TACTGGCAGT tag f
48		
49	0	0 TACTGGCGGTATATTGCTATAAAGAGAGCT
50	0	0 GTGCACGTTCCGGTCTTGCGACTGTGGCTC
51		
52	0	0 GTCTTCACG tag p
53	7	3 GTGTGGGAG tag g
54		
55	3	7 GCACAGGTTC long g
56	0	0 GTGTCCTGGCTCCCTTGCGGGCACGCCGGC
57		
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0 GTGCACCGGTCTCTTGCGAGAAGGACACCT  
2 GGATCACGGTTCCTTGCGGGCACCCCAAC/  
6 GTGGCACACCCTCGAAGGCGACCCACTTTG/  
0 GTGCAGGTTCTCTTTGAGCACCAAACCATC/  
0 AACCACAAGTTCTCCGAAGAGCACCCCCGCA/  
4 GTGTTCTGGC tag f  
0 CCCATAGAAT long f  
4 GTATCCAAGC long o  
5 GTGTTCCCGC tag g  
0 GTGTTGTATC long f  
0 TGCAGACAGGAGCCGGTTACCCGGATCATC/  
0 CGACTCCTGTCTCTTGCGAGAAGGCGATATT/  
6 GTGTCCCGGT long c  
3 GTACTAGCTCTCTTGCGAGTCGTTCCCTTTG/  
0 GTGTATGCTGATATTGCTATCTCGTCAGACT/  
0 CGACTCCCGT tag o  
0 TGCATCGTGC long f  
0 GTGTTCCAGT tag c  
6 11 GTACAAGCTCCCGAAGGTCGTTCCCTTTTCA/  
0 GTGCACGTTCCACCCGAAGGCGTCAATGAC/  
4 5 GGGGCGAGTTTTATTAATATTATTAATTTGT/  
0 GTGTTCCGACCTATTGCTAGGAGGAGTCCA/  
0 GTCTTCTGGTCTCCTTGTGGGAGAGGGCCC/  
2 3 GTGTGGGAGCCAGCCGAAGTGAAGGATCA/  
0 TTGTCTATCTCATACTAATTCTCTAATAGACT/  
0 GTGTGGCGTCCGGCCGAACCGACTCCCAGA/  
0 GTGCGGAGT(long g  
3 4 GTGCATGTTCCACCCTTGCGGGTGTGGCCG/  
0 TCTCACTAGC tag g  
2 0 GTGCAGGTT long g  
7 6 GTAATAGCTC long f  
0 GTGTGGAGGTTCTCTTTGAGCACCAAACCA/  
0 AGTTTCGTGTCATTGCTGAAGGGATCCTTTG/  
0 GTGTGTAGG1 long g  
4 5 GCTAAGAAATTAATCAAAAAAAGGAAA/  
4 0 GTGCACGTTTCACCCGAAGGCAGATTACTC/  
0 GTGCACGTT long f  
0 GTGTCTGAGT tag o

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3			
4	0	0 GTGTGCAGG1long	g
5	0	0 GTCTCTCGGTTGTATTGCTACAAAGACTGTA	
6	7	7 CCCATCCGATCCTCTGAAGGGCCTTCTCGTC	
7			
8	0	0 GTGTATCGGT long	c
9	4	3 GTCTCCAAGT long	p
10	0	0 GTGTGGCGTCCAGCCGAAGTGAAGGAGCA	
11	4	5 GTGTTCTAGC tag	o
12	0	5 TGCTTCGTGTCCCTTGCGGGCCTGCCACCTT	
13	0	0 GTGTTCCGGCCTATTGCTAGGAGGAATCCA	
14			
15	0	0 ATACAGAAGTCCTTTCGGACGATATCATTTT	
16	0	0 GTCTTCCGGTCGTATTGCTACGAAAGCCGT	
17	0	0 AGTTTCGCGCCCTTGCGGGAAGTCTGCTTTC	
18	0	0 CCCATAGAATCAAGAAAGAGCTCTCAAATC	
19	0	0 GTAAACCGACTCTTGCGAGCTACGACATCTC	
20	0	0 GTAAAGGCTCCCCGAAGGGTCGCTCAGCTT	
21	0	0 AAGTGACAG(long	o
22	0	0 GTGCCCAGG1tag	g
23	4	2 GTGCAGGAGGTCCCTTGCGGGAAGCGACCA	
24	0	2 GTTTTCAGGT long	f
25	4	6 GTGTTCAAAT tag	g
26	6	0 GTGTTTCGCGT long	o
27	3	3 GTGTTACGGC tag	f
28	0	0 GTTTAGGCTCCCCGAAGGGTCGATCCGCTT	
29	2	6 GTGTTTAGATTTCTTTTCGGACACAATTCCA	
30	3	0 CCACTACGGCCCCGAAGGGAAGATGCATCT	
31	3	2 GTGTTCAGGCTCCCTTGCAAGGCACTCCCGA	
32	4	3 GTGTTTCGCGCTCCCGAAGGCACCTTCGACT	
33	0	4 CTGCATGTGTCCGAAGAATATGAGCTTTCA	
34	5	10 GTGCTCCTCC tag	k
35	0	0 GTGTCACGGT long	g
36	0	0 GTGTGCAGGTTCTCTTTCGAGCACCACCCCA	
37	0	0 GTGTCCAGGT tag	c
38	0	0 GTGTTAGCGTTCTTGCGGACGTATTCCCTTT	
39	0	0 GTGCGGCCGCCTTTCGGAAGGTACATCTCTC	
40	5	2 GTCTCCAGGTCCCCGAAGGGAAGACCTACT	
41	0	0 GTGCTAGAAGTTATTTTTTTAACTCAAAGAA	
42	0	0 CGACTGGACC tag	c
43	0	3 GTCACCGATC tag	o
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0 4 GTGTCCTAGCTCCCTTGCGGGCACATCCACC  
0 0 CGACACCAGCCCTTGCGGGCCCCTACATCTC  
3 0 GTGTGGGAG(long o  
0 2 GTGAGTGTGTCTTGCGAACCTCAGGCTTTC/  
0 0 GTGTTCAGGC tag g  
0 0 TGTTTTGTGTCCTTACGGACTAATTCATCTCT  
0 0 GTGCACTTGCCTTGCGGAGGGTGTATTTCT/  
0 0 GTGCACAGACTCCGAAGAGCTATAACATCTC  
0 0 GTCACTGGTCCAGCCGAAGTGAAGGATACC  
1 0 GTATTCAGGCTCCCTTGCGGGCACTCCCGA/  
6 3 GTGAATCTGCCCTTGCGGGAAGGAATATCTC  
2 4 GTCACCGCGCCTCCGAAGAGGACCATCGAT  
0 0 GTGCACGTTGTACCCTTGCGGGCCTCATTCC  
0 0 GCACTAAGTATTTTATAATTAACGCTCTAAT  
0 0 GTAAACAAGCTCTTGCGAGAAGACCATTTC  
0 2 TGAAAATTGT long g  
0 0 TGCAAGCGGCCATTGCTGGCTGCAAACCTTC  
0 8 GTACTAGCTC long f  
0 0 GCTAGGAAATTAAGTATCAAAAAAAAAAGAAA  
0 0 GTGAGCAGGTTCTCTTTCGAGCACCAAACCA/  
3 6 GTGATCGCGCTCCGAAGAGGGAAACGTGTTT  
0 0 GTGTGCAGGTTCTCTTCCGAGCACCAAACCA/  
0 0 GTATAGGGCCCAGCCGAAGTGAAGAATCC  
0 0 GTGTGGCGTC tag g  
0 0 GTCTCTGGGC long f  
0 0 TGCAGGCAG(long o  
0 0 GTGTCTTGGT tag f  
2 4 GTGCATGTTCCACCCAGAGGGTGTGGCTCC  
0 0 TGCAATCGGTCTCCGAAGAGAAGGCCACCT  
2 0 GTGCAGGAGCCGGCCGAACCGAAGGTCCA  
0 0 GTCTCCGGTC tag g  
3 0 GTAGAAGGT tag f  
0 0 CTCCAAGTGCCCTTGCGGGAAACCACTTTCA  
0 7 GTGCACGTTC long g  
0 0 GTGGTAGCTTCCGGACTGGATACCGTTGGG  
2 4 GTGCACGTTGTACTCTTGCGAGCCTCATTCC  
0 0 GTGTCCTGGC long f  
0 0 GTGTCCAGGT long f

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3		
4	7	0 GTCCCAGTGCCCCGGAGGGAAACCGACTTT
5	0	0 GTGTCCTGGT tag f
6	0	0 GTGCTTGTTCCACTCTTGCGAGTGTGGCTCC
7	0	0 TCCACGGAATCGAGAAAGAGCCTTCAGTCC
8	0	2 GTGTGGACG(long g
9	0	5 GTGTCCACTTTCCCTTTCGGGCACCTAATCC/
10	0	0 GTTATTAAATACTCTTTCAGTATATTATATAT
11	0	0 GTGTGCAGGTTCTCTTTTGAGCACCAAACCA
12	0	0 CCCACTTAAT(tag g
13	0	2 GTGCTCTCTCCGGCCGAACCGAAGGACTCC/
14	0	0 GTGCTCCACCCTCGAAGGCCTCCCGGTTTCC
15	0	0 GTCTCTCTGTTGTATTGCTACAAAGACTGTA
16	0	0 GTGTTCCGGC tag c
17	0	0 GTCAGTGGTC tag o
18	0	0 GTATACCGAC tag c
19	3	3 GTGCAGGTT(long g
20	4	6 CGCACCCGGCCCCGAAGGGCTGACACCTTT/
21	0	0 GTCAGTATC long f
22	0	0 GTCTCTCGGT tag c
23	2	7 GTGCAAGCTC tag f
24	0	0 GTGCCCCGGTTCTCTTTCGAGCACTCCCACA
25	0	2 GTAACGGCTCCCGAAGGTCGGTCCACTTTCC
26	0	0 GTGTGCAGGTTCTCTCTCGAGCACCAAACCA/
27	0	2 TTGAGAGAA(long g
28	0	0 GTGTGCAAGTTCTCTTTCGAGCACCAAACCA
29	0	5 GTGTCCAGGT tag f
30	0	0 TGTAAATTGCTCCGAAGAGAGTTCCAGTTTC
31	0	0 TGTATCGAGTCCCGAAGGACGATCCCCTTTC
32	0	0 TGCACTCTGTTCTTGCGACCAACGAACCTTCC
33	2	1 CCCATAGAATCAAGAAAGGACCATCAACCT/
34	0	5 GTGCAGATTCCGACTCCGAAGAGCTGTCAC/
35	5	4 GTAGACAAGCTCTTGCGAGAAGACCATTTC
36	0	0 TGTAACCTGT tag f
37	0	0 GCATGAGCTAAAAAAATAATTTAATCTAA/
38	0	0 GTGTCCAGGTTCCCGAAGGCACCAATCCATC
39	0	0 GTAGGAAACCCTTACGGACCCACCATCTCTC
40	0	4 GTGCAAACCTC long c
41	0	0 GTGTTCCAGT tag f
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0 GTGTCCCAGT tag g  
0 GTGTTTCAGGC long g  
0 GTGTCCAGGT tag c  
2 3 ATGTAACAGTACCGAAGTAAAATACCCTTT  
3 2 TGAATCAGCCCCAAAGGGCGATCACCTTT  
0 0 GTGGCGGCTCCCTTGCGGGTCGTCGGGCTT  
0 0 GTCAAAGAGTCCCGTGAGGGAAGGAATCC/  
0 0 CGACTTCAGTCCCTTGCGGGAAATCCATGT  
0 0 GTGTTCCGAGCTCCGAAGAGAAAGTTCCAT/  
3 2 GTGTTCTCGCCAGCCGAAGTGAAGGATCCC/  
0 0 GTGTTTCAGGCTCCCTTGCGGACACTCCCGA/  
3 0 GTCACCGGTC tag g  
0 3 GTACAGACTCCCGAAGGTCGTTCCGCTTTCA  
0 0 GTCTCCGGGT tag o  
3 4 CTAGACCAATCAAGAAAGAACTCTCAATCT/  
0 0 GTCTCGGGG tag g  
0 0 GTATCCGGTC long g  
0 0 GTCCCACTGC long g  
10 0 CCCAAAGAAT long g  
0 0 TGAAAATTGT tag g  
0 0 GTATAGAGGCCTTGCGGAAGCACCATCTCT/  
0 3 GTGTCTGCTTCGGATTGGATACCGTTCCGG/  
2 2 GTAATCGCTCCCCGAAGGGTCGTTCCACTTT  
0 0 GTGCAAACCTCCCTTGCGGGGTCATTACCTT  
0 0 GTGTGCAGGTTCTCTTCGAGCACCAGACC/  
0 0 CGACTCCCGT tag o  
0 7 GTACAGGCTCCCGAAGGTCGTTCCGGCTTTCA/  
0 2 GTGTTTCAGGCTCCCTTGCGGGCACTCCCGA/  
0 0 GTGCATGTTC tag g  
6 2 GTGCTCAAATTCCTTTTCAGGCACATCCCTA/  
0 0 GTCTCAGCGCTCCCGAAGGCACCCCTTAATT  
0 11 GTGCATGTTCCATTCTTGCGATTGTCATTGA/  
0 2 GTCTCTGCGC tag g  
0 0 GTGTTTCAGGCTCCCTTGCGGCACTCCCGAA/  
2 3 GTATAAGCTCCCGAAGGTCGTTCCGCTTTCC  
0 0 GTGCATGTTC tag g  
0 0 GTCTTCACGTCTTCCTTGTTGGGAAGAGGGC/  
0 0 GTATACAGGCCCCGAAAGGCTATACCGTCT/

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3		
4	0	0 GTGTAGGTTCCACCCGAAAGCGTCAGCGAC
5	0	0 GTGCATGTTc long g
6	0	0 GTGTACGTTCCATTCTTGCGATTGTCATTCC
7	0	0 GTGTGCAGG1long g
8	0	0 GTGATTGTTTCACCCGAAGGCAGAGTTATC
9	0	0 GTGCCAGGTTCCGGATTGGATAACCGTTCGT
10	0	0 CTATCGGCAACCGACTTTACGGTTCATCGCT
11	0	0 ATACTAGCGT tag p
12	0	2 GTGCATGTTCCACCCTTGCGGGTGTGGCTC
13	0	0 GTGTCCCGTC tag g
14	2	0 GTGTGGAAGCCAGCCGAAGTGAAGAAAGG
15	4	2 GTGTATCTGCCTATTGCTAGGGGTCCAAAC
16	0	3 GTCACCGGTC long f
17	0	0 GTGTTCCGGT long c
18	2	2 GTCTCTCGGT tag c
19	5	0 GTCTCAGAGT tag g
20	0	4 GTGCAGCAG1tag k
21	0	0 ATACAGAAGTCCTTTCCGGACGAAGCCATTT
22	0	0 GTCTCGGGGTTCTCGCGGCACTGCCCATC
23	0	0 GTGGAGCACCTCGAAGGCGACCGGCTTTC
24	0	0 GTGTCCCGAT tag g
25	0	2 GTGCACGTTCCGGTCTTGCGACTGTGGCTT
26	2	2 GTGCACCAGC long g
27	0	4 TGTTCGTGTCCCGAAGGAAAAACGGCTTT
28	6	0 GTGCGGGAG1long o
29	0	0 GTGTCCTCCGTCCCTTGCGGGTCTAGCCTGT
30	3	0 GTGCACGCTCCCTTGCGGGTCATCACCTTT
31	0	0 GTGTGAGAC tag p
32	0	3 TCCATCAAATCAAGAAAGAGCTATCAATCT
33	0	0 GTGTGTGATC long g
34	0	0 ACAAACGAATCATGAAAGATCTTTCAGTCT
35	0	0 GTGCACGCTACCCTTGCGGGTTCGTTACGC
36	0	2 GTACGCGTTCGGACTGGATAACCGTTCGTA
37	0	0 GTGCTTGTTCCGGTCTTGCGACTGTGGCTCT
38	0	8 GTGTCAGTGT long g
39	5	5 ATATAACAGTCCTTGCGGAACTCTTCATTT
40	0	0 GTGCATGTTCCACCCTTGCGGGTGTACTCC
41	0	0 CGACTACAGTCCCCGAAGGGAAAGCCCATG
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0 3 GTGTAGAACC tag g  
0 0 GTGTGCAGGTTCTCCTTCGAGCACCAAACCA/  
0 0 GTGTCTTAATTTCTTTTCGGACACTTTTACAT  
0 0 GTGCTGGGTTCCGGATTGGATAACCGTTCGC  
0 0 GTGTCCTGGT tag g  
0 0 GTAGTAGGTTCCGGATTGGATAACCGTTCGC/  
0 0 GTGTGCGGGTTCTCTTTCGAGCACCAAACCA/  
0 0 GAGTGCAGGTTCTCTTTCGAGCACCAAACCA/  
0 0 GTGTGCAGGTTCCCTTTCGAGCACCAAACCA/  
0 0 GTGCATGTTCCGGCCTTGCGGCTGTGGCCTC/  
0 0 GTGTCCAGGCTCTCTTTCGAGCACTCCTAAA  
0 0 AGTTTCGTGTCATTGCTGAAGGGTGGCTTTT/  
0 0 CTACTAGCAT tag f  
0 0 GTCTCCAGGT long g  
0 0 GTCACGGCTCCTTGCGGTCCGGTTCGGTTTCC/  
4 0 GTTATACCCACCCGAAGTGAGAGCTATGT  
0 1 GTGTTCAAGCTCCCTTGCGGGCACTCCCGA/  
0 0 GTGTGGAAG tag f  
0 0 GTCTTCGGGCCAGCCTTGTTGGGCTGGGGGC  
0 3 CTCCGAGTGTCTTGCGGAAAACCACTTTCA  
32 2 3 GGTCTGGCGGCCTCGAAGGACTTCTTATTT/  
0 0 GTGTGCAGGTTCTCTTTCGGGCACCAAACCA/  
0 0 CGACTGGACC long f  
0 0 GTGTCAGAG long g  
0 0 GTCACCGGTC tag o  
0 0 GTGTTAGCGC long f  
0 3 GTCTCCGCGTCCCGAAGGACCTTCCGCTTTC  
0 0 GTGTGACACCCTCGAAGGCGACCGGCTTTTC/  
43 0 4 CGACAGCGGCCCCGAAGGGAAAGTACATCT  
0 0 GTGTCCAGACTCCCTTTCGGGCACCAAGCCA/  
0 0 GTACCAAGTC tag g  
0 0 GTGTTCAAATTCTCTTTCGAGCACGATTTCA  
0 2 GTGCTAGTTGTTCCCCTTGCGGGGCCCTACTC  
50 2 0 GTCTCTGCGTTCCTTTCGGCACACCAGCCTC  
0 0 GTACCAAGTCCCCTCTTGCGAGGTTCCCCTG  
0 0 GTGTGCAGGTTCTCTTTCGAGCATCAAACCA/  
0 0 GTGCAAAGCGTATGTATTGCTACATACTAAC  
0 0 GTCTCTGGATTCCCTTGCGGGCACGCCAACCT



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3			
4	0	0 CCCACAAAAT tag	k
5	0	0 TACATTCTGTGTATTGCTACAAAAATCCCTT	
6	0	0 GTGATCAGGTag	c
7	0	0 GTGTCCAGGTag	f
8	0	0 GTGTCCAGGTag	f
9	0	0 GTGACCGTTGTACCCTTGCGGGCCTACTCCC	
10	0	0 GTCACCGGTC tag	o
11	0	0 GTGCCCAGGTTCCCGAAGGCACAATCCCAT	
12	0	0 CTACACGGGTag	o
13	0	0 TGTTTTGGGCCAGTAACTGGCGATCGGTA	
14	0	0 TGAAAGACGTCCTTGCGGAAAGAAACCTTT	
15	0	0 GTGCACCTCCCACCCGAAGTGAAGGAATCC	
16	0	13 TCCATAGGAT long	g
17	4	4 GTCTTGGCGTCCTTTCGGAACCTGCTTTC	
18	0	0 GTGTTACGGC tag	g
19	3	3 GTGTTCCAGC tag	f
20	0	0 GTGTTCTGGT long	f
21	2	0 TGTTTCGTGTCCCAGGAAAGTCTCCTTTC	
22	0	0 GTCTCCGGTC long	g
23	0	0 GTGTGCAGGTTCTCTTTCGAGCACCAAACA	
24	0	2 CGCACGCAGTag	f
25	0	0 GTGTCCAGGTag	f
26	3	3 CTAAACCAATCAAGAAAGAACTCTCAATCTC	
27	0	0 GTCTATAGGTCTCTTACGAGAAGACCCGATC	
28	0	0 GTGTCCTGGCTCTCTTTCGAGCACCAAGCCA	
29	0	0 CGATTGCCGT tag	o
30	0	0 GTGTCCCAGT long	g
31	0	2 GTGTTCAGACTCCCTTGCGGGCACTCCCGA	
32	0	0 GTGTTAGCGTCCTTGCGGACGTATTCCCTTT	
33	0	0 GTGCACGTTCCACCCAGAGGGCGTCATTGA	
34	0	0 GTGCACGGAATCCGAAGAGGGGCTCACGT	
35	0	0 GTGCAAGCTC tag	c
36	2	0 CCCACGAAAT long	c
37	0	0 GTGTCCAGGCTCCCTTTCGAGCACCAAGCC	
38	0	0 GCACTAAGTATCTAATATTTAACTTTATAAA	
39	0	0 GTCTCATGGTTCCTTGCGGCACTCCCACATC	
40	0	0 GTGAAAAAGTag	g
41	0	0 GTGCTCCTCCCACCCGAAGTGAAAGACCCCT	
42	0	0 TGTTTTGAGTCCATTGCTGGAAAATCGGCTT	
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0 GTGTGGGAGGTCTCTTGCGAGAAAGATCCA  
0 GTGCAAGAGCTCCCGAAGGCACCCCGCCCT  
0 TGCCAATTGC tag f  
5 GTGCATCCGCCTTTCGGAGGGTGTATCTCTA  
0 GTGTCCAGGT tag o  
0 GTGGATGCGCCTTGCGGACCTCAGGCTTTC  
0 GTGCCTGTTCCGGTCTTGCGACTGTGGCCCT  
0 GTGCAAGCTCCCGAAGGTCGTTCCCTTTCG  
6 GTGCACGTTC tag g  
0 GTGTCCCTTGTCTCTTGCGAGCCTATCCCTA  
0 GTGTGACGTCCGGCCGAACCGACTCCCCGC  
4 GTGTTCCGACCTATTGCTAGGAGGATCCCA  
5 GTCACGGCTC tag f  
0 GTGTCCAGGC tag g  
1 GTGTTCAGGCCCCCTTGCGGGCACTCCCGA  
0 GTCTCAATGT long g  
0 GTGCAAAGCTCCCGAAGGGCACTCCCCG  
0 GTGTTCCGGTCCCTTTCGGGCACTCCCGCA  
0 GAGTTCAGGCTCCCTTGCGGGCACTCCCGA  
6 CTAGACCAATCAAGAAGGAACTCTCAATCT  
0 GTGCACTAGTCCCGAAGGAAAGACACCTTT  
1 GTGTTCAGGCTCCCTTGCGGGGACTCCCGA  
0 GTGTTCCGGT tag o  
0 GTGTTCCGGCTCCCTTGCGGGCACTCCCGA  
2 GTGCAGGCTCCCGAGGGTCGGTCCCTTTC  
3 CCCAACCGATCCTCTGAAGGGCCTTCTCGTC  
4 GTGCTCTCCCCGGCCGAACCGAAGAACCTG  
0 GTGCAGAAGTCCTTGCGGAAAGCACTATCT  
0 GTGTTCAGGC tag g  
0 CCACCGCGGTCCCGAAGGGAGGACCTCAT  
0 GTACAGCGGCCCGAAGGCGACTACATCTCT  
0 GTGTCCCAGT tag g  
0 GTGCATGTTCCACTCTTGCGAGCGTGGCCCC  
0 GTGACCGAGCTCCGAAGAGCTGACCAGGTT  
3 CGCACCCGGCCCCGAAGGGCTGGCACCTTT  
0 GTGCGATAGCCTTTCGGAGGATGCATCTCT  
0 GTGTGCAGGTTCTCTTTCGAGCACCTATGTA  
0 GTGAACAGACCCTCGCGGGCTCATGTATCT

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4	0	0 GTGTACACTGGTATTGCTACCTCGTCACCCCT
5	0	0 GTCCAACCGTTCTTGCGAACTGCTCACGTTT
6	2	0 GTGTTCTGGCTCCCTTGCGGGCACTCCCGA/
7	0	0 GTGTTAGCGTCCTTGCGGACGCATGCCCTT
8	0	0 GTCTCTGCGCTCCTTGACAGGCACTCCCACC
9	0	0 GTGCTAGCTCCGTATTTCTACGGTCGTCCCC
10	0	0 GTCTTACGGTTCCTCGAAGGCACTTCCGCATC
11	0	0 GTGTAGGCTT tag f
12	0	0 GTGTTACAGGCTCCCTTGCGGGCACTCCCGA/
13	2	0 GTGACAGTCTCCGACTGGATACCGGCCCC
14	0	0 GTCATACTGCTGTATTGCTACAGAAAAGTGA/
15	0	2 GTCTCTGGATTCCCTTACGGGCACGCCGACT
16	2	2 CCCATAGAATCAAGAAAGGACCGTCAACCT.
17	1	5 CCCATAGAATCAAGAAAAGACCGTCAACCT.
18	3	0 CCCATGGAATCAAGAAAGGACCGTCAACCT
19	0	2 AACCACAGATTCCCCGAAGGGCACCTCATC
20	0	0 GTGTTCTCGC long o
21	0	0 GTGCAGGTTC long g
22	0	0 GTGTTACGGT long f
23	0	0 GTGTCCCGAC long g
24	0	7 GCTATCGGATCAAGAAAGCGCTATCAAACCT.
25	0	0 CGACTCGACTCCCTTGCGGGATAACCATGT
26	2	2 GTGTGTTAGCCAGCCGAAGTGAAGGAAGG
27	0	0 GTGTTCCGAC long g
28	2	2 GTATCCGGTC tag o
29	0	0 GTCTCACGGT long g
30	0	0 GTGCTACACCCTCGAAGGCGGCTCCGATTT
31	0	1 GTGTTACAGGCTCCCTCGCGGGCACTCCCGA/
32	0	0 ATATAGCGGCCCCGAAGGCGCAAACATCTCT
33	0	0 CCCACAGAAATTAAGAAAGAGCTATCAATC
34	2	2 CTGCAGATGT long o
35	2	3 GTCTCTTGGCTCCTTTCGGCACTTCCGCCTC
36	0	0 GTCACCGGTC tag g
37	0	2 GTGTACCGGCCCTTGCGGGCGACGACATTT
38	0	0 AGTTTCGTGT tag f
39	0	0 GTGTAGGCTCTCCGAAGAGTCGTTCCCCTTT
40	0	0 GTGTCCAGGCTCTCTTTTGAGCACGAATCCA
41	0	0 TACTAGCGACGTATTGCTACGCTATAAGCTT
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0 TGCTTTGTGT tag f  
4 GTAATATTAAATTAATAATAAAT  
3 GTGCATGTTCCACCCTTGCGGGCGTCATCC  
4 GTGTGGACGCCAGCCGAAGTGAAGAACGG  
0 AGTTTCGCGT tag f  
0 CCCACACAATCATGAAAGATCTATTAGTCTG  
0 GTGACGACCCCTTGCGGGACTCCCGGCTC  
0 AACTACGAGTTCTCAAAAGAGCACCCCGAT  
0 GTGTTCCAGC tag g  
2 GTGTACGTTC long k  
0 GTGTTCGCGCTCCTTACGGCACTCCGACCTT  
0 TACTGGCGGTGTATTGCTACAAAACCCCTT  
2 CTGGACCAATCAAGAAAGAACTCTCAATCTC  
2 GTGCACGTTCCACCCGAAGGCGTCAGTGAC  
0 CCCATAAAAT tag c  
0 GTGTGCAGGTTCTCTTTCGAGCACAAAACCA  
0 GTGATTGTTACCCTCTTGCGAGGAATCAATC  
0 GTACTAGGCTCCTCCATTGCTGGAGTTCGTT  
0 GTGTTCAGGCTCCCTTGCGGGCACTCCCGA  
0 AGTTTCGTGT tag g  
2 TGTTTCGTGTCCCGAAGGAATGCTCCCTTTC  
0 GTGTCCAGACTCTCTTTCGAGCACTCCTAAA  
7 GTGTATGTTGTAAGTCAAGAGCCTCACTGAC  
0 GTTCACGAGT tag f  
0 GTGTTCCAGC long f  
3 TGGAAGCAGCTATTGCTAGCTCATAAGTTTC  
2 TGCTTTGTGT long k  
0 CTCACTACATTTCTTGCGGACACTCCGATA  
0 CTCATGGAGTCAAGAAAGAGCTATCAATCTC  
0 GTCTCCGGTCCGGCCGAACCGAAGGTCCGG  
0 GTAGCAGGTTCCGGACTGGTTACCGTTGGC  
0 GTGTTCAGATTCTCTTTCGAGCACGATCTCA  
0 TGATACAGGCCCCGAAGGGATATCTGCTTT  
5 CTAGACCAATCAAGGAAGAACTCTCAATCTC  
0 GTGCAGAGACTCTTACGAGAGACGCCGTTT  
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0 CCCATCCAATCCTCTGAAGGGCCTTCTCGTC

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8	0	0 CTCATGGAATCAAGAAGGAGCTATCAATCTC
9	0	0 GTGCCAGGTTCCGGACTGGTTACCGTTCGCT
10		
11	1	1 ATGTTTCAGGCTCCCTTGCGGGCACTCCCGA/
12	4	3 GTTTAGCAGCCATTGCTGGAAATACTATTTTC
13	0	0 GTGTTCTAGC long g
14		
15	0	0 TGCAGACAGGAGCCGGTTACCCGGATCGCC
16	3	0 GCGCATGTTCCACCCTTGCGGGTGTGGCTCT
17	0	0 CCCATCCGATCCTCTGAAGGCCTTCTCGTCTC
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19	2	0 GTGTTTAGGCTCCCTTGCGGGCACTCCCGA/
20	0	0 GTGTGCAGGTTCTTTTTTCGAGCACCAAACCA
21		
22	0	0 GTCTCGGGG( tag g
23	3	0 CCCATAGAATCAAGAAGGGACCGTCAACCT
24	0	0 GTGCAAAAG( long g
25		
26	0	0 GTGCTTGTTCCACCCAAAGGGCGTGGCCTC
27	0	0 CCCACCAAAT tag p
28	0	0 CCCATAGAAT tag f
29		
30	0	0 GTGTTTCAGGCTCCCTTGCGGGCGCTCCCGA/
31		
32	0	0 GTGTCCCGGT tag g
33	0	0 GTGTGGTATC long f
34		
35	0	0 GTGCAAAGGCCCGAAGGGAGACGCTATTTC
36	0	0 AACCACAGATTCTCCGAAGAGCACCCCGAG
37	0	0 GTGCATGCTCCCGAAGGGTCCATCAGCTTTC
38		
39	0	0 GTGCAAATAATTACTCAAAAAGAGTATTTA/
40	0	0 CCCACTAAAT long g
41	0	0 GTGAAGACCCGGCCGAACCGAAAAAGTAG/
42		
43	0	0 GTGTTCCAGC tag g
44		
45	0	2 GTGTCCAGGCTCTCTTTCGGGCGACGAATCCA/
46	0	0 GTGCTTGTTTCACTCTTGCGAGTAGTCTCCA/
47	0	0 GTCCACCAGCCATAAAGGAGAGTGTATCTC
48		
49	0	0 GTGTGACGTC tag g
50	0	0 CCCACCGAATCAAGGAAGAGCTCTCAATCTC
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52	0	0 TGTTTCGTGTCTATTGCTAGAAAGACTCCTT
53	0	0 GTGTGATATCCAGCCGAAGTAAAGCCCCA
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56	0	3 GTGCAGCAGCCCCGAAGGGAAATACCATCT
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0 3 GTATTAGAGT tag f  
3 0 CCATTTAATCAAGAAAGGGCTATCAACCTGT  
0 2 GTGTTCAGGCTCCCTTGCGGGCACTCCCGG/  
4 0 CTAGACCAATCAAGAAAGTACTCTCAATCTC  
0 0 GTAACCGCTCCCCGAAGGGTCGTTCCGCTT  
0 0 GTCTATCAGCCTGAAAGGAAGGCGTATCTC  
0 0 TGAAAATTGT long g  
0 0 GTGTAGGGC tag f  
0 0 GTGTGGGAGCCAGCCGAAGGATCA  
0 0 TGGAATCAGCCCCGAAGGGCGATCACCTTT  
2 0 GTGTACAGACCCTTGCGGGCTAAACTGTCTC  
0 0 CGCATCGTGCCCCGAAGGGAGATCGGCTTT  
3 0 GTGTGTGGTCCAGCCGAAGTACGGCTATA  
0 0 GTGAACCGACCCTTGCGGGCGGGGACATTT  
0 0 GTGTTCAGGCTCCCTTTCGGGCACCCCCACC  
0 0 GTCACCGCGT tag g  
3 3 GTGCAAACCGGGTATTGCTACCCTAGCCTG  
1 3 CTAGACCAATCAAGAATGAAGTCTCAATCTC  
0 3 CTAGACCAATCAAAAAAGAACTCTCAATCTC  
0 0 GTCTCAGAGC tag o  
2 0 GTGTTCAGGCTCCCTTGCGGGCACTCCTGA/  
0 0 GTGTGCAGG1 long g  
0 0 GTGCAGCAGTCCCGAAGGAAGGGTGCCTTT  
2 0 GTTACAGCTT tag g  
0 0 GTGCAATAGCTCCCTTGCGGGCACCCCCACC  
0 0 GTGTGCAGGATCTCTTTCGAGCACCAAACCA/  
2 2 GTGTACAGTCCCCGAAGGGCTCCAATATCTC  
0 0 GTGTGGAAGCCAGCCGAAGTGAAGAGGTC/  
0 0 GTATACCGCC tag o  
0 0 GTCTCGGGG tag g  
0 0 CTCATGGAATCAAGAAAAAGCTATCAATCTC  
0 0 GTGCACGTTCCGGTCTTGCGACTGTGGCCCC  
0 0 GTACGCGTTCCGGAAGTGGTACCGTTCTGTA  
0 2 GTGTTCAGGTTCTCTTACGAGCACTCCCAAA  
0 0 GTCTCCGGTC tag g  
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0 0 AACCACAGATTCTCCGAAGAGCACCTCATC

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5	0	0 CCCATCCGATCCTCTGAAGGGTCTTCTCGTC
6	0	0 GTGTTCCGGTCCCCGAAGGGAACGCCTCAT
7	0	4 GTCTTCGTGTTCCCTTGTTGGAAGGAGCGGC
8	0	4 GTGTGGAAG(tag f
9	0	0 TACAGACTGTGTATTGCTACAAAACCTCTT
10	0	0 GTCTTTGGGTCCTCTTGTTGAGGAGGGCCT
11	0	0 GTGCACGTTCCACTCTTGCGAGCGTCATCTC
12	0	0 TACGATCTGT long f
13	0	0 GTGTCCCCGG long c
14	0	0 GTGTCCAGGTTCCCTTTCGAGCACGAATCCA
15	0	0 CCCACCGAAT tag p
16	0	0 GTGCTCACGTCCCTTGCGGGAAAACCTGCAT
17	0	0 GTCTCGGGG(tag g
18	3	0 ATATAACAGTCCTTGCGGAAATAACCATCTC
19	0	0 GTTCTAGACCCGGCCGAACCGACGCGACCA
20	0	0 GTGCTCCTCC long f
21	0	0 GTGTGTAGGTTCTCTTTCGAGCACCAAACCA
22	0	0 GTGCACGTT long g
23	0	2 GTGCACGTTG tag f
24	0	3 GTCTCCAAGT long p
25	0	6 AGTTGAAACTGGTAAGGTTTTTCGCGGATC
26	0	6 GTGCAGCAGTCCCGAAGGAAGACACTATCT
27	0	2 GTCTCGGGGCTCCTTTCGGCACCCCCATCTC
28	0	2 TGAGAACCGTCCGAAGAAAGATCTGTTTCC
29	0	0 GTGCAAGCTC long f
30	0	0 GTGATCAGGCTCCCTTGCGGGCACTCCCGA
31	2	0 CTAGACCAACCAAGAAAGAACTCTCAATCTC
32	2	0 CTAGACCAATCAAGAAAGAACTCTCAATCTC
33	0	1 GTGTTCAGGCTCCATTGCGGGCACTCCCGA
34	0	0 GTGTGCAGG1tag g
35	0	2 GTGCAACAG(tag f
36	0	0 GTCTAGCCGTCCCGAAGGAAAATCCTGGTT
37	0	0 GTCTCACGGT long f
38	0	0 GTGTCCTGTCCGGCCGAACCGACAGACCCG
39	0	0 GTTACATCCATCTCGAATTTATTTTAAATTCA
40	0	0 GTCTCACGGC tag f
41	0	0 GTGACACTGTCTTGCGAACCTCAGGCTTCA
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0 GTACTGGGTTCGGGTTGGATACCGTTCGT  
0 GTGATGGTTACTCTTGCGAGTAATCGAT/  
0 GAACCACCGc long o  
3 2 GTCTCCTGGCTCCCCGAAGGGGCACCCAC  
0 ATGTCCAGGCTCTCTTTCGAGCACTCCTAAA  
0 GTGCACGTTc tag g  
0 GTACAAATTAATAAATAAACTAATTTAATAA  
0 GTGTCCGGCTCCGGGCTGGATACCGTTCG  
0 GTGTACAGGCTCCCTTGCGGGCACTCCCGA/  
0 GTGTTCAGGTTCTCTTGCGAGCACTCCCGAA  
0 TGTTTTGTGCTCTTGCGAGAGAGTACATTT  
3 0 CTAGACCAATCAAGAAAGAACTCCCAATCTC  
0 GTGTTCTCGC long c  
2 0 CCCATAGAATCAAGAAAGGATCGTCAACCT/  
0 GTGCTTGTTCCACTCTTGCGAGTGTATCAC  
0 GTCTCTCGATTCTTCTTGCGAAGGCACCCC  
0 GTGTCCAGGCTCTCTTTCGAGCACCCCTAAA  
0 GTCTTCCGGTTGTATTGCTACAAAAACGTA  
0 GTGTTCAAGTCCCGAAGGCACTTCTACATC  
0 GTGTGCAGGTTCTCTTTCGAGCACCGAACC/  
0 TACTACCTGTATATTGCTATAAAATCCCCTT  
0 GTGTCCAGGCTCTCTTCAAGCACTCCTAAA  
0 3 CCCATCCGATCCTCTGAAGGGCCTTCTCGTT  
0 TGTAAATTGT tag g  
0 GTGTGCAGGtag g  
0 GTGTCTAAATTCCCTTTCGGGCACTTTTGCA  
0 GTGCTTGTTCCACCCGAAGGACGTGGCCTC  
2 2 GTGTTCTGGCTCCCGAAGGCAACCTCGCCTC  
0 0 CCCACCGAATCAAGAAGAGCTCTCAATCTG  
0 GTCTCTGCGT tag g  
0 TACCAGCGGtag f  
0 ATCGCAGGCtag g  
0 2 GTCTCTCGGT tag f  
0 2 GTGTACAGTCCCCGAAGGGCTCCGATATCTC  
2 0 GTGGACCGGCCTTGCGGCTGCCACGTCTC  
0 GTGCAAATGtag p  
0 GTGCAGCAGTCCCTAAGGAAAGGTCCATCT  
0 GTGTGCAGGTTCTCTTTCGAGTACCAAACCA



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5	0	0 GTGCAGACTT long c
6	0	0 GTGTCTAGGTTCCCTTTCGGGCACCCCCACA
7		
8	0	0 GTGTTCCAAT tag g
9	0	0 GTGTGCAGG long g
10		
11	0	0 CCCATCCGATCCTCTGAAGGGCCTTCTCATC
12	0	0 GTGTACGACC tag g
13	0	2 GTGTTCAAGGCTCCCTTGCGGGCACTCCCGT/
14		
15	0	0 GTGTTCCAGC tag c
16	0	0 GTTATACCCACCCGAAGTGAAATCTACGT
17		
18	0	0 GTCTCGGGG long g
19	0	0 TACTGGCAGT long f
20		
21	0	0 GTATACGAGT long g
22	0	0 CCCACCGAAT tag p
23	0	0 GTATTCCGGCTCTCTTTCGAGCACTCCCAAA
24		
25	0	0 GTCTCCTCTGTCTCTTGCGAGCCCATCTCTA
26	0	0 GTGTAAGCT tag c
27		
28	0	0 GTGGCCGGTTCGGGGCTGGATACCGTTTCGC
29	0	0 GTCACCGCGT long g
30	0	5 GTGCCCAGAT tag f
31		
32	0	0 TCGCCGGGCTCCCTTGCGGGTCGTGCGGGCTT
33	0	0 GTACAGGGGGCCTATTGCTAGGCTGCGATAT
34		
35	2	0 GTGTTCAAGGCTCCCTTGCGGGCACTTCCGA/
36	0	3 GTCTTTGGGC tag p
37		
38	4	0 CCCATCCGATCCTCTGAAGGGCCATCGCTCA
39	0	0 GTTCACAGAC long g
40	0	0 GTGCTTGTTCCACTCGAAGGGCGTGGCCTC
41		
42	0	0 GTCTCTCGGT tag g
43	0	2 GTAATAGCTCCCTTGCGGGACACGAACTT
44		
45	0	2 CCCATCCGATCCTCCGAAGGGCCTTCTCGTC
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47		
48	0	0 CCCACCGAATCAAGAAAGAGCTCCCAATCT
49	0	0 TGTTTTGGGCCAGTAACCTGGCTGTTGGCA
50	0	0 GTGTGCAGG long g
51		
52	0	0 GTGTTCAAGGCTCCCTTGCGGGCACTCCGAA
53	0	1 CAAGACCAATCAAGAAAGAACTCTCAATCT
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55	0	0 GTGTGCAGGTTTTCTTTCGAGCACCAAACCA
56	2	0 CGCACCCGGCCCCGAAGGGCTGTACAGTTT
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0 ATACAGACGC long o  
0 GTCTCGGGG tag g  
0 GTGCTGGTTCCGGACTTGCGACTGTGGCTC  
0 GTGCTGGTTCCGGTCTTGCGACTATGGCTC  
0 GTTACATCCATCTCGAATTTATTTTAAATTA  
0 GTGTCACGGC long f  
0 GTGCCTATTCCGGTCTTGCGACTGTGGCCCC  
0 GTTTAGCGCTTGATTGCTACAATTATTACCA  
0 GTCTTCCGGTTGATTGCTACAAAAATCGTA  
0 GTCTTGTCGTTCCCGAAGGCACCCCTCATC  
0 GTGCACGTTCCACCCAAGGGCGTCAATGAC  
0 GTGCATGTTc tag c  
0 GTGCAGCAGTCCCGAAGGAAGCTCTATCTC  
0 GTGCATGTTCCGACTCCGAAGAGCTGTTACCA  
0 TGTAAAGTGTCCGAAGAAAAAACTGTTTCCCA  
0 GTGTGCAGGtag g  
2 GTGTTCAGACCCTTGCGGGCTAAACTATCTC  
2 GTCTCCACGTTGATTGCTACAAAAAATACA  
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2 AACCGCAGGTTCTCCGAAGAGCACCCCCAA  
2 GTGCAGCAGtag g  
2 GTGTTCAGGCTTCCTTGCGGGCACTCCCGA  
2 GAGCACGCTGGCATTGCTACCTCGTCAGGC  
2 GTGCACAGCtag g  
2 GTGCAGGTCACACCCGAAGGTAATCAGCCA  
2 CTAGACCAATCAAGAAAAAACTCTCAATCTC  
2 TGTTCGAGTCTCCGGTTTCCCCTCGACGAC  
0 AACCACAAGTTCTCCGAAGAGCACCCCCATC  
0 AGTTTCGTGT long g  
0 GTGATGGTGlong f  
0 GTGCAATTGTCCAAACCGAAGTTTGGAAAG  
0 GTATCCAGGCTCTCTTCGAGCACTCCTAAA  
0 GTGTCCAGGCTCCCTTTCGGGCACGAGTCCCA  
2 CTAGACCAATCAAGAAAGAACTCTCAATCTC  
0 GTATAACGGCCCTTGCGGGCGACGACATTT  
0 GTCACCGGTCtag f  
0 GTTCACAGGCGTATTGCTACGCTACGACATC  
1 GTGTTCAGGCTCCCTTGCTGGCACTCCCGAA

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5	2	0 GTGCAAATGTCTAAACCGAAGCTTAGAAAA
6	2	0 GTGTACGTTGTACCCGAAGGCCTCATCAATC
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8	0	0 GTGTCCAGGc long c
9	0	0 CCCAAAGAATCAAGAAAGGACCGTCAACCT
10	0	0 GTGTGGACGCCAGCCGAAGAGCCTC
11	0	0 GTGTCCCTGG long f
12	0	0 GGGGATAGTTAAACAGTTGTATTTTAAAT
13		
14	0	0 GTCTCCTGTCtag g
15	0	0 GTGCATGTTC long g
16		
17	0	2 GTGCAGCAGtag g
18		
19	0	2 CCCATAGAATCAAGAAAGGACTGTCAACCT
20	0	0 GTGTTTCAGGCTCCCTTGCGAGCACTCCCGA
21	0	0 GTGTATGCTGtag c
22	0	0 GTGCTTATTCCACCCGAAGGGCGTGGCCTC
23	0	0 GTGTTCTAGCCAGCCGAAGTGAAGAATCC
24	0	0 GTGTCCAGGCTCCCTTTCGGGCACAAATCC
25	0	0 TGTTCAGGTCATTGCTGACTTACTCATCTC
26	0	0 GTAGCAGGTTCCGGACTGGATACCGTTCGT
27	0	0 CTCATGGAATCAAGGAAGAGCTATCAATCT
28	0	0 GCGTGCAAGtag g
29	0	0 GAGTCCAGGCTCTCTTTCGAGCACTCCTAA
30	0	0 GTACCAGCTTCCGGATTGGATACCGTTCGT
31	0	0 GTGCTTGTTCCACCCGAAGGGCGTGGCCTC
32	0	0 GTGTCCAGGCTCTCTTTCGAGCACTCCTAAT
33	0	0 GTATACCGAC long f
34	0	0 CCCATTTATTCAAGAAAGGGCTATCAACCT
35	0	0 GTGTATGTTCCACCCTTGCGGGTGTGGCTC
36	1	3 GTGTTTCAGGTTCCCTTGCGGGCACTCCCGA
37	0	0 GTGTGCAGGTTCTCTTCTAGCACCAAACCA
38	0	2 TGTTCGAGTCTCCAGTTTCCCTTCGACGAC
39	0	2 GTCACCGGTC long g
40	0	0 GTGCGTGTTCCACCCTTGCGGGTGTGGCTC
41	0	0 GTGCTCAGGCTCCCTTGCGGGCACTCCCGA
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43	0	0 AGTTTTGTGCTCCGAAGAGAAATCCGCTTTC
44	0	0 CTCATGGAATCAAGAAAGAGCTATCAATCT
45	0	0 TGTAAGCGGtag f
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6 0 0 GTGTCACGGTlong f  
7 0 0 GTGCAGACTCCCCTTGCGGGGTCATCACCT  
8 0 0 GTGTCCTGGT tag f  
9 0 0 AGTTTCGCGC tag o  
10 0 0 CCCATCCGATCCTCTGAAGGGCCCTCTCGTC  
11 0 0 GTGTTTCAGGCTCCCTTGCGGGCACTCCCGA  
12 0 0 CGATAGCACCCCTTGCGGGCAAGGACTTTC  
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14 0 0 CTAGACCAATCAAGAAAGAACTCTCGATCT  
15 0 0 GTCTCCAGGT tag g  
16 0 0 CCCATAGAATCAAGAAAGGACCGTCAACCT  
17 0 0 CCCATAAAAT tag k  
18 0 0 GTGTAGGCTCCCTTGCGGGCACTCCCGAAT  
19 0 4 GTGCAGCAGCCCCAAAGGGAAATACCATCT  
20 0 4 GTGTTTCAGGCTCCCTTGCGGGCACTCCCTAA  
21 0 4 TGCTTCAGGTCTATGGTTTCCCATAGAGAAA  
22 0 4 TGTTTTGTGTCCCGAAGGAAATTCCGCTTTC  
23 0 0 GTGCAGCAGCCCCGAATGGAAATACCATCT  
24 0 0 CCCATAGAGTCAAGAAAGGACCGTCAACCT  
25 0 0 AGTTTCAGGTCATTGCTGACTGACTTCTTTC  
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27 0 2 GTGTTTCAGGCTCCTTGCGGGCACTCCCGAA  
28 0 2 ATGTACAGACCCTTGCGGGCTAAACTATCTC  
29 0 0 GTGTGCTGGTTCTCTTTCGAGCACCAAACCA  
30 2 0 GTGTTTCAGGCTCCCTTGAGGGCACTCCCGA  
31 0 0 GTGTTCCAGG long f  
32 0 0 GTGCAACAGCCCCGAAGGGAAATACCATCT  
33 0 0 GTAATATTAAATTAAAAAAAATAATAAA  
34 3 0 CCTATAGAATCAAGAAAGGACCGTCAACCT  
35 3 0 CTAGACCAATTAAGAAAGAACTCTCAATCTC  
36 3 0 CTAGACCGATCAAGAAAGAACTCTCAATCTC  
37 3 0 CCAGACCAATCAAGAAAGAACTCTCAATCTC  
38 2 0 CTAGACTAATCAAGAAAGAACTCTCAATCTC  
39 0 0 GTGTTCCGAC long g  
40 0 0 CTAGACCAATCAAGAAAGAACTCTCAATTT  
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3		
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5	0	0 CTAGACCAATCAAGTAAGAACTCTCAATCTC
6	0	0 GTTCATGTTG long g
7	0	0 GTGTGCAGGTTCTCTTTGGAGCACCAAACCA
8	0	0 TGTGCAGGTTCTCTTTGAGCACCAAACCAT
9	0	0 GTGTGCAGGTTCTCTTTGAGCACCAAACCA
10	0	0 GTGTGGCGTCCGGCCGAACCGACTCCCCGC
11	0	0 GTGTGGCGTCCGGTCTTACGACTGTGGCTCT
12	0	0 AACCACAGGTTCCCCGAAGGGAACCCCGAA
13	0	0 CCCATAGAAT tag k
14	0	0 GTGTTCCGAT long g
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16	0	0 TCCATAGAAT tag k
17	0	0 GTAAACCGG tag f
18	0	0 GTGCTGGTTACACCCGAAGGCAATCCCTCC
19	0	0 GTGCTGGTTCCGGTCTTGCAACTGTGGCTCT
20	0	0 GAGCAGGAT long g
21	0	0 GTGCTCTATG long f
22	0	0 GTGTCCTGGTTACCTTGCGGCACTCCAGCTT
23	0	0 GTGACCATTGTACCCTTGCGGGCCTACATCT
24	0	0 GTGCTGGTTCCGGTCTTGCGAATGTGGCTCT
25	2	0 CTAGACCAATCAAGAAAGGACTCTCAATCTC
26	0	0 GTGTCCAGGCTCCCTTGCGGGCACTCCCGA
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30	0	0 GTGTACCGACCCTTGCGGACGACGACATTT
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0 GTGCAAAGTTlong c  
0 GTGCAGGTTtag g  
0 TACAATCTGTtag f  
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0 GTGCTCCGGC long g  
0 CTCATGGAATCAAGAAAGAGCTATCATCTG  
0 GTGTCTTAATTCCCTTTCGGGAACCTTTGCA  
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0 GTGACGCCTCCCTTGCGGGTCGGGAATGTT  
0 CCCACCGAAT tag p  
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0 AACCACAGGTTCCCCGAAGGGCACCCCAAA  
0 GTGTTCAGATTCTCTTTCGAGCACACTCTCA  
0 GTCTCCACGT long g  
0 GTATTCCGGCTCCCTTTCGGGCACACCCAAA



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5	0	0 CGACTTCGAT long f
6	0	0 GTCTCCGATC tag g
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41	0	0 GTATACCGAC tag f
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0 TGTTCGTGTCCCTTGCGGGAAGAGTCCATT  
0 CCCATTTAATCAAGAAAGGGCTATCAACCT

1		
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3		
4	0	0 GTGGACAGACCCTTGCGGGCTAAACTATCTC
5	0	0 GTGTTCTCGCCAGCCGAAGTGAAGGAAGTC
6	0	0 GTGTTCCGGCCCTCTTTTCGAGCACTCCCAAA
7	0	0 CCCATAGAATCAAGAAAGGTCCGTCAACCTC
8	0	0 GTGTGCAGGTTCTCTTTTCGAGCACCAAACCT
9	0	0 GTGTGCAGGTTCTCTTTTCGAGCACCATACCA
10	0	0 GTGTGCAGGTTCTCTTTTCGAGCACCAAACCAT
11	0	0 GTGTGCAGGTTCTCTTTTCGAGACCAAACCA1
12	0	0 GTGTGCGGTTCTCTTTTCGAGCACCAAACCAT
13	0	0 GTGTGAGGTTCTCTTTTCGAGCACCAAACCA1
14	0	0 CTCATAGAATCAAGAAAGGACCGTCAACCTC
15	1	0 GCCATAGAATCAAGAAAGGACCGTCAACCT
16	1	0 CTAGACCAATCAAGAAAGAACTCTCATTCTC
17	0	0 CTAGACCAATCAAGAAAGAACTATCAATCTC
18	0	0 GTGTGCAGGTTCTCTTTTCGAGCACCAAATCA
19	0	0 GTGTGCAGGTTCTCTTTTCGTGCACCAAACCA
20	0	0 TGCAGGTTCTCTTTTCGAGCACCAAACCATCT
21	0	0 GTGTCCAGGCTCTCTTTTCGAGCACTCATAAA
22	0	0 GTGACCAGGCTCTCTTTTCGAGCACTCCTAAA
23	0	0 GTGTCCAGGCTCTCTTTTCGAGCACTCCTAAC
24	0	0 GTGTCCAGGCTCCCTTTTCGGGCACGAATCGA
25	0	0 GTGTGCAGGTCGGAAGTACCCGACAAGGA
26	0	0 GTGTGCAGGTTCACTTTTCGAGCACCAAACCA
27	0	0 GTGTGCACG tag g
28	0	0 CTCATAGAAT tag k
29	0	0 CACACCGAATCAAGAAAGAGCTCTCAATCTC
30	0	0 GTGTTCAGGCTCCCTTGCGGGCAGCCCCGA
31	0	0 CTCATGGAATCAAGAAAGAGCTATCAATCTC
32	0	0 CTCATGGAATCAAGAAAGAGCTACCAATCTC
33	0	0 CCCATAGGATCAAGAAAGGACCGTCAACCT
34	0	0 GTGTTCAGGCTCCCCTTGCGGGCACTCCCCGA
35	0	0 GTGTTCAGGCTCCCTTGCGGGCACTCCCCGA
36	0	0 CCCATAGAATCAAGAAAGGCCCGTCAACCTC
37	0	0 GCGTTCAGGCTCCCTTGCGGGCACTCCCCGA
38	0	0 CTAGACCAATCGAGAAAGAACTCTCAATCTC
39	0	0 GTGTTCAGGCTCCCTAGCGGGCACTCCCCGA
40	0	0 GTGTTAAGGCTCCCTTGCGGGCACTCCCCGA
41	0	0 CTCATGGAATCAAGAAAGAGCTATCAATCTC
42	0	
43	0	
44	0	
45	0	
46	0	
47	0	
48	0	
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53	0	
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0 CCCACCGAAT tag p  
0 CTCATGGAATCAAGAAAGGGCTATCAATCTC  
0 CTCATGGAATCAAGAAAGAGCTAACAATCTC  
0 GTGTTCAGGCTCCCTTGCGGGCACTCCCCGA  
1 CTAGACCAATCAAGAGAGAACTCTCAATCTC  
0 GTGTTCAGGCTCCCTTGCGGGCACTCCCCA  
1 CTAGACCAATCAAGAAAGAACTCTCAAACCTC  
0 CTAGACCAATCAAGAAAGAACTCTCAATCTC  
1 CCCATCCGATCCTCTGAAGGGCCTTCTCGTC  
0 GTGTTCAGGCTACCTTGCGGGCACTCCCCGA  
1 GTGTTCAGGCTCCCTTGCGGGCAGTCCCCGA  
1 GTGTTCAGGCTCCCTTGCGGGCACTCCAGAA  
0 GTGTTGAGGCTCCCTTGCGGGCACTCCCCGA  
0 CCCATAGAATCAAGAAAGGACAGTCAACCTC  
0 CACATCCGATCCTCTGAAGGGCCTTCTCGTC  
0 CTAGACCAATCATGAAAGAACTCTCAATCTC  
0 GTGTGCAGGTTCTCTTTCGAGCACCAAACCTA  
0 GTGTGCAGGTTCTCTTTCGAGCACCAAACCA  
0 GTGTGCAGGTTCTCTTTCGAGCACCAAACCA  
0 GTGTGCCGGTTCTCTTTCGAGCACCAAACCA  
0 GTGTGAAGGTTCTCTTTCGAGCACCAAACCA  
0 GTGTGCATGTTCTCTTTCGAGCACCAAACCA  
0 GTGTGCAGGTTGTCTTTCGAGCACCAAACCA

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4		taxon_data	long	long_total	long_this	support	confidence
5		g	GACGACAGC	8	8	744	0.96774194
6		g	GACGACAGC	12	12	20	1
7		g	AAGAACGGC	12	12	181	1
8		g	AAGAACGAC	12	12	8	1
9		o	AAGAACGGC	12	12	3	1
10		f	GACGACGGC	6	6	7	1
11		TG	AAGAACGGC	7	7		
12		p	AAGAACGGC	7	7	14	1
13		GC	GACGACAGC	12	12		
14		o	AAGAACGGC	12	12	5	1
15		TCT	GACGACAGC	8	8		
16		ATC	GACGACAGC	6	6		
17		CTA	GACGACAGC	7	7		
18		g	GACGACAGC	12	12	354	0.98022599
19		g	GACGACAGC	10	10	5	1
20		g	GACGACAGC	12	12	4	1
21		g				15962	1
22		g	GACGACAGC	6	6	10	0.9
23		TC	GACGACAGC	10	10		
24		g				74	0.98648649
25		g	GACGACAGC	12	12	270	0.92962963
26		AC					
27		CTG	GACGACAGC	6	6		
28		f				13696	1
29		g	GACGACAGC	12	12	9	1
30		g	GACGACAGC	10	10	7	1
31		AA	GACGACAAC	6	6		
32		CA	AAGAACGGC	12	12		
33		g	GACGACAGC	12	12	22	0.95454545
34		c	AAGAACGGC	11	11	4	1
35		g	GACGACAGC	12	12	218	0.87155963
36		g	GACGACAGC	12	12	100	0.97
37		f	GACGACAGC	11	11	8	1
38		GC	GACGACAGC	12	12		
39		TCA	AAGAACGGC	6	6		
40		g	GACGACAGC	12	12	20	1
41		AG	GACGACAGC	6	6		
42							
43							
44							
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3						
4	GA	GACGACAGC	12	12		
5	g	GACGACAGC	12	12	2	1
6	g	GACGACAGC	11	11	620	0.97903226
7						
8	TC	GACGACAGC	12	12		
9	g	AAAAGCGGC	10	10	422	1
10	AC	GACGACAGC	12	12		
11						
12	TC	AAAAACGGC	12	12		
13						
14	g				336	0.9702381
15	TGT	AAGAACGGC	12	12		
16	g	GACGACAGC	12	12	3	1
17						
18	CAC	GACGACAGC	7	7		
19	TCT	GACGACAGC	6	6		
20						
21	g	GACGACAGC	6	6	4	1
22	f				30	1
23						
24	o	GACGACAGC	12	12	2	1
25	p	AAGAACGGC	12	12	4	1
26	f	AAGAACGGC	11	11	283	1
27	g	GACGACAGC	12	12	3	1
28						
29	AC	GACGACAGC	6	6		
30	g	GACGACAGC	6	6	11	1
31	g	GACGACAGC	6	6	2	1
32	g	GACGACAGC	6	6	3	1
33	g	GACGACAGC	6	6	3	1
34	c	GACGACAGC	12	12	3	1
35						
36	f				7	1
37	g				49	0.87755102
38						
39	TTT	GACGACAGC	12	12		
40	f	GACGACAGC	6	6	3	1
41						
42	CTA	GACGACAGC	7	7		
43	c	GACGACAGC	12	12	19	1
44	TC	GACGACAGC	11	11		
45						
46	ATT	GACGACAGC	6	6		
47						
48	o				36	0.97222222
49	f	GACGACAGC	6	6	2	1
50	g	GACGACAGC	12	12	19	0.94736842
51	g	AAGAACGGC	6	6	76	0.90789474
52	f	GACGACAGC	12	12	10	0.9
53						
54	g	AAAAGCGGC	6	6	49	1
55	o	GACGACAGC	12	12	6	1
56						
57						
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2						
3						
4	CAC	GACGACAGCC	6	6		
5	CT	GACGACAGCC	6	6		
6	f	GACGACAGCC	6	6	10	1
7	TT	GACGACAGCC	12	12		
8						
9	g	GACGACAACC	6	6	4	1
10						
11	g	GACGACAGCC	7	7	6	1
12	f	GACGACAGCC	12	12	2	1
13						
14	g	GACGACAGCC	12	12	4	1
15	CTC	AAGAACGGCC	6	6		
16	TT	GACGACAGCC	12	12		
17						
18	CAC	GACGACAGCC	6	6		
19	CTA	GACGACAGCC	12	12		
20						
21	TC	GACGACAGCC	11	11		
22	TTT	GACGACAGCC	6	6		
23						
24	g	GACGACAGCC	12	12	8	1
25	f	GACGACAGCC	7	7	4	1
26						
27	o	GACGACAGCC	12	12	78	0.97435897
28	TTT	GACAACAGCC	6	6		
29	f	GACGACAGCC	12	12	24	1
30						
31	f	GACGACAGCC	6	6	7	1
32	p	AAGAACGGCC	9	9	23	1
33	f	GACGACAGCC	12	12	31	0.96774194
34						
35	g	GACGACAGCC	12	12	11	1
36	c	GACGACAGCC	12	12	12	1
37	TCA	GACGACAGCC	6	6		
38						
39	f				58	0.98275862
40	o	GACGACAGCC	6	6	7	1
41						
42	g	GACGACAACC	5	5	348	0.99712644
43	TT	GACGACAGCC	9	9		
44						
45	g	GACGACAGCC	12	12	2	1
46	g	GACGACAGCC	12	12	79	0.98734177
47						
48	o	GACGACAGCC	6	6	12	1
49	GT	AAGATCGGCC	7	7		
50						
51	g				3	1
52	f	GACGACAGCC	12	12	3	1
53						
54	g				322	1
55	CCC					
56	TGT	GACGACAGCC	7	7		
57						
58						
59						
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f	GACGACAGCC	10	10	202	0.97029703
TC	GACGACAGCC	7	7		
g	GACGACAGCC	12	12	5	1
p	ACGAACGACC	12	12	78	1
TCAG	GACGACAGCC	6	6		
f	GACGACAGCC	12	12	52	1
f	GACGACAGCC	7	7	3	1
TC	GACGACAGCC	6	6		
g	GACGACAGCC	11	11	11	1
CAC	GACGACAGCC	6	6		
o	GACGACAGCC	12	12	6	1
g	AAGAACGGCC	10	10	5	1
g	GACGACAGCC	7	7	6	1
g	GACGACAGCC	6	6	3	1
.AAA	GACGACAGCC	12	12		
g	AAGAACGGCC	10	10	8	1
CT	GACGACAGCC	6	6		
AAG	GACGACAACC	6	6		
g	GACGACAGCC	12	12	158	0.99367089
TTC	GACGACAGCC	6	6		
g	GACGACAACC	5	5	10	0.9
AT	GACGACAGCC	6	6		
f	GACGACGGCC	6	6	2	1
AG	GACGACAACC	6	6		
TG	GACGACAGCC	6	6		
g	GACGACAGCC	6	6	2	1
g	GACGACAGCC	7	7	3	1
f	GACGACAGCC	6	6	4	1
TCG	GACGACAACC	6	6		
g	AAGAACGGCC	6	6	3	1
f	GACGACAGCC	11	11	45	1
CTG	GACGACAGCC	6	6		
AATC	GACGACAGCC	6	6		
GAC	GACGACAGCC	6	6		
g	GACGACAGCC	10	10	49	0.97959184
g	GACGACAGCC	12	12	114	0.98245614
f	GACGACAGCC	6	6	4	1
CTA	GACGACAGCC	12	12		



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3						
4	TTTC	GACGACAGCC	6	6		
5	p	GACGACAGCC	12	12	4	1
6	g	GACGACAGCC	5	5	294	0.82653061
7	g	GACGACAGCC	4	4	152	0.96052632
8	g	GACGACAGCC	4	4		
9	f	GACGACAGCC	6	6	3	1
10	o	GACGACAGCC	6	6	10	1
11	CAC	GACGACAGCC	12	12		
12	TG	GACGACAGCC	7	7		
13						
14	TG	GACGACAGCC	7	7		
15	g	GGAAACGGCC	6	6	53	1
16	g				1789	0.92901062
17						
18	TC	GACGACGGCC	10	10		
19	TTCC					
20						
21	TTC	GACGACAGCC	7	7		
22	TC	GACGACAGCC	12	12		
23	o	GACGACAGCC	12	12	2	1
24						
25	TC	GACGACAGCC	5	5		
26	g				13	1
27	f				16	1
28						
29	g	GACGACAGCC	6	6	81	0.96296296
30	g	GACGACAGCC	4	4	130	0.99230769
31						
32	TTTC	GACGACAGCC	6	6		
33						
34	ATC					
35	o				11	1
36	g	GACGACAGCC	11	11	266	0.9887218
37	f	GACGACAACC	6	6	4	1
38						
39	ATCT	GACGACAGCC	6	6		
40	g	GACGACAGCC	10	10	704	0.98295455
41	ATG	GACGACAGCC	6	6		
42						
43	TAC	GACGACAGCC	6	6		
44						
45	GCA	GACGACAACC	6	6		
46	GTC	AAGAACGGCC	6	6		
47	g	GACGACAGCC	10	10	824	0.99029126
48	c	GACGACAGCC	6	6	2	1
49						
50	g	GACGACAGCC	6	6	4	1
51	f	GACGACAGCC	6	6	3	1
52						
53	f	GACGACAGCC	7	7	4	1
54						
55	CGTC	GACGACAGCC	6	6		
56	TAA	GACGACAGCC	6	6		
57						
58						
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3						
4	CAC	GACGACAGCC	6	6		
5	g	GACGACAGCC	6	6	48	0.97916667
6	f	GACGACAGCC	6	6	4	1
7						
8	TTTC					
9	ATG					
10						
11	TCG	GACGACAGCC	6	6		
12	TCT	GACGACAGCC	6	6		
13	g	GACGACAGCC	6	6	2	1
14	g				5	1
15	TT	GACGACAGCC	6	6		
16	f	GACGACAGCC	10	10	4	1
17	p	AACAACGGCC	6	6	3	1
18	g				6	1
19	g				132	0.9469697
20	o	GACGACAGCC	12	12	2	1
21	CTA	GACGACAGCC	6	6		
22	AA					
23	g	GACGACAGCC	6	6	15	0.93333333
24	g	GACGACAGCC	6	6	108	0.9537037
25	f	GACGACAGCC	6	6	2	1
26	g	GACGACAGCC	12	12	94	0.93617021
27	g	GACGACAGCC	12	12	12	1
28	TCG	GACGACAGCC	12	12		
29	f	GACGACAGCC	6	6	4	1
30	g				14	1
31	TC	GACGACAGCC	6	6		
32	f	GACGACAGCC	6	6	2	1
33	g	GACGACGGCC	6	6	53	0.8490566
34	ATA					
35	f	GACGACAGCC	11	11	44	0.95454545
36	g	GACGACAGCC	4	4	4	1
37	TC	GACGACAGCC	11	11		
38	g	GACGACGGCC	6	6	8	1
39	TCT	GACGACAGCC	8	8		
40	g	GACGACAGCC	4	4	17	1
41	f	GACGACAGCC	5	5	7	1
42	p	GACGACAGCC	6	6	2	1
43	TC	GACGACAGCC	6	6		
44						
45						
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3						
4	g	GACGACAGC	12	12	650	0.85538462
5	TC	GACGACAGC	7	7		
6	CAG	GACGACAGC	6	6		
7	GATC	GACGACAGC	6	6		
8						
9	g	GACGACAGC	10	10	1238	0.99434572
10	g	GACGACAGC	6	6	17	1
11	CTT	GACGACAGC	11	11		
12	TC	GACGACAGC	6	6		
13						
14	g	GACGACAGC	7	7	29	1
15	g	GACGACAAC	6	6	53	1
16						
17	TTTC	GACGACAGC	6	6		
18	CTT	GACGACAGC	6	6		
19						
20	AG	GACGACAGC	6	6		
21	AA	GACGACGGC	6	6		
22						
23	f				12	0.91666667
24	g	GACGACAGC	6	6	2	1
25						
26	ACT	GACGACAGC	6	6		
27	TC	GACGACAGC	6	6		
28	TC	AACAACGGC	6	6		
29						
30	g				10	1
31	CCT	GACGACAGC	6	6		
32	GC	GACGACAGC	7	7		
33						
34	g	GACGACAGC	6	6	27	0.92592593
35	CTA	GACGACAGC	6	6		
36	GG	GACGACAGC	11	11		
37						
38	f	GACGACAGC	6	6	6	1
39	g	GACGACAGC	12	12	22	1
40	TC	GACGACAGC	12	12		
41	TC	GACGACAGC	12	12		
42	TC	GACGACAGC	6	6		
43	AG	GACGACAGC	9	9		
44						
45	f	GACGACAGC	11	10	7	1
46	CTG					
47	CTC	GACGACAGC	9	9		
48	TTC	GACGACAGC	6	6		
49						
50	f	GACGACAGC	6	6	5	1
51	f	GACGACAGC	6	6	33	0.90909091
52	GG	GACGACAGC	6	6		
53						
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2							
3							
4	g	GACGACAGCC	8	8	40	0.975	
5	f	GACGACAGCC	6	6	11	0.81818182	
6	f				18	0.88888889	
7							
8	TC	GACGACAACC	12	12			
9	TCG						
10							
11	g	GACGACAGCC	6	6	3	1	
12	f	GACGACAGCC	6	6	5	1	
13	TT	GACGACAGCC	6	6			
14	f	GACGACAGCC	6	6	4	1	
15	CTG	GACGACAGCC	6	6			
16							
17	g	GACGACGGCC	6	6	17	1	
18	g	GACGACAGCC	9	9	150	0.84666667	
19	TAA	GACGACAGCC	6	6			
20	GTT	GACGACAGCC	6	6			
21	o	GACGACAGCC	6	6	2	1	
22	TC	GACGACAGCC	6	6			
23	f	GACGACAGCC	10	10	3	1	
24	ATC	GACGACAGCC	6	6			
25	TCG	GACGACAGCC	10	10			
26	g	GACGACAACC	7	7	4	1	
27	AGG	GACGACAGCC	6	6			
28	TC	GACGACAGCC	6	6			
29	TC	GACGACAGCC	6	6			
30	CAC	GACGACAGCC	6	6			
31	TT	GACGACAGCC	6	6			
32	CTG	GACGACAGCC	6	6			
33	o	GACGACAGCC	6	6	5	1	
34	TC	GACGACGGCC	8	8			
35	o	GACGACAGCC	6	6	15	1	
36	f	GACGACAGCC	10	10	3	1	
37	AAA	GACGACAGCC	6	6			
38	TCG	GACGACAGCC	6	6			
39	g				97	0.90721649	
40	TC	AAGAACGGCC	6	6			
41	c	GACGACAGCC	6	6	388	0.98969072	
42	o	GACGACAGCC	6	6	7	1	
43	g	GACGACAGCC	12	12	2	1	
44	g	GACGACAGCC	6	6	12	1	
45							
46							
47							
48							
49							
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3						
4	g	GACGACAGC	6	6	43	1
5	ΓCT	GACGACAGC	6	6		
6	f	GACGACAGC	7	7	7	0.85714286
7						
8	TT	GACGACAGC	6	6		
9	f	GACGACAGC	6	6	3	1
10						
11	f	GACGACAGC	6	6	2	1
12	ΓCC	GACGACAGC	6	6		
13						
14	f	GACGACAGC	12	12	27	0.96296296
15	c	GACGACAGC	11	11	6	1
16	CTC	GACGACAGC	11	11		
17	ACT	GACGACAGC	7	7		
18						
19	g	GACGACGGC	5	5	334	0.99401198
20	TTTC	GACGACAGC	6	6		
21						
22	g	GACGACAGC	6	6	2	1
23	g	GACGACAGC	11	11	25	1
24						
25	CAG	GACGACAGC	6	6		
26	GTC	AAGAACGGC	6	6		
27	CTT	GACGACAGC	6	6		
28						
29	ΓTC	AAGAACGGC	6	6		
30	g	GACGACAGC	6	6	168	0.99404762
31	f	GACGACAGC	6	6	4	1
32						
33	ΔTC	GACGACAGC	10	10		
34	ΔATA	GACGACAGC	6	6		
35						
36	o				36	0.97222222
37	CAG	GACGACAGC	6	6		
38						
39	g	GACGACAGC	5	5	23	0.86956522
40	AGA	GACGACAAC	6	6		
41						
42	g	GACGACAAC	6	6	81	0.98765432
43	TC	GACGACAGC	6	6		
44						
45	g	GACGACAGC	6	6	3	1
46	g				5341	0.96498783
47	TC	GACGACAGC	6	6		
48						
49	g	GACGACAGC	7	7	2404	0.92720466
50	ΓTT	GACGACAGC	5	5		
51						
52	ΔAC	GACGACAGC	11	11		
53	CTC					
54						
55	ΔTG	GACGACAGC	6	6		
56	g				10	1
57						
58						
59						
60						

g	GACGACAGC	6	6	3	1
CATC	GACGACAGC	6	6		
f	GACGACAGC	6	6	19	1
f	GACGACAGC	6	6	11	1
.TC	GACGACAGC	6	6		
f	GACGACAGC	6	6	2	1
g	GACGACAGC	6	6	2564	0.96411856
TTC	GACGACAGC	12	12		
GTC	GACGACAGC	6	6		
g	GACGACAGC	8	8	100	0.96
g	GACGACGGC	6	6	3	1
CTT	GACGACAGC	11	11		
GATT	GACGACAGC	8	8		
CA	AAGAACGGC	11	11		
p	GACGACAGC	6	6	2	1
AA	TGCGACAGC	9	9		
g	GACGACAGC	5	5	15	0.93333333
g	AAGAACGGC	6	6	35	0.85714286
g	GACGACAAC	6	6	10	1
ΓTC	GACGACAGC	6	6		
f	GACGACAGC	6	6	12	1
ATC	GACGACAGC	6	6		
g				2	1
ΓCA	AAGAACGGC	7	7		
o	GACGACAGC	6	6	4	1
c	GACGACAGC	10	10	39	0.84615385
CCT	GACGACAGC	6	6		
o	GACGACAGC	6	6	7	1
AG	GACGACAGC	6	6		
CTT	GACGACAGC	6	6		
CTC	GACGACAGC	7	7		
ICA	GACGACAGC	6	6		
TCT	GACGACAGC	6	6		
TT	GACGACAGC	6	6		
ΓTT	GACGACAGC	6	6		
ΓTC					
CTG	GACGACAGC	6	6		
TGT	GACGACAGC	6	6		

1						
2						
3						
4	CA	GACGACAGCC	6	6		
5	f	GACGACAACC	7	7	41	0.97560976
6	g	GACGACAGCC	6	6	41	1
7	g	GACGACAGCC	6	6	3	1
8	g	GACGACAGCC	6	6	17	0.94117647
9	g	GACGACAGCC	6	6		
10	AAT					
11	g	GACGACAGCC	5	5	36	0.86111111
12	TT	GACGACAGCC	6	6		
13	g	GACGACAGCC	5	5	5	1
14	CAC	GACGACAGCC	8	7		
15	f	GACGACAGCC	8	8	2	1
16	TA	GACGACAGCC	6	6		
17	TTT	GACGACAGCC	5	5		
18	CT	GACGACAGCC	5	5		
19	g	GACGACAGCC	6	6	34	0.97058824
20	g	GACGACAGCC	3	3	1039	0.99230029
21	CC	GACGACAACC	7	7		
22	g	GACGACAGCC	10	10	9	0.88888889
23	c	GACGACAGCC	6	6	12	0.91666667
24	TTT					
25	TTT	GACGACAGCC	6	6		
26	c	GACGACAGCC	6	6	3	1
27	ATC	GACGACAGCC	6	6		
28	AT	GACGACAGCC	5	5		
29	g	GACGACAGCC	9	9	2	1
30	GTC	AAGAACGGCC	9	9		
31	CTG	GACGACAGCC	11	11		
32	CA	GACGACAGCC	8	8		
33	GATC	GACGACAGCC	6	6		
34	AT	GACGACAGCC	5	5		
35	TGT	GACGACAGCC	7	6		
36	CGG	GACGACAACC	6	6		
37	ATC	GACGACAGCC	6	6		
38	f	GACGACAGCC	6	6	3	1
39	CT	GACGACAGCC	5	5		
40	GTC	AAGAACGGCC	6	6		
41	g				447	1
42	g	GACGACAGCC	6	6	2	1
43						
44						
45						
46						
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48						
49						
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60						

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3						
4	g	GACGACGAC	11	11	10	1
5	CGG	GACGACAGC	5	5		
6	p	GACGACAGC	5	5	36	0.94444444
7	GT	AAGAACGGC	5	5		
8						
9	f	GACGACAGC	6	6	2	1
10						
11	g				14	0.92857143
12	g	GACGACAGC	7	7	8	1
13	f	GACGACAGC	6	6	2	1
14						
15	g	GACGACAGC	6	6	2	1
16	f	GACGACAGC	6	6	4	1
17						
18	TCT	GACGACAGC	6	6		
19	TG	GACGACAGC	10	10		
20						
21	GAA					
22	TC	GACGACAGC	6	6		
23	f	GACGACAGC	6	6	5	1
24	f	GACGACAGC	6	6	2	1
25						
26	TC					
27	CT					
28						
29	TTT	GACGACAGC	8	8		
30	g	GACGACGGC	6	6	3	1
31	f	GACGACAGC	6	6	3	1
32						
33	g	GACGACAGC	6	6	3	1
34	CTC	GACGACAGC	6	6		
35						
36	ATT	GACGACAGC	3	3		
37	f	GACGACAGC	6	6	7	0.85714286
38						
39	f				11	1
40	GTC	AACAACGACC	6	6		
41						
42	TTC	GACGACAGC	6	6		
43						
44	g				87	0.8045977
45	CTT	GACGACAGC	9	9		
46	AG	GACGACAGC	5	5		
47						
48	g	GACGACAGC	7	7	2	1
49	c	GACGACAGC	6	6	11	1
50	g	GACGACAGC	9	9	2	1
51						
52	TTC	GACGACAGC	9	9		
53	g	GACGACAGC	5	5	380	0.95526316
54	GTC	GACGACAGC	4	4		
55						
56	g				60	0.86666667
57						
58						
59						
60						



1						
2						
3						
4	\TA					
5	CAC	GACGACAGC	8	8		
6	GTC	AAGAACGGC	5	5		
7						
8	.TCT	GACGACAGC	9	9		
9	f	GACGACAGC	6	6	9	0.88888889
10						
11	g				31	0.93548387
12	f	GACGACAGC	6	6	12	1
13						
14	g				94	0.84042553
15	\TA					
16	p	GACGACAGC	6	6	2	1
17	g	GACGACAGC	6	6	4	1
18						
19	o	GACGACAGC	6	6	16	0.875
20						
21	f	GACGACAGC	6	6	2	1
22	.TG	GACGACAGC	6	6		
23						
24	g	GACGACAGC	6	6	18	0.88888889
25	g	GACGACAGC	6	6	12	1
26	.AC	GACGACAGC	6	6		
27						
28	TT	GACGACAGC	5	5		
29	c	GACGACAGC	5	5	2	1
30	.TG	GACGACAGC	10	10		
31						
32	g				83	1
33	TTC	GACGACAGC	6	6		
34	CTT	GACGACAGC	6	6		
35						
36	.ACC	GACGACAGC	5	5		
37						
38	g	GACGACAGC	6	6	59	1
39	TC	GACGACAGC	5	5		
40	f	GACGACAGC	5	5	6	1
41						
42	g	GACGACAGC	4	4	3	1
43	AC	GACGACAGC	6	6		
44						
45	f	GACGACAGC	9	9	10	1
46	f	GACGACAGC	5	5	24	0.91666667
47	\TC	GACGACAGC	6	6		
48						
49	.TT	GACGACAGC	4	4		
50	p	GACGACAGC	6	6	11	0.90909091
51	o	GACGACAGC	6	6	2	1
52						
53	f				8	0.875
54	.CG	GACGACAGC	9	9		
55						
56	o	GACGACAGC	5	5	24	0.875
57						
58						
59						
60						

f				2	1
g	GACGACAGC	6	6	3	1
ATC	GACGACAGC	6	6		
CA	GACGACAAC	6	6		
CAA	GACGACAGC	6	6		
g	GACGACAGC	6	6	87	0.96551724
ATC	GACGACAGC	5	5		
CCC	GACGACAGC	6	6		
f	GACGACAGC	6	6	3	1
g				22	0.90909091
CC					
p	GACGACAGC	6	6	2	1
g	GACGACAGC	6	6	2	1
CGC	GACGACAGC	6	6		
TCT	GACGACAGC	6	6		
CCC	GACGACAGC	5	5		
f	GACGACAGC	8	8	7	1
g	GACGACAGC	7	7	2	1
CTG	GACGACAGC	7	7		
f	GACGACAGC	5	5	3	1
g	GACGACAGC	6	6	2	1
g	GACGACAGC	5	5	6	1
AT					
TC					
AGC	GACGACAGC	6	6		
o	GACGACAGC	6	6	5	1
f	GACGACAGC	6	6	9	1
g	GACGACAGC	6	6	316	0.99050633
TTT	GACGACAGC	6	6		
CC					
g	GACGACGGC	6	6	5	1
f	GACGACAGC	6	6	10	1
TC	GACGACAAC	6	6		
ATC	GACGACAGC	5	5		
g	AAGAACGGC	6	6	4	1
CT	GACGACAGC	6	6		
o	AAGAACGGC	4	4	181	0.94475138
AT					

1						
2						
3					187	0.98395722
4	f					
5	ITC					
6	ATC	GACGACAGCC	5	5		
7	ATC	GACGACAGCC	6	6		
8	ATC	GACGACAGCC	6	6		
9	TGA	GACGACAGCC	5	5		
10	GT	AAGAACGGCC	6	6		
11	CGTC	GACGACAGCC	6	6		
12	g	AAGAACGGCC	5	5	23	1
13	ATT	GACGACAGCC	4	4		
14	TC					
15	TC	GACGACAGCC	5	5		
16	f	GACGACAGCC	6	6	2	1
17	g	GACGACAGCC	6	6	64	0.96875
18	p	GACGACAGCC	6	6	2	1
19	GA	GTCGACAGCC	5	5		
20	g				23	1
21	ATCT	GACGACAGCC	6	6		
22	f				47	0.89361702
23	g				89	0.87640449
24	g				4851	0.85075242
25	g	GACGACAGCC	8	8	8	1
26	AC	GACGACAGCC	6	6		
27	f	GACGACAGCC	5	5	5	0.8
28	TG	GACGACAGCC	6	6		
29	GTC	AAGAACGGCC	4	4		
30	CGA	GACGACAGCC	6	6		
31	f	GACGACAGCC	5	5	6	0.83333333
32	ATC	GACGACAGCC	6	6		
33	ATC	GACGACAGCC	5	5		
34	TCT	GACGACAGCC	7	7		
35	f				13	0.92307692
36	g				65	0.98461538
37	ITC	GACGACAGCC	6	6		
38	ICC	GACGACAGCC	5	5		
39	p	GACGACAGCC	5	5	3	1
40	g				5	1
41	g	GACGACAGCC	7	7	2	1
42	TTT					
43						
44						
45						
46						
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48						
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54						
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56						
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60						

TTC	GACGACAGC	7	7		
ATT	GACGACAGC	6	6		
GTG	GACGACAGC	5	5		
TC	GACGACAGC	6	6		
CTT					
g	GACGACGGC	5	5	2	1
f	AAGAACGGC	6	6	292	0.96232877
o	GACGACAGC	5	5	2	1
g				2	1
g	GACGACAGC	4	4	24	1
TC	GACGACAGC	5	5		
TC	GACGACAGC	6	6		
f	GACGACAGC	6	6	4	1
CG	GACGACAGC	5	5		
TT	GACGACAGC	5	5		
o	GACGACAGC	4	4	2	1
f	GACGACAGC	6	6	2	1
f				18	1
GT	GACGACAGC	4	4		
CTT	GACGACAGC	6	6		
TC					
TCT	GACGACAGC	4	4		
ACT					
CATC					
C					
TCT	GACGACAGC	5	5		
g	GACGACAGC	5	5	10	0.9
AAC					
g	GACGACAGC	4	4	2	1
g	GACGACAGC	10	9	29	0.96551724
f	GACGACAGC	5	5	22	0.95454545
ATC	GACGACAGC	6	6		
AG	GACGACAGC	5	5		
g	GACGACAGC	4	4	182	0.98351648
AAT					
AGG	GACGACAGC	7	7		
f	GACGACAGC	4	4	2	1
g				7314	0.97429587

1						
2						
3						
4	g	GACGACAGC	5	5	2	1
5	.TC	GACGACAGC	3	3		
6	TA					
7						
8	g	GACGACAGC	4	4	3	1
9	p	GACGACAGC	5	5	2	1
10	GGTC	GACGACAGC	5	5		
11						
12	g				36	0.83333333
13	TC	GACGACAGC	4	4		
14	TTT	GACGACAGC	5	5		
15	.TG	GACGACAGC	4	4		
16	.TC					
17						
18	.AC	GACGACAGC	4	4		
19	TGA					
20	CTG	GACGACAGC	4	4		
21	TCA					
22						
23	o	GACGACAGC	4	4	6	0.83333333
24	g	GACGACGGC	4	4	4	1
25	ATCT	GACGACAGC	6	6		
26	g	GACGACAGC	4	4	4	1
27					6	1
28	o	GACGACAGC	4	4	2	1
29	g				365	0.97534247
30						
31	CA	GACGACAGC	7	7		
32	TC					
33	CTG	GACGACAGC	4	4		
34	ATC					
35	CTC	GACGACAGC	4	4		
36	CCC					
37	f				4	1
38	g	GACGACAGC	4	4	11	1
39	ATC	GACGACAGC	5	5		
40	g	GACGACAGC	5	5	3	1
41	CG	GACGACAGC	5	5		
42	GCA	GACGACAAC	5	5		
43	TTC	GACGACAGC	4	4		
44	.TA	GACGACAGC	4	4		
45	o	GACGACAGC	4	4	8	1
46	o				7	1
47						
48						
49						
50						
51						
52						
53						
54						
55						
56						
57						
58						
59						
60						

1						
2						
3						
4	TT					
5	CTG	GACGACAGC	5	5		
6	f	GACGACAGC	6	6	16	0.9375
7						
8	ACC					
9	g				11	1
10	G					
11						
12	ACA	GACGACAGC	5	5		
13	CTG	GACGACAGC	4	4		
14	GTC	GACGACAGC	4	4		
15	ATC	GACGACAGC	6	6		
16	CTA	GACGACAGC	4	4		
17	CTC	GACGACAGC	6	6		
18	CTG	GACGACAGC	4	4		
19	TA	GACGACAGC	4	4		
20	GG	GACGACAGC	5	5		
21	g	GACGACAAC	4	4	5	0.8
22	CAT	GACGACAGC	4	4		
23	f	GACGACAGC	5	5	3	1
24						
25	AAA					
26	ATC	GACGACAGC	5	5		
27	CCA					
28	ATC	GACGACAGC	5	5		
29	ATC	GACGACAGC	4	4		
30						
31	g				2	1
32	f	GACGACAGC	4	4	9	0.88888889
33	o	GACGACAGC	5	5	3	1
34	f				7	1
35						
36	TGT	GACGACAGC	6	6		
37	TTC	GACGACAGC	4	4		
38	TGTT					
39	g				11	1
40	f				2	1
41						
42	ATG	GACGACAGC	4	4		
43	g	GACGACAGC	4	4	58	1
44	GTA	GACGACAGC	5	5		
45	TG	GACGACAGC	6	6		
46	g	GACGACGGC	5	5	8	1
47	g	GACGACGGC	5	5	131	0.99236641
48						
49						
50						
51						
52						
53						
54						
55						
56						
57						
58						
59						
60						

1							
2							
3							
4	CAC	GACGACAGC	4	4			
5	g				32		1
6	AC	GACGACAGC	5	5			
7							
8	GTC						
9	g	GACGACAGC	5	5	3		1
10	AT						
11	A	GAGGACAAC	3	3			
12	ATC	GACGACAGC	4	4			
13							
14	g	AAAAACGGC	3	3	2		1
15	ATC	GACGACAGC	6	6			
16	CG	GACGACAGC	4	4			
17							
18	TC	GACGACAGC	4	4			
19							
20	f				4		1
21							
22	g				5		1
23	f				100		0.97
24							
25	g	GACGACAGC	7	7	8		1
26	CAG	GACGACAAC	5	5			
27							
28	g	GACGACAGC	4	4	134	0.92537313	
29	o				160	0.9625	
30	f				4		1
31							
32	TC	GACGACGGC	4	4			
33	TTT	GACGACAGC	5	5			
34	ATC	GACGACAGC	4	4			
35							
36	g	AAAAGCGGC	4	4	44		1
37	ATC	GACGACAGC	6	6			
38							
39	f				4		1
40	CT	GACGACAGC	3	3			
41	AG	GACGACAGC	4	4			
42							
43	AT						
44	GTC	AAGAACGAC	8	8			
45							
46	CCC	GACGACAGC	4	4			
47	TGA	GACGACAGC	4	4			
48							
49	f				4		1
50	AA						
51	CTC						
52							
53	AT						
54	c	GACGACAGC	4	4	2		1
55							
56	g				130	0.96923077	
57							
58							
59							
60							

g					170	0.82352941
g	GACGACAGC	3	3		58	0.98275862
g					113	1
AG						
CAG	GACGACAGC	5	5			
TCA	GACGACAGC	5	5			
ATCT	GACGACAGC	3	3			
TC	GACGACAGC	4	4			
CTC	GACGACAGC	3	3			
GTC	GACGACAGC	5	5			
ATC						
g					10	1
ACT	GACGACAGC	4	4			
o	GACGACAGC	5	5		2	1
ATC	AAGAACGGC	5	5			
g					2	1
g	GACGACAGC	4	4		774	0.93023256
g	GACGACAGC	5	5		18	1
g	AAGAACGGC	3	3		82	0.85365854
g					308	1
GGT						
CA	GACGACAGC	4	4			
CG	GACGACAGC	4	4			
TT	GACGACAGC	3	3			
ATC	GACGACAGC	4	4			
f	GACGACAGC	4	4		35	0.91428571
ACC	GACGACAGC	4	4			
ATC	GACGACAGC	5	5			
g	GACGACAGC	4	4		2	1
TT						
TC	GACGACAGC	4	4			
TG						
g	GACGACAGC	5	5		2	1
CT	GACGACAGC	5	5			
CT	GACGACAGC	5	5			
g					12	1
CCA						
CTG						



1						
2						
3						
4	CTT	GACGACAGC	5	4		
5	g	GACGACAGC	4	4	2	1
6	FG	GACGACAGC	4	4		
7						
8	g	GACGACAGC	5	5	3	1
9	CCT	GACGACAGC	5	5		
10						
11	TCC					
12	AC	GACGACAGC	3	3		
13						
14	p				3	1
15	TGA					
16						
17	g				5	1
18	CATC					
19	TTT	GACGACAGC	5	5		
20						
21	g	GACGACAGC	4	4	100	0.98
22	o	GACGACAGC	4	4	4	1
23						
24	c				10	1
25	g				95	0.91578947
26	g	GACGACAGC	4	4	2	1
27						
28	CTG	GACGACAGC	4	4		
29	TCT	GACGACAGC	4	4		
30	GCC	GACGACAGC	4	4		
31						
32	g				29	0.93103448
33	CCC	GACGACAGC	4	4		
34						
35	g	GACGACAGC	4	4	9	1
36	CAC	GACGACAAC	4	4		
37	f	GACGACAGC	4	4	10	1
38						
39	TT	GACGACAGC	3	3		
40	CA					
41						
42	o				4	1
43	gTC	AAAAACGGC	3	3		
44						
45	g	GACGACAGC	2	2	20	1
46	gTC	AAAAACGGC	5	5		
47						
48	TTT					
49	CGT					
50	AC					
51						
52	g	GACGACAGC	3	3	40	0.925
53	TG					
54	CC	GACGACAGC	5	5		
55						
56	TTT					
57						
58						
59						
60						

g					11	1
ATC	GACGACAGC	4	4			
C						
TCC						
g					6	1
ACC						
ATC	GACGACAGC	5	5			
ATC	GACGACAGC	5	5			
ATC	GACGACAGC	3	3			
CCC	GACGACAGC	3	3			
TA						
CAC	GACGACAGC	4	4			
f					2	1
g	GACGACAGC	2	2		10	0.8
CT	GACGACAGC	3	3			
ITC						
ATC						
f					3	1
CTG						
ATG						
TA	GACGACAGC	4	4			
ATC	GACGACAGC	5	5			
f	GACGACAGC	4	4		2	1
g	GACGACAGC	2	2		4279	0.99252162
g					8	1
f	GACGACAGC	2	2		2	1
AC	GACGACAGC	3	3			
ACC						
CTG						
ATC	GACGACAGC	3	3			
g					2	1
TC						
TA	GACGACAGC	3	3			
TC						
CG						
ATC	GACGACAGC	5	5			
CG	GACGACAGC	4	4			
TT	GACGACAGC	4	4			

1						
2						
3						
4	p	AAGAACGGC	3	3	124	1
5	TC	GACGACAGC	2	2		
6	c				3	1
7	f	GACGACAGC	4	4	9	1
8						
9	AC					
10	g				4	1
11	CTC					
12						
13	o				27	1
14	TTA					
15	CGG					
16	ATT	GACGACAGC	3	3		
17	g	AAGAACGGC	1	1	2	1
18	AC					
19	g				4	1
20	f				26	1
21						
22	g	GACGACGGC	2	2	33	1
23	AG					
24	g	GACGACAGC	4	4	2	1
25	CT					
26	f	GACGACAGC	4	4	9	1
27	g				66	0.96969697
28	CTC					
29	CTC					
30	CTC					
31	o				9	0.88888889
32	g	GACGACAGC	3	3	28	0.92857143
33	ATC					
34	CG	GACGACAGC	3	3		
35	CCT	GACGACAGC	5	5		
36	CTCT					
37	c				15	1
38	f	AAGAACGGC	3	3	200	0.995
39	ATC	GACGACAGC	3	3		
40	TA					
41	TC	GACGACAGC	3	3		
42	g				5	1
43	TTT	GACGACAGC	3	3		
44	TC					
45						
46						
47						
48						
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51						
52						
53						
54						
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60						

1							
2							
3							
4	ATCT						
5	TTC						
6	f				3		1
7							
8	ACA						
9	o				111	0.93693694	
10	GCC	GACGACAGC	3	3			
11	AC						
12	GT						
13							
14	g				10		1
15	TC	GACGACAGC	2	2			
16	TCT	GACGACAGC	4	4			
17	TTT						
18	f				2		1
19							
20	g				213	0.82159624	
21							
22	ATC	GACGACAGC	4	4			
23	g	GACGACAGC	2	2	7331	0.99686264	
24	CTT	GACGACAGC	3	3			
25	TC	GACGACAGC	3	3			
26	ATC	GACGACAGC	3	3			
27	GTC	AAGAACGGC	2	2			
28	CAA						
29	ATC	GACGACAGC	4	4			
30	o				4		1
31	ATC	GACGACAGC	4	4			
32	GGT						
33	TG						
34	ATC						
35	CTA						
36	g				2		1
37	CTC						
38	GCA						
39	g				139	0.92086331	
40	AC	GACGACAGC	3	3			
41	TCC	GACGACAGC	2	2			
42	CAG						
43	GCA						
44	TT						
45	CTA						
46							
47							
48							
49							
50							
51							
52							
53							
54							
55							
56							
57							
58							
59							
60							

1						
2						
3						
4	TT					
5	CC					
6	ATC	GACGACAGC	4	4		
7						
8	CA					
9	TT	GACGACAGC	1	1		
10	CT					
11	ATC	GACGACAGC	2	2		
12						
13	f				653	0.99846861
14						
15	ATC	GACGACAGC	4	4		
16	CCG	GACGACAGC	3	3		
17	ATT					
18						
19	TTT					
20	ATC	AAGAACGAC	4	4		
21						
22	GTC					
23	GTC	AAGAACGAC	3	3		
24						
25	CTT					
26	o	GACGACAGC	3	3	4	1
27						
28	g	GACGACAGC	2	2	5	1
29	g	GACGACAGC	3	3	473	0.98520085
30	g	GACGACAGC	3	3	2	1
31						
32	GTC	AAGAACGGC	2	2		
33						
34	TC					
35	ATC					
36	g	GACGACAGC	3	3	6	1
37	o				10	0.8
38						
39	g	GACGACAGC	2	2	27	0.85185185
40	CTC	GACGACAGC	2	2		
41						
42	ATC	GACGACAGC	4	4		
43	GCT	GACGACAGC	2	2		
44						
45	TGA					
46	o	GACGACAGC	3	3	19	1
47	TC	GACGACAGC	4	4		
48						
49	g				28	1
50	CTG	GACGACAGC	3	3		
51						
52	f				2	1
53	CG	GACGACAGC	4	4		
54						
55	ATC					
56	TC	GACGACAGC	2	2		
57						
58						
59						
60						

g				6	1
TT					
GTG					
AATC	GACGACAGC	3	3		
f				12	1
TC	AAGAACGGC	1	1		
GCA					
GTT					
g				42	0.83333333
c	GACGACAGC	3	3	2	1
TC	GACGACAGC	2	2		
TC	GACGACAAC	3	3		
GTG	AAGAACGGC	4	4		
CTT					
g	AAGAACGGC	3	3	15	0.93333333
ATC	GACGACAGC	3	3		
GGG	GACGACAGC	2	2		
AC					
ACC					
g				8	1
AG					
TC					
GT	GACGACAGC	1	1		
g				303	0.99669967
f	GACGACAGC	2	2	11	0.90909091
CC	GACGACAAC	2	2		
f	GACGACAGC	3	3	8	1
TT	GACGACAGC	3	3		
GTC					
GTG	GACGACAGC	1	1		
CCC					
TC					
CAC	GACGACAAC	2	2		
GTG					
CTG					
CTG	GACGACAGC	2	2		
TT					
TG	AAGAACGGC	3	3		

1							
2							
3							
4	TGC	GACGACAGC	3	3			
5	AT	GACGACAGC	3	3			
6	TG						
7	GTC	AAGAACGGC	3	3			
8	CCC						
9	ATC						
10	ATC						
11	TA	GACGACAGC	2	2			
12	g	GACGACAGC	2	2	4		1
13	CTCA						
14	TGC						
15	GT						
16	ATC	GACGACAGC	4	4			
17	ATC						
18	g				17		1
19	GTC						
20	g	GACGACAGC	2	2	3		1
21	TCT	GACGACAGC	3	3			
22	p	AAGAACGGC	2	2	167	0.9760479	
23	g				102	0.95098039	
24	ATC	GACGACAGC	4	4			
25	g				2		1
26	g	GACGACAGC	2	2	31	0.93548387	
27	TCTA	GACGACAGC	3	3			
28	ACT	GACGACAGC	2	2			
29	TCA						
30	AA	GACGACAGC	1	1			
31	g	AAAAACGGC	2	2	3		1
32	ATCT	GACGACAGC	2	2			
33	g				4		1
34	ATC						
35	CG	GACGACAGC	2	2			
36	TAC						
37	g				11		1
38	GTC	AAGAACGGC	2	2			
39	TC	GACGACAGC	2	2			
40	TCT	GACGACAGC	1	1			
41	TGA						
42	CTA						
43							
44							
45							
46							
47							
48							
49							
50							
51							
52							
53							
54							
55							
56							
57							
58							
59							
60							

f				2	1
CA					
ATC	GACGACAGC	4	4		
TC					
CA					
TAC	GACGACAGC	2	2		
g	GACGACAACC	1	1	6	1
f				16	0.9375
CATT					
CAG					
TA	GACGACAGC	3	3		
CAC	GACGACAGC	1	1		
TCT	GACGACAGC	2	2		
CTG	GACGACAGC	2	2		
TT					
g				34	1
CTT	GACGACAGC	2	2		
TC	AAGAACGGC	3	3		
TC	AAGAACGGC	2	2		
g				9	1
ATC	GACGACAGC	4	4		
g	GACGACAGC	1	1	2	1
CAG					
g				35	1
TT					
ATC					
TA	GACGACAGC	3	3		
AATC					
f				5	1
g	GACGACAGC	2	2	18	0.88888889
TC	AAGAACGGC	2	2		
CGC					
GT					
TC	GACGACAGC	2	2		
g				8	1
GTC	AAGAACGAC	3	3		
TC	GACGACAGC	3	3		
TT	GACGACAGC	2	2		



1						
2						
3						
4	CTA					
5	TG	AAGAACGGC	2	2		
6	CTC	GACGACAGC	2	2		
7	TTT	GACGACAGC	2	2		
8						
9	f				3	1
10	TC	GACGACAAC	2	2		
11	GCT	GACGACAGC	2	2		
12						
13	.TG	GACGACAGC	2	2		
14						
15	g	GACGACAGC	2	2	12	1
16	o	GACGACAGC	2	2	4	1
17						
18	\TC	GACGACAGC	2	2		
19	p	AAGAACGGC	2	2	2	1
20						
21	ITC					
22	g				7	1
23						
24	.TG					
25	ATC	GACGACAGC	1	1		
26	f	GACGACAGC	1	1	2	1
27						
28	\TC	GACGACAGC	2	2		
29	g	GACGACAGC	2	2	6	1
30	f	GACGACAGC	2	2	2	1
31						
32	p	GACGACAGC	2	2	8	1
33	ATC	GACGACAGC	1	1		
34	CTA	GACGACAGC	1	1		
35						
36	TG					
37	AGA	GACGACAAC	3	3		
38						
39	g	GACGACAGC	2	2	3	1
40	ATC					
41						
42	ITC	AAGAACGGC	3	3		
43						
44	ICC					
45	ATC					
46	g				2	1
47	g	GACGACAGC	2	2	2	1
48						
49	TCC	GACGACGGC	2	2		
50	g	GACGACAGC	1	1	13	1
51	GTC	GACGACAGC	1	1		
52						
53	.T	GACGACAAC	2	2		
54	g	GACGACAGC	2	2	7	1
55						
56	\CC	GACGACAGC	2	2		
57						
58						
59						
60						

1							
2							
3							
4	TCC						
5	AGG	GACGACAGC	2	2			
6	o	GACGACAGC	2	2	6		1
7							
8	TCC	GACGACAGC	2	2			
9	TC	GACGACGGC	2	2			
10							
11	g				73	0.87671233	
12	TT	GACGACAGC	1	1			
13	CCC	GACGACAGC	2	2			
14							
15	ATC						
16	ATA						
17							
18	TG						
19	GTC	AAGAACGGC	2	2			
20							
21	g	GACGACAGC	2	2	9		1
22	GTC						
23	TG	GACGACAGC	2	2			
24							
25	AC						
26	TC	GACGACGGC	2	2			
27							
28	TC						
29	TC	GACGACAGC	1	1			
30	ATC	GACGACAGC	1	1			
31							
32	C						
33	TC						
34							
35	TG	AAGAACGGC	2	2			
36	g				106	0.90566038	
37					3		1
38	g						
39	TC	GACGACAGC	2	2			
40	CT	GACGACAGC	2	2			
41							
42	CTC						
43	TCA						
44							
45	g				6		1
46	g				8	0.875	
47	g				57		1
48							
49	f				5		1
50	CTA	GACGACAGC	2	2			
51	TGC	GACGACAGC	2	2			
52							
53	p				2		1
54	CTG	GACGACAGC	2	2			
55							
56	ATC	GACGACAGC	2	2			
57							
58							
59							
60							

1						
2						
3						
4	CTG	GACGACAGC	2	2		
5	c	GACGACAGC	2	2	2	1
6	.TC	GACGACAGC	2	2		
7						
8	g				137	0.96350365
9	g	GACGACAGC	3	3	2	1
10	TG					
11						
12	g				25	0.92
13	.TC					
14						
15	o				19	1
16	TC					
17						
18	g	GACGACAGC	1	1	8	1
19	f	GACGACAGC	1	1	2	1
20						
21	g	GACGACAAC	1	1	2	1
22	p	AAGAACGGC	1	1	5	1
23	TC					
24						
25	TC					
26	c	GACGACAGC	1	1	6	1
27	CCC	GACGACAGC	1	1		
28						
29	g	GACGACAGC	2	2	20	1
30	f				30	0.93333333
31						
32	TCA	GACGACAGC	2	2		
33	CTC	GACGACAGC	2	2		
34	.TC					
35						
36	p	GACGACAGC	2	2	2	1
37	.AC					
38						
39	g	GACGACAGC	1	1	2	1
40	TCT	GACGACAGC	2	2		
41						
42	g	GACGACAGC	2	2	39	0.87179487
43	TCA	GACGACAGC	2	2		
44						
45	.TG					
46	.TT	GACGACAGC	2	2		
47	GTC	AAGAACGGC	2	2		
48						
49	TAT	GACGACAGC	2	2		
50	g	GACGACAGC	3	3	2	1
51	TCT					
52						
53	GTC	AAGAACGGC	2	2		
54	.TC	GACGACAGC	2	2		
55						
56	CCA					
57						
58						
59						
60						

o	GACGACAGC	2	2	5	1
g	GACGACAGC	1	1	11	1
TAC	GACGACAGC	1	1		
AC					
T	GAGGACAAC	1	1		
g	GACGACAGC	1	1	2	1
AC	GACGACAGC	1	1		
AT	GACGACAGC	1	1		
.TC	GACGACAGC	2	2		
TC	GACGACAGC	2	2		
CTT	GACGACAGC	2	2		
c				2	1
CTA					
CT	GACGACAGC	2	2		
AGA					
g				1533	0.99086758
CTA					
.TC					
GTC	AAGAACGAC	2	2		
TTT					
g				2	1
ATC					
TTT					
g	GACGACAGC	2	2	3	1
.ACT	GACGACAGC	2	2		
TC	AAGAACGGC	2	2		
TC	GACGACAGC	2	2		
CTT					
g	GACGACAGC	2	2	136	0.99264706
f	GACGACAGC	2	2	7	1
CTA					
TC					
ATC					
AC					
CTG	GACGACAGC	1	1		
g				24	0.91666667
GC	GACGACAGC	1	1		
ATC					

1							
2							
3							
4	GTC	AAGAACGAC	2	2			
5	ATA						
6	TTT						
7							
8	o	GACGACAGC	2	2	2		1
9	GTC	AAGAACGAC	2	2			
10	ATC	GACGACAGC	2	2			
11	ATC	GACGACAGC	2	2			
12	f	GACGACAGC	2	2	2		1
13	AT	GACGACAGC	2	2			
14							
15	g				9		1
16	g	GACGACAGC	2	2	5		1
17					5		1
18	g						
19	GTC	AAGAACGAC	2	2			
20	ATC						
21							
22	c				5		1
23	CT						
24	ATC	GACGACAGC	2	2			
25	ATC						
26	ATC						
27	AG	GACGACAGC	2	2			
28	TCC	GACGACAGC	2	2			
29	GTC	AAGAACGGC	2	2			
30							
31	g				2		1
32	ATC	GACGACGGC	1	1			
33	ATC	GACGACAGC	1	1			
34	ATC	GACGACAGC	1	1			
35	TAT	GACGACAGC	1	1			
36	CT						
37							
38	g	GACGACAAC	2	2	28	0.92857143	
39	ATC						
40	ATC	GACGACAGC	2	2			
41	ATC	GACGACAGC	2	2			
42	ATC						
43	ATC	GACGACAGC	2	2			
44	ATC						
45	TC						
46	g	GACGACAGC	2	2	7	0.85714286	
47	ATC						
48	ATC						
49	ATC						
50	ATC						
51	ATC	AAGAACGGC	2	2			
52	ATC	GACGACAGC	2	2			
53	ATC	AAGAACGGC	2	2			
54	ATC	AAGAACGGC	2	2			
55	f	GACGACAGC	1	1	2		1
56							
57							
58							
59							
60							

1						
2						
3						
4	GCG	GACGACAGCC	1	1		
5	CTC					
6	g	GACGACAGCC	1	1	13	1
7	TTT					
8						
9	f	GACGACGGCC	1	1	2	1
10	f				3	1
11						
12	TTG	AAGAACGGCC	2	2		
13	TTT	GACGACAGCC	2	2		
14	ATC	GACGACAGCC	1	1		
15	GTC	AAGAACGACC	1	1		
16	GTC	AAGAACGGCC	2	2		
17						
18	g				15	0.93333333
19	GCC	AAGAACGACC	2	2		
20	o	AAGAACGGCC	1	1	533	1
21	CTC	GACGACAGCC	1	1		
22	CTG	GACGACAGCC	1	1		
23	ATC	GACGACAGCC	1	1		
24	ATG	GACGACAGCC	1	1		
25	AC	GACGACAGCC	1	1		
26	CTG					
27	GTC					
28	AA					
29	TTT	GACGACAGCC	2	2		
30	TCT	GACGACAGCC	2	2		
31	CTA	GACGACAGCC	2	2		
32	ATC	GACGACAGCC	2	2		
33	ATC	GACGACAGCC	2	2		
34	f	GACGACAGCC	1	1	3	1
35	CTG					
36	ATT					
37	GTC	AAGAACGACC	1	1		
38	GTC	AAGAACGGCC	1	1		
39	GTC	AAGAACGGCC	1	1		
40	GTC	AAGAACGGCC	1	1		
41	GTC					
42	g	GACGACAGCC	1	1	7	1
43	GTC	AAGAACGGCC	1	1		
44	ACC	GACGACAGCC	1	1		
45						
46						
47						
48						
49						
50						
51						
52						
53						
54						
55						
56						
57						
58						
59						
60						

1							
2							
3							
4	CTC	AAGAACGGCC	1	1			
5	CTC	AAGAACGGCC	1	1			
6	g	GACGACAGCC	1	1	4		1
7	ATC	GACGACAGCC	2	2			
8							
9	CT						
10	CTC	GACGACAGCC	2	2			
11	TTT	GACGACAGCC	1	1			
12	TTT	GACGACAGCC	1	1			
13	AC	GACGACAGCC	1	1			
14	AC	GACGACAGCC	1	1			
15	CTT	GACGACAGCC	1	1			
16	g	AAGAACGGCC	1	1	28		1
17	g	GACGACAGCC	1	1	10		0.8
18	f	GACGACAGCC	1	1	2		1
19	f	GACGACAGCC	1	1	30		1
20	p	AAAAACGGCC	1	1	30		1
21	f	GACGACAGCC	1	1	11		1
22							
23	ACT						
24	AC						
25	AC						
26	g	GACGACAGCC	1	1	22	0.95454545	
27	g	GACGACAGCC	1	1	13		1
28	g	GACGACAGCC	1	1			
29	TT	GACGACAGCC	1	1			
30	AC	GACGACAGCC	1	1			
31	AC	GACGACAGCC	1	1			
32	TAC	GACGACAGCC	1	1			
33	CTC	AAGAACGGCC	2	2			
34	ATC						
35							
36	CAG	GACGACAACC	1	1			
37	CTG	GACGACAGCC	1	1			
38	CTG	GACGACAGCC	1	1			
39	TTCC	GACGACAGCC	1	1			
40	CTG						
41	TTT	GACGACAGCC	1	1			
42	TCC						
43	TCC						
44	CTC	AAGAACGGCC	1	1			
45	c	GACGACAGCC	1	1	18	0.94444444	
46	GG						
47	ATC	GACGACAGCC	1	1			
48							
49	AA						
50	CTC	AAGAACGGCC	1	1			
51	ATT	GACGACAGCC	1	1			
52	ATT	GACGACAGCC	1	1			
53	ATT	GACGACAGCC	1	1			
54	TCA	AAGAACGGCC	1	1			
55							
56							
57							
58							
59							
60							

TC	GACGACGGC	1	1		
o				6	1
o	GACGACAGC	1	1	3	1
CATT					
TA	GACGACAAC	1	1		
c	GACGACAGC	1	1	2	1
g	GACGACAGC	1	1	2	1
g	GACGACAGC	1	1	92	0.98913043
ATA					
GG	GACGACAGC	1	1		
TTT	GACGACAGC	1	1		
TT	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
ATC					
TC	GACGACAGC	1	1		
TA	GACGACAGC	1	1		
TC					
f				14	0.85714286
TGC	GACGACAGC	1	1		
GTG	GACGACAGC	1	1		
AC	GACGACAGC	1	1		
CC					
TC					
ATA					
TC					
TC	GACGACAGC	1	1		
TCAG					
GTC	AAGAACGGC	1	1		
CTG	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
g	GACGACAGC	1	1	120	0.98333333
TC	GACGACAGC	1	1		
AAT					
CTT	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
GTC	AAGAACGGC	1	1		
CCC	GACGACAGC	1	1		
TTT	GACGACAGC	1	1		



1						
2						
3						
4	GGC	GACGACAGC	1	1		
5	ATC	GACGACAGC	1	1		
6	CTC	GACGACAGC	1	1		
7						
8	ATC	GACGACAGC	1	1		
9	f				2	1
10						
11	AA					
12	TCC	GACGACAGC	1	1		
13	TT					
14						
15	CAC	GACGACAGC	1	1		
16	f	GACGACAGC	1	1	9	1
17	TTT	GACGACAGC	1	1		
18						
19	GTC	AAGAACGGC	1	1		
20						
21	TC					
22	ATC					
23	ATC					
24						
25	GTC	AAGAACGGC	1	1		
26	g	GACGACAGC	1	1	31	0.93548387
27						
28	TGC					
29	TGC	GACGACAGC	1	1		
30	AG	GACGACAAC	1	1		
31						
32	CTG	GACGACAGC	1	1		
33	GTC	AAGAACGGC	2	2		
34	GTC	AAGAACGAC	2	2		
35						
36	TA					
37	GTC	AAGAACGGC	1	1		
38						
39	ATC	GACGACAGC	1	1		
40	CTC	GACGACAGC	1	1		
41						
42	TTT	GACGACAGC	1	1		
43	AT	GACGACAGC	1	1		
44	CA	GACGACAGC	1	1		
45						
46	c				3	1
47	p	AAGAACGGC	1	1	4	1
48						
49	p	AAGAACGGC	1	1	3	1
50	GTC	AAGAACGGC	1	1		
51	TT	GACGACAGC	1	1		
52						
53	CTG	GACGACAGC	1	1		
54						
55	g				13380	0.99379671
56	ATC	GACGACAGC	2	2		
57						
58						
59						
60						

ATC						
p					1026	0.99902534
ACT	GACGACAGC	1	1			
GTC	AAGAACGAC	1	1			
ACA	GACGACAGC	1	1			
g					2	1
TTT	GACGACAGC	1	1			
CA	GACGACAGC	1	1			
TGT	GACGACAGC	1	1			
GTC	AAGAACGGC	1	1			
TC	GACGACAGC	1	1			
TT	GACGACAGC	1	1			
TG	GACGACAGC	1	1			
TA	AAGAACGGC	1	1			
ATC	GACGACAGC	1	1			
GTC	AAGAACGGC	1	1			
p	AAGAACGGC	1	1		3	1
f					3	1
ATC	GACGACAGC	1	1			
o					4	1
GTT						
g					19	1
f					17	1
TTT	GACGACAGC	1	1			
TG						
TCC						
GTT	AAGAACGGC	1	1			
TCA	AAGAACGGC	1	1			
TGT						
GTC	AAGAACGGC	1	1			
AATC	GACGACAGC	1	1			
TT	GACGACAGC	1	1			
g	AAGAACGGC	1	1		21	1
TC	GACGACAGC	1	1			
f	GACGACAGC	1	1		2	1
g	GACGACAGC	1	1		8	1
GTC	AAGAACGAC	1	1			
g	GACGACAGC	1	1		2	1

1						
2						
3						
4	.TG	AAGAACGGC	1	1		
5	TC	GACGACAGC	1	1		
6	FGC	GACGACAGC	1	1		
7						
8	g				6	1
9	ATC					
10	TGT	AAGAACGGC	1	1		
11						
12	CAC					
13	CTG					
14						
15	CC	GACGACAGC	1	1		
16	CT					
17						
18	CCC					
19	g				4	1
20	AAT					
21						
22	.TC	GACGACAGC	1	1		
23	ATC	GACGACAGC	1	1		
24						
25	.GG	GACGACAGC	1	1		
26	CT	GACGACAGC	1	1		
27						
28	CTA	GACGACAGC	1	1		
29	CTC	GACGACAGC	1	1		
30	CG	GACGACAGC	1	1		
31						
32	g	GACGACAAC	1	1	2	1
33	CTG	GACGACAGC	1	1		
34	CT	GACGACAGC	1	1		
35						
36	CTG					
37	TT	GACGACAGC	1	1		
38	CTG	GACGACAGC	1	1		
39						
40	TCT					
41						
42	f	GACGACAGC	1	1	11	1
43	TTT	GACGACAGC	1	1		
44						
45	TTC					
46	TCA					
47	CC	GACGACAGC	1	1		
48	TCA					
49						
50	FGC					
51						
52	TCT	GACGACAGC	1	1		
53	TTC	GACGACAGC	1	1		
54	IGTC	GACGACAGC	1	1		
55	GTC	AAGAACGGC	1	1		
56						
57						
58						
59						
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ATC	GACGACAGC	1	1		
TGT					
CTT					
ATC	GACGACAGC	1	1		
CT					
g	AAGAACGGC	1	1	13	1
g	GACGACAGC	1	1	29	0.96551724
CC	GACGACAGC	1	1		
.TC	GACGACAGC	1	1		
CTG					
g	GACGACAGC	1	1	42	0.83333333
ACT	GACGACAGC	1	1		
GTC	AAGAACGGC	1	1		
TT	GACGACAGC	1	1		
CTG	GACGACAGC	1	1		
TG	GACGACAAC	1	1		
TT					
TT					
AG	GACGACAGC	1	1		
ATG					
TG	GACGACAGC	1	1		
CT	GACGACAGC	1	1		
g	GACGACAGC	1	1	780	0.93076923
CAC					
CT	GACGACAGC	1	1		
CTA	GACGACAGC	1	1		
CTA	GACGACAGC	1	1		
TT	GACGACAGC	1	1		
AG	GACGACAGC	1	1		
AC					
C					
CTA	GACGACAGC	1	1		
TT					
GTC	ACGAACGAC	1	1		
GTC	AAGAACGAC	1	1		
TTA					
CTA	GACGACAGC	1	1		
CTG	GACGACAGC	1	1		

1				
2				
3				
4	5TC	AAGAACGGCC	1	1
5	3AT	GACGACAGCC	1	1
6	5TC			
7				
8	3TT	GACGACAGCC	1	1
9	3TG	AAGAACGGCC	1	1
10	5AC	GACGACAGCC	1	1
11	5GA	GACAACAGCC	1	1
12	5CT	GACGACAGCC	1	1
13	TTT	GACGACAGCC	1	1
14	3TA	GACGACAGCC	1	1
15				
16	GTG			
17				
18	3TG	GACGACAGCC	1	1
19	3A	GACGACAGCC	1	1
20	5GC	GACGACAGCC	1	1
21	5CA	AAAAACGGCC	1	1
22	TC	GACGACAGCC	1	1
23	3AA	GACGACGGCC	1	1
24	5TC	GACGACAGCC	1	1
25	GAC	AAGAACGACC	1	1
26	5TC	AAGAACGGCC	1	1
27	3CT	GACGACAGCC	1	1
28	3TC	GACGACAGCC	1	1
29	5AC	GACGACAGCC	1	1
30	5TC	GACGACAGCC	1	1
31	TC	GACGACAGCC	1	1
32	5TC			
33	TG	GACGACAGCC	1	1
34	f	GACGACAGCC	1	1
35	ATT	GACGACAGCC	1	1
36	5AC	GACGACAGCC	1	1
37	TC			
38	CTT	GACGACAGCC	1	1
39	TC	GACGACAGCC	1	1
40	5TT	GACGACAGCC	1	1
41	TC	GACAACAGCC	1	1
42	5TT	GACGACAGCC	1	1
43	5GC	GACGACAGCC	1	1
44	5TG	GACGACAGCC	1	1
45				
46				
47				
48				
49				
50				
51				
52				
53				
54				
55				
56				
57				
58				
59				
60				

16 1

1							
2							
3							
4	GTC						
5	TT	GACGACAGC	1	1			
6	TT						
7							
8	AG	GACGACAGC	1	1			
9	TT	GACGACAGC	1	1			
10	TTA						
11	CCA						
12	TG						
13	CAC	GACGACAGC	1	1			
14	GATC	GACGACAGC	1	1			
15	AT						
16	ATC	GACGACAGC	1	1			
17							
18							
19							
20	g				66	0.98484848	
21	ATG						
22							
23	TG	AAGAACGGC	1	1			
24							
25	g				36		1
26	f				2		1
27	c	GACGACAGC	1	1	2		1
28	TG	GACGACAGC	1	1			
29	TA	GACGACAGC	1	1			
30	TTT	GACGACGGC	1	1			
31	CTA	GACGACAGC	1	1			
32	GATC	GACGACAGC	1	1			
33	TTT						
34	TTC	GACGACAGC	1	1			
35	AGC	GACGACAGC	1	1			
36	ATC						
37	ATC						
38	ATC						
39	ATC						
40	ATC						
41	ATC						
42	ATC						
43	ATC						
44	ATC						
45	ATC						
46	CTT						
47	f	GACGACAGC	1	1	2		1
48	ATC	AAGAACGGC	1	1			
49	TG	GACGACAGC	1	1			
50	TG	AAGAACGGC	1	1			
51	TC	GACGACAGC	1	1			
52	ATC	GACGACAGC	1	1			
53	CTA	GACGACAGC	1	1			
54							
55							
56							
57							
58							
59							
60							

1					
2					
3					
4	GCT	GACGACAGC	1	1	
5	CTC	GACGACAGC	1	1	
6	g				7454 0.92125034
7					
8	TC	GACGACAGC	1	1	
9	GATC	GACGACAGC	1	1	
10					
11	g	GACGACAGC	1	1	23 0.95652174
12	AA				
13	AG				
14					
15	TC	GACGACAGC	1	1	
16	CTT	GACGACAGC	1	1	
17	ATC	GACGACAGC	1	1	
18					
19	CTC				
20					
21	ATC				
22	ATC	GACGACAGC	2	2	
23	ATC	GACGACAGC	2	2	
24					
25	CAA				
26	GTT				
27					
28	AAA	GACGACAAC	1	1	
29	AA				
30	CT	GACGACAGC	1	1	
31					
32	TCG	GACGACAGC	1	1	
33					
34	ATC				
35					
36	ATT				
37	TTT	GACGACAGC	1	1	
38					
39	CGC	GACGACAGC	1	1	
40					
41	CTC				
42	ATA	GACGACAGC	1	1	
43	TAC	GACGACAGC	1	1	
44					
45	ATC	GACGACAGC	1	1	
46					
47	TC				
48	g				7 1
49	ATC				
50	GTG	GACGACAGC	1	1	
51	TTT	GACGACAGC	1	1	
52					
53	ACT				
54					
55	CTA	GACGACAGC	1	1	
56	ATC	GACGACAGC	1	1	
57					
58					
59					
60					

CT	GACGACAGC	1	1		
g	GACGACAGC	1	1	643	0.99222395
TC	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
g	GACGACAGC	1	1	4	1
TC					
ATC					
g	AAGAACGGC	1	1	9	1
g				163	0.98773006
TT	GACGACAGC	1	1		
TC					
ACC	GACGACAGC	1	1		
f	GACGACAGC	1	1	2	1
CTC	GACGACAGC	1	1		
TCT	GACGACAGC	1	1		
TTT	GACGACAGC	1	1		
CTA	GACGACAGC	1	1		
TCT					
TC	GACGACAGC	1	1		
g				3	1
CA	GACGACAGC	1	1		
g	GACGACAGC	1	1	6	1
ATC					
g	GACGACAGC	1	1	19	0.94736842
TCT					
g	GACGACAGC	1	1	12	1
CTC					
TC					
TC	GACGACAGC	1	1		
CG					
TCT	GACGACAGC	1	1		
f	GACGACAGC	1	1	2	1
CTA	GACGACAGC	1	1		
TCT	GACGACAGC	1	1		
TAC					
GT	AAGAACGGC	1	1		
f	GACGACAGC	1	1	4	1



1						
2						
3						
4	CC	GACGACAGC	1	1		
5	g	GACGACAGC	1	1	369	0.97831978
6	g	GACGACAGC	1	1	3	1
7						
8	CT					
9	GCTT	GACGACAGC	1	1		
10	CT					
11	CAT	GACGACAGC	1	1		
12						
13	p				2	1
14	CA	GACGACAGC	1	1		
15						
16	ITC					
17						
18	TA					
19	TC	GACGACGGC	1	1		
20						
21	g	GACGACAGC	1	1	6	1
22	TA	GACGACAGC	1	1		
23						
24	TC					
25	AC	GACGACAGC	1	1		
26	TTT	GACGACGGC	1	1		
27						
28	TC	GACGACAGC	1	1		
29	TAC	GACGACAGC	1	1		
30	CAC	GACGACAGC	1	1		
31						
32	CT	GACGACAGC	1	1		
33	TTT	GACGACAGC	1	1		
34						
35	TTT	GACGACAGC	1	1		
36	GTC	AAGAACGGC	1	1		
37	CT	GACGACAGC	1	1		
38						
39	CAC	GACGACAGC	1	1		
40	ATC					
41						
42	TT	GACGACAGC	1	1		
43	AC	GACGACAGC	1	1		
44						
45	ATC	GACGACAGC	1	1		
46	CA	AAGAACGGC	1	1		
47	TGT	AAGAACGGC	1	1		
48						
49	AG	GACGACAGC	1	1		
50	GCT	GACGACAGC	1	1		
51						
52	CAC					
53	TC	GACGACAGC	1	1		
54						
55	p				75	1
56	g	GACGACAGC	1	1	4	1
57						
58						
59						
60						

g	GACGACAGC	1	1	24	0.83333333
TTT					
TAC	GACGACAGC	1	1		
.CC	GACGACGGC	1	1		
TCG	GACGACAGC	1	1		
CAC	GACGACAGC	1	1		
TTT	AAGAACGGC	1	1		
f	GACGACAGC	1	1	2	1
g	GACGACAGC	1	1	5	1
TCC	AAGAACGGC	1	1		
TC	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
TCT	GACGACAGC	1	1		
CTA	GACGACAGC	1	1		
TCC	GACGACAGC	1	1		
TCA	GACGACAGC	1	1		
ATG	GACGACAGC	1	1		
GTC	AAGAACGGC	1	1		
TTT	GACGACAGC	1	1		
CCC					
CT	GACGACAGC	1	1		
TAA					
CCC	GACGACAGC	1	1		
ATC					
CAC	GACGACAGC	1	1		
g	GACGACAGC	1	1	2	1
AC	GACGACAGC	1	1		
CCC	GACGACAGC	1	1		
TCT	GACGACAGC	1	1		
g	GACGACAGC	1	1	5	1
TCC	GACGACAGC	1	1		
p	AAGAACGGC	1	1	766	1
GA	GACGACAGC	1	1		
GTC	AAGAACGGC	1	1		
.CTT	GACGACAGC	1	1		
TT	GACGACAGC	1	1		
g	GACGACAGC	1	1	2	1
ATC					

1						
2						
3						
4	CTC	GACGACAGC	1	1		
5	f	GACGACAGC	1	1	2	1
6	g	GACGACAGC	1	1	256	0.97265625
7						
8	ATG	GACGACAGC	1	1		
9	TC	GACGACAGC	1	1		
10	TC	GACGACAGC	1	1		
11	CTG	GACGACAGC	1	1		
12						
13	f	GACGACAGC	1	1	28	1
14						
15	TC					
16	CA	GACGACAGC	1	1		
17	TTT	GACGACAGC	1	1		
18						
19	ATC					
20	TT	GACGACAGC	1	1		
21						
22	g	GACGACAGC	1	1	9	0.88888889
23	g				24	0.95833333
24						
25	TTC	GACGACAGC	1	1		
26	f	GACGACAGC	1	1	24	0.83333333
27	GTC	AAGAACGGC	1	1		
28						
29	CT	GACGACAGC	1	1		
30	ATC					
31						
32	ATC	GACGACGGC	2	2		
33	TCT	GACGACAGC	1	1		
34	TTT	GACGACAGC	1	1		
35						
36	ATT	GACGACAGC	1	1		
37						
38	AAA					
39	AA					
40	CT	GACGACAGC	1	1		
41						
42	TC	GACGACAGC	1	1		
43	TGC	GACGACAGC	1	1		
44						
45	TTT					
46	ATC	GACGACAGC	1	1		
47	AA	GACGACAAC	1	1		
48						
49	ATA	GACGACAGC	1	1		
50						
51	ATC					
52	ATC	GACGACAGC	1	1		
53	TT	GACGACAGC	1	1		
54	CAC	GACGACAGC	1	1		
55						
56	g				7	1
57						
58						
59						
60						

GTC	AAGAACGAC	1	1		
TTT					
AA					
TC	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
GTC	AAGAACGAC	1	1		
GGC	GACGACAGC	1	1		
CAT	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
CTC					
TC	GACGACAGC	1	1		
CAA	GACGACAGC	1	1		
CTC	GACGACAAC	1	1		
TTT					
CTG	GACGACAGC	1	1		
ATC					
ATC	GACGACAGC	1	1		
CAT	GACGACAGC	1	1		
GTC					
TG	GACGACAGC	1	1		
GATC	GACGACAGC	1	1		
TG	AAGAACGGC	1	1		
TC	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
CAT					
CTA	GACGACAGC	1	1		
CAT	GACGACAGC	1	1		
TGTC	GACGACAGC	1	1		
TCG	GACGACGGC	1	1		
TCA	GACGACAGC	1	1		
TCC	GACGACAGC	1	1		
TC	GACGACAAC	1	1		
TCA	GACGACAGC	1	1		
p	AAGAACGGC	1	1	2	1
f	GACGACAGC	1	1	8	1
GTC	AAGAACGGC	1	1		

1						
2						
3						
4	ATC	GACGACAGC	1	1		
5	TCT	GACGACAGC	1	1		
6	CT	GACGACAGC	1	1		
7						
8	g				137	0.95620438
9	ATT	GACGACAGC	1	1		
10	TTT	GACGACAGC	1	1		
11	TTT	GACGACAGC	1	1		
12	g	GACGACAGC	1	1	2	1
13	TTT	GACGACAGC	1	1		
14	TTT	GACGACAGC	1	1		
15	GAC	AAGAACGGC	1	1		
16	TC	GACGACAGC	1	1		
17						
18	p	AAGAACGGC	1	1	5	1
19	TTT	GACGACAGC	1	1		
20	TTT	GACGACAGC	1	1		
21	TTG	GACGACAGC	1	1		
22	TTT	GACGACAGC	1	1		
23	TTT	GACGACAGC	1	1		
24	TTT	GACGACAGC	1	1		
25	CG	GACGACAGC	1	1		
26	AG					
27	CATC					
28	TTAC					
29	TTAC					
30	ACT					
31						
32	AGG	GACGACAGC	1	1		
33	CA	GACGACAAC	1	1		
34	TGT	AAGAACGGC	1	1		
35	TC	GACGACAGC	1	1		
36	TC	GACGACAGC	1	1		
37	TGT	AAGAACGGC	1	1		
38	TC	GACGACAGC	1	1		
39	TC	GACGACAGC	1	1		
40	ATC					
41	TCG	GACGACAGC	1	1		
42	TC	GACGACAAC	1	1		
43	TCG	GACGACAGC	1	1		
44	TTC	GACGACAGC	1	1		
45	TTC	GACGACAGC	1	1		
46	TTT					
47	TTT					
48	g	GACGACAGC	1	1	5	1
49	TC					
50	TTT	GACGACAGC	1	1		
51	TTT	GACGACAGC	1	1		
52	TTT	GACGACAGC	1	1		
53	TCT	GACGACAGC	1	1		
54	GTT	GACGACAGC	1	1		
55						
56						
57						
58						
59						
60						

ATC	GACGACAGC	1	1		
TC					
TCT					
ATC					
g	GACGACAGC	1	1	2	1
TGC					
TCT	GACGACAGC	1	1		
TCT	GACGACAGC	1	1		
ATC					
TCT	GACGACAGC	1	1		
TTT	GACGACAGC	1	1		
TC	GACGACGGC	1	1		
TC	GACGACGGC	1	1		
TCA	GACGACAGC	1	1		
TTA					
TC	GACGACGGC	1	1		
CGC	GACGACAGC	1	1		
TCA	AAGAACGGC	1	1		
CTG	GACGACAGC	1	1		
TTT	GACGACAGC	1	1		
ACG	GACGACAGC	1	1		
GCC	GACGACAGC	1	1		
ATC					
TTT	GACGACAGC	1	1		
f	GACGACAGC	1	1	4	1
ATC					
TC					
CTT	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
TC	GACGACAGC	1	1		
g	GACGACAGC	1	1	18	1
TGA	GACGACAGC	1	1		
ATC	GACGACAGC	2	2		
AG					
ATC	AAGAACGGC	1	1		
GCT	GACGACAGC	1	1		
AG	GACGACAGC	1	1		
TC					

1				
2				
3				
4	CTG	GACGACAGC	1	1
5	AG			
6	ACT	GACGACAGC	1	1
7	TTT	GACGACAGC	1	1
8	TTT			
9	TC	GACGACAGC	1	1
10	CTC			
11	CTC			
12	TC			
13	TC			
14	TC			
15	TC			
16	TC	GACGACAGC	1	1
17	ATT	GACAACAGC	1	1
18	ATC	AAGAACGGC	1	1
19	ATC	GACGACAGC	1	1
20	GATA			
21	CT			
22	ACC	GACGACAGC	1	1
23	CTG	AAGAACGGC	1	1
24	GTT			
25	GTC			
26	ATC	GACGACAGC	1	1
27	TT	GACGACAGC	1	1
28	GTC	AAGAACAGC	1	1
29	g	AAGAACGGC	1	1
30	CT	GACGACAGC	1	1
31	CAA	GACGACAGC	1	1
32	CA	AAGAACGGC	1	1
33	CTC			
34	TG			
35	GTC	GACGACAGC	1	1
36	CC	GACGACAGC	1	1
37	CT	GACGACAGC	1	1
38	TC	GACGACAGC	1	1
39	CTG	GACGACAGC	1	1
40	GTC			
41	AAA			
42	TA	GACGACAGC	1	1
43	CTG	GACGACAGC	1	1
44	AT	GACGACAGC	1	1
45				
46				
47				
48				
49				
50				
51				
52				
53				
54				
55				
56				
57				
58				
59				
60				

865 0.97572254

TC						
TAC	GACGACAGC	1	1			
TCA	AAGAACGGC	1	1			
CTC						
CTC	GACGACAGC	1	1			
GTC						
CTG						
g	GACGACAGC	1	1	21		1
TC						
TA						
CTC						
ATA						
CTT	GACGACAGC	1	1			
TG						
TAC	GACGACAGC	1	1			
TTT	GACGACAGC	1	1			
ATC						
c	GACGACAGC	1	1	4		1
TC						
CTC	AAGAACGGC	1	1			
TCT	GACGACAGC	1	1			
TC	GACGACAAC	1	1			
ATC	GACGACAGC	1	1			
g	GACGACAGC	1	1	26		1
TGC						
TGC	GACGACAGC	1	1			
TT	GACGACAGC	1	1			
CA	GACGACAGC	1	1			
TAC	AAAAAAGGC	1	1			
ACT	GACGACAGC	1	1			
AG	GACGACAGC	1	1			
TCT	GACGACAGC	1	1			
C	GACGACAGC	1	1			
CTC						
CTC	AAGAACGGC	1	1			
g	GACGACAGC	1	1	29		1
TCT	GACGACAGC	1	1			
CTC	AAAAACGGC	1	1			



1						
2						
3						
4	ATC	GACGACAGC	1	1		
5	TCT	GACGACAGC	1	1		
6	TCTA	GACGACAGC	1	1		
7						
8	CTA					
9	CTA	GACGACAGC	1	1		
10	GTC	AAGAACGGC	1	1		
11						
12	TCC					
13	CTA	GACGACAGC	1	1		
14	g	GACGACAGC	1	1	17	0.82352941
15	CTA	GACGACAGC	1	1		
16	g	GACGACAGC	1	1	189	1
17	AC	GACGACAGC	1	1		
18						
19	TG					
20						
21	g	GACGACAGC	1	1	2	1
22	GAT					
23	f	GACGACAGC	1	1	5	1
24	f	GACGACAGC	1	1	3	1
25	p	AAGAACGGC	1	1	3	1
26	GTC	AAGAACGGC	1	1		
27	TC					
28	CTA	GACGACAGC	1	1		
29	TTC	GACGACAGC	1	1		
30	CT	GACGACAGC	1	1		
31	TTT	GACGACAGC	1	1		
32	AC	GACGACAGC	1	1		
33	f				4	1
34	ACC	GACGACAGC	1	1		
35	ATC					
36	CTC	AAGAACGGC	1	1		
37	p	AAGAACGGC	1	1	2	1
38	f	GACGACAGC	1	1	4	1
39	g				6	1
40	g				3	1
41	TCT					
42	f	GACGACAGC	1	1	7	1
43	TC					
44	TC	GACGACGGC	1	1		
45	TC					
46						
47						
48						
49						
50						
51						
52						
53						
54						
55						
56						
57						
58						
59						
60						

CT	GACGACAGC	1	1		
GTC	AAGAACGGC	1	1		
GGC	GACGACAGC	1	1		
GCT	GACGACAGC	1	1		
GTC					
GTC					
TGT	AAGAACGGC	1	1		
GGC	GACGACAGC	1	1		
c	AAGAACGGC	1	1	4	1
ATC					
f	GACGACAGC	1	1	2	1
GTC	AAGAACGGC	1	1		
ATC					
AC	GACGACAAC	1	1		
g	AAGAACGAC	1	1	3	1
f	GACGACAGC	1	1	5	1
.TC	GACGACAGC	1	1		
CTG					
GTC					
CT					
TGT	GACGACAGC	1	1		
CTA	GACGACAGC	1	1		
GC	GACGACAGC	1	1		
TT					
GG	GACGACAGC	1	1		
.TC	GACGACAGC	1	1		
TG	AAGAACGGC	1	1		
GGC					
CA					
GTC	AAGAACGGC	1	1		
.TC	GACGACAGC	1	1		
f	GACGACAGC	1	1	3	1
GTC					
ATC	GACGACAGC	1	1		
CTA	GACGACAGC	1	1		
TT					
GCT	GACGACAGC	1	1		
GCA	AAGAACGGC	1	1		

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4	TCG	GACGACAGCC	1	1		
5	CAC	GACGACAGCC	1	1		
6	g	GACGACAGCC	1	1	16	1
7	CTT	GACGACAGCC	1	1		
8						
9	CA	GACGACGGCC	1	1		
10	TT	GACGACAGCC	1	1		
11	CTA	GACGACAGCC	1	1		
12	CTC	GACGACAGCC	1	1		
13						
14	GTG					
15	CT					
16						
17	ATC	GACGACAGCC	1	1		
18	CAC	GACGACAGCC	1	1		
19						
20	o	GACGACAGCC	1	1	5	1
21	ATC	GACGACAGCC	1	1		
22						
23	GA	GACGACAGCC	1	1		
24	TGT	AAGAACGGCC	1	1		
25						
26	TCA					
27						
28	TC	GACGACAGCC	1	1		
29	TG	GACGACAGCC	1	1		
30	GA	GACGACAGCC	1	1		
31						
32	p	AAGAACGGCC	1	1	5	1
33	CTC	GACGACAGCC	1	1		
34	GC	GACGACAGCC	1	1		
35						
36	ATC					
37	ATT	GACGACAGCC	1	1		
38						
39	TC	GACGACAGCC	1	1		
40	TG	AAGAACGGCC	1	1		
41						
42	TC	GACGACAGCC	1	1		
43	TCA	AAGAACGGCC	1	1		
44						
45	g				4	1
46	ATT	GACGACAGCC	1	1		
47	TCTC	GACGACGGCC	1	1		
48						
49	TCA	AAGAACGGCC	1	1		
50	TCA	AAGAACGACC	1	1		
51	CTC	AAGAACGGCC	1	1		
52						
53	g	GACGACAGCC	1	1	2	1
54	GGT					
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56	GTG	AAGAACGACC	1	1		
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4	TCT	GACGACAGC	1	1		
5	TC					
6	TC	GACGACAGC	1	1		
7	ATC	AAGAACGGC	1	1		
8	ATC					
9	ATC					
10	ATC	GACGACAGC	1	1		
11	ATC					
12	ATC					
13	GGT	GACGACAGC	1	1		
14	ATT	GACGACAGC	1	1		
15	ATT	GACGACAGC	1	1		
16	ATT	GACGACAGC	1	1		
17	TTC	GACGACAGC	1	1		
18	TTC	GACGACAGC	1	1		
19	TCT	GACGACAGC	1	1		
20	g				55	1
21	TGA					
22	TGA					
23	TG	GACGACAGC	1	1		
24	CTG					
25	CTG					
26	g	GACGACAGC	1	1	13	1
27	TCT					
28	TCT					
29	GTC	AAGAACGAC	1	1		
30	CTG	GACGACAGC	1	1		
31	CTG	GACGACAGC	1	1		
32	TA	GACGACAGC	1	1		
33	TTT					
34	TAC	GACGACAGC	1	1		
35	TAC	GACGACAGC	1	1		
36	CTG	GACGACAGC	1	1		
37	CAC	GACGACAGC	1	1		
38	CAC					
39	TGG					
40	CAC					
41	TGC					
42	TGC					
43	TC	GACGACAGC	1	1		
44	TC					
45	ATC	GACGACAGC	1	1		
46	ATC	GACGACAGC	1	1		
47	AC	GACGACAGC	1	1		
48	TCT	GACGACAGC	1	1		
49	TCT					
50	TA					
51	g				2	1
52	g	GACGACAGC	1	1	11	1
53	g	GACGACAGC	1	1		
54	TC	GACGACAAC	1	1		
55	TC	GACGACAAC	1	1		
56	TGT	AAGAACGGC	1	1		
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4	CTA	GACGACAGC	1	1		
5	ATC					
6	.TC					
7						
8	GTC	AAGAACGAC	1	1		
9	CT					
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11	.TC	GACGACAGC	1	1		
12	CT					
13	CT					
14	CT					
15	CT	GACGACAGC	1	1		
16	CT	GACGACAGC	1	1		
17						
18	GTC	AAGAACGAC	1	1		
19	GTC	AAGAACGAC	1	1		
20	GTC	AAGAACGGC	1	1		
21	GTC	AAGAACGGC	1	1		
22	GTC	AAGAACGGC	1	1		
23	.TC	GACGACAGC	1	1		
24	.TC	GACGACAGC	1	1		
25	CT					
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27	.TC	GACGACGGC	1	1		
28	.TC					
29	TC	GACGACGGC	1	1		
30	ATC	GACGACAGC	1	1		
31	ATT					
32	ATC	GACGACAGC	1	1		
33						
34	g				65	1
35	f	AAGAACGGC	1	1	4	1
36	GTC	AAGAACGGC	1	1		
37	ATC	GACGACAGC	1	1		
38	GAC	AAGAACGGC	1	1		
39	GTC	AAGAACGGC	1	1		
40	GTC	AAGAACGAC	1	1		
41	ATC	GACGACAGC	1	1		
42	ATT	GACGACAGC	1	1		
43	GTC	AAGAACGAC	1	1		
44	ATC	GACGACAGC	1	1		
45	ATC	GACGACAGC	1	1		
46	GTC					
47	ATC	GACGACAGC	1	1		
48	GTC					
49	ATC	GACGACAGC	1	1		
50	GTC					
51	ATC	GACGACAGC	1	1		
52	ATC					
53	GTA					
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p	AAGAACGGC	1	1	2202	0.99954587
GTC	AAGAACGGC	1	1		
GTC					
CTC	GACGACAGC	1	1		
GTC					
ATC					
GTC	AAGAACGGC	1	1		
GTA					
TC	AAGAACGGC	1	1		
ATC	GACGACAGC	1	1		
ATC	GACGACAGC	1	1		
ATC					
ATC					
GTC	AAGAACGAC	1	1		
GTG	AAGAACGGC	1	1		
GTC	AAGAACGGC	1	1		
ATC	GACGACAGC	1	1		
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ATC	GACGACAGC	1	1		

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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Comamonas	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac	
Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymenophorea		
Eukaryota	Gracilipodida				Filamoeba	
Eukaryota	Discosea	Flabellinia	Dactylopodida			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae		
Eukaryota	Metazoa					
Eukaryota	Discosea	Flabellinia	Vannellida			
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Zoogloea	
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio	
Bacteria	Proteobacteri	Betaproteobacteria			Thiobacillus	
Eukaryota						
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae		
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiracea	Nitrospira	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Thauera	
Eukaryota						
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac	
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiracea	Nitrospira	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Candidatus Ac	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17		
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc	

Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Proteobacteri	Gammaproteobacteria			
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetoplastina		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Nitrosomonas	Nitrosomonas
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Eukaryota					
Eukaryota					
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineac	Ornatilinea
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Dongia
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Azovibrio
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Dechloromon
Bacteria	Planctomycet	BD7-11			
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteria	Massilia
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Bacteria	Planctomycet	OM190			
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	PHOS-HE51	
Bacteria	Proteobacteri	Betaproteobacteria			
Eukaryota	Cercozoa		Euglyphida		
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetoplastina		
Bacteria	Cyanobacteri	Melainabacte	Obscuribacterales		



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Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Blvii28 waste
Bacteria	Proteobacteri Alphaproteob Rhodospirilla Rhodospirilla Defluviicoccus
Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomona Nitrosomonas
Bacteria	Proteobacteri Betaproteoba Rhodocyclace Rhodocyclace Zoogloea
Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae
Bacteria	Proteobacteri Betaproteobacteria
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Proteobacteri Gammaproteob Xanthomonas Xanthomonadaceae
Eukaryota	
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Ferruginibacte
Bacteria	Planctomycet OM190
Bacteria	Chloroflexi Anaerolineae Anaerolineales Anaerolineaceae
Bacteria	Proteobacteri Deltaproteob Myxococcales
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteria Chryseobacte
Bacteria	Planctomycet Phycisphaera Phycisphaera Phycisphaera SM1A02
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Proteobacteri Betaproteobacteria
Bacteria	Proteobacteri Betaproteoba Nitrosomona Nitrosomona Nitrosomonas
Bacteria	Proteobacteri Alphaproteob Rhodospirilla Rhodospirillaceae
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteriaceae

Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae	
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Eukaryota	Metazoa				
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Chloroflexi		Anaerolineae	Anaerolineaceae	
Bacteria	Proteobacteri	Alphaproteob	Caulobacteri	Hyphomonad	Woodsholea
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3		
Eukaryota	Discosea	Flabellinia	Vannellida		Vannella
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Eukaryota	Tubulinea	Arcellinida	Echinamoebida		Echinamoeba
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia	Bosea
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	CL500-3
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae	Haliangium
Bacteria	Chlorobi	Ignavibacteri	Ignavibacteri	BSV26	
Eukaryota	Ciliophora	Intramacronu	Conthreep	Phyllopharynx	Tokophrya
Bacteria	Chloroflexi				
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacte	Meganema
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	

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Bacteria	Chloroflexi	
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonada Brachymonas
Bacteria	Proteobacteri	Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Bacteroidetes	Flavobacteriia Flavobacteria NS9 marine group
Bacteria	Acidobacteria	Acidobacteria Subgroup 17
Eukaryota	Heterolobose Tetramitia	Naegleria
Bacteria	Proteobacteri	Gammaprote Aeromonadal Aeromonada Aeromonas
Bacteria	Acidobacteria	Acidobacteria Subgroup 3
Bacteria	Proteobacteri	Alphaproteob Rhodospirilla Rhodospirilla Ferrovibrio
Bacteria	Bacteroidetes	Flavobacteriia Flavobacteria NS9 marine group
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonadaceae
Bacteria	Proteobacteri	Gammaprote Pseudomona Pseudomona Pseudomonas
Bacteria	Acidobacteria	Acidobacteria Subgroup 3
Bacteria	Proteobacteri	Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Proteobacteri	Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Proteobacteri	Alphaproteob Caulobactera Caulobactera Brevundimon
Bacteria	Planctomycet	OM190
Bacteria	Proteobacteri	Betaproteoba Rhodocyclale Rhodocyclaceae
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Chloroflexi	Anaerolineae Anaerolineale Anaerolineaceae

Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Candidatus Acidithiobacillus
Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonas	Xanthomonadaceae	
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	Chitinophagales	Ferruginibacter
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacteriales	Hyphomonadaceae	Woodsholea
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	Chitinophagaceae	
Eukaryota					
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Thauera
Bacteria	Chloroflexi	Thermomicrobium	JG30-KF-CM45		
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	Chitinophagaceae	
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteraceae	
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	Chitinophagaceae	
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacteriales	Rhodobacteraceae	
Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	Phaselicystidae	Phaselicystis
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	Chitinophagaceae	
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriia	Flavobacteriia	Flavobacterium
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Pelomonas
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Oxalobacteraceae	
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadaceae	
Bacteria	OC31				

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobia
Bacteria	Proteobacteri	Gamma	Xanthomonas	Thermomonas
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales	Reynanella
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Nitrosomonadaceae
Bacteria	Proteobacteri	Gamma	Xanthomonas	Candidatus
Bacteria	Planctomycet	Planctomycet	Planctomycet	Schlesneria
Bacteria	Proteobacteri	Betaproteoba	Burkholderia	Oxalobacter
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteob	Caulobacter	Phenylobacte
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	NS9 marine group
Bacteria	Proteobacteri	Alphaproteob	Sphingomonas	Sphingomonadaceae

Bacteria	Proteobacteri Alphaproteob Rhizobiales
Bacteria	Proteobacteri Betaproteoba Hydrogenoph Hydrogenophilaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 4 DS-100
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Dongia
Bacteria	Proteobacteri Alphaproteob Rhizobiales JG35-K1-AG5
Bacteria	Bacteroidetes
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Azospira
Bacteria	Actinobacteri Actinobacteri PeM15
Bacteria	Proteobacteri Deltaproteob Myxococcales mle1-27
Bacteria	Actinobacteri Actinobacteri Kineosporiale Kineosporiace Kineosporia
Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	Actinobacteri Actinobacteri PeM15
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Singulisphaera
Bacteria	Cyanobacteri Chloroplast
Bacteria	Proteobacteri Gammaproteobacteria
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pirellula
Bacteria	Acidobacteria Holophagae Holophagales Holophagace Geothrix

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Devosia
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae	
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Proteobacteria				
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad	Diaphorobact
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangiaceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Plasticicumula
Eukaryota	Ascomycota				
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad	Delftia
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces

Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	mitochondria
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas Stenotrophon
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad
Bacteria	Chloroflexi			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderiac
Eukaryota	Ochrophyta	Diatomea	Bacillariophyt	Bacillariophyc
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteriu
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Cryomorphac
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	
Bacteria	Chloroflexi	Ardenticatenia		
Bacteria	Cyanobacteri	Melainabacte	Obscuribacterales	



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Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Caulobacteral	Hyphomonad
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Thauera
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Sphingobacte Nubsella
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Proteobacteri	Alphaproteob	Caulobacteral	Hyphomonad Hirschia
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Alcaligenaceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Candidatus Cc
Bacteria	Chloroflexi			
Bacteria	Planctomycet	OM190		
Bacteria	Chloroflexi	Chloroflexia	Chloroflexale	Roseiflexacea Roseiflexus
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga Ferruginibacte

Bacteria	Spirochaetae Spirochaetes Spirochaetales Leptospiraceae Turnerella
Bacteria	Chloroflexi
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillaceae
Bacteria	Actinobacteria Actinobacteria Micrococcales Microbacteriaceae Leucobacter
Bacteria	Verrucomicrobia Verrucomicrobia Verrucomicrobia Verrucomicrobia Prosthecobacter
Bacteria	Bacteroidetes Sphingobacteriales Sphingobacteriales Saprospiraceae
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales Rhodospirillales Defluviicoccus
Bacteria	Verrucomicrobia Verrucomicrobia Verrucomicrobia DEV007
Bacteria	Bacteroidetes Sphingobacteriales Sphingobacteriales Saprospiraceae
Bacteria	Bacteroidetes Sphingobacteriales Sphingobacteriales env.OPS 17
Bacteria	Proteobacteria Betaproteobacteria Burkholderiales Comamonadaceae Comamonas
Bacteria	Proteobacteria Alphaproteobacteria Rhodospirillales B79
Bacteria	Planctomycetes Planctomycetes Planctomycetes Planctomycetes Planctomyces
Bacteria	Proteobacteria Alphaproteobacteria Sphingomonadales
Bacteria	Chlorobi Chlorobia Chlorobiales OPB56
Bacteria	Planctomycetes Planctomycetes Planctomycetes Planctomycetes Planctomyces
Bacteria	Proteobacteria Rhizobiales Hyphomicrobia Rhodoplanes
Bacteria	Verrucomicrobia OPB35 soil group
Bacteria	Proteobacteria Betaproteobacteria Nitrosomonas Nitrosomonas Nitrosomonas
Bacteria	Proteobacteria Alphaproteobacteria Rhizobiales Phyllobacteriaceae Mesorhizobium
Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae

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Bacteria	Bacteroidetes Sphingobacte Sphingobacteriales
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Singulisphaera
Bacteria	Proteobacteri Betaproteoba Neisseriales Neisseriaceae
Bacteria	Proteobacteri Betaproteoba Burkholderiales
Bacteria	Chloroflexi
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonada Comamonas
Bacteria	Proteobacteri Betaproteoba TRA3-20
Bacteria	Bacteroidetes Sphingobacte Sphingobacte NS11-12 marine group
Bacteria	Acidobacteria Holophagae Holophagales Holophagaceae Geothrix
Bacteria	Proteobacteri Alphaproteob Caulobactera Caulobacteraceae
Bacteria	Planctomycet Pla4 lineage
Bacteria	Actinobacteri Actinobacteri Micrococcales Microbacteriaceae
Bacteria	Nitrospirae Nitrospira Nitrospirales Nitrospiraceae Nitrospira
Bacteria	Proteobacteri Alphaproteob Caulobactera Hyphomonadaceae
Bacteria	Proteobacteri Deltaproteob Myxococcales Nannocystaceae Nannocystis
Bacteria	Bacteroidetes Sphingobacte Sphingobacteriales
Bacteria	Proteobacteri Alphaproteob Rhizobiales MNG7
Bacteria	SHA-109
Bacteria	Acidobacteria Acidobacteria Subgroup 4
Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Proteobacteri Betaproteoba SC-I-84

Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12 marine group
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Denitratisoma
Bacteria	Armatimonadetes			
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderiac Lautropia
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Acidobacteria	Holophagae	Subgroup 10	ABS-19
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Gemmata
Bacteria				
Bacteria	Proteobacteri	Gammaproteobacteria		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ Sphaerotilus
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Eukaryota	Discosea	Flabellinia	Vannellida	
Eukaryota	Metazoa	Silicispongia	Demospongiae	

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Bacteria	Proteobacteri	Alphaproteobacteria			
Eukaryota	Tubulinea	Arcellinida	Echinamoebida		Vermamoeba
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Diaphorobact
Bacteria	Candidate division	BRC1			
Bacteria	Bacteroidetes	Flavobacteriæ	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderia	Pandora
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Acidovorax
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	F0723	
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Armatimonadetes				
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Ferrovibrio
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Isosphaera

Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Eukaryota	Phragmoplast	Embryophyta		Liliopsida
Bacteria	Proteobacteri	Alphaproteob	DB1-14	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhodoplanes
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteraceae
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillal Reyranelia
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae Haliangium
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Chlorobi	Chlorobia	Chlorobiales	SJA-28
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona Sphingomona
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Gammaprote	Pseudomonadales	

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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Comamonas
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Candidate division	BRC1			
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales		
Bacteria	Acidobacteria	Holophagae	Subgroup 7		
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Sphaerotilus
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteræ	Rhodobacteraceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomona	Nitrosomonas
Bacteria	Proteobacteri	Betaproteoba	SC-I-84		
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria					
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Thermomona
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Acidobacteria	Acidobacteria			
Bacteria	Proteobacteri	Alphaproteob	DB1-14		

Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Oxalobacteria Massilia
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria Flavobacteria Flavobacteriu
Bacteria	Chlorobi	Chlorobia	Chlorobiales SJA-28
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal Rhodospirilla Defluviicoccus
Bacteria	Proteobacteri	Gammaprote	Xanthomonac Xanthomonadaceae
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales Xanthobacter Labrys
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycetaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Planctomyces
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Comamonadaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial Comamonadaceae



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Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla
Eukaryota	Tubulinea	Euamoebida		Saccamoeba
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales	
Bacteria	Actinobacteri	Actinobacteria		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomonadaceae
Bacteria	Proteobacteri	Gammaproteobacteria		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Verrucomicro	OPB35 soil group		
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae

Bacteria Proteobacteri Alphaproteob Caulobacteri Caulobacteria Brevundimon  
Bacteria Proteobacteri Betaproteoba Burkholderial Oxalobacteria Massilia  
Bacteria Proteobacteri Betaproteobacteria

Bacteria Proteobacteri Alphaproteob Rhizobiales Rhizobiales In Bauldia

Bacteria Proteobacteri Gammaprote Xanthomonadales

Bacteria Proteobacteri Gammaprote Xanthomonac Xanthomonac Candidatus Co

Bacteria Proteobacteri Alphaproteob Rhizobiales Brucellaceae Ochrobactrun

Bacteria Proteobacteri Alphaproteob Rhizobiales Hyphomicrob Hyphomicrob

Eukaryota Ciliophora Intramacronu Conthreep Oligohymeno Tetrahymena

Bacteria Bacteroidetes Flavobacteriiz Flavobacteria Flavobacteria Cloacibacteriu

Bacteria Acidobacteria Acidobacteria Subgroup 3

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Schlesneria

Bacteria Proteobacteri Gammaprote Legionellales Coxiellaceae Aquicella

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces

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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ	Comamonas
Bacteria	OC31				
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla	Defluviicoccus
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Phyllobacteriaceae	
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Proteobacteri	SPOTSOCT00m83			
Bacteria	Proteobacteri	Gammaprote	Chromatiales	Chromatiaceæ	Rheinheimera
Bacteria					
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace	Denitratisoma
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales		
Bacteria	Actinobacteria				
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiaceae	Rickettsia
Bacteria	Proteobacteri	Gammaprote	Thiotrichales	Thiotrichacea	Thiothrix

Bacteria	Actinobacteri	Acidimicrobii	Acidimicrobia	lamiaceae	lamia
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Ideonella
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Steroidobacte
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149	
Bacteria	Proteobacteri	Gammaprote	Pseudomona	Pseudomona	Pseudomonas
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales		
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	SM1B06	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata

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Eukaryota				
Bacteria	Chloroflexi	KD4-96		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 17	
Eukaryota	Choanomona	Craspedida	Codonosigidae	Sphaeroeca
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Oxalobacteria
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Xanthobacteraceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla
Bacteria	Bacteroidetes	Flavobacteriiz	Flavobacteria	NS9 marine group
Bacteria	Proteobacteri	Betaproteobacteria		Rhodocyclaceae
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona
Bacteria	Verrucomicro	OPB35	soil group	
Eukaryota	Ascomycota	Sordariomycetes		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet
				Pirellula

Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12 marine group
Bacteria	Proteobacteri	Betaproteoba	TRA3-20	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Pir4 lineage
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderial Thiomonas
Bacteria	Proteobacteri	Gammaprote	Pseudomona	Pseudomona Pseudomonas
Bacteria	Proteobacteri	Betaproteoba	SC-I-84	
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclace Candidatus Ac
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera Caulobacter

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Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteob	DB1-14	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales	
Bacteria	Proteobacteri	Gammaprote	Enterobacteri	Enterobacteri
Bacteria	Proteobacteri	Gammaprote	Enterobacteri	Enterobacter
Bacteria	Acidobacteria	Acidobacteria	Subgroup 6	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiales
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17

Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Bacteroidetes Sphingobacte Sphingobacte PHOS-HE51
Bacteria	Proteobacteri Betaproteoba Rhodocyclale: Rhodocyclace Dechloromon
Bacteria	
Eukaryota	Phragmoplast Embryophyta
Bacteria	Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Rikenella
Bacteria	Actinobacteri Actinobacteri Micrococcale: Microbacteriaceae
Bacteria	Proteobacteri Alphaproteob Rhizobiales MNG7
Bacteria	



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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobact	Meganema
Bacteria	Proteobacteri	Gamma	Xanthomonas	Xanthomonas	Candidatus C
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Eukaryota	Metazoa				
Eukaryota				Thraustochytriaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Alcaligenaceae	MWH-UniP1
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Eukaryota	Tubulinea	Euamoebida			BOLA868
Bacteria	Proteobacteri	Alphaproteob	Caulobacteral	Hyphomonad	Woodsholea
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Amaricoccus

Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellaceae
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria
Bacteria	Actinobacteri	Acidimicrobi	Acidimicrobia	Sva0996 marine group
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona
Bacteria	Proteobacteri	Gammaprote	Methylococcales	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada
Bacteria	Chlorobi	Chlorobia	Chlorobiales	Chlorobiaceae
Bacteria	Actinobacteri	Actinobacteri	Frankiales	
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla

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Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	TK34
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Proteobacteri	Alphaproteobacteria		
Eukaryota	Metazoa			
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Candidatus Cc
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Candidate division	BRC1		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadæ Comamonas
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteraceae
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae
Bacteria	Proteobacteri	Gammaprote	Enterobacteri	Enterobacteriaceae

Bacteria	Proteobacteri Deltaproteob GR-WP33-30
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Pir4 lineage
Bacteria	Proteobacteri Alphaproteobacteria
Bacteria	Bacteroidetes Flavobacterii; Flavobacteria Flavobacteria Flavobacteriu
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonad; Comamonas
Bacteria	Proteobacteri Gammaprote Legionellales Coxiellaceae Aquicella
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Actinobacteri Acidimicrobii; Acidimicrobia Acidimicrobia Candidatus M
Bacteria	Proteobacteri Deltaproteob Myxococcales; 0319-6G20
Bacteria	TM6

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Bacteria	Verrucomicro OPB35 soil group
Bacteria	Proteobacteri Betaproteoba Hydrogenoph Hydrogenoph Thiobacillus
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadæ Comamonas
Bacteria	Actinobacteri Acidimicrobiiæ Acidimicrobia Acidimicrobia CL500-29 mar
Bacteria	Proteobacteri Alphaproteobacteria
Bacteria	Proteobacteri Gammaprote Xanthomonac Xanthomonac Candidatus Cc
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Actinobacteri Actinobacteri Micrococcale Intrasporengi Tetrasphaera
Eukaryota	Metazoa
Bacteria	Verrucomicro OPB35 soil group
Bacteria	Proteobacteri Alphaproteob Sphingomona Sphingomona Novosphingot
Bacteria	Proteobacteri Betaproteoba Burkholderial Alcaligenaceae
Bacteria	Armatimonadetes
Bacteria	Spirochaetae Spirochaetes Spirochaetale Spirochaetac Spirochaeta
Bacteria	Proteobacteri Deltaproteob Myxococcales Cystobacterac Anaeromyxob
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadæ Comamonas

Bacteria	Acidobacteria	Acidobacteria Subgroup 6
Bacteria	Proteobacteri	Gammaprote Xanthomonac Xanthomonac Candidatus Cc
Bacteria	Proteobacteri	Gammaprote Xanthomonac Xanthomonadaceae
Bacteria	Planctomycet	OM190
Bacteria	Proteobacteri	Betaproteoba Burkholderial Burkholderiac Limnobacter
Bacteria	Chlamydiae	Chlamydiae Chlamydiales Parachlamydi Candidatus Pr
Bacteria	Spirochaetae	Spirochaetes Spirochaetale Spirochaetac Spirochaeta
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Sphingobacte Sphingobacte
Bacteria	Actinobacteri	Thermoleoph Solirubrobact 480-2
Bacteria	Proteobacteri	Alphaproteob Rhizobiales Phyllobacteriaceae

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Bacteria	Proteobacteri	Betaproteobacteria
Bacteria	Proteobacteri	Alphaproteob Rhizobiales Beijerinckiaceae
Bacteria	Proteobacteri	Alphaproteob Rhodobacter Rhodobacter Amaricoccus
Bacteria	Planctomycet	Planctomycet Planctomycet Planctomycet Schlesneria
Bacteria	Chlamydiae	Chlamydiae Chlamydiales Parachlamydi Candidatus Pr
Bacteria	Verrucomicro	OPB35 soil group
Bacteria	Proteobacteri	Betaproteoba Burkholderial Comamonada Comamonas
Bacteria	Actinobacteri	Actinobacteri Micrococcale Intrasporangiaceae
Bacteria	Proteobacteri	Alphaproteob Rhizobiales Phyllobacteri Mesorhizobiu
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Saprospiraceae

Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacteriales	
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac Steroidobacte
Eukaryota				
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacteriaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob Pedomicrobiu



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Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Eukaryota					
Bacteria	Proteobacteri	Gamma	proteobacteria		Pseudomonas
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	aceae
Eukaryota					
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae	
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobiaceae	
Bacteria	Verrucomicro	OPB35	soil group		

Eukaryota

Bacteria Acidobacteria Acidobacteria Subgroup 17

Bacteria Planctomycet 028H05-P-BN-P5

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Isosphaera

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae

Bacteria Acidobacteria Acidobacteria

Bacteria Proteobacteri Alphaproteob Rhizobiales Bradyrhizobiaceae

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Bacteria      Proteobacteri   Betaproteoba   Burkholderial   Comamonadaceae

Bacteria      Proteobacteri   Betaproteoba   Rhodocyclale   Rhodocyclaceae

Bacteria      Proteobacteri   Betaproteoba   Rhodocyclale   Rhodocyclaceae

Bacteria  
Eukaryota      Metazoa  
Eukaryota      Metazoa

Bacteria      Proteobacteri   Gammaproteobacteria

Eukaryota	Metazoa				
Bacteria	Cyanobacteri	Cyanobacteri	SubsectionIII	FamilyI	Leptolyngbya
Eukaryota	Metazoa				
Eukaryota					
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Eukaryota					
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	Lewinella

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Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Acetobacteria	Roseomonas
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteria	Leucobacter
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	

Eukaryota

Bacteria Proteobacteri Alphaproteob Rhizobiales Hyphomicrob Hyphomicrob

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Sediminibacte

Bacteria Proteobacteri Gammaprote Enterobacteri Enterobacteri Cronobacter

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For Peer Review

Bacteria      Proteobacteri   Betaproteoba   Hydrogenoph   Hydrogenophilaceae

Bacteria	Proteobacteri	Betaproteoba	Methylophila	Methylophila	Methylophilu
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Hyphomicrob
Bacteria	Proteobacteria			Nitrosomonadaceae	
Bacteria	Verrucomicro	OPB35 soil group			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	



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Bacteria	Proteobacteri	Gammaproteob	Enterobacteri	Enterobacteriaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiaceae	Shinella
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Hyphomonad	Woodsholea

Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacte
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacte
Eukaryota				
Archaea	Euryarchaeot	Methanomicr	Methanosarci	Methanosarci
Archaea	Euryarchaeot	Methanomicr	Methanosarci	Methanosarci
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet
Bacteria	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellacea
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionella
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobiaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Planctomyces
Eukaryota				
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Eukaryota				
Eukaryota	Metazoa			
Bacteria	Proteobacteri	Gammaprote	Pseudomona	Moraxellacea Perlucidibaca

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Isosphaera

Bacteria

Bacteria Proteobacteri Alphaproteob Rhizobiales Methylocysta Methylocystis

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Gemmata

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Gemmata

Eukaryota Metazoa

Bacteria Proteobacteri Alphaproteob Rhizobiales Xanthobacter Labrys

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Bacteria	Acidobacteria	Acidobacteria Subgroup 3	SJA-149
Bacteria	Proteobacteria	Alphaproteobacteria Rhizobiales	Brucellaceae Ochrobactrun
Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteria env.OPS 17
Bacteria	Proteobacteria	Betaproteobacteria Rhodocyclales	Rhodocyclaceae
Bacteria	Proteobacteria	Gammaproteobacteria Legionellales	Legionellaceae Legionella
Bacteria	Proteobacteria	Alphaproteobacteria Rhizobiales	
Bacteria	Actinobacteria	Actinobacteria Micrococcales	Microbacteriaceae

For Peer Review

Eukaryota      Metazoa  
Bacteria      Proteobacteria      Alphaproteobacteria      Rhizobiales      Xanthobacteraceae

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Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Rhizobiales In Nordella
Eukaryota	Metazoa			
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellaceae Legionella

Bacteria Proteobacteri Alphaproteob Rhodobacter Rhodobacter Paracoccus

Bacteria Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae

Bacteria Proteobacteri Gammaprote Xanthomonac Xanthomonadaceae



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Eukaryota    Ascomycota    Dothideomyc    Pleosporales

Bacteria Proteobacteria Betaproteobacteria Nitrosomonas Nitrosomonas Nitrosomonas

Bacteria Verrucomicrobia

Bacteria Bacteroidetes Sphingobacteriales Sphingobacteriales Chitinophagaceae

Bacteria Bacteroidetes Sphingobacteriales Sphingobacteriales Saprospiraceae Haliscomenella

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Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales	Novosphingot
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiracea Nitrospira
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae Haliangium
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Betaproteobacteria		
Eukaryota	Metazoa			
Bacteria	Chloroflexi	Anaerolineale	Anaerolineaceae	
Eukaryota	Metazoa			
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Gemmata
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Gemmata
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12 marine group

Eukaryota	Gracilipodida	LEMD267	
Bacteria	Planctomycet	Planctomycet	Planctomycetaceae
Eukaryota	Heterolobose	Tetramitia	Vahlkampfia
Bacteria	Proteobacteri	Gammaprote	Legionellales Legionellaceae
Bacteria	Bacteroidetes		

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Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Candidatus Cc
Bacteria	Proteobacteri	Alphaproteob	DB1-14		
Eukaryota	Metazoa				
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus

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20	Bacteria	Proteobacteri Alphaproteob Rhizobiales
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26	Bacteria	Planctomycet Planctomycet Planctomycet Planctomycetaceae
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51	Bacteria	Proteobacteri Alphaproteob Rhizobiales Methylocysta Pleomorphon
52	Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirilla Ferrovi
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tag	Flocs Control 1	Flocs Control 2
TTGCCATTAGTTGCTACATTCAAGTTGAGCACTC	15	18
TTGCCATTAGTTGCTACATTCAAGTTGGGCACTC	2	5
TTGTCATTAATTGCCATCATTGAGTTGGGCACT	19417	3325
TAACCTGCTAACTAGTATTACTATCCCAAATAG	2	2
TTGTCATTAGTTGCTACGAAAGGGCACTCTAAT	4345	20967
TAGCCTACTAAATAGTTCGCCGACACCTCTTGT	6723	3139
TTACTGCTAGTTGCTAACAGGAAAGCTGAGAAC	23	16
TTGTCGTTAATTGCCATCATTTAGTTGGGCACT	1200	1078
TTGTCATTAGTTGCCAGCATTCAAGTTGGGCACT	2658	2648
CTGCTTTCAGTTGCTACCGGGTCATGCCGAGCA	1022	1640
TTGTCGTTAATTGCCATCATTAAAGTTGGGCACT	912	756
TTGTCCCTAGTTGCCAGCGGTTGCGCCGGGAAC	198	285
TTGTCATTAATTGCCATCATTTAGTTGGGCACT	1084	1106
TTGTCACTAGTTGCCATCATTTGGTTGGGCACT	934	426
CTGTTGTTAGTTGCCATCGAGTCAAGTCGGGAA	0	0
CGAGAGGGTGTTGAGGTTATTATTGAGGGATG	2198	1109
TTGTCATTAATTGCCATCATTCAAGTTGGGCACT	634	709
TTGTCACTAATTGCCATCATTTGGTTGGGCACT	785	1750
CAGTGGGAGGGACGCTCAATTCATCTCATAATG	0	0
TTGTCGTTAATTGCCATCATTTGGTTGGGCACT	961	1014
TTGTCCTTAGTTGCCAGCACGTAATGGTGGGAA	548	1200
CTCCTTATTAAGTAGTGTGGCTCGCGGCCATAA	352	375
TAGCCTGCTAAATAGTCCGTGATCTTCCGAGAT	2004	941
CGACTTGTTAACTAGTCCGGCGCAGCCTGCAAG	953	806
CGAGAGGGTGTTGAGGTTATTATTGAGGGGTG	1311	626
CAGTGGGAGGGACGCTCAATCAATAGTCTTATT	0	0
TTACCGTGAGTTACCATCATTCAAGTTGGGGACT	515	722
TTGTCACTAATTGCCATCATTAAAGTTGGGCACT	449	261
CTATCGTTAGTTGCCTGGCGCAAGCCGGTACTC	16	27
TTGTCATTAATTGCCATCCTTAAGTTGGGCACT	0	0
TCGTCCTGTGTTGCTAACCGAAAGGTGCACTCT	459	468
TTGTCATTAGTTGCCATCATTAAAGTTGGGCACT	720	551
TCGCTGTATGTTACATGTGTCATACAGGACCGC	0	0
CTGTCGTTAGTTGCTCACAGGTTATGCTGAGTA	776	404
CTCCTTATTAAGTAGTGTGGCTCGCGGCCGTAA	5	4
TCATTGCCAGTTACAAGTGTCTGGCGAGACTGC	0	0
CTACCATTAGTTGCCAACAGGTAAAGCTGGGGGA	533	463

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4	CAGCCTACTAAATAGCTATGCAGATTTGATTAT	47	65
5	CCATCACTAGTTGCCATCAGGTAACGCTGGGAA	514	309
6	CTATTGCCAGTTACCATCATTGAGTTGGGGACT	0	0
7	TAACCTGCTAAATATGTCACCGGTAGACTTCTG	576	143
8	TTGTCCCTAGTTGCCAGCATTTTCGGATGGGAAC	4	6
9	CAGTGGGAGGGGACACTCAATTCATCTCATAATG	0	0
10	CTATTCTTAGTTGCCAGCATGTAATGGTGGGGA	259	271
11	CAGTGGGAGGGGACACTCAATTCATTGAAAGATG	0	0
12	TCGCCTTTAGTTGCCACGCAAGTGGATCTCTAG	279	193
13	CAGTGGGAGGGGACACTCTTTTCATCACAAAGATG	0	0
14	CTACCATTAGTTGCTAACATTTAGTTGAGGACT	0	0
15	CTATCACTAGTTGCCATCAGGTAATGCTGGGAA	260	331
16	TTGCCGTTAGTTACTAACGGGTAAAGCCGAGGA	277	427
17	TCGTCTTCAGTTGCCATCGGGTAGGGCCGGGCA	318	488
18	CTATTCTTAGTTGCCAGCATGTTATGGTGGGGA	0	0
19	CTATCTTTAGTTGCCAGCGAGTAATGTCGGGGA	138	193
20	CTGTGCTTAGTTGCTCGGCGAAAGCCAGTACTC	261	406
21	TTACCGTGAGTTACCATCATTTAGTTGGGTACT	365	387
22	TTGCCATTAGTTGCTACGAAAGGGCACTCTAAT	308	239
23	TTATCATTAGTTGCCAACATTTAAGGTGGGAAC	2	0
24	CTATCTTCAGTTGCCATCATTAGTTGGGCACT	5	12
25	TTGTCACTAGTTGCCATCATTTAGTTGGGCACT	6	3
26	CTGTGCTTAGTTGCCAGCATTAAGTTGGGCACT	0	0
27	CGGCCTGCTAAATAGTGCTCTGAACTCTTCGGG	194	434
28	CTGTCACTAGTTGCTAACATTAAGTTGAGGACT	0	0
29	TGGTCTACTAACTAGTATTTATCATTTAGCAAC	131	458
30	TTATTTGTTAATTAGATGAAGCAACAGGATTGT	200	231
31	CGAGAGGGTGGTTGAGGTTATTAATGAGGGATG	389	202
32	CTATTCTTAGTTGCCAGCATGTCATGGTGGGGA	18	13
33	CTGTCCATAGTTGCCAGCAAGTTAGTTGGGGA	191	266
34	CAGTGGGAGGGACGCATTGGAAAGAGTTTTTTC	0	0
35	TTACCCTATGTTGCCAGCATTTAGTTGGGCACT	232	165
36	TCACTTGCTAACTAGTCGCAGCTAAAACCTAGC	265	393
37	CTATCGCTAGTTGCCAGCGCGTCAAGGCGGGGA	0	0
38	CGGCTTACTAAATAGTCTAAAGTTCGCAGGGAC	46	42
39	TCGTGCGGTGTTATATGTGTACGCGAGACCGC	150	146
40	TCGGTGTGCGTTACAAGTGTCGCACACAACTGC	0	3
41	CTGTCCTCAGTTACCACCGTTCAGTCGGGGACT	152	271
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4	TTGTCGCTAGTTACAAGTGTCTAGCGAGACTGC	186	206
5	CTATCGTTAGTTGCTCGGAGCAATCCAGTACTC	111	331
6	TAACCTGCTAAATAGTCAGGCCGCTTTGGCTG	53	944
7			
8	CTACCATTAGTTGCTAGCAGGTCATGCTGAGGA	19	16
9	CTATTGCCAGTTACCATCATTTAGTTGGGGACT	0	0
10			
11	CAGCCTACTAAATAGTAATGCAAACCTTTACTAA	347	63
12	TTATCTTCTGTTACCAACGCGTAAAGGCGGGGA	0	0
13			
14	CTGTCACTAGTTGCCATCATTAAAGTTGGGGACT	111	742
15	CAGCCTGCTAAATAGTTATGCGAATTTTACTAC	151	231
16	TAACCTGCTAACTAGTACTTTGATTTTCAATCG	14	370
17			
18	CCGTTGTTAGTTGCCATCAGGTAATGCTGGGCA	128	203
19	CTGTTGTTAGTTGCCAGCGAGTGATGTCGGGAA	37	66
20			
21	CTGTCCTTAGTTGCCATCATTAGTTGGGCACT	103	92
22	TCGTGTCCAATTGCCATCATTAAAGTTGGGGACT	0	0
23			
24	TTGCCATTAATTGCCATCATTTAGTTGGGCACT	140	250
25	CTATTGCCAGTTACAAGTGTCTGGCGAGACTGC	164	220
26	TAACCTGCTAAATAGACATGCCGGCTTTGGCTG	70	683
27			
28	CCGTGTCCAGTTGCCAGCATTAAAGTTGGGGACT	0	0
29	CTGTTGTTAGTTGCCAGCATTAGTTGGGCACT	140	256
30			
31	CTATCTTTAGTTGCCATCAGGTAATGCTGGGAA	141	230
32	CTATCGTTAGTTGCTCACGCAAGTAGTACTCTA	72	55
33			
34	TTGTCCCTAGTTGCCAGCACTTCGGGTGGGAAC	0	7
35	TAACCTACTAAATAGTTACGAAAATATTGCTAT	301	8
36	CAGTGGGAGGGACGCTCATCACATGAATAATGA	0	0
37			
38	TCGCCGTTAGTTGCTTCGCAAGAAGATCTCTAA	19	14
39	TCGCCGTATGTTACATGTGTCATACGGGACCGC	29	18
40	TTGCCCTGTGTTGCCACTCCGAAAGGAAGCACT	166	181
41			
42	TTGTCACTAGTTGCCAGCATTAAAGTTGGGCACT	97	76
43	TCGCCTCCTGTTGCCAACAGATAATGCTGGGCA	124	132
44			
45	TCGTTCCATGTTGCCAGCACGTAGTGGTGGGGA	72	161
46	TTGTCCTCAGTTACCACCATTAGTTGGGGACT	133	188
47			
48	CAGTGGGAGGGACGCATTGAGAAGAATCACTTT	0	0
49	CTATTTTCAGTTGCCAGCACATAATGGTGGGAA	149	91
50	CTACCATTAGTTACCAACGGGTAAAGCCGGGCA	26	29
51			
52	TTACCGTGAGTTACCATCATTTAGTTGGGGACT	75	230
53	CTATCTTTAGTTGCCACCAGGTAATGCTGAGCA	0	0
54			
55	CCGCCTGCTAAATAGCGCAGCCTTGGCTCGTCC	2	0
56	CTGTTTCTAGTTGCCAGCGAGTAAAGTCGGGCA	78	215
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4	CCGCCTGCTAAATAGCGCTGGCCTTGGCTTGTC	0	0
5	TCATCCTCAGTTGCCATCGGGTTCGGCCGGGCA	0	0
6	TCACGAGATAATAGGTCGAGAAAAGGAACTTT	0	0
7			
8	TTGTCCTGTGTTGCCATCATTAGTTGGGCACT	90	103
9	CTATCTCTAGTTGCCAGCGGGTAATGCCGGGGA	0	0
10			
11	CTATCGTTAGTTGCTCGGCGCAAGCCAGTACTC	49	82
12	CTGTGCTTAGTTGCCAGCATTAGTTGGGCACT	133	146
13	TTGTCATTAGTTGCCATCATTTAGTTGGGCACT	87	58
14			
15	CTGTGTCCTGTTGCCACCGGGATGAGAGTCCCCG	0	0
16	TTGTCATTAGTTGCTACGAAAGAGCACTCTAAT	83	160
17	TTGCCCTTAGTTGCTACGCAAGAGCACTCTAGG	58	168
18			
19	CAGTTAATAAATAGGGGACATAATTCATTGAAT	0	11
20	TCGTCGCTAGTTACACGTGTCTAGCGAGACCGC	22	40
21			
22	CTATCTTCTGTTACCATCGCGTAAAGGCGGGGA	5	291
23	TTGTCATTAATTGCTACCATTTAGTTGGGCACT	108	75
24	TCGTCCTATGTTGCCAGCACGTGATGGTGGGAA	0	0
25			
26	TCACGAGATAATAGGTCGGGAAAAGGAACTTT	0	0
27			
28	TAACCTGCTAAATAGTCCATGTTTGGTTCGCCC	42	5
29	TTGTCATTAGTTGCCAGCATTAAAGTTGGGCACT	143	94
30			
31	CTACCAATAGTTGCCAGCGGTTTCGGCCGGGGAC	100	52
32	TAGCCTGCTAAATAGTACGCCGATCCTTAGTCG	41	219
33	TCGTCCTTAGTTGCCATCATTAGTTGGGCACT	7	9
34			
35	TAACATGCTAACTAGCCGACGCGCGTCTGCCCT	0	6
36	CAGTGGGAGGGACGCAATGATCATTTTTCTTAA	0	0
37	TTACTGCCAGTTACAAGTGTCTGGCGGGACTGC	13	24
38			
39	TTGTCACTAATTGCCATCATTAGGTTGGGCACT	142	95
40	CTGTCCACAGTTGCCACCATTAGTTGGGAACT	51	128
41			
42	TCGTGGCTAGTTACAAGTGTCTAGCCAGACTGC	47	112
43	TTACCAGCTAAATAGTAATTATTTGATTTATC	0	30
44	TCGCCCCTAGTTGCCATCATTAGTTGGGAACT	52	47
45			
46	TAGCCTATTAATTAGGGCTTTATAACTCGGCCG	0	0
47	TCGCCGCGTGTTATACGTGTCACGCGGGACCGC	35	90
48			
49	CCATCTTCAGTTGCCAACGGGTCATGCCGGGAA	44	89
50	CTGTGCTAGTTACCATCAGGTTATGCTGGGGA	67	124
51	TTGTCATTAATTGCCATCATTTGGTTGGGCACT	32	50
52			
53	ACACTTTCAGTTGCCATCATTAGTTGGGCACT	38	37
54	CTATCTTTAGTTGCCAGCATTAAAGTTGGGCACT	0	0
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56	CTGCCGTTAGTTGCCAACGGGTTATGCCGGGAA	0	0
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4	TTATCGCCAGTTACAAGTGTCTGGCGAGACTGC	39	126
5	CTATTGATAGTTGCTAACATTAAGTTGAGAACT	69	49
6	TCGTCCTGTGTTGCTACCCGCAAGGGGCACTCT	37	83
7	TTGTCATTAGTTGCTACATTCAGTTGAGCACTC	0	7
8	TCGTTCTATGTTGCCAGCACGTAATGGTGGGAA	46	110
9	CCATCATTAGTTGCCATCAGGTAAAGCTGGGAA	87	59
10	CTATCTTTAGTTGCCATCAGGTTTGGCTGGGCA	0	0
11	TTGTCCTGTGTTGCAACCCGCAAGGGGCACTCT	67	77
12	CTATCCTATGTTGCCACCCGCGCAAGCGGCGCA	24	127
13	TCGGCGTTAGTTACAAGTGTCTAACGCGACTGC	0	0
14	CTATTGACATTTGCCATCATTAAAGTTGGGGACT	0	0
15	CTATCGTATGTTGCTAACGGGTAATGCCGAGCA	0	0
16	TCGTCTCCAGTTGCCATCAGGTTAAGCTGGGCA	80	80
17	TCGCCTTTAGTTGCTCCGCAAGGAGATCTCTAG	69	68
18	TTGCCCTAGTTGCCAGCACGTAATGGTGGGAA	42	81
19	TCGGCGTTAGTTACACGTGTCTAACGCAACTGC	0	0
20	TCGCTATTAGTTGCCATCAGGTTAAGCTGGGCA	70	62
21	TAATTTTTAAATAGTTTCCATCAAGGCAACTTG	0	2
22	CTATCGTTAGTTGCTCACGGGTCATGCCGAGTA	65	85
23	TCGTTCTATGTTGCCAGCGCGTTATGGCGGGGA	4	0
24	TAGCCTGCTAACTAGCTACGCGCGTCGTGCGGC	0	89
25	TTACCGTCAGTTACAAGTGTCTGGCGGGACTGC	30	57
26	TTACCAGCTAAATAGTGATTATTATGATTTATC	0	31
27	TCGCCTCTAGTTGCCATCATTTAGTTGGGCACT	5	5
28	CTGTCCTTAGTTGCCATCATTAAAGTTGGGGACT	0	0
29	TAACCTGCTAACTAGTACACTTATTTTCCATAG	2	130
30	CAGTTAATAAATAGGGGATATAATCTTTACTGA	0	0
31	CAGTTAATAAATAGGGGACATAATCTTTTAGAT	0	0
32	TCGTCTTCAGTTGCCATCAGGTTTGGCTGGGCA	49	91
33	TCGCCCTTAGTTGCCATCATTAGTTGGGCACT	15	57
34	CTATTGCTAGTTGCCATCAGTTCGGCTGGGCAC	15	143
35	TTACCATTAGTTGCCATCATTAGTTGGGCACT	68	51
36	TCGTCTTATGTTGCCAGCGGGTCATGCCGGGAA	29	100
37	TTGTCCTGTGTTGCAACCCGCGAGGGGGCACT	49	57
38	CTGTCGCTAGTTACTAACAGGTAATGCTGAGGA	55	76
39	TCGTGTTCAAGTTGCCAGCAAGTAAAGTTGGGGA	9	10
40	TCATCCCTAGTTGCCATCATTAGTTGGGCACT	0	0
41	CTATCGTTAGTTGCCAGCGGTCCGGCCGGGCAC	0	0
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4	TAACCTGCTAACTAGTATTAGTATCCCAAATAC	3	122
5	TCGTGCGGTGTTATACGTGTCACGCGAGACCGC	19	18
6	TTGTCACTAGTTGCCAGCGGGTAATGCCGGGGA	34	72
7	TCGTGCTATGTTGCCAGCGGATAATGCCGGGGA	57	33
8	TTGTCCTCAGTTGCCATCATTAGTTGGGCACT	20	48
9	TCGTGCGCAGTTACACGTGTCTGCCGAGACCGC	17	28
10	AAGCTGTCCAGTAGGAGTCTAAATTGTTTTTTT	0	0
11	CTACCATTAGTTGCTAACAGGTAATGCTGAGGA	37	72
12	CAGTTAATAAATAGGGGATACTAATAGTAATGT	0	0
13	TCTTGTTAGTTGCCAACAGGTAATGCTGGGGA	61	36
14	CGACTTGTTAAGTAGGTGCGGCTATCCTGTGAA	50	40
15	TTGTCATTAGTTGCTACATTAGTTGGGCACTC	28	27
16	CTACACTTAGTTGCCATCAGGTAATGCTGGGCA	67	58
17	CTAGTATTATTTATTTAATAGTTTAGATAATAC	35	46
18	TCATCTTCAGTTGCCATCATTTAGTTGGGCACT	2	9
19	TTACCAGCTAAATAGTAATTTTTATGACTTGTC	0	6
20	TTACCGTTAGTTGCTAACAGGAAAGCTGAGCAC	33	22
21	TTAGCGCCAGTTACAAGTGTCTGGCGCGACTGC	26	48
22	TTGCCCTGTTTTGCCATCATTAAAGTTGGGAACT	53	45
23	TCGCTACTAGTTGCCATCAGGTTAAGCTGGGCA	0	3
24	TCGCTACGTGTTACATGTGTCACGTAGGACCGC	25	51
25	CTATTTTCAGTTGCCAACGGGTAATGCCGGGAA	12	69
26	CTGTTGTTAGTTGCCAGCATTAAAGTTGGGCACT	18	60
27	CTATCTTTAGTTGCCAGCGGGTAATGCCGGGGA	0	0
28	TCATCCTCTGTTGCTAACAGGTAATGCTGAGAA	0	0
29	TTGTCATTAAATTGCTATCATTAAAGTTGGGCACT	39	56
30	CTGCGGTTTGTTGCCAGCATTAAAGTTGGGCACT	0	0
31	CTATCATTAGTTGCCATCAGGTAGTGCTGGGAA	0	0
32	TTGTCATTAAATTGCCATCATTAAAGTTGGGCACT	15	16
33	TTAATTATTAATTAGTTAAATATATAGTAATAT	46	30
34	TTGTCCCTAGTTGCCAGCACGTAAAGGTGGGAA	40	55
35	CTATCTTCTGTTACCATCATTAAAGTTGGGGACT	25	44
36	ACACTTCCAGTTGCCATCATTAGTTGGGCACT	0	0
37	TCGTCCCTAGTTACCAGCGGGTCATGCCGGGCA	37	39
38	AAGCTGCCCAGTAGAAACCAAAATCTCTAAACA	0	0
39	TTACCTCTAGTTGCCAGCGAGTCAAGTCGGGAA	30	29
40	TCGCCTTCAGTTGCCATCAGGTAAAGCTGGGCA	0	0
41	CTATCGTTAGTTGCCAGCGTAAAGTCGGGCACT	15	52
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4	CAACCTACTAACTAGTACGACGTGAACAACGTT	17	30
5	TTGTTGTTAATTGCCATCATTTAGTTGGGCACT	47	23
6	TTGTCCTTAGTTGCCATCATTAGTTGGGAACT	32	41
7	TTATCATTAGTTGCTACGCAAGGGCACTCTAAT	28	46
8	TCGCCCTTAGTTGCCATCATTAAGTTGGGCACT	21	42
9	TTACCAGCTAAATAGTGATTATTTTGATTTATC	0	10
10	CCGCCTGCTAAATAGCGCACGCCGGGCACGTCC	0	0
11	TCGTCGCTAGTTATACGTGTCTAGCGAGACCGC	28	34
12	CTACTGCTAGTTGCCAGCGGATAATGCCGGGGA	0	5
13	TTGTCATTAGTTGCTACCGCAAGGAGCACTCTA	41	36
14	TTGTCATTAGTTGCCAGCATTGAGTTGGGCACT	48	51
15	ACACTCTTAGTTGCCAGCATTAGTTGGGCACT	39	15
16	CTGTCCCTAGTTGCCAGCGCGTGAAGGCGGGAA	0	0
17	TCACCTTCAGTTGCCATCAGGTTAAGCTGGGCA	2	4
18	TCATCATTAGTTGCCATCAGGTTTGGCTGGGCA	0	0
19	TCATTTTTAGTTGCCTTATGGAAGCTCTAAAAAG	0	0
20	CTATCTTCAGTTGCCATCATTGAGTTGGGCACT	0	0
21	CTATCGTCTAGTTGCCAGCGGTTGCGCCGGGCA	5	3
22	CTGTGCTTAGTTACTAACAGGTAATGCTGAGGA	15	35
23	TTGTCACTAATTGCCAGCATTAGGTTGGGCACT	3	0
24	TTACCAGCTAAATAGTAATTATTATGACTTGTC	2	4
25	CTGTCTTTAGTTGCCATCATTAAGTTGGGCACT	8	3
26	TTACCGTCAGTTATACGTGTCTGGCGGGACTGC	18	24
27	TAGCCTACTAAATAGTTCGCCGACACCTCTCGT	40	7
28	TAACCTATTAAATAGTCACGCTTATCCTTCGGG	40	21
29	TTGCCCTGTTTTGCCATCATTAGTTGGGAACT	22	48
30	TCACCTTCAGTTGCCAGCGGTTGCGCCGGGGCAC	0	4
31	CTATCTTTAGTTGCCAACAGGTTAAGCTGGGGA	0	2
32	TTGTCACTAATTGCCATCATTGAGTTGGGCACT	1	0
33	CTATCATTAGTTACCAACGGATAAAGCCGGGCA	18	35
34	TTGTCGATAGTTGCCAGCATTTGGTTGGGCACT	25	31
35	TCGTCCTTAGTTGCCATCATTTAGTTGGGCACT	8	19
36	TCGTCGTTAGTTACAAGTGTCTAACGAGACTGC	22	50
37	CTATCATTAGTTACCAACGGGTAAAGCCGGGCA	27	42
38	CTGTGCTTAGTTGCTAACGCGTTATGGCGAGGA	0	0
39	CCGGGGTCAGTTACACGTGTCTGGCCCGACTGC	0	0
40	TCGTCGTCAGTTGCCACCATTCAGTTGGGCACT	9	57
41	TCGTCTTCAGTTGCCATCATTTAGTTGGGCACT	0	0
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4	CCATCCTATGTTGCCATCATTAGTTGGGCACT	0	26
5	AAGCTGCCCAGTAGGAACCAGGATTGTCCATTA	0	0
6	TTAATTATTAATTAGTTAAATATATTTTTTATA	23	14
7	TTGTCATTAGTTGCCATCATTTGGTTGGGCACT	36	30
8	TCGCTGCGTGTTATACGTGTCACGCAGGACCGC	16	11
9	TCGGCGTTAGTTACAAGTGTCTAACGCAACTGC	20	24
10	TCGCCTTTAGTTGCCATCATTTAGTTGGGCACT	0	0
11	TTGTCACTAGTTGCCATCATTAAGTTGGGCACT	0	0
12	CCGTCCTTAGTTGCTACCATTAGTTGAGCACT	21	54
13	TTACCTTATGTTGCCATCATTAGTTGGGCACT	0	0
14	TTGTCCTTAGTTGCTACCATTAGTTGAGCACT	0	0
15	TTGTCCTTAGTTACCAGCACGTTATGGTGGGCA	2	91
16	CTATTTTTAGTTGCCAGCGAGTCATGTCGGGGA	3	24
17	TCGCCCTTAGTTGCCAGCATTAAAGTTGGGCACT	0	3
18	CCGCCTGCTAAATAGCGCAGCCTTGGCCCGTCC	0	0
19	CTATCATTAGTTGCCATCAGGTCAAGCTGGGAA	0	0
20	CTATCTTTAGTTGCTACCGGGTCAAGCCGGGCA	0	0
21	CTATCGTTAGTTGCCTGGCGAAAGCCGGTACTC	12	25
22	CTATCATTAGTTACCAGCGGGTCATGCCGGGAA	34	15
23	TCACGAGATAATAGGTCGAGGAAAGGAACTTT	0	0
24	TTGCCATTAGTTGCCACACTTCGGGTGGGCACT	10	42
25	CTATCTTTAGTTGCCAGCACATAATGGTGGGAA	0	5
26	TCATTCTCTGTTGCTACCAGGTTAAGCTGAGCA	35	21
27	CTGTCGTCAGTTACATGTGTCTGACGAGACTGC	10	28
28	CAGTTAATAAATAGGGGGTATTATTCATTGAAT	0	0
29	TCGTGTTCAAGTTGCCAGCAGGTAAAGCTGGGGA	13	6
30	CTATTAACAGTTGCCATCATTAAGTTGGGAACT	25	26
31	TTGTACTTAGTTGCCATCAAGTGAAGTTGGGGA	45	21
32	TTGTCGTTAGTTGCTAACAGGTAATGCTGAGGA	0	0
33	TCGCCCTTAGTTGCCAGCATTAGTTGGGCACT	9	21
34	CTGTCGCCAGTTTCAGGTGTCTGGCGAGACTGC	16	30
35	CTATCCTTAGTTGCTAACAGGTGAAGCTGAGCA	10	36
36	TTGTCCTTAGTTGCCAGCGGGTAATGCCGGGGA	0	0
37	AAGCTGCCCAGTAGGAACCAGGATTGTCCAAAA	0	0
38	CTGTGTCCTGTTGCCACCGGAACGCGAGTTCCG	19	18
39	CTGTTCTCAGTTACCACCGTTAGTCGGGGACT	13	22
40	TAACCTGCTAACTAGTACCCTGATCCTCAATCG	15	15
41	TCGCCCTTAGTTGCCATCATTTAGTTGGGCACT	10	14
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4	TTACCAGCTAAATAGTGATTATTATGACTTGTC	0	3
5	CTACCATTAGTTGCCAGCGGTTCTGGCCGGGGAC	28	13
6	TCGTGTTCAATTGCCATCAAGTAAAGTTGGGGA	28	13
7	CTATTGCTAGTTATACGTGTCTAGCGAGACTGC	13	26
8	TTGTCATTAGTTGCTACGCAAGAGCACTCTAAT	20	25
9	CTGTTGTTAGTTGCCAACGAGTCAAGTCGGGAA	0	0
10	CTGTTGTTAGTTGCCAGCGAGTAATGTCGGGAA	0	4
11	TCGCCTTTAGTTGCCATCACGTTTGGGTGGGCA	0	2
12	CCGCCTGCTAAATAGCGCTGGCCTTGGCTCGTC	0	5
13	TTGTCCCTAGTTGCTACGCAAGGGCACTCTAGG	8	21
14	CTACACTTAGTTGCCATCAGGTTATGCTGGGCA	24	24
15	TTACCTCTAGTTGCCAGCGGTTCTGGCCGGGAAC	13	55
16	CCATGTTCAAGTTGCCATCATTAAAGTTGGGGACT	21	20
17	TCGCCCCCTAGTTGCCAGCATTAGTTGGGCACT	0	0
18	TTGTCACTAGTTACCAGCGGGTAATGCCGGGAA	22	28
19	CTATCCTTAGTTGCCAGCATGTCTAGGTGGGGA	18	31
20	CTGTTGTTAGTTGCCAGCGAGTCAAGTCGGGAA	26	6
21	CTGTGCTAGTTGCTCGGCGCAAGCCAGTACTC	24	26
22	CTGTTGCTAGTTACAAGTGTCTAGCAAGACTGC	0	0
23	TTTTCCCATGTTGCAATTGCATCTAAACCGTAA	4	32
24	TCGCCTCCTGTTGCCAACAGGTCAAGCTGGGCA	14	20
25	TCACCTTCAGTTGCCATCATTTAGTTGGGCACT	4	7
26	CTATTGACAGTTGCCAATATTAAGTTAGGAACT	26	17
27	CTATCTTCTGTTGCCAATATTAAGTTAGGCACT	2	0
28	TCACGAGATAATAGGTCGGAAAAAGGAACTTT	0	0
29	TTGTCACTAGTTGCTACGAAAGGGCACTCTAGT	10	13
30	CTACTGTGTGTTGTATCACTCACACGGGACTGC	18	24
31	TCGTCTATGTTGCCAGCGGATAATGCCGGGGA	22	18
32	TTGCCAATAGTTGCCATCATTGAGTTGGGCACT	15	22
33	CTGTCACTAGTTGCCATCATTAGTTGGGGACT	4	49
34	CTGTCCTTAGTTGCCATCAGGTTAAGCTGGGCA	0	0
35	CTGCCCTTAGTTGCCATCGGTTCTGGCCGGGCAC	18	21
36	TTGTGCTAGTTACCATCAGGTTATGCTGGGGA	21	20
37	TCATCTTCAGTTGCCATCAGGTTAAGCTGGGCA	0	0
38	CTGTGCTAGTTACCATCAGGTAATGCTGGGGA	17	17
39	TTGTCCTGTGTTGCCACTCCGCAAGGAAGCACT	22	15
40	TCGCCTCTAGTTGCCATCATTAGTTGGGCACT	0	0
41	TTGCCTCTAGTTGCCAGCGAGTCATGTCGGGAA	18	18
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4	CTGTTGTTAGTTGCCAGCGGTTCGGCCGGGCAC	13	22
5	TCGCCATTAGTTGCCATCATTTAGTTGGGAACT	2	6
6	CAGTTAATAAATAGGGGATACTATTCATTGAAT	0	0
7	TCGTCCTATGTTGCCAGCGGGTAATGCCGGGAA	0	8
8	CTGTGTCCTGTTGCCACCCCTTAAATGGGAGCA	20	17
9	TTATTTGTTAATTAGATGAATCAACATTATTGA	23	9
10	CAGTTAATAAATAGGGGATACTATCTTTTAGAT	0	0
11	CTGTCTCCAGTTGCCAGCATTAGTTGGGGACT	12	15
12	CTATCTTTAGTTGCCAACAGGTAATGCTGGGAA	0	0
13	CAGTTAATAAATAGGGGATATTAGTTTTTACT	0	0
14	CCTTGTTGAGTTGCCAGCATTAAAGTTGGGGACT	0	0
15	TCGCTTCTAGTTGCCAGCATTTAGTTGGGCACT	0	0
16	TCGCCTTTAGTTGCCATCATTCAGTTGGGCACT	0	0
17	TTGTCCCTGGTTGCCAGCACTTCGGGTGGGAAC	0	0
18	CAGTTAATAAATAGGGGATATTATTCATTGAAT	0	0
19	CTGGGGTTCAGTTACACGTGTCTGGCCCGACTGC	0	0
20	CAACTTGCTAAATAGTCGCACTAGTCTTCTAAA	10	17
21	CTGTCCTTAGTTGCCATCAGGTAAAGCTGGGCA	9	9
22	TCGCTTTTAGTTGTTTTTTAAAAGGACTGCCTG	24	5
23	CTGTTGCCAGTTACAAGTGTCTGGCGAGACTGC	10	18
24	TTGTCATTAGTTGCCACGAAAGGGCACTCTAGT	16	14
25	CTATCGTATGTTGCCATCATTTAGTTGGGCACT	0	0
26	TTACCAGCTAAATAGTAATTATTATGATTTATC	0	13
27	CCGTTGTTAGTTGCCATCAAGTAATGTTGGGCA	12	23
28	CTGCTGCCAGTTACCATCATTTAGTTGGGGACT	0	0
29	TTGTCACTAGTTACCAGCGGGTAAAGCCGGGCA	5	7
30	CTGTCGTTAGTTGCTAACGCGTCATGGCGAGGA	0	3
31	TCGTCGTTAGTTGCTAACGGTTCGGCCGAGCAC	12	19
32	CTGTCTCCAGTTGCCAGCGAGTCATGTCGGGGA	11	22
33	CTGTTGTCAGTTGCCACCAGGTCAAGCTGGGCA	16	13
34	TTACCGTGAGTTACCATCATTAAGTTGGGGACT	15	15
35	TCACGAGATAATAGGCCGGGAAAAGGAACTTT	0	0
36	CTGCCGTTAGTTGCTAACAGGTCATGCTGAGCA	0	0
37	TCGCCTTCAGTTGCCATCGGGTTAAGCTGGGCA	7	22
38	TTACCAGCTAAATAGTGATTGTTTTGATTTATC	0	0
39	CTGTGGGTAGTTAGATGATCTACCCAGACTGCC	9	14
40	CTATTTCCAGTTGCCAGCGAGTAATGTCGGGGA	12	23
41	TCGCCACTAGTTGCCAGCATTAGTTGGGCACT	0	0
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CTATCACTAGTTACCAGCGGGTAAAGCCGGGGA	0	0
TCGCCATTAGTTGCCATCATTAGTTGGGCACT	7	22
TTATCGCTAGTTGCCATCAGGTTGGGCTGGGCA	0	0
TTATCATTAGTTGCCAACACTTAGGGTGGGAAC	0	0
CCATTTCTAGTTGCCAGCGGGTAATGCCGGGGA	0	0
TTGTCACTAGTTGCCAGCGGGTTATGCCGGGAA	9	16
CAACCTATTAAATAGTGTAATAGAAAATTTCA	36	9
TCGTCTTATGTTGCCAGCGGGTAATGCCGGGAA	7	28
CAACCTATTAAATAGTGTAATAGAAAATTTCT	31	5
TTTTTTTAAGTTACTAATTTAATGATTAAATGT	0	28
CTACTCTTAGTTGCCAGCATGTAATGGTGGGGA	10	16
CTTTCTTTAGTTGCCATCAGGTAATGCTGGGGA	0	0
CTATCTTCAGTTGCCATCATTTAGTTGGGCACT	0	0
TCGGGAGTAGTTACAAGTGTCTACTCCGACTGC	0	0
TTGCCGCTAATTGCCATCATTAGTTGGGCACT	0	5
CTACTTACTAAATAGTTTGTAGTATTTTCA	0	0
CTGCCTGCTAAATAGTCTGGCGAGTGTTTTTCA	0	0
CTATCTTTAGTTGCCATCGGGTAATGCCGGGAA	6	15
TTGTCATTAATTGCCACCATTTAGTTGGGCACT	18	13
TTGTCATCAGTTGCTACGAAAGGGCACTCTGAT	0	0
TTGTCATTAGTTGCTACATTTGGTTGGGCACTC	2	0
CTATCTTTAGTTGCTAACCCGCAAGGGAGGACT	2	0
TTGCCGCTAGTTACCAGCGAGTAAAGTCGGGGA	0	0
CTGTCTGTTAGTTGCTCACGGGTAATGCCGAGCA	0	0
TTGTCATTAATTGCCATCATTGAGTTGGCACTT	9	0
CAGTTAATAAATAGGGGGTAGTATCTTTACTGA	0	0
TCGCCATTAGTTGCCATCATTAAAGTTGGGCACT	0	4
CGAGAGGGTGGTTGAGGTTATTATTGAGGGGCG	14	12
TCGTCTGCTGTTGCCATCAGGTTAAGCTGGGCA	8	8
TTGCCCTTAGTTACCAGCGAGTAAAGTCGGGGA	2	0
CTACTACCAGTTACCAGCGGGAAAGCCGGGGAC	0	0
TTGCTATTAGTTGCTACATTCAGTTGAGCACTC	0	0
CAGTTAATAAATAGGGGACATAATCTTTACTGA	0	0
CTATCTTTGGTTGCCATCATTAAAGTTGGGCACT	0	0
TCGTTCTATGTTGCCAGCACGTAATGGTGGGGA	0	0
CTATCATTAGTTGCCATCAGGTTATGCTGGGGA	15	7
TTGCCAATAATTGCCATCATTAGTTGGGCACT	0	0
TTGTCCTGTGTTGCCATGGCGCAAGCCGGAAC	10	24

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4	CTATGAATAGTTGCCAGCATGTAATGGTGGGGA	0	0
5	TTGTCACTAATTGCCATCATTTAGTTGGGCACT	11	20
6	TTTCCTTATGTTGCTACCAGTTCGGCTGGGCAC	0	3
7	TTGCCCTGTGTTGCCACCCGAAAGGGAGCACT	9	10
8	TCGCTGCCAGTTACCATGTCTGGCGGGACCGCC	7	11
9	TCGTTTCCAGTTGCCAGCGAGTAATGTCGGGGA	0	0
10	TAACCTGCTAAATAGCCCGTATTGCTTTGGCAG	0	13
11	TCGTTCGTTAGTTACAAGTGTCTAACGATACTGC	3	25
12	CTGTCCTTAGTTGCCACCATTAAAGTTGGGCACT	5	3
13	TCATCCTTAGTTGCCATCAGGTAATGCTGGGCA	0	0
14	CGGCCTGCTAACTAGTGCGTGGCGCGCCGCGAG	5	19
15	TCATTGCCAGTTATAAGTGTCTGGCGAGACTGC	0	0
16	ACGCCTTTAGTTGCCATCATTCAGTTGGGCACT	8	24
17	CAGTTAATAAATAGGGGATACTAGTTTTTTTACT	0	0
18	CAGCCTGCTAATTAGTTATATAAATTAATACAC	2	10
19	TTGTACTTAGTTGCCATCAAGTGAAGTTGGGAA	18	10
20	TTGTCCGTAGTTGCCATCATTCAGTTGGGCACT	8	19
21	CTGTCCTTAGTTACCAGCGCGTAATGGCGGGAA	0	0
22	CACTTGGTGTTGTTATCGATTTTTTTTATAAAAC	0	0
23	TTATTCTATGTTGCCAGCGGGTAATGCCGGGGA	0	0
24	CTATCGTTAGTTGCCATCATTCAGTTGGGCACT	0	0
25	AAGCTGCCCAGTAGAAGCCAGGATTGTCTTTTC	0	0
26	TCATCCTTATTTGCCATCAGGTTATGCTGGGGA	0	0
27	CTGTTGTTAGTTGCCAGCGAGTCATGTCGGGAA	8	10
28	TTGTCCCTAGTTGCCAGCACTTTGGGTGGGAAC	7	17
29	TTATCATTAGTTGCCAACGGGTAATGCCGGGGA	0	0
30	CTGTGATTTGTTGCCACCCGTTTTCCGGAGCA	15	5
31	CTGTCCGTAGTTACTAACGCGTCATGGCGAGGA	11	10
32	CTATCTTTAGTTGCCATCAGGTTATGCTGGGGA	16	4
33	CTATCTTTAGTTGCCAGCACGTAATGGTGGGAA	0	6
34	TTACCTGTAGTTGCCAGCGGTTCGGCCGGGAAC	0	2
35	TTGTCTTATGTTGCCAGCACGCCCTTCGGGGTG	12	19
36	CTGTGATTTGTTGCCACCCAGTTTACTGGAGCA	6	12
37	TTGTCATTAATTGCCATTATTGAGTTGGGCACT	6	3
38	TCGGGGGTAGTTACAAGTGTCTACCGCGACTGC	0	0
39	AAGCTGCCCAGTTAGGAACCAGGATTGTCCCAA	0	0
40	TCGCCTTTAGTTGCCAGCATTCAGTTGGGCACT	0	2
41	TCGCGTCCAATTGCCAGCAGGTAAAGCTGGGGA	7	14
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4	TTGCCATTAATTGCCATCATTGAGTTGGGCACT	3	0
5	CCATCTCTAGTTGCCAGCGGGTAATGCCGGGGA	0	0
6	TCGTTGTATAATACGAGGCGCTAGTTTTTTCGT	13	4
7	TAACCTGCTAAATAGTCACTGGAACTGCTGCA	4	2
8	TTGTCACTAGTTGCCAGCGAGTAATGTCGGGGA	0	6
9	CTATCTTTAGTTGCCAGCGCGTCATGGCGGGGA	8	6
10	CTGTGTCCTGTTGCCACTCGGATGAGAGTCCGA	0	0
11	CTATCTCTAGTTGCCATCAGGTAATGCTGGGGA	8	7
12	TTGTCCTTATTTGCCAACAGGTAATGCTGGGAA	0	0
13	TAACCTGCTAAATAGAACTTCTATAACTTAGA	8	13
14	CTACGGTCAGTTACCTGTGTCTGGCCGGACGGC	7	7
15	TTGCCGCTAATTGCCATCATTTAGTTGGGCACT	0	3
16	TTGCCATTAGTTGCTACATTCAGTTGGCACTCT	0	0
17	TAACCTGCTAAATAGACACGCCGGCTTTGGCTG	5	31
18	CTGTTGTTAGTTGCCATCGAGTCAAGTCGGGAG	0	0
19	TTGTCCTTAGTTGCCATCATTCAGTTGGGCACT	14	4
20	TCGCCTTTAGTTGCCACGTAAGTGGATCTCTAG	4	0
21	TTGTCGCTAGTTGCCAACAGGTAATGCTGGGGA	5	11
22	TTGCTATTAGTTGCTACATTCAGTTGGGCACTC	0	0
23	TTGTCGCTAGTTGCCAGCGGGTAATGCCGGGGA	6	5
24	TTGTTCTTAGTTGCCATCATTAAGTTGGGCACT	5	5
25	CTGCTTTAGTTGCTACCGGGTCGTGCCGAGCA	2	5
26	TTATTGCCAGTTACAAGTGTCTGGCGAGACTGC	0	0
27	TCGCTTCTAGTTGCCATCATTCAGTTGGGCACT	6	10
28	TTGTCTTTAGTTGCGACCATTTAGTTGAGCACT	4	9
29	CAGTTAATAAATAGGGGATATAATCTTTTAGAT	0	0
30	TTGTCCTTAGTTGCCAGCGGGTCATGCCGGGGA	0	2
31	CTGCGTCCAGTTGCCACCCCTTAATTGGGAGCA	12	3
32	TCGTCCCTAGTTACCAGCGGGCAAAGCCGGGCA	6	9
33	CTATCCTTAGTTGCCAGCGGATGATGCCGGGCA	3	14
34	TTTTCTCTAGTTGCTAACGGATTATGCCGAGAA	10	9
35	CTGTCTTCAGTTACCAACGGGTCATGCCGGGAA	7	13
36	TTGTCCTATGTTGCCAGCGGGTAATGCCGGGGA	0	2
37	TTACCGTGAGTTACTACCATTCAGTTGAGGACT	10	2
38	CTATTGTTAGTTACCAGCACGTAAAGGTGGGGA	0	4
39	TTGTCATTAATTGCCATCATTGAGTTGGGCACC	9	0
40	CAGTTAATAAATAGGGGGTAATATCTTTTAGAT	0	0
41	AAGCTGCCCAGTAGGAACCAAAATCGCTTGAGA	0	0
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4	TCATCCTTAGTTGCCAACACCTCGGGTGGGAAC	0	12
5	CTTTCTTTAGTTGCCATCAGGTTATGCTGGGGA	8	13
6	CAGCCTGCTAACTAGCTATGTGGAGGTGACCTT	0	0
7	TAACCTGCTAACTAGACTTGCTCACCTTGGTGG	8	4
8	TCGCCTTCAGTTGCCATCACTTTCAGGTGGGCA	0	0
9	TCATTCTCTGTTGCTAACAGGTTAGGCTGAGCA	0	2
10	TTGTCCCTAGTTGCCAGCGAGTCATGTCGGGGA	11	2
11	CCGCCTGCTAACTAGTCGCCTGAATGCCTAGCA	0	0
12	CTACCATTAGTTGCCATCAGGTAAAGCTGGGGA	0	0
13	TTGCCGTTAGTTGCCAGCAGGTCAAGCTGGGCA	0	0
14	CTGTTGTTAGTTGCCAGCAAGTAAAGTTGGGGA	16	3
15	CTGTCCCTAGTTGCCAGCGAGTAAAGTCGGGGA	0	5
16	TCGTCCCTAGTTACCAGCGGGTTATGCCGGGCA	2	10
17	TCGTCTTTGTTGCCAGCGATTAAAGTCGGGAA	0	0
18	CTATTGTTAGTTGCCAGCGGGTCATGCCGGGAA	8	20
19	TTATCAACAGTTGCCATCATTAAAGTTGGGAACT	19	2
20	TCGTCTATGTTGCCAGCACGTTATGGTGGGAA	0	0
21	TCGCCATTAGTTGCCAGCATTAGTTGGGCACT	0	3
22	TCGTCTTCAGTTGCCATCAGGTTATGCTGGGCA	0	0
23	CTGTTTCTAGTTGCCACCGGGTAATGCCGAGCA	0	0
24	CTAGTGCCAGTTACAAGTGTCTGGCGCGACTGC	0	3
25	TTATCCTCAGTTGCCAATGGGTAGAGCCAGGAA	7	0
26	CTACCTTTAGTTGCCAGCATTAAAGTTGGGCACT	7	5
27	TCGCCTCCAGTTGCCAGCATGTTTGGGTGGGCA	5	11
28	CTGTGCTACTTGCTAACGAGTAATGTCGAGGA	2	7
29	TTGCCATTAGTTGCTACATTAGTTGAGCACTT	0	0
30	CTATTGCTAGTTACACGTGTCTAGCGATACTGC	0	0
31	CAACCTGCTAAATAGGAAGTTTGATGGGGGAAT	9	4
32	TTGTTATTAATTGCCATCATTGAGTTGGGCACT	3	0
33	CTGTTCTTAGTTGCCAGCGAGTAAAGTCGGGGA	6	3
34	TTACCAGCTAAATAGTGATTGTTTTGATTTTTC	0	0
35	CTATCATCAGTTGCCAGCGGGTCATGCCGGGGA	0	0
36	TCGTCTATGTTACCAGCGAGTAAAGTCGGGGA	2	15
37	TCGTGTCAGTTGCCCCATTAAGTTGAGCACT	0	0
38	TCGCCATTAGTTGCCCTTATTAAGTTAGGCACT	10	9
39	CTGTGACTAGTTGCCAGCGCGTCAAGGCGGGGA	0	0
40	CTGCCTTTAAATAGAGATGATTATGAGAAATCA	0	0
41	TTGTCATTAATTGTCATCATTGAGTTGGGCACT	1	0
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TCGTTCTATGTTGCCAGCACGTTATGGTGGGAA	0	7
CTCCTTATTAAGTAGTGCGGCCCGCGGCCGTAA	9	8
CTGTCGTTAGTTGCCAGCGAGTAATGTCGGGAA	0	0
CCTTGTTCAAGTTGCCAGCAAGTAAAGTTGGGGA	5	15
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CTGTCGTTAGTTGCCAGCATTGAGTTGGGAACT	0	0
CTATCGTCTGTTGCCATCATTAGTTGGGAACT	0	0
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TCGCTACTAGTTGCTACCAGGTTAAGCTGAGCA	5	9
TTGTCTTTAGTTGCCAGCATTAAAGTTGGGCACT	0	9
CTATCATTAGTTGCCAGCGATTCCGGTCGGGCAC	0	18
CTATGAACTGTTGCCAGCGGGTAATGCCGGGGA	0	0
TTGTTATTAGTTGCCAGCATTAGTTGGGCACT	10	4
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CTGCCTTTAAATAGAGATAGTTATAAGAAATTA	0	0
CTACTGTATGTTGCTAACGGATAATGCCGAGCA	0	6
TCATCCTCAGTTGCCATCGGGTTAAGCCGGGCA	0	0
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TTGTCCTTAGTTGCCAGCATTAGTTGGGGACT	4	8
TTGTCCCTAGTTGCCAGCACGTAATGGTGGGAA	0	4
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TTGTCCTTAGTTGCCAGCGAGTAATGTCGGGGA	0	0
AAGCCTTTAACTAGCCGTAGGCCTTTTCCTTCG	0	0
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CTACCATTAGTTGCTAGCAGGTAATGCTGAGGA	0	0
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TCATCTTCAGTTACTAACGGGTAAAGCCGAGGA	0	0
TCGCCTTTAGTTGCCAGCATTAAAGTTGGGCACT	4	3
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ACGTCCTTAGTTGCCATCATTAAAGTTGGGCACT	0	0



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8	TTACCATACTAACTAGTTATATGTATACTTCTG	16	0
9	TAACCTGCTAAATAGCCCGTACTGCTTTGGCAG	5	16
10			
11	CAGCCTGCTAATTAGTTATATAAATTAATACGC	7	9
12	CGGCTTACTAAATAGTCTAAAGTTCGAAGGGAC	3	3
13	TCACGAGACAATAGGCCAGATAAAGGAACTTT	0	0
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15	TCGTCTTTAGTTGCCAGCACGTCATGGTGGGGA	0	0
16	TTGTCACTAGTTGCCAGCGAGTCATGTCGGGGA	3	9
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18	CTACCTTCAGTTGCCATCACTTCTAGGTGGGCA	0	2
19	TTGTCCTCTGTTGCCACCCCGAAAGGGAGCACT	4	0
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21	TTGTCCTTAGTTGCCAGCGGTTGCGCCGGGAAC	4	3
22	TTGTCCTTAGTTGCTACGCAAGAGCACTCTAAG	4	14
23	CTTTCCTATGTTGCCAGCGGTTGCGCCGGGGAC	0	0
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25	TTGCCATTAGTTGCTACATTCAGTTGGGCACTT	0	0
26	TCGTCCTATGTTGCCAGCGAGTAATGTCGGGAA	2	5
27			
28	TTATCATTAGTTGCCAACACGTAAGGTGGGGAC	7	3
29	TTACCAGCTAAATAGTGATTGCTTTGATTTATC	0	0
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31	TAATTTTTAAATAGTTTTCTTTACTTTTCGAGT	0	0
32	CTGTCCTTAGTTGCCAGCATTCACTTGGGCACT	0	11
33	TCGTTATTTATTGCTTAATCTTTATAGTATAAA	0	5
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35	TCGTTATTTATTGCTTAATCTTTAAAAAAGAAG	7	7
36	CCATGGTCAGTTGCGGATGTTTCTGGCCAGACT	4	6
37	TTGTCATTAATTGCCATCATTGAGTTGGGTACT	2	0
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39	TCCTCTTCAGTTGCCATCGGGTAGGGCCGGGCA	0	6
40	CTATTCCTAGTTGCCAACACTTCGGGTGGGCAC	0	0
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42	TCGTCCTATGTTGCCAGCGGTTGCGCCGGGAAC	3	6
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46	TGCCATTAGTTGCTACATTCAGTTGGGCACTCT	0	0
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54	TAACCTGCTAACTAGTATTACTATCCTAAATAG	0	0
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56	TTGCCTTTAGTTGCCAGCATTAGTTGGGCACT	3	6
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7	CTGCCTTTAAATAGAGATAGTTATGAGAAATCA	0	0
8	TTGTCATTAATTGCCATCATTGAGTTGGGCATT	0	0
9	TCGTCCTATGTTGCCAGCGGGTTATGCCGGGGA	4	5
10	CTATCATTAGTTGCCAGCGAGTAATGTCGGGGA	2	10
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12	CTACCATTAGTTGCCAGCGAGTAATGTCGGGGA	5	7
13	TTGTCATTAATTACCATCATTGAGTTGGGCACT	2	0
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15	TTGTCCTTAGTTACCAGCGGGTTATGCCGGGCA	0	0
16	CTGTCGTTAGTTGCCAGCCTTAAGTGGGGCACT	6	3
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18	TCATCCCTAGTTGCCATCATTAAAGTTGGGCACT	6	6
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21	TTATCATTAGTTGCCAACATTTTCGGATGGGAAC	9	2
22	AAGCTGCCCAGTAGGGGTCTGAATTGTCTCTGA	0	0
23	CAGATTCTAGTTGTGGGTATTAGTGCCAAATTT	5	0
24	TCGTCCTTAGTTGCCAATATTAAGTTAGGCACT	0	0
25	TTGTCCTTAGTTGCCAGCGAGTAATGTCGGGAA	0	2
26	TTGCCAATAGTTGCCAGCGAGTCATGTCGGGAA	0	0
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28	TTGTCACTAGTTGCCATCATTGAGTTGGGCACT	0	0
29	TCATCCTTATTTGCCAGCGGTTAGGCCGGGAAC	11	0
30	TTGTCCCTAGTTGCCAGCACCTCGGGTGGGAAC	0	0
31	TCGCCCTTAGTTGCCACCATTTAGTTGGGCACT	3	5
32	CTGCCTTTAAATAGAGATGACTATAAGAAATTA	0	0
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34	CCATGGCCAGTTACTCGTGTCTGGCCAGACTGC	0	3
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38	TTGTCATTAATTGCCATCATTGTTGGGCACTTT	0	0
39	CTGCCTTTAAATAGAGATGACTATGAGAAATCA	0	0
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41	TAACCTGCTAACTAGTATTACTATTCCAAATAG	0	0
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5	CCGCCTGCTAACTAGTCGCCTTAATGCCTAGCA	0	0
6	CTACGGTCAGTTACTTGTGTCTGGCCGGACTGC	0	4
7	TCATCGCTAGTTACAAGTGTCTAGCGAGACTGC	0	3
8	TTGCCATTAGTTGCTACATTCAGTTGGGTA	0	0
9	TCGTTCTATGTTGCCAGCGGTTCCGGCCGGGAAC	0	0
10	TTGATTATTAATTAGTTTAAACAGATATGTATAA	5	2
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14	CTGTCGTCAGTTGCCAACACGTTATGGTGGGCA	3	3
15	CTCCTTATTAAGTGTGGCTCGCTGACCATA	0	0
16	TTGTCACTAGTTGCCAGCGAGTCAAGTCGGGGA	0	5
17	TCGTCCTCTGTTGCCATCAGGTTAAGCTGGGCA	0	4
18	TAACCTGCTAACTAGAACTATCCCAAATAG	0	0
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20	TTGCCATTAGTTGCTACATTCGTTGAGCACTC	0	0
21	TCGCCTTTAGTTACCATCATTTAGTTGGGGACT	3	5
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24	CTGCGTCCAGTTGCCAACGGGTCAAGCCGGGGA	0	0
25	TAATCTGCTAACTAGTATTACTATCCCAAATAG	0	0
26	TTACCGTATGTTGCTATCAGGTAATGCTGAGCA	0	0
27	TAACCTGCTAACTAGTATTACTATCCCAAATAG	0	0
28	TAACCTGCTAAATAGAAACATCTATAACTTAGA	0	0
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30	CAGTTAATAAATAGGGGGTATAATTCATTGAAT	0	0
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35	TCATTGTGTGTTATACGTGTCACACAAGACTGC	0	0
36	TTGTCCCTAGTTACCAGCGGGTAAAGCCGGGCA	4	4
37	TTGTCATTAATTGCCATCATTGAGTTGGGCGCT	0	0
38	CTATCCTTAGTTGCTATCAGTTTACTGAGCTCT	0	8
39	TTGCCATTAGTTGCTACATTCGTTGGGCACTC	0	0
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CTGTGTCCTGTTGCCACCCGGGAAACCGGAGCA	2	4
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5	TTACCCTATGTTGCCACGTCTGTAATGGACAGC	0	6
6	CTATCGTTAGTTACCAGCACGTAAAGGTGGGGA	0	0
7	CCGGGGTCAGTTAGACTGTCTGGCCCCGACTGCC	2	2
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9	CTATCGTTAGTTGCCAGCGTAAAGACGGGGCACT	0	0
10	CAGTTAATAAATAGGGGGTAATATTCATTGGAT	0	0
11	CTATCTTCAGTTGCCATCAGGTCAAGCTGGGCA	0	0
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25	CTGTGCTAGTTGCTAACGAGTAATGTCGAGGA	0	0
26	TAACCTGCTAACTAGTATTATTATCCCAAATAG	0	0
27	TTGTCATTAGTTGCTATGAAAGGGCACTCTAAT	0	1
28	CTGCTTTCAGTTGCTACCGCGTCATGCCGAGCA	3	4
29	TTGTCCTTAGTTGCCAGCATTAAAGTTGGGCTCT	2	2
30	CCTAACTTAATTATAAGTTTACTGCTTAGGAAA	0	0
31	TCGCCCTCAGTTGCCATCAGGTAGAGCTGGGCA	0	0
32	CTGTCCCTAGTTGCCAGCACGTAATGGTGGGAA	0	0
33	TTATCCCTAGTTGCTACCGGGTAAAGCCGGGCA	0	0
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38	TTACCATACTAACTAGTTATATATACTTCTG	2	0
39	CTACCCTGAGTTGCAACCGCAAGGGCACTCTCG	0	2
40	TAACCTGCTAACTAGTATTACTATCCCAATTAG	0	0
41	TTGTCGCTAGTTACTAACGAGTCAAGTCGAGGA	4	0
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5	TTGTCTCTAGTTGCCAGCGAGTAATGTCGGGGA	0	0
6	TTGTCATTAATTGCCATCATAGAGTTGGGCACT	2	2
7	TTGTCATTAATTGCCATCATCGAGTTGGGCACT	0	0
8	TAGCCATTAGTTGCTACATTGAGTTGAGCACTC	0	0
9	TTGCCGTATGTTATATATGTCATGCGGAACTGC	0	0
10	CTGTTGCTAGTTTCAGGTGTCTAGCAAGACTGC	3	0
11	TTGCCCTTCAGTTGCCATCGGGTAGGGCCGGGCA	0	3
12	TTATTGCTAGTTACCAACGGGTAAAGCCGGGGA	0	0
13	TCGTCATTAATTGCCATCATTGAGTTGGGCACT	2	0
14	TCGTTATTTATTGCTTAATCTTTCTACGAAAGA	0	0
15	TTGTCCTTAGTTACCAGCACCTCGGGTGGGCAC	0	0
16	CTGCCCTTAGTTGCCAGCGGTTGCGCCGGGCAC	0	0
17	TTGTCATTAATTGCCATCATTGGGCACTTTAAT	0	0
18	ACACTTCCAGTTGCCAGCATTGAGTTGGGCACT	0	3
19	TTGTCACTAGTTGCTACATTTAGTTGGGCACTC	0	0
20	TTACCATATAACTAGTTATATATACTTATG	0	0
21	TTATCCTTAGTTGCTACGCAAGGGCACTCTAGG	3	0
22	TAGCCTACTAAATAGTTCGCCGACATCTCTTGT	2	0
23	TTGTCATTAATTGCCACCATTGAGTTGGGCACT	1	0
24	TTGTCCCTAGTTGCCAGCATTGAGTTGGGCACT	0	3
25	TTAATTATTAATTAGTTAAATATATAGCAATAT	0	0
26	TAGCCTGCTAAATAGAACGAGGATAAACCTTTT	0	0
27	CTGTCTTCAGTTGCCATCATTAGTTGGGCACT	0	5
28	CTATCTTCAGTTGCCATCATTAGTTGGGGACT	0	5
29	TCATTGTCTGTTGCCACCATTGAGTTGGGCACT	0	0
30	TTCCCATTAGTTGCTACATTGAGTTGAGCACTC	0	0
31	TTGCATTTTGTGTTGCCACCTTCGCGCGAGCGAAG	2	0
32	TCGCCTCTAGTTGCCAGCATTGAGTTGGGCACT	0	0
33	ACGTCGCGTGTACAAGTGTACGCGAGACTGC	0	2
34	TAACCTGCTAACTAGTATTACTATCCCGAATAG	0	0
35	TTGTCCTTAGTTACCAGCACGTCATGGTGGGGA	0	5
36	TTATTCTTAGTTGCCAGCGCGTAAAGGCGGGAA	0	2
37	TTGTCTCCAGTTGCCAGCACTTCGGGTGGGGAC	0	0
38	CTATTGCCAGTTACCATCGGGTAGAGCCGGGGA	0	0
39	TAGCCTACTAAATAGTTCGCTGACACCTCTTGT	0	3
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41	CGGCCTGCTAAATAGCTACGCCGACCCCGCTAT	3	2
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5	TTGCCATTTGTTGCTACATTCAAGTTGAGCACTC	0	0
6	TTGCCATTAGTTGCCAGCATTTAGTTGGGCACT	0	0
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9	TAACCTCTAAATAGCGCCGCTAGCCTTGTGCTG	0	0
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13	TAACCTGCTAAATAGCCACGTTGCTTTGGCAG	0	0
14	TTGTCATTAATTGCCTTCATTGAGTTGGGCACT	1	0
15	TCATCTCCAGTTACCAGCGGGTAATGCCGGGGA	0	0
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23	TAACCTGCTAACTAGTATTGCTATCCCAAATAG	0	0
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26	CTATCATTAGTTGCCATCAGGTAAAGCTGGGAA	0	5
27	TTGCCGTTAGTTGCTACATTCAAGTTGGGCACTC	0	0
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40	TCGTGCTAGTTACCAACATGTAATGATGGGGA	0	0
41	TTGCCATCAGTTGCTACATTCAAGTTGGGCACTC	0	0
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45	CTGTTGTTAGTTGCTAACGGTTCGGCCGAGCAC	0	0
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47	CTACGGTCAGTTATCCGTATCTGGCCGGACTGC	0	0
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54	TCATCTTTAGTTGCCAGCATTTCAAGTTGGGCACT	0	0
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8	TTGCCATTGGTTGCTACATTGAGTTGAGCACTC	0	0
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22	TTGCCCTTAGTTACTAACGAGTAATGTCGAGGA	0	0
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25	CAGTGAGAGGGGACACTCATCACATGAATAATGA	0	0
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36	TTGCCATTAGTTGCCACATTGAGTTGGGCACTC	0	0
37	TAACCTGCTAACTAGTATTTCTATCCCAAATAG	0	0
38	TCGTCCATAGTTGCCAGCAAGTAATGTTGGGGA	4	2
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41	TTGTCCTATGTTGCCAGCAATTCGGTTGGGGAC	0	6
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27	CGGCACTCCGAATAGCGCGGGCGGACGTCGCGGC	3	0
28	TCGCCTTTAGTTGTTATGTAAGTGGATTTTATG	0	0
29	TCGCCTTCAGTTGCCAGCAGGTAAAGCTGGGCA	0	0
30	CTATCATTAGTTACCAACGGGTAAAGCCGGGAA	0	0
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32	CTGTTGCCTGTTACAAGTGTGAGGCAAGACTGT	0	0
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36	CTACCATTAGTTGCCATCAGTTCGGCTGGGCAC	0	0
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38	TCGTTGCCTGTTATAAGTGTGAGGCGAGACTGC	0	0
39	TCATCTTCAGTTACTAACGGGTAAATGCCGAGGA	0	0
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13	GGGATTGATAAATAGGGCGGCCGCGGGCGCGAG	2	0
14	TTGCCATTAGTTACTACATTCAGTTGAGCACTC	0	0
15	TAGTCTACTAAATAGTTGCGCCGACACCTCTTGT	3	0
16	CTGTTTTTGGTTGCCATCATTAAAGTTGGGCACT	0	2
17	TCGCCTCCAGTTGCCATCATTGGTTGGGCACT	0	0
18	CTACCCTCAGTTGCTAATTATAGGACTCTGGGG	0	3
19	TTGCCATTAGTTGCTACATCCAGTTGGGCACTC	0	0
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8	TTGTCCTTAGTTGCCACCAGTTCGGCTGAGCAC	0	0
9	TGATTTATTAATTAGTTGATCGTAGATTTAATT	0	0
10	TTGTCATTAATTGCCATTATTGAGTTGGGCATT	0	0
11	TTGCCATCAGTTGCTACATTCACTGGGCACTC	0	0
12	CAGTGAGAGAGATGCATTGAGAAGAAGTGATTC	0	0
13	CAGTGGGAGGGACGCATTGGAAAGAGTTTTTTT	0	0
14	CGACCTGCTAAATAGTGCGGCCACGCTTCGGC	0	0
15	CCGCCTGCTAAATAGCGCTGGCCTTGGCTCGCC	0	0
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18	TAGTCATTAATTGCCATCATTGAGTTGGGCACT	0	0
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21	TTGTCGTTAGTTGCCAGCATTAGTTGGGAACT	0	0
22	TTGTCATTAATAGCCATCATTGAGTTGGGCACT	2	0
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25	TTGTCATTAGTTGCCATCATTGAGTTGGGCACT	0	0
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5	CGACCTGCTAAATAGCTCGGCGAATCTTTCGGG	0	0
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7	TAACCTGCTAACTAGTATTACTTTCCCAAATAG	0	0
8	CTACTGCTAGTTGCTAACAGGAAAGCTGAGCAC	4	0
9	TTACCATACTAACTAGTTATATATATACATTTG	4	0
10	TAGCCTGCTAAATAGTTCGTGATCTTCCGAGAT	4	0
11	TTACCCTTAGTTGCAACCGCAAGGGCACTCTAG	4	0
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17	CTGTCATTAATTGCCATCATTGAGTTGGGCACT	0	0
18	TTGTCATTAGATGCTACGAAAGGGCACTCTAAT	0	4
19	TTATCTTTAGTTGCCAGCATTAAAGTTGGGCACT	0	4
20	TTACCATACTAACTAGTTATATTTATATTTTT	0	4
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22	TTGCCATTAGTTGCTACATTCAGTTGGACTC	0	0
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39	TAGCTTACTAAATAGTTCGCCGACACCTCTTGT	0	0
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7	TAACCTGCTAACTAGTATTACTATCCCAGATAG	0	0
8	TAACCTGCTAACTAGCATTACTATCCCAAATAG	0	0
9	TTGTCTTTAATTGCCATCATTGAGTTGGGCACT	0	0
10	CAGCCTACTAAATAGTTCGCCGACACCTCTTGT	1	2
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12	TTGTCACTAATTGCTATCATTTGGTTGGGCACT	0	3
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14	TTACCTCTAGTTGCCAGCGAGTAAAGTCGGGGA	0	3
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36	CTGCTTTCAGATGCTACCGGGTCATGCCGAGCA	0	0
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ACGCTGTTAGTTGCTAGCAGGTAAAGCTGAGCA	0	2
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TAGCCTGCTAAATAGTCCGTGATCTTCCGGGAT	0	2
TTAGCCCCCGTTACAAGTGTCTGGGGCGACTGC	0	2
TTGCCATTAATTGCTATCATTTAGTTGGGCACT	0	2
CTGTTGCTAGTTACAAGTGTCTAGCGAGACTGC	0	2
TCGTGTCCAGTTGCCAGCAAGTAATGTTGGGGA	0	2
CTGTGTCTAGTTACCAGCGGTTTCGGCCGGGAAC	0	2
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TTGTTATTAATTGCCATCCTTAAGTTGGGCACT	0	0
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9	TTGCCTTTAGTTGCTACATTCAGTTGAGCACTC	0	0
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46		66930	68795
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Flocs Control 3	Flocs Treated 1	Flocs Treated 2	Flocs Treated 3
11	17	15	3
2	0	0	3
6137	20399	13736	19414
10	4	3	5
22577	5378	5928	1772
6526	4466	2109	5067
20	27	44	30
1052	1847	1296	1120
2378	1815	1447	1711
1536	749	890	1133
700	659	541	645
296	166	164	179
1407	975	617	1017
542	490	387	712
0	0	0	0
1418	613	745	1801
798	591	448	437
1219	944	874	692
0	0	0	0
1400	1032	574	884
1626	816	488	699
415	263	313	290
1038	528	191	541
965	879	652	714
815	361	442	1001
0	0	0	0
654	471	342	421
206	105	127	365
18	15	7	5
0	0	0	0
473	371	277	362
646	530	198	563
0	0	0	0
608	440	250	584
4	4	3	2
0	0	0	0
653	501	250	430

58	50	31	19
524	387	270	441
0	0	0	0
354	310	137	616
7	0	0	2
0	0	0	0
247	170	109	190
0	0	0	0
233	170	131	201
0	0	0	0
0	0	0	0
293	207	180	216
408	276	232	199
520	248	236	260
0	0	0	0
210	160	112	107
387	341	239	213
299	262	187	315
320	241	135	217
0	0	0	0
12	9	5	4
2	2	0	5
0	0	0	0
332	200	232	174
0	450	551	301
264	194	285	98
300	208	202	154
245	118	127	333
10	11	7	14
362	217	144	238
0	0	0	0
343	269	142	220
282	171	151	82
0	0	0	0
118	69	36	55
209	274	221	193
2	0	0	0
269	205	147	145



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4	299	144	158	172
5	257	171	161	114
6	92	5	112	5
7	12	7	14	13
8	0	0	0	0
9	0	0	0	0
10	135	81	37	239
11	0	0	0	0
12	323	10	29	0
13	227	174	155	159
14	132	127	358	12
15	178	120	144	124
16	32	86	96	455
17	70	56	37	48
18	0	0	0	0
19	201	140	165	124
20	229	147	117	124
21	138	16	125	4
22	0	0	0	0
23	208	117	113	139
24	247	130	99	71
25	63	60	33	56
26	4	2	0	3
27	187	122	8	288
28	0	0	0	0
29	35	30	11	17
30	21	38	31	42
31	175	132	95	125
32	103	154	122	169
33	125	220	105	140
34	179	138	173	100
35	172	141	110	97
36	0	0	0	0
37	154	159	99	144
38	29	24	27	35
39	76	73	69	92
40	0	0	0	0
41	2	7	11	3
42	169	120	113	57
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2	12	65	9
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0	0	0	0
136	84	64	113
0	0	0	0
74	49	45	32
135	72	78	96
62	57	54	59
2	2	2	3
112	74	79	109
117	116	96	77
0	2	3	0
39	17	24	16
42	31	156	3
85	90	65	83
0	172	58	266
0	0	0	0
20	14	4	42
90	65	64	94
138	85	44	113
121	41	96	34
9	4	0	2
0	0	0	0
0	0	0	0
28	19	16	17
97	35	35	97
91	85	79	45
93	36	57	35
6	4	22	0
118	63	30	54
0	0	0	0
73	63	65	35
69	75	44	42
102	68	52	54
61	34	32	27
64	58	40	24
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0	0	0	0

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4	110	61	63	45
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6	66	53	27	44
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9	89	51	59	47
10	86	71	37	62
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14	75	64	90	14
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18	0	0	0	0
19	0	0	0	0
20	77	60	39	48
21	90	63	51	41
22	99	55	47	59
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24	3	0	0	0
25	68	60	33	48
26				
27	0	0	0	0
28				
29	70	55	41	43
30	0	3	2	0
31	3	3	192	0
32	46	35	46	38
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34	0	4	11	0
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37	0	0	0	0
38				
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44	35	18	20	12
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47	79	41	27	61
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21	42	40	28	31
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28	41	47	14	49
29	7	2	5	4
30	44	41	44	35
31	64	51	31	18
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45	0	0	0	0
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26	0	0	0	0
27	2	4	2	5
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32	2	0	2	0
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46	48	29	21	18
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49	25	26	16	18
50	26	29	25	17
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52	0	0	0	0
53	3	5	0	0
54	46	16	27	14
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9	26	36	30	26
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15	31	12	14	15
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35	23	27	7	26
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1150	888	807	827
1066	1395	1421	919
2639	1544	1223	1823
985	827	836	664
1280	823	967	976
954	1392	2436	590
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740	441	408	360
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888	1599	970	706
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308	208	188	176
454	415	369	241
623	715	553	471
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781	482	240	668
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Granules Treated 2	Granules Treated 3	tag	use	taxon_level
0	0	TTGCCATTAG	long	g
0	0	TTGCCATTAG	long	c
13670	15571	TTGTCATTAA	long	c
16034	24834	TAACCTGCTAACTAGTATTACTATCCCAAAT		
17	13	TTGTCATTAG	long	o
0	0	TAGCCTACTAAATAGTTCGCCGACACCTCTT		
2990	2218	TTACTGCTAG	long	o
657	649	TTGTCGTTAA	long	f
20	22	TTGTCATTAG	long	c
673	726	CTGCTTTCAG	long	g
887	1338	TTGTCGTTAA	long	g
1138	1122	TTGTCCCTAG	long	g
526	661	TTGTCATTAA	long	f
561	714	TTGTCACTAG	long	g
759	1965	CTGTTGTTAG	long	f
6	0	CGAGAGGGTGGGTTGAGGTTATTATTGAGGC		
384	532	TTGTCATTAA	tag	c
13	17	TTGTCACTAA	long	g
935	1038	CAGTGGGAGGGACGCTCAATTCATCTCATA		
13	18	TTGTCGTTAA	long	f
18	71	TTGTCCTTAG	tag	f
388	674	CTCCTTATTAAGTGTGGCTCGCGGCCAT		
0	0	TAGCCTGCTAAATAGTCCGTGATCTTCCGAG		
0	0	CGACTTGTTAACTAGTCCGGCGCAGCCTGCA		
4	0	CGAGAGGGTGGGTTGAGGTTATTATTGAGGC		
681	692	CAGTGGGAGGGACGCTCAATCAATAGTCTT		
126	138	TTACCGTGAG	long	o
207	405	TTGTCACTAA	long	g
335	458	CTATCGTTAGTTGCCTGGCGCAAGCCGGTA		
388	584	TTGTCATTAA	long	g
91	102	TCGTCCTGTG	long	f
0	0	TTGTCATTAG	long	k
399	631	TCGCTGTATG	long	g
2	0	CTGTCGTTAGTTGCTCACAGGTTATGCTGAG		
420	539	CTCCTTATTAAGTGTGGCTCGCGGCCGT		
400	288	TCATTGCCAGTTACAAGTGTCTGGCGAGAC		
0	0	CTACCATTAG	long	f

303 392 CAGCCTACTAAATAGCTATGCAGATTTGATT  
23 28 CCATCACTAG long f  
329 208 CTATTGCCAGTTACCATCATTGAGTTGGGG/  
46 69 TAACCTGCTAAATATGTCACCGGTAGACTTC  
277 472 TTGTCCCTAG long c  
374 432 CAGTGGGAGGGACACTCAATTCATCTCATA/  
149 68 CTATTCTTAG tag o  
380 393 CAGTGGGAGGGACACTCAATTCATTGAAAG  
137 252 TCGCCTTTAG long o  
361 348 CAGTGGGAGGGACACTCTTTTCATCACAAG/  
300 44 CTACCATTAGTTGCTAACATTTAGTTGAGGA  
103 80 CTATCACTAG tag g  
49 46 TTGCCGTTAGTTACTAACGGGTAAAGCCGA/  
0 0 TCGTCTTCAG long g  
284 133 CTATTCTTAG long f  
95 294 CTATCTTTAG tag p  
2 3 CTGTCGTTAG tag g  
0 0 TTACCGTGAG long k  
61 45 TTGCCATTAG long f  
200 363 TTATCATTAG tag g  
164 207 CTATCTTCAG long f  
133 218 TTGTCACTAG long g  
241 164 CTGTCGTTAG long g  
0 0 CGGCCTGCTAAATAGTGCTCTGAACTCTTCG  
0 0 CTGTCACTAG long f  
0 3 TGGTCTACTAACTAGTATTTATCATTTAGCA/  
10 26 TTATTTGTTAATTAGATGAAGCAACAGGATT  
0 2 CGAGAGGGTGTTGAGGTTATTAATGAGG(  
209 121 CTATTCTTAG long f  
0 2 CTGTCCATAGTTGCCAGCAAGTTAGGTTGG(  
217 220 CAGTGGGAGGGACGCATTGGAAAGAGTTT  
0 0 TTACCCTATGTTGCCAGCATTTAGTTGGGCA  
0 0 TCACTTGCTAACTAGTCGCAGCTAAAACCTA  
206 224 CTATCGCTAG long g  
116 175 CGGCTTACTA long p  
3 4 TCGTCGCGTG long f  
133 98 TCGGTGTGCGTTACAAGTGTCGCACACAAC  
0 0 CTGTCCTCAG long o

1			
2			
3			
4	0	0 TTGTCGCTAG long	k
5	4	3 CTATCGTTAGTTGCTCGGAGCAATCCAGTAC	
6	0	0 TAACCTGCTA long	g
7			
8	143	119 CTACCATTAG long	f
9	143	104 CTATTGCCAG long	g
10			
11	33	63 CAGCCTACTAAATAGTAATGCAAACCTTTACT	
12	185	218 TTATCTTCTGTTACCAACGCGTAAAGGCGGC	
13	0	0 CTGTCACTAG long	f
14			
15	0	0 CAGCCTGCTAAATAGTTATGCGAATTTTACT	
16	0	0 TAACCTGCTA long	g
17			
18	20	42 CCGTTGTTAG long	o
19	51	4 CTGTTGTTAG tag	g
20			
21	73	100 CTGTCCTTAG long	g
22	149	130 TCGTGTCCAATTGCCATCATTAAAGTTGGGG/	
23	0	0 TTGCCATTAA long	f
24			
25	0	2 CTATTGCCAG tag	f
26	0	0 TAACCTGCTA long	g
27			
28	115	251 CCGTGTCCAG long	f
29	0	0 CTGTTGTTAG long	o
30			
31	5	6 CTATCTTTAG tag	o
32	73	45 CTATCGTTAGTTGCTCACGCAAGTAGTACTC	
33	119	117 TTGTCCCTAG long	g
34			
35	0	0 TAACTTACTAAATAGTTACGAAAATATTGCT	
36	121	138 CAGTGGGAGGGACGCTCATCACATGAATAA	
37			
38	118	128 TCGCCGTTAGTTGCTTCGCAAGAAGATCTCT	
39	99	121 TCGCCGTATG long	f
40	0	0 TTGCCCTGTG long	f
41			
42	16	17 TTGTCACTAG tag	p
43	0	0 TCGCCTCCTG long	o
44	0	0 TCGTTCCATG long	f
45			
46	0	0 TTGTCCTCAGTTACCACCATTGAGTTGGGGA	
47	115	142 CAGTGGGAGGGACGCATTGAGAAGAATCA/	
48			
49	0	0 CTATTTTCAGTTGCCAGCACATAATGGTGGC	
50	78	85 CTACCATTAG long	c
51			
52	19	24 TTACCGTGAG long	o
53	112	148 CTATCTTTAGTTGCCACCAGGTAATGCTGAG	
54	156	224 CCGCCTGCTAAATAGCGCAGCCTTGGCTCG	
55			
56	0	0 CTGTTTCTAGTTGCCAGCGAGTAAAGTCGG/	
57			
58			
59			
60			

93 349 CCGCCTGCTAAATAGCGCTGGCCTTGGCTTC  
98 116 TCATCCTCAGTTGCCATCGGGTTCGGCCGGC  
89 96 TCACGAGATAATAGGTCGAGAAAAGGAAA  
14 18 TTGTCCTGTG` long f  
98 67 CTATCTCTAG` long f  
43 56 CTATCGTTAG` long g  
2 0 CTGTCGTTAG tag g  
25 39 TTGTCATTAG` long c  
54 112 CTGTGTCCTGTTGCCACCGGGATGAGAGTC  
6 2 TTGTCATTAG` long g  
0 0 TTGCCCTTAG` long g  
90 125 CAGTTAATAAATAGGGGACATAATTCATTG/  
65 44 TCGTCGCTAG tag f  
8 11 CTATCTTCTG1 long c  
8 22 TTGTCATTAA` long g  
14 10 TCGTCCTATG` long f  
69 89 TCACGAGATAATAGGTCGGGAAAAGGAAA  
56 80 TAACCTGCTA long g  
0 4 TTGTCATTAG` long g  
3 2 CTACCAATAG tag f  
0 0 TAGCCTGCTA long p  
47 64 TCGTCCTTAG` tag c  
94 34 TAACATGCTAACTAGCCGACGCGCTCTGC  
83 87 CAGTGGGAGGGACGCAATGATCATTTTTCT  
53 54 TTAGTGCCAG tag f  
0 0 TTGTCACTAATTGCCATCATTAGGTTGGGCA  
0 0 CTGTCCACAGTTGCCACCATTAGTTGGGA/  
12 12 TCGTGGCTAG tag c  
51 46 TTACCAGCTAAATAGTAATTATTTTGATTTA1  
3 6 TCGCCCCTAG long g  
57 82 TAGCCTATTAATTAGGGCTTTATAACTCGGC  
12 16 TCGCCGCGTG long g  
4 0 CCATCTTCAG` long f  
0 0 CTGTCGCTAGTTACCATCAGGTTATGCTGGC  
19 37 TTGTCATTAA` tag c  
16 26 ACACTTTCAG` long f  
53 62 CTATCTTTAG` tag c  
38 94 CTGCCGTTAGTTGCCAACGGGTTATGCCGGC

1			
2			
3			
4	0	0 TTATCGCCAG tag	p
5	0	0 CTATTGATAG tag	o
6	12	17 TCGTCCTGTGTTGCTACCCGCAAGGGGCAC	
7			
8	61	26 TTGTCATTAG tag	o
9	2	0 TCGTTCTATG tag	g
10			
11	3	0 CCATCATTAG long	g
12	50	51 CTATCTTTAG tag	f
13	0	0 TTGTCCTGTGTTGCAACCCGCAAGGGGCAC	
14			
15	0	0 CTATCCTATG long	o
16			
17	48	81 TCGGCGTTAG long	f
18	54	32 CTATTGACATTTGCCATCATTAAGTTGGGGA	
19	30	110 CTATCGTATGTTGCTAACGGGTAATGCCGAC	
20	0	2 TCGTCTCCAG long	g
21			
22	0	0 TCGCCTTTAG long	o
23	0	0 TTGCCCTAG long	f
24			
25	60	63 TCGGCGTTAGTTACACGTGTCTAACGCAACT	
26	4	2 TCGCTATTAG long	g
27			
28	51	57 TAATTTTTAAATAGTTTCCATCAAGGCAACT	
29	0	0 CTATCGTTAGTTGCTCACGGGTCATGCCGAC	
30	36	45 TCGTTCTATG long	g
31			
32	3	3 TAGCCTGCTAACTAGCTACGCGCGTCGTGCC	
33	15	10 TTACCGTCAGTTACAAGTGTCTGGCGGGAC	
34			
35	40	41 TTACCAGCTAAATAGTGATTATTATGATTTA	
36	43	38 TCGCCTCTAG long	o
37	35	68 CTGTCCTTAG long	f
38			
39	0	0 TAACCTGCTAACTAGTACACTTATTTTCCATA	
40	57	63 CAGTTAATAAATAGGGGATATAATCTTTACT	
41			
42	45	71 CAGTTAATAAATAGGGGACATAATCTTTTAC	
43	0	0 TCGTCTTCAG long	g
44			
45	15	11 TCGCCCTTAG tag	o
46	0	0 CTATTGCTAGTTGCCATCAGTTCGGCTGGGC	
47	0	0 TTACCATTAG tag	o
48			
49	0	0 TCGTCTTATGTTGCCAGCGGGTCATGCCGGC	
50	0	0 TTGTCCTGTGTTGCAACCCCGCGAGGGGGC	
51	0	0 CTGTCGCTAGTTACTAACAGGTAATGCTGAC	
52			
53	39	28 TCGTGTTTCAG long	f
54	23	14 TCATCCCTAG long	o
55			
56	41	49 CTATCGTTAG long	g
57			
58			
59			
60			

0 TAACCTGCTAACTAGTATTAGTATCCCAAAT.  
0 TCGTCGCGTG long g  
0 TTGTCACTAG long c  
0 TCGTCGTATG long o  
8 TTGTCCTCAGTTGCCATCATTGAGTTGGGCA  
25 TCGTCGGCAGTTACACGTGTCTGCCGAGAC  
63 AAGCTGTCCAGTAGGAGTCTAAATTGTTTT  
0 CTACCATTAGTTGCTAACAGGTAATGCTGAC  
53 CAGTTAATAAATAGGGGATACTAATAGTAA  
0 TCTTGTTGAGTTGCCAACAGGTAATGCTGGC  
2 CGACTTGTTA long c  
12 TTGTCATTAG tag f  
0 CTACACTTAG long f  
6 CTAGTATTATTTATTTAATAGTTTAGATAAT/  
21 TCATCTTCAG long f  
38 TTACCAGCTAAATAGTAATTTTTATGACTTG  
11 TTACCGTTAGTTGCTAACAGGAAAGCTGAG  
0 TTAGCGCCAGTTACAAGTGTCTGGCGCGAC  
3 TTGCCCTGTT long f  
15 TCGCTACTAG long g  
0 TCGCTACGTGTTACATGTGTACGTAGGACC  
0 CTATTTTCAG long f  
0 CTGTTGTTAG long o  
35 CTATCTTTAG tag k  
51 TCATCCTCTG tag f  
0 TTGTCATTAATTGCTATCATTAAGTTGGGCA  
76 CTGCGGTTTGTGTTGCCAGCATTAAGTTGGGC/  
22 CTATCATTAGTTGCCATCAGGTAGTGCTGGC  
27 TTGTCATTAA long o  
2 TTAATTATTAATTAGTTAAATATATAGTAAT/  
0 TTGTCCCTAG long g  
8 CTATCTTCTGTTACCATCATTAAGTTGGGGA  
43 ACACTTCCAG long f  
0 TCGTCCCTAG long f  
29 AAGCTGCCCCA tag g  
0 TTACCTCTAG long f  
28 TCGCCTTCAG tag o  
0 CTATCGTTAGTTGCCAGCGTAAAGTCGGGC

1			
2			
3			
4	0	0	CAACCTACTAACTAGTACGACGTGAACAAC
5	0	0	TTGTTGTTAATTGCCATCATTTAGTTGGGCA
6	0	0	TTGTCCTTAG` long o
7	0	0	TTATCATTAG` long c
8	0	0	TTATCATTAG` long c
9	4	6	TCGCCCTTAG` tag o
10			
11	13	15	TTACCAGCTAAATAGTGATTATTTTGATTTA`
12	29	52	CCGCCTGCTAAATAGCGCACGCCGGGCACG
13	9	2	TCGTCGCTAG` tag f
14			
15	26	23	CTACTGCTAG` tag f
16	0	0	TTGTCATTAG` long g
17	0	2	TTGTCATTAG` long g
18	0	2	TTGTCATTAG` long g
19	0	0	AACTCTTAG` tag f
20			
21	20	30	CTGTCCCTAGTTGCCAGCGCGTGAAGGCGG
22	20	24	TCACCTTCAG` long o
23			
24	30	32	TCATCATTAG` tag g
25	17	10	TCATTTTCTAG` long c
26	19	37	CTATCTTCAG` long f
27			
28	18	28	CTATCGTCTA` tag f
29	5	3	CTGTCTTAGTTACTAACAGGTAATGCTGAC
30			
31	13	32	TTGTCACTAATTGCCAGCATTAGGTTGGGCA
32	18	26	TTACCAGCTAAATAGTAATTATTATGACTTG`
33	11	16	CTGTCTTTAG` tag k
34	7	8	TTACCGTCAG` tag g
35			
36	0	0	TAGCCTACTAAATAGTTCGCCGACACCTCTC
37	0	0	TAACCTATTAAATAGTCACGCTTATCCTTCC
38			
39	0	0	TTGCCCTGTT` long f
40	10	24	TCACCTTCAG` long f
41			
42	21	12	CTATCTTTAG` long f
43	18	18	TTGTCACTAA` long f
44			
45	0	0	CTATCATTAGTTACCAACGGATAAAGCCGG
46	0	0	TTGTGATAGTTGCCAGCATTGTTGGGCA
47			
48	10	3	TCGTCCTTAG` long f
49	0	0	TCGTCGTTAG` tag c
50	0	0	CTATCATTAGTTACCAACGGGTAAAGCCGG
51			
52	23	16	CTGTCTTAGTTGCTAACGCGTTATGGCGAC
53	21	16	CCGGGGTCA` tag f
54	0	0	TCGTCGTCAG` long f
55			
56	22	16	TCGTCTTCAG` long f
57			
58			
59			
60			

12 15 CCATCCTATGTTGCCATCATTAGTTGGGCA  
30 31 AAGCTGCCCAGTAGGAACCAGGATTGTCCA  
0 0 TTAATTATTAATTAGTTAAATATATTTTTTAT  
0 0 TTGTCATTAG` long c  
0 0 TCGCTGCGTGTTATACGTGTCACGCAGGAC  
6 7 TCGGCGTTAG long f  
11 7 TCGCCTTTAG` long f  
13 5 TTGTCACTAG` long f  
0 0 CCGTCCTTAG` long g  
14 8 TTACCTTATGTTGCCATCATTAGTTGGGCA  
45 13 TTGTCCTTAG` long g  
0 0 TTGTCCTTAG` long g  
7 5 CTATTTTATAGTTGCCAGCGAGTCATGTCGGC  
6 3 TCGCCCTTAG` long o  
29 44 CCGCCTGCTAAATAGCGCAGCCTTGGCCCC`  
18 19 CTATCATTAG` long g  
17 14 CTATCTTTAGTTGCTACCGGGTCAAGCCGGC  
0 0 CTATCGTTAGTTGCCTGGCGAAAGCCGGTA  
0 0 CTATCATTAG` long g  
22 24 TCACGAGATAATAGGTTCGAGGAAAGGAA  
0 0 TTGCCATTAG` long f  
21 19 CTATCTTTAG` long f  
0 0 TCATTCTCTGTTGCTACCAGGTTAAGCTGAG  
0 0 CTGTCGTCAG tag p  
19 32 CAGTTAATAAATAGGGGGTATTATTCATTG/  
8 17 TCGTGTTTCAG long f  
0 0 CTATTAACAG long o  
0 0 TTGTACTTAGTTGCCATCAAGTGAAGTTGGC  
15 18 TTGTCGTTAG` tag f  
5 3 TCGCCCTTAG` long o  
0 2 CTGTCGCCAG long f  
0 0 CTATCCTTAG` long f  
14 23 TTGTCCTTAG` tag f  
19 8 AAGCTGCCCCA long g  
8 9 CTGTGTCCTG` tag c  
0 0 CTGTTCTCAGTTACCACCGTTCAGTCGGGGA  
0 0 TAACCTGCTAACTAGTACCCTGATCCTCAAT  
8 11 TCGCCCTTAG` long o



1		
2		
3		
4	16	9 TTACCAGCTAAATAGTGATTATTATGACTTG
5	0	0 CTACCATTAG` tag f
6	0	0 TCGTGTTCAA` long f
7	0	4 CTATTGCTAGTTATACGTGTCTAGCGAGACT
8	2	8 TTGTCATTAG` long o
9	6	34 CTGTTGTTAGTTGCCAACGAGTCAAGTCGGC
10	7	7 CTGTTGTTAG` tag f
11	10	10 TCGCCTTTAG` long f
12	0	0 CCGCCTGCTAAATAGCGCTGGCCTTGGCTCC
13	0	6 TTGTCCCTAG` long o
14	0	0 CTACACTTAGTTGCCATCAGGTTATGCTGGC
15	0	0 TTACCTCTAG` long g
16	0	0 CCATGTTTCAGTTGCCATCATTAAAGTTGGGG/
17	12	10 TCGCCCCTAG long o
18	0	0 TTGTCACTAGTTACCAGCGGGTAATGCCGGC
19	0	0 CTATCCTTAG` long f
20	4	8 CTGTTGTTAG` tag f
21	0	0 CTGTCGCTAGTTGCTCGGCGCAAGCCAGTA/
22	10	12 CTGTTGCTAG long f
23	0	0 TTTTCCCATGTTGCAATTGCATCTAAACCGT/
24	0	0 TCGCCTCCTGTTGCCAACAGGTCAAGCTGGC
25	11	9 TCACCTTCAG` long o
26	0	0 CTATTGACAG long o
27	10	24 CTATCTTCTGTTGCCAATATTAAGTTAGGCA/
28	12	17 TCACGAGATAATAGGTTCGGAAAAAGGAAA/
29	8	3 TTGTCACTAG` long g
30	2	2 CTA CTGTGTG tag c
31	0	0 TCGTCCTATG` long c
32	0	0 TTGCCAATAGTTGCCATCATTGAGTTGGGCA/
33	0	0 CTGTCACTAG long g
34	12	19 CTGTCCTTAG` long k
35	0	0 CTGCCCTTAG` tag k
36	0	0 TTGTCGCTAG tag k
37	13	16 TCATCTTCAG` tag g
38	0	0 CTGTCGCTAG tag g
39	0	0 TTGTCCTGTG` long o
40	7	14 TCGCCTCTAG` long o
41	0	0 TTGCCTCTAGTTGCCAGCGAGTCATGTCGGC
42		
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59		
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0 CTGTTGTTAG long g  
0 TCGCCATTAG long g  
11 18 CAGTTAATAAATAGGGGATACTATTTCATTG/  
10 12 TCGTCCTATG tag o  
0 0 CTGTGTCCTG long c  
3 0 TTATTTGTTAATTAGATGAATCAACATTATT  
17 15 CAGTTAATAAATAGGGGATACTATCTTTTAC  
0 0 CTGTCTCCAG long g  
7 12 CTATCTTTAG long g  
13 22 CAGTTAATAAATAGGGGATATTAGTTTTTTA  
16 13 CCTTGTTTCAG long f  
16 10 TCGCTTCTAG long g  
10 17 TCGCCTTTAG long o  
10 19 TTGTCCCTGG long f  
10 30 CAGTTAATAAATAGGGGATATTATTTCATTG/  
13 16 CTGGGGTCAGTTACACGTGTCTGGCCCCGAC  
0 0 CAACTTGCTAAATAGTCGCACTAGTCTTCTA  
7 8 CTGTCCTTAG long g  
0 2 TCGCTTTTAGTTGTTTTTTAAAAGGACTGCC  
0 0 CTGTTGCCAG long p  
0 0 TTGTCATTAG long g  
16 16 CTATCGTATG long o  
5 10 TTACCAGCTAAATAGTAATTATTATGATTTA  
0 0 CCGTTGTTAG long o  
21 20 CTGCTGCCAGTTACCATCATTTAGTTGGGGA  
7 2 TTGTCACTAG long f  
10 12 CTGTCGTTAGTTGCTAACGCGTCATGGCGA  
0 0 TCGTCGTTAG long g  
3 0 CTGTCTCCAG tag f  
0 0 CTGTTGTCAGTTGCCACCAGGTCAAGCTGG  
0 0 TTACCGTGAG long o  
12 8 TCACGAGATAATAGGCCGGGAAAAGGAAA  
8 6 CTGCCGTTAGTTGCTAACAGGTCATGCTGA  
0 0 TCGCCTTCAGTTGCCATCGGGTTAAGCTGG  
7 5 TTACCAGCTAAATAGTGATTGTTTTGATTTA  
7 4 CTGTGGGTAGTTAGATGATCTACCCAGACT  
0 0 CTATTTCCAGTTGCCAGCGAGTAATGTCGG  
17 7 TCGCCACTAGTTGCCAGCATTCAAGTTGGGC/

1		
2		
3		
4	11	12 CTATCACTAGTTACCAGCGGGTAAAGCCGG
5	0	2 TCGCCATTAG long f
6	12	11 TTATCGCTAGTTGCCATCAGGTTGGGCTGGC
7	9	26 TTATCATTAG tag g
8	10	9 CCATTTCTAG long f
9	0	0 TTGTCACTAGTTGCCAGCGGGTTATGCCGGC
10	0	0 CAACCTATTAAATAGTGTAATAGAAAATTT
11	0	0 TCGTCTTATG tag p
12	0	0 CAACCTATTAAATAGTGTAATAGAAAATTT
13	2	3 TTTTTTAAAGTTACTAATTTAATGATTAAATG
14	0	0 CTACTCTTAGTTGCCAGCATGTAATGGTGGC
15	4	13 CTTTCTTTAG tag f
16	4	20 CTATCTTCAG tag g
17	9	12 TCGGGAGTAC long f
18	10	0 TTGCCGCTAA tag p
19	8	6 CTACTTACTAAATAGTTTAGTTAGTGATTTTC
20	4	3 CTGCCTGCTAAATAGTCTGGCGAGTGTTTTT
21	3	3 CTATCTTTAGTTGCCATCGGGTAATGCCGGC
22	0	0 TTGTCATTAATTGCCACCATTTAGTTGGGCA
23	9	16 TTGTCATCAG long f
24	8	9 TTGTCATTAG long o
25	8	13 CTATCTTTAG tag f
26	5	13 TTGCCGCTAGTTACCAGCGAGTAAAGTCGG
27	11	14 CTGTCGTTAGTTGCTCACGGGTAATGCCGAC
28	7	0 TTGTCATTAATTGCCATCATTGAGTTGGCAC
29	7	22 CAGTTAATAAATAGGGGGTAGTATCTTTACT
30	5	10 TCGCCATTAG long f
31	0	0 CGAGAGGGTGTTGAGGTTATTATTGAGGC
32	4	0 TCGTCTGCTGTTGCCATCAGGTTAAGCTGGC
33	11	6 TTGCCCTTAG long g
34	8	5 CTACTACCAGTTACCAGCGGGAAAGCCGGG
35	0	0 TTGCTATTAGTTGCTACATTCAGTTGAGCAC
36	6	16 CAGTTAATAAATAGGGGACATAATCTTTACT
37	13	10 CTATCTTTGGTTGCCATCATTAAAGTTGGGCA
38	4	12 TCGTTCTATG tag c
39	0	0 CTATCATTAG long k
40	5	16 TTGCCAATAA long g
41	0	0 TTGTCCTGTG long c
42		
43		
44		
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49		
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5 0 CTATGAATAG long f  
0 0 TTGTCACTAA' tag g  
3 12 TTTCTTATGTTGCTACCAGTTCGGCTGGGC  
0 0 TTGCCCTGTGTTGCCACCCCGAAAGGGAGC  
6 2 TCGCTGCCAG long c  
5 5 TCGTTTCCAGTTGCCAGCGAGTAATGTCGGC  
5 5 TAACCTGCTA tag c  
2 0 TCGTCGTTAG long c  
5 4 CTGTCCTTAG' tag g  
8 0 TCATCCTTAGTTGCCATCAGGTAATGCTGGC  
0 0 CGGCCTGCTAACTAGTGCGTGGCGCGCCGC  
6 3 TCATTGCCAGTTATAAGTGTCTGGCGAGAC  
0 0 ACGCCTTTAG long g  
7 12 CAGTTAATAAATAGGGGATACTAGTTTTTTA  
2 4 CAGCCTGCTAATTAGTTATATAAATTAATAC  
0 0 TTGTACTTAGTTGCCATCAAGTGAAGTTGGC  
0 0 TTGTCCGTAG long o  
6 4 CTGTCCTTAG' long p  
7 13 CACTTGGTGTGTTATCGATTTTTTTATAAA/  
10 11 TTATTCTATG' long g  
5 8 CTATCGTTAG' tag k  
6 0 AAGCTGCCCAGTAGAAGCCAGGATTGTCTT  
7 17 TCATCCTTATTTGCCATCAGGTTATGCTGGG  
0 0 CTGTTGTTAG long g  
0 0 TTGTCCCTAG' tag c  
6 6 TTATCATTAGTTGCCAACGGGTAATGCCGGC  
0 0 CTGTGATTTG' tag k  
0 2 CTGTCGGTAGTTACTAACGCGTCATGGCGA  
0 0 CTATCTTTAG' tag f  
7 4 CTATCTTTAG' long f  
11 5 TTACCTGTAG' long g  
0 0 TTGTCTTATGTTGCCAGCACGCCCTTCGGGC  
0 0 CTGTGATTTG' long f  
2 4 TTGTCATTAATTGCCATTATTGAGTTGGGCA  
10 7 TCGGGGGTAGTTACAAGTGTCTACCGCGAC  
4 4 AAGCTGCCCAGTTAGGAACCAGGATTGTCC  
2 4 TCGCCTTTAG' tag p  
0 0 TCGCGTCCAA long f

1			
2			
3			
4	4	8 TTGCCATTAA' tag	c
5	4	9 CCATCTCTAG' tag	f
6	0	0 TCGTTGTATAATACGAGGCGCTAGTTTTTGC	
7			
8	0	12 TAACCTGCTAAATAGTCACTGGAAACTGCTC	
9	4	6 TTGTCACTAG' tag	f
10			
11	0	2 CTATCTTTAG' tag	k
12	6	7 CTGTGTCCTGTTGCCACTCGGATGAGAGTCC	
13	0	0 CTATCTCTAG' long	f
14			
15	9	10 TTGTCCTTATTTGCCAACAGGTAATGCTGGC	
16	0	0 TAACCTGCTAAATAGAACTTCTATAACTTA	
17			
18	3	0 CTACGGTCAGTTACCTGTGTCTGGCCGGAC	
19	5	3 TTGCCGCTAA long	k
20	0	0 TTGCCATTAGTTGCTACATTCAGTTGGCACT	
21			
22	0	0 TAACCTGCTAAATAGACACGCCGGCTTTGG	
23	10	9 CTGTTGTTAGTTGCCATCGAGTCAAGTCGG	
24	0	0 TTGTCCTTAG' tag	k
25			
26	3	7 TCGCCTTTAGTTGCCACGTAAGTGGATCTCT	
27			
28	3	0 TTGTCGCTAGTTGCCAACAGGTAATGCTGG	
29	0	0 TTGCTATTAGTTGCTACATTCAGTTGGGCAC	
30	0	0 TTGTCGCTAG tag	f
31			
32	0	0 TTGTTCTTAG' long	k
33	2	5 CTGCTTTCAGTTGCTACCGGGTCGTGCCGAC	
34	7	4 TTATTGCCAG' long	p
35	0	0 TCGCTTCTAG' long	f
36			
37	0	0 TTGTCTTTAGTTGCGACCATTTAGTTGAGCA	
38			
39	6	9 CAGTTAATAAATAGGGGATATAATCTTTTAC	
40	5	9 TTGTCCTTAG' tag	f
41	0	0 CTGCGTCCAG long	c
42			
43	0	0 TCGTCCCTAGTTACCAGCGGGCAAAGCCGG	
44	0	0 CTATCCTTAGTTGCCAGCGGATGATGCCGG	
45			
46	0	0 TTTTCTCTAGTTGCTAACGGATTATGCCGAG	
47	0	0 CTGTCTTCAG' long	g
48			
49	3	10 TTGTCCTATG' tag	p
50	0	0 TTACCGTGAGTTACTACCATTTCAGTTGAGGA	
51			
52	4	11 CTATTGTTAG' tag	g
53	3	4 TTGTCATTAATTGCCATCATTGAGTTGGGCA	
54			
55	5	7 CAGTTAATAAATAGGGGGTAATATCTTTTAC	
56	2	5 AAGCTGCCCCA long	g
57			
58			
59			
60			

0 TCATCCTTAGTTGCCAACACCTCGGGTGGG/  
0 CTTTCTTTAGtag f  
0 CAGCCTGCTA long c  
0 TAACCTGCTAACTAGACTTGCTCACCTTGGT  
2 TCGCCTTCAGTTGCCATCACTTTCAGGTGGG  
2 TCATTCTCTGTTGCTAACAGGTTAGGCTGAG  
3 TTGTCCCTAGtag f  
3 CCGCCTGCTA long g  
5 CTACCATTAGtag g  
5 TTGCCGTTAGTTGCCAGCAGGTCAAGCTGG  
0 CTGTTGTTAGtag g  
0 CTGTCCCTAGtag g  
0 TCGTCCCTAG long f  
0 TCGTCCTTTGTTGCCAGCGATTAAAGTCGGC  
0 CTATTGTTAG long g  
0 TTATCAACAG long o  
0 TCGTCCTATG long f  
4 TCGCCATTAGtag c  
7 TCGTCTTCAG long f  
4 CTGTTTCTAG long f  
0 CTAGTGCCAGtag f  
3 TTATCCTCAGTTGCCAATGGGTAGAGCCAGC  
0 CTACCTTTAGtag o  
0 TCGCCTCCAG long f  
0 CTGTCGCTACTTGCTAACGAGTAATGTCGAG  
0 TTGCCATTAGtag c  
3 CTATTGCTAGTTACACGTGTCTAGCGATACT  
0 CAACCTGCTAAATAGGAAGTTTGATGGGGG  
6 TTGTTATTAATTGCCATCATTGAGTTGGGCA  
0 CTGTTCTTAGTTGCCAGCGAGTAAAGTCGGC  
4 TTACCAGCTAAATAGTGATTGTTTTGATTTT  
3 CTATCATCAGTTGCCAGCGGGTCATGCCGGC  
0 TCGTCCTATGTTACCAGCGAGTAAAGTCGGC  
4 TCGTCGTCAGTTGCCCCATTAAGTTGAGCA  
0 TCGCCATTAG long g  
2 CTGTGACTAGTTGCCAGCGCGTCAAGGCGG  
8 CTGCCTTTAAATAGAGATGATTATGAGAAAT  
1 TTGTCATTAATTGTCATCATTGAGTTGGGCA

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4	5	0 CTGCCTTTAAATAGAGATGATTATAAGAAA1
5	0	0 CTATCTTTAG <sup>-</sup> long g
6	6	9 TCACGAGATAATAGGCCGAGAAAAGGAAA1
7		
8	3	7 TTATACTTAG <sup>-</sup> long f
9	2	0 TCGTTCTATG <sup>-</sup> tag f
10		
11	0	0 CTCCTTATTA/ tag g
12	0	3 CTGTCGTTAG long g
13	0	0 CCTTGTTTCAGTTGCCAGCAAGTAAAGTTGG1
14	0	3 TTACCGTATGTTGCTAGCAGGTAATGCTGAC1
15		
16	3	5 CTGTCGTTAG tag g
17	2	5 CTATCGTCTG <sup>-</sup> tag o
18		
19	6	4 TCGTCGTCTG <sup>-</sup> tag c
20	6	5 TCGTCTGCTGTTGCCATCAGGTTATGCTGG1
21	0	0 TCGCTACTAG long g
22	0	5 TTGTCTTTAG <sup>-</sup> long f
23		
24	0	0 CTATCATTAGTTGCCAGCGATTTCGGTCGGG1
25	0	5 CTATGAACTG long f
26	0	0 TTGTTATTAG <sup>-</sup> tag o
27		
28	0	0 TAACCTGCTA long g
29		
30	9	2 CTGCCTTTAA/ tag o
31	0	0 CTA CTGTATGTTGCTAACGGATAATGCCGAC1
32	3	5 TCATCCTCAGTTGCCATCGGGTTAAGCCGG1
33		
34	0	0 TAACCTATTAATTAAGTTTTTTGAATTTTTAA
35	0	0 TTGTCCTTAG <sup>-</sup> tag g
36	2	6 TTGTCCTTAG <sup>-</sup> tag c
37		
38	6	7 CTATCTTTAG <sup>-</sup> tag k
39	0	0 TCGCGTCCTGTTGCCACTCCGTCGCAAGACC1
40	3	7 TTGTCCTTAG <sup>-</sup> long g
41	0	0 AAGCCTTTAA long g
42		
43	0	0 ACACTTCTAG <sup>-</sup> tag g
44	0	0 TTGCCATTAGTTGTTACATTCAGTTGAGCAC1
45		
46	0	0 TCATTCTCTGTTGCTAACAGGTTAAGCTGAG1
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48	6	0 CTACCATTAGTTGCTAGCAGGTAATGCTGAC1
49	0	0 CCACGTCCAGTTGCCAGCATTAAAGTTGGGG1
50		
51	4	3 TCATCTTCAG <sup>-</sup> long g
52	0	0 TCGCCTTTAG <sup>-</sup> tag p
53		
54	2	0 TTAATTATTAATTAGTTAAATATATTTTTATA
55	7	0 ACGTCCTTAG tag k
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0	0	CCATCCTGTGTTGCCAGCTCGCAAGAGCGC/
2	0	TCACCTTTAG` tag f
0	0	TTACCGTATGTTGCTAACGGGTAATGCCGA/
0	0	TTACCATACTAACTAGTTATATGTATACTTCT
0	0	TAACCTGCTA long f
6	0	CAGCCTGCTAATTAGTTATATAAATTAATAC
0	4	CGGCTTACTA long p
0	3	TCACGAGACAATAGGCCAGATAAAGGAAAC/
2	6	TCGTCTTTAG` tag p
2	0	TTGTCACTAG` tag f
0	3	CTACCTTCAG` long f
0	0	TTGTCCTCTGTTGCCACCCCGAAAGGGAGC/
0	0	TTGTCCTTAG` tag f
0	0	TTGTCCTTAG` long g
5	3	CTTTCCTATG` long o
0	0	TTGCCATTAGTTGCTACATTCAGTTGGGCAC
0	0	TCGTCCTATG` long p
0	0	TTATCATTAG` tag g
4	4	TTACCAGCTAAATAGTGATTGCTTTGATTTA`
4	10	TAATTTTTTAAATAGTTTTCTTTACTTTTCGAG
0	0	CTGTCCTTAG` tag k
0	0	TCGTTATTTATTGCTTAATCTTTATAGTATAA
0	0	TCGTTATTTATTGCTTAATCTTTAAAAAAGA/
0	0	CCATGGTCAGTTGCGGATGTTTCTGGCCAG/
4	5	TTGTCATTAATTGCCATCATTGAGTTGGGTA
0	0	TCCTCTTCAG` long g
4	2	CTATTCCTAG` long o
2	0	TCGTCCTATG` tag c
0	5	CTGTCGCGTGTTACACGTATCACGCGAGAC/
0	0	CTGTCTTCAG` long g
0	0	TGCCATTAGTTGCTACATTCAGTTGGGCACT
3	8	TCGTTCTATG` long c
0	0	TTGCCATTAGTTGCTATATTCAGTTGGGCAC
0	0	CTGTGTCTAGTTACCAGCGCGTCATGGCGG/
4	2	TCACGAGACAATAGGCCAGATAAAGGAGAC/
0	0	TTGCCATTAGTTGCTATATTCAGTTGAGCAC
6	8	TAACCTGCTAACTAGTATTACTATCCTAAAT/
0	0	TTGCCTTAG` tag g



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	2	7 CTGCATCCAGTTGCGACCGGGAAAGCCGAG
	0	0 TCGTTTTTTATTTTTTGTATTTCAAAAAA
	2	2 CTGTCCTTAG` tag p
	0	0 TCGCCTTAG` tag g
	0	0 CTATCGCCAG long g
	4	3 CAGTTAATAAATAGGGGGTATTATCTTTAG
	0	0 ACGTTGTTAG long f
	0	0 TCGTCCATAGTTGCCAGCACGTAATGGTGG
	0	0 TTGCCATTAG` long c
	2	3 CTGCCTTTGGTTGCCATCATTAAGTTGGGCA
	4	0 TCATCCTCAG` long g
	0	0 TTGTCCTTAG` tag c
	0	0 TTGCCATTAG` long f
	0	0 CAGCCTGCCAAATAGCCATGCGGACGCCTC
	2	5 TTGTCTTCTG` long o
	0	0 CCATTTCCTAGTTACCAGCACGTCATGGTGGC
	3	4 TTGTCATTAG` tag k
	0	0 TTGCCCTTAG` tag k
	0	0 CTA CTGTATGTTGCTAGCAGGTAATGCTGAC
	0	0 CTGTCGTGTGTTTCACGTGTCACACGAGACT
	0	0 CTATCTTGTAGTTGCCAACAGGTAATGCTGC
	0	0 TTGCCTCCTG` tag o
	2	2 TTATCATTAATTGCCATCATTGAGTTGGGCA
	2	3 TTATCCTATG` tag o
	0	0 CTACCATTAGTTGCTACCAGGTAATGCTGAC
	2	5 CTGTGTCTAG tag g
	0	0 CTATCATTAG` tag o
	4	5 TTGTCCTTAG` tag c
	0	0 TTGTGTCCTGTTGCCACTCAAACGAGAGTTT
	2	0 TTGTCCTTAG` long g
	0	0 CAACCTGCTAAATAGGAAGTTTGATAGGGG
	4	0 TTGTCCTGTG` long o
	0	0 CTGTGTCCTG` long c
	0	0 TCATTTTTTATTACGTACGTGATTTGTTTTTG
	0	2 CTGTCGTCAG long g
	0	7 CTTGGAGAA` tag f
	0	0 TTATCCTTAG` tag k
	0	0 TTGTCCTGTGTTGCTATCCGCAAGGAGCACT

0 TTGCCATTAGTTGCTACATTCAGTTGAGTAC  
2 CTACTGCCAG long f  
1 TTGTCATTAATTGCTATCATTGAGTTGGGCA  
0 CTGCCTTTAAATAGAGATAGTTATGAGAAAT  
5 TTGTCATTAATTGCCATCATTGAGTTGGGCA  
0 TCGTCCTATG long f  
0 CTATCATTAG tag o  
2 CTACGGCCAG tag g  
0 CTACCATTAG long f  
0 TTGTCATTAATTACCATCATTGAGTTGGGCA  
4 TCGGTGCGTGTTACAAGTGTCACGCACAAC  
4 TTGTCCTTAG tag g  
0 CTGTCGTTAG long g  
15 CAAGAGAGTGTTTTGTGCTTCCTTGTCAAAG  
0 TCATCCCTAG long g  
3 CAGTTAATAAATAGGGGACATAATCTATTAC  
0 CTGTCTCCAGTTGCCAGCGAGTAAAGTCGG  
0 TTATCATTAG tag f  
0 AAGCTGCCCAGTAGGGGTCTGAATTGTCTC  
0 CAGATTCTAGTTGTGGGTATTAGTGCCAAAT  
2 TCGTCCTTAG tag g  
0 TTGTCCTTAG long f  
0 TTGCCAATAGTTGCCAGCGAGTCATGTCGG  
0 TTGCCATTAGTTGTTACATTCAGTTGGGCAC  
3 TTGTCACTAG long g  
0 TCATCCTTAT long g  
2 TTGTCCCTAG long g  
0 TCGCCCTTAG long g  
4 CTGCCTTTAAATAGAGATGACTATAAGAAAT  
3 TTACCAGCTAAATAGTAATTATTATGATTTA  
0 CCATGGCCAGTTACTCGTGTCTGGCCAGACT  
0 TCGTCCCTAG tag g  
3 TTGTCACTAG tag f  
0 CTATGACCTGTTGCCACTCCGAGTAATCGGA  
2 TTGTCATTAATTGCCATCATTGTTGGGCACT  
4 CTGCCTTTAAATAGAGATGACTATGAGAAAT  
0 TCATTCTCTGTTGCCATCATTAAGTTGGGCA  
2 1 TAACCTGCTAACTAGTATTACTATTCCAAAT

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4		2	2 TCGTTCCTAG` tag g
5		0	0 TCGGGTCCAGTTACAAGTGTCTGGAGCGAC
6		0	3 TCGTCCTTAG` tag k
7		0	0 CCGTCCTTAG` long f
8		0	0 TTGTCATTAATTGCCACATTGAGTTGGGCAC
9		3	0 TTATCCTTAG` tag c
10		0	0 CCATCACTAG long g
11		0	0 TTGTCCCTGGTTGCCAGCCGTAAGAGGGGA
12		4	3 TTACCAGCTAAATAGTAATTGCTTTGATTTA`
13		2	0 TTGTCTCTAG` tag f
14		2	0 TTGCCTTTAG` tag k
15		2	4 CTGCCTTTAG` long g
16		0	0 CGAGAGGGTGGTTGAGGTTATTATTGAGGC
17		0	0 CTATCTTCAG` long f
18		0	0 TCGTCGCATAATAGAAGGCGTCATTGAATTG
19		0	0 TCGTTATTTATTGCTTAATCTTTCTTTAAAGA
20		4	7 TAACCTGTAACTAGTATTACTATCCCAAAT/
21		0	0 TCGTCTTTAGTTGCCATCACGTTATGGTGGG
22		2	5 TCGGTGTTAG long f
23		0	0 TAACCTGCTAAATAGACATGCCGGCTTTGAC
24		0	2 CTATTCTTAG` tag p
25		0	0 TCGCCACTAGTTGCCATCACGTTGGGGTGGG/
26		3	4 TTGGCGTATGTTTCACGTGTCATGCGCAACT
27		2	0 TCATCCCTTGTTGCTAACAGGTAATGCTGAG
28		0	0 CTGTCGCTAG tag g
29		3	2 CTACTTTTAG` tag p
30		0	0 CTATTTTTAGTTACCAGCGCGTTATGGCGGG
31		0	0 TCGTCCTATGTTGCCAGCACTAACGGTGGG/
32		0	0 TCGTCTTCAGTTACCAGCGGTTTTGGCCGGG
33		1	1 TTGACATTAATTGCCATCATTGAGTTGGGCA
34		0	0 CTGTCGCTAGTTGCTCGGCGCAAGCCTGTAC
35		0	0 CTGTCGCTAGTTGCTCGGTTCCGCCAGTACTC
36		0	0 TCGCGATTAG long g
37		0	0 CTATTATTAGTTGCCATCAGGTCATGCTGGG
38		0	0 TCGCCCTTAG` long o
39		0	0 TTGCCCTGTG` long f
40		0	0 TTGCCTTCAGTTGCCAACGGGTAAAGCCGG/
41		3	2 CTATTGCCAG tag k
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0 CTGTCGTTAG tag g  
3 CCGCCTGCTA tag g  
0 CTACGGTCAG tag g  
2 TCATCGCTAG tag f  
0 TTGCCATTAGTTGCTACATTCAGTTGGGTAC  
0 TCGTTCTATG' long f  
0 TTGATTATTAATTAGTTTAACAGATATGTAT/  
2 CTGTGTCTAG tag g  
0 TCATCTTCAG' tag g  
10 0 TAACCTGCTA tag g  
0 CTGTCGTCAGTTGCCAACACGTTATGGTGGC  
0 3 CTCCTTATTAAGTAGTGTGGCTCGCTGACCA  
0 0 TTGTCACTAG' long g  
0 2 TCGTCCTCTG' tag o  
5 4 TAACCTGCTAACTAGAACTTACTATCCCAAAT/  
4 4 TTACCTTATGTTGCTACCATTTAGTTGAGCA/  
0 0 TTGCCATTAG' long c  
0 0 TCGCCTTTAG' tag g  
0 0 TTACCATTAG' tag p  
0 4 CTACTTTCAGTTGCTACCAGGTTAAGCTGGC  
0 2 CTGCGTCCAGTTGCCAACGGGTCAAGCCGG  
2 3 TAATCTGCTAACTAGTATTACTATCCCAAAT/  
0 5 TTACCGTATGTTGCTATCAGGTAATGCTGAG  
2 1 TAACTTGCTAACTAGTATTACTATCCCAAAT/  
0 11 TAACCTGCTAAATAGAAACATCTATAACTTA  
0 0 TTACCATTAG' tag f  
2 4 CAGTTAATAAATAGGGGGTATAATTCATTG/  
0 0 TTGCCATTAGTTGCTACATTCAGTTGAGCAT  
0 0 CTGTCTCTAG' tag g  
0 0 CTGCCGTTAG tag g  
0 0 TCGTTCTATG' tag c  
0 0 TCATTGTGTGTTATACGTGTCACACAAGACT  
0 0 TTGTCCCTAG' tag f  
2 0 TTGTCATTAATTGCCATCATTGAGTTGGGCG  
0 0 CTATCCTTAG' tag f  
0 0 TTGCCATTAGTTGCTACATTCGGTTGGGCAC  
4 2 CTATCTTTAGTTGCCAGCAAGTAATGTTGGC  
0 9 CTGGCTTTGGTTGCCATCATTAGTTGGGCA

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4	0	0 TCGTTGCCAG tag	k
5	0	0 TTGTCTCATG` tag	o
6	0	2 CTGTCGCCAGTTACCATCATTGAGTTGGGG/	
7	0	0 TGCCATTAGTTGCTACATTGAGTTGAGCACT	
8	0	0 CTGGGAATA` long	g
9	0	0 CTGTGTCCAGTTGCCACTCGAACTTTGTTCG	
10	0	3 TTGATTTTAATTATTTAAAATCAAGGATTG`	
11	0	0 TTGTCATTAG` tag	f
12	2	5 TTATTGCCAGTTACACGTATCTGGCGAGACT	
13	0	0 CTGTCGCCAG long	c
14	3	2 CTGTCGTCAG tag	p
15	0	0 TCGCCATTAG long	g
16	0	0 TTGTCATTAATTGCCATCATTGAGTTTGGCA/	
17	0	0 TAACCTATTAATAAGTACGCTTATCCTTTCC	
18	0	0 TCGTCCTGTG` tag	p
19	0	0 TTGCCATTAGTTGCTACATTGAGTTGGGCAT	
20	0	0 CTGCCCCTAGTTGCCAGCGAGTAGAGTCGG	
21	0	3 TTATCCTTAGTTACCAACGAGTAGAGTCGGC	
22	0	0 TCACTCTTAG` tag	f
23	2	3 CTGCCGCTAG tag	c
24	0	0 TTGCCATTAGTCGCTACATTGAGTTGAGCAC	
25	0	0 CTATTGTTAG` long	c
26	0	0 TCGCCTTCAG` long	g
27	0	0 TTACCTTCAG` long	g
28	0	0 CTACCATTAG` tag	c
29	0	0 TTGTCATTTATTGCCATCATTGAGTTGGGCA	
30	0	2 CTGTCGTTAGTTGCTCACGGGTTATGCCGAC	
31	1	4 TTGTCATTAA` tag	f
32	0	3 TTGTCGTTAA` long	g
33	0	0 TTACCATTAG` long	o
34	0	0 TTATTATTAGTTGCCCCAATTAAGTTTGGCA/	
35	0	0 TTGCCATAGTTGCTACATTGAGTTGGGCACT	
36	5	0 TAACCTGCTAACTAGTCGCCTTTACATCATA/	
37	0	0 CTATCAATAG tag	f
38	0	2 TCGTCGCTAG tag	c
39	0	0 TTTTCCTTATT long	f
40	0	0 CTGTGTCCTGTTGCCACCCGGGAAACCGGA/	
41	4	0 TCGTCTCCAG` long	g
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2 0 TTGCCCTGTGTTGCTAGTCTGGTTTCGATCA  
0 0 TTACCCTATGTTGCCACGTCTGTAATGGACA  
0 2 CTATCGTTAGTTACCAGCACGTAAAGGTGGC  
0 0 CCGGGGTCAGTTAGACTGTCTGGCCCCGACT  
2 2 TAACCTGCCAACTAGTATTACTATCCCAAAT  
0 0 CTATCGTTAGTTGCCAGCGTAAAGACGGGC  
3 4 CAGTTAATAAATAGGGGGTAATATTCATTG  
0 3 CTATCTTCAG` tag f  
0 0 CTATCGTTAGTTGCTCAGCGCAAGCTAGTAC  
0 0 TTGTCCTGTG` tag o  
4 0 TTGTCATTAATTGCCATCATTGAGTTGGACA  
0 0 CTATTCTTAGTTACCAGCGGGTCAAGCCGGC  
0 0 CTGTTGTTAG` tag f  
0 4 TCGCCGTTAGTTGCTTCGTAAGAAGATCTCT  
2 0 TTGTCATTAATTGCCAACATTGAGTTGGGCA  
0 0 TTGTCCTGTG` tag o  
0 0 CTGTGATCAG long g  
0 0 TTGTCGCTAG tag k  
0 0 TTGCCATAGTTGCTACATTGAGTTGAGCACT  
2 0 CTTTTATCAG` long f  
0 0 TCGCCATTAGTTGCTACATTGAGTTGGGCAC  
0 0 CTGTCGCTAGTTGCTAACGAGTAATGTCGAC  
2 2 TAACCTGCTAACTAGTATTATTATCCCAAAT  
0 0 TTGTCATTAG` tag o  
0 0 CTGCTTTCAGTTGCTACCGCGTCATGCCGAG  
0 0 TTGTCCTTAG` long f  
0 0 CCTAACTTAATTATAAGTTTACTGCTTAGGA  
0 2 TCGCCTTCAGTTGCCATCAGGTAGAGCTGGC  
0 2 CTGTCCCTAG` tag c  
0 0 TTATCCCTAGTTGCTACCGGGTAAAGCCGGC  
0 3 TTGTCATTAATTGCCATCATTGTGTTGGGCA  
0 0 CTATCCTTAG` tag g  
0 3 CTGTCGTTAGTTGCTAACGGGTAAAGCCGAC  
0 0 TTGTTATTAG` long o  
0 0 TTACCATACTAACTAGTTATATATACTTCT  
0 0 CTACCCTGAGTTGCAACCGCAAGGGCACTC  
0 1 TAACCTGCTAACTAGTATTACTATCCCAATT  
0 0 TTGTCGCTAGTTACTAACGAGTCAAGTCGAC

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4		4	TCGCCATTAG tag c
5	0	0	TGGTCTACTAACTAGTATTTATCTTTAGCAA
6	0	0	TTACCCTCAG tag g
7	0	0	TCGTCCTATG long g
8	0	4	TAACCTGCTAACTAGTATTACTATCCAAAAT
9	0	0	TTACCTTTAG long g
10	0	0	CAGCCTGCTA tag k
11	0	5	TAACCTGCTAACTAGTATTACTATCCCAATA
12	0	0	TTGCATTAGTTGCTACATTGAGTTGAGCACT
13	2	2	CTGCCTTTAAATAGAGATGATTATGAGAAAT
14	0	0	TTATCATTAG tag g
15	0	0	CAGCCTTTAA tag g
16	0	0	TTGCCATTAG long g
17	0	0	TTATCTTTAG tag g
18	0	0	TTGTCATAAATTGCCATCATTGAGTTGGGCA
19	0	0	CTATCATTAG long f
20	0	0	TTGTTCCATG tag c
21	0	0	TTGCCATTAGTCGCTACATTGAGTTGGGCAC
22	0	0	TTGCCTTTAG long g
23	0	0	TTACCATACTAACTAGTTATATTTATACTTTT
24	0	0	TAACCTGCTAACTAGTATTACTATCTCAAAT
25	0	0	TTGCCATTAGATGCTACATTGAGTTGAGCAC
26	0	0	TCATCTTCAGTTACCATCGGTTCGGCCGGGC
27	0	0	TTGTTTTTTGTTACCACTCTTTGAGAGAACT
28	0	0	TTATTCTAATTTTATTCGACTAGTTGGTACGT
29	0	0	TTGCCTCTAACTAGAACAGTGTATGGGCAC
30	2	2	TAACCTGCTAATTAGTATTACTATCCCAAAT
31	0	0	TTACTACTAG long f
32	0	0	CTGTCGTCAGTTGCCAACGGGTCAAGCCGG
33	0	3	CTATCTTCAG tag f
34	0	0	CTATCGTTAG tag p
35	0	0	TCGTCCTATG tag c
36	0	0	TTGTCATTAAGTCCATCATTGAGTTGGGCA
37	5	0	TTACCGTTAGTTACAAGTGTCTAACGGGAC
38	0	0	CTGTTGTTAGTTGCCATCGAGTCAAGTCGGC
39	0	0	TTGCCATTAGTTGCTACACTGAGTTGGGCAC
40	0	0	TTGTCATTAG long o
41	0	4	TTGTCATTAATTGCCATCATTGAGCTGGGCA
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0 TCACCCTTAGTTGCCAACAGGTTATGCTGGC  
0 TTGTCTCTAG<sup>-</sup> long f  
0 TTGTCATTAATTGCCATCATAGAGTTGGGCA  
0 TTGTCATTAATTGCCATCATCGAGTTGGGCA  
0 TAGCCATTAGTTGCTACATTAGTTGAGCAC  
4 TTGCCGTATGTTATATATGTCATGCGGAACT  
0 CTGTTGCTAGTTTCAGGTGTCTAGCAAGACT  
0 TTGCCTTCAG<sup>-</sup> tag o  
0 TTATTGCTAGTTACCAACGGGTAAAGCCGGI  
3 0 TCGTCATTAATTGCCATCATTGAGTTGGGCA  
0 TCGTTATTTATTGCTTAATCTTTCTACGAAAG  
0 TTGTCCTTAG<sup>-</sup> tag o  
0 CTGCCCTTAG<sup>-</sup> tag f  
0 TTGTCATTAATTGCCATCATTGGGCACTTTA/  
0 ACACTTCCAG long g  
3 0 TTGTCACTAG<sup>-</sup> tag f  
0 TTACCATACTAACTAGTTATATATACTTAT  
0 TTATCCTTAG<sup>-</sup> long g  
0 TAGCCTACTAAATAGTTCGCCGACATCTCTT/  
2 0 TTGTCATTAATTGCCACCATTGAGTTGGGCA  
0 TTGTCCCTAG<sup>-</sup> long g  
0 2 TTAATTATTAATTAGTTAAATATATAGCAAT/  
2 0 TAGCCTGCTA tag p  
0 CTGTCTTCAG<sup>-</sup> tag c  
0 CTATCTTCAGTTGCCATCATTAAGTTGGGGA  
2 0 TCATTGTCTG<sup>-</sup> tag o  
0 TTCCCATTAGTTGCTACATTAGTTGAGCAC<sup>-</sup>  
0 TTGCATTTTGTTGCCACCTTCGCGCGAGCGA  
0 TCGCCTCTAG<sup>-</sup> long o  
0 ACGTCGCGTG<sup>-</sup> tag g  
1 0 TAACCTGCTAACTAGTATTACTATCCCGAAT/  
0 TTGTCCTTAGTTACCAGCACGTCATGGTGGC  
0 TTATTCTTAG<sup>-</sup> long g  
0 TTGTCTCCAG<sup>-</sup> long g  
0 CTATTGCCAGTTACCATCGGGTAGAGCCGGI  
0 TAGCCTACTAAATAGTTCGCTGACACCTCTT/  
0 2 CTGTCGTTAG long c  
2 0 CGGCCTGCTAAATAGCTACGCCGACCCCGC<sup>-</sup>



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4	0	0	TTGTCATTAG` long f
5	0	0	TTGCCATTTGTTGCTACATTCAGTTGAGCAC`
6	2	3	TTGCCATTAG` tag p
7	0	0	TTGTCACTAATTGCCATCATTTGGTTGGGCA
8	0	0	TAACTCTAA` long g
9	0	0	TTGTCGTTAG` long g
10	0	0	CTATCTTCAGTTACCATCATTGAGTTGGGCA`
11	0	0	TAACTGCTAAATAGCCCACGTTGCTTTGGC
12	0	3	TTGTCATTAATTGCCTTCATTGAGTTGGGCA
13	0	0	TCATCTCCAG` long f
14	2	5	TAACTGCTAACTAGTATTACTATCCAAATA`
15	0	0	CTGGGGATA` long g
16	0	0	TTGCCATTGGTTGCTACATTCAGTTGGGCAC
17	0	0	TTACCAGCTAAATAGTGATTGTTTTGAGTTT
18	0	4	TAACTGCTAACTAGTATTGCTATCCCAAAT,
19	0	0	CTGTCGTTAGTTGCCAGCGTAAAGACGGGC
20	0	0	CTATCATTAG` long f
21	0	0	TTGCCGTTAGTTGCTACATTCAGTTGGGCAC
22	0	0	CTGTCGTCAGTTACCATCAGGTAAAGCTGGC
23	0	0	TTGTCATTAG` tag o
24	0	0	CTGCCACTAGTTGCTAACGGGTGAAGCCGA
25	4	0	CAACCTGCTAACTAGTATTACTATCCCAAAT,
26	0	0	TTGCCATTAGCTGCTACATTCAGTTGAGCAC
27	0	0	TTCCCATTAGTTGCTACATTCAGTTGGGCAC
28	2	0	TTACTGCTAGTTGCTAACAGGAGAGCTGAG
29	0	3	TCATCCTCAGTTGCCATCGGGTTAAGCTGGC
30	0	0	TCGTCGCTAGTTACCAACATGTAATGATGGC
31	0	0	TTGCCATCAGTTGCTACATTCAGTTGGGCAC
32	0	0	TAGCCATTAGTTGCTACATTCAGTTGGGCAC
33	0	0	CTGTTGTTAGTTGCTAACGGTTCGGCCGAGC
34	3	1	TAACTGCTAACTAGTATTACCATCCCAAAT,
35	2	0	CTACGGTCAGTTATCCGTATCTGGCCGGACT
36	0	0	TCGCCCCTAG tag k
37	0	0	TTGTCATTAATTGCCGTCATTGAGTTGGGCA
38	0	0	TTGCCATTAGTTGCTTCATTGAGTTGAGCAC`
39	0	0	TTGTCATCAG` tag o
40	0	0	TCATCTTTAG` tag k
41	2	1	TAACTGCTGACTAGTATTACTATCCCAAAT,
42			
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2 TAGCCTGCTAACTAGTATTACTATCCCAAAT,  
0 TTATCTCTAGTTGCCAACACGTAATGGTGGC  
0 CTGTCGTTAGTTACTAACGGGTAAAGCCGA  
0 TCATCCTCAG` long f  
0 TTGCCATTGG long g  
2 TAACCTGCTAACTAGTACTACTATCCCAAAT,  
0 TAACCTGCTAACTAGTATTACAATCCCAAAT,  
0 TTGTCATTAATTGCCATCATTGAGTTGGGCT  
0 TTGCCATTAGTTGCTACATTCAGCTGAGCAC  
0 CTATCTTCTGTTGCCATCATTGAGTTGGGCA  
0 CTATCATTAGTTGCCAACGAGTAAAGTCGG  
0 CTGCTGCCAGTTACCAGCATTGAGTTGGGG  
0 CTGCCATTAG tag c  
0 CTGTGTCCTGTTGCCACCGGAATGCAAGTTC  
2 CTATCCTTAGTTACCAGCGGGTCAAGCCGG  
2 TTATCGCTAG tag c  
0 TTGCCATTAGTTGCTACATTCAGTTGACCAC  
3 TAACCTGCTAACCAGTATTACTATCCCAAAT,  
0 TTGCCCTTAGTTACTAACGAGTAATGTTCGAG  
2 ACGTCCTTAG tag g  
2 TTATTCTATG` tag f  
0 CAGTGAGAGGGACACTCATCATGAATAA  
0 TTGTCCTTAG` tag k  
2 TGTCATTAATTGCCATCATTGAGTTGGGCAC  
0 TTATCACTAGTTGCTAACAGGAAAGCTGAG  
1 TAACCTGCTAACTAGTATCACTATCCCAAAT,  
2 TCATCCTTAG` tag g  
4 TTGTTGTCTGTTGCCATCAGGTTAAGCTGGC  
2 TTGTCATTAATTGCCATCATTGAGATGGGCA  
0 CTGTTGCTAGTTGCCAACGAGTAAAGTCGG  
0 CTGTGTCCTG` tag c  
0 TTGCCATTAGTTGCTACATTCAGTTGGGCTC  
0 TTGCCATTAG` long o  
4 TAACCTGCTAACTAGTATTTCTATCCCAAAT/  
0 TCGTCCATAGTTGCCAGCAAGTAATGTTGGC  
0 TTGTCATTAATTGCCATCGTTGAGTTGGGCA  
0 TCGTCCTTAG` long o  
0 TTGTCCTATG` long f

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4	0	0 TTGCCATTAG` long f
5	0	0 TTGCCATTAGTTGCTACATTCAGTGAGCACT
6	0	0 TTGTCGTTAGTTACCAGCGCGTAATGGTGGC
7	0	0 TTACCATACTAACTAGTTATATATATACTTTT
8	0	0 TCGCCCCTAG tag o
9	0	0 CTATTGCTAGTTACAAGTGTCTAGCGATACT
10	0	0 TTGTCATTAG` long o
11	0	0 TCATCCTTAT` tag f
12	3	2 TCATCCTTATTTGCCAGCGGGTAATGCCGGC
13	0	0 CGAGAGGGTGTTGAGGTTATTATTGAGGC
14	0	0 CCGCCTGCTAAATAGCCCGACGTTCTGTGG/
15	0	0 TTACCTTTAGTTGCCAGCGAGTGAAGTTGGC
16	0	0 TTGTCATTAG` long o
17	0	0 TTGCCATTAGTTGCTGCATTCAGTTGAGCAC
18	2	0 TTGTCATTAATTGCCATCATTGAGTTAGGCA
19	0	0 CTGTGGTCAG` long g
20	0	0 TTGCCATTAGTTGCTACATTCAATTGGGCAC
21	0	0 TTGCCATTAGTAGCTACATTCAGTTGGGCAC
22	2	2 TAACCTGCTAACTAGTATTACTAACCCAAAT
23	0	0 CTGCCATTAGTTGCTACATTCAGTTGGGCAC
24	0	2 CCGGGGTTAGTTACAAGTGTCTAACCCGAC`
25	0	2 TTGTCACTAG` long f
26	0	0 CTATCGTTAG` tag k
27	0	0 CGGCACTCCGAATAGCGCGGCGGACGTCGC
28	2	0 TCGCCTTTAGTTGTTATGTAAGTGGATTTTT/
29	0	0 TCGCCTTCAGTTGCCAGCAGGTAAAGCTGG/
30	0	0 CTATCATTAGTTACCAACGGGTAAAGCCGG/
31	0	0 TAACGTGCTAACTAGTATTACTATCCCAAAT
32	0	0 CTGTTGCCTGTTACAAGTGTCAAGGCAAGAC`
33	0	0 CTATTCTTAG` tag p
34	1	3 TTGTCATTATTTGCCATCATTGAGTTGGGCA
35	0	0 CTGTCTCCAGTTGCCAGCAAGTAATGTTGGC
36	0	0 CTACCATTAG` tag o
37	0	3 TTGCCATTAG` long c
38	0	3 TCGTTGCCTG` tag p
39	0	0 TCATCTTCAG` tag g
40	0	0 TTGCCATTAGTTGCTACTTTCAGTTGGGCAC
41	0	0 CTGTGTCCTGTTGCCACTCAGGTGCAAACCT
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0 3 TACCTGCTAACTAGTATTACTATCCCAAATA  
0 0 CTGCATTTAGTTGCCAGCATTTAGTTGGGCA  
0 0 CTATCGTTAGTTGCTCACGGGTAAAGCCGA  
0 0 TTGTCATTAG' long o  
0 0 TTGTCGTTAATTGCCACCATTAAGTTGGGCA  
0 0 CTGCCATTAG long f  
0 5 TAACCTACTAAATAGTTACGGTAATATTGCT  
0 0 TCGCCTTCAG' tag g  
0 0 TTGCCACTAG long f  
0 0 GGGATTGATAAATAGGGCGGCCGCGGGCG  
0 0 TTGCCATTAGTTACTACATTCAGTTGAGCAC  
0 0 TAGTCTACTAAATAGTTTCGCCGACACCTCTT  
0 0 CTGTTTTTGGTTGCCATCATTAAAGTTGGGCA  
2 0 TCGCCTCCAGTTGCCATCATTTGGTTGGGCA  
0 0 CTACCCTCAGTTGCTAATTATAGGACTCTGG  
0 0 TTGCCATTAGTTGCTACATCCAGTTGGGCAC  
0 0 CTGTCGTCAGTTGCCAACAGGTCAAGCTGG  
0 0 TTGTCTCCAG' tag f  
2 0 CTATCATTAG' tag o  
0 0 CTATTGTTAG' long f  
0 0 CTGTTGTTAGTTGCCAGCGAGTGATGTCGG  
0 0 TTGTCGTTAATTGCCATCATTTAGTTGGGTA  
0 0 TCGTCCTATG' long c  
2 0 TCCTCTTCTGTTGCCAGCGAGTAATGTCGGC  
2 0 TAACCTGCTAACTAGTAATACTATCCCAAAT  
0 0 TTGCCATTAGCTGCTACATTCAGTTGGGCAC  
0 0 TTGCCATTAGTTGCTGCATTCAGTTGGGCAC  
0 0 TTGCCATTAGTTGCTACATTCAGTAGGGCAC  
0 0 TCGCCTTTAG' tag f  
0 0 TTGTCGTTAATTGCCATTATTTAGTTGGGCA  
0 0 TCGTTCTATG' tag g  
2 2 TAACCTGCAAACCTAGTATTACTATCCCAAAT  
2 2 TCATCCTCAGTTGCCATCGGGTTCGGCCGGC  
0 0 TTGTCATTAATCGCCATCATTGAGTTGGGCA  
0 0 CTATCACTAG' long g  
0 0 CAGTGGGAGGGACACTCAATTTATCTCATA  
0 0 CTGTCGCTAGTTGCTAACAGGTAATGCTGA  
0 0 CTGTTGTTAGTTGCCATCGAGTCAAGTCGG

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4	0	0 TATCCTGCTAACTAGTATTACTATCCCAAAT/
5	0	1 TTGTCATTAATTGCCATCATTGAGTAGGGCA
6	1	0 TGACCTGCTAACTAGTATTACTATCCCAAAT,
7		
8	0	0 TTGCCATTAGTTGCTACATTCAGTGGGCACT
9	0	0 TTGTCCTTAG` long g
10	0	0 TGATTTATTAATTAGTTGATCGTAGATTTAA`
11	0	0 TTGTCATTAATTGCCATTATTGAGTTGGGCA
12	0	0 TTGCCATCAGTTGCTACATTCAGTTGAGCAC
13	0	0 CAGTGAGAGAGATGCATTGAGAAGAAGTG,
14	0	0 CAGTGGGAGGGACGCATTGGAAAGAGTTT
15	0	0 CGACCTGCTAAATAGTGCGGCCACGCTTCC
16	0	0 CCGCCTGCTAAATAGCGCTGGCCTTGGCTCC
17	0	0 TTGTTCTCAGTTACCACCATTGAGTTGGGGA
18	0	0 TTGCCTTTAG` long g
19	0	0 TAGTCATTAATTGCCATCATTGAGTTGGGCA
20	0	0 TCATCTTCAG` long f
21	0	2 CCGCCTGCTA tag g
22	0	2 TTGTCGTTAG` tag o
23	0	0 TTGTCATTAATAGCCATCATTGAGTTGGGCA
24	0	0 CTTTTCTTAGTTGCCAGCGATTCCGGTCGGGC
25	0	0 TTGCCTTTAGTTGCTACATTCAGTTGGGCAC
26	0	1 TTGTCATTAG` tag k
27	0	0 AAGCTGCCCAGTAGAAGCCAGGATTGTCTT`
28	0	0 TTGTCCCTAGTTGCTAGCGGTTTCGGCCGGG/
29	0	0 TTGTCCTTAG` tag p
30	0	0 CTACCATTAG` long f
31	0	0 TTGCCATTAGTTGCTACTTTTCAGTTGAGCAC`
32	0	0 TCGCCTTTAG` long g
33	0	0 TCGCCTTTAG` long g
34	0	0 CTATCTTTAG` tag f
35	0	0 TCGTCCTGTG` long f
36	0	0 CTGCCTTCAGTTGCTACCGGGTCATGCCGAC
37	0	0 CTGTTGTTAGTTGCCATCGAGTCAAGTCGGC
38	0	0 TCGTGCCTAGTTGCTGATGTTTCTAGGCAGA
39	0	0 TTGTCCTTAG` long p
40	0	0 TTAGTGCTAGTTGCTAGCAGGAAAGCTGAG,
41	0	0 TCATTGTCAGTTGCTAACAGGTAATGCTGAC
42	0	0 TTATTGTCAGTTACCAGCATGTAATGATGGC
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0 TCGTCCTCTG` long f  
2 CGACCTGCTA tag g  
2 AAACCTGCTAACTAGTATTACTATCCCAAAT/  
1 TAACCTGCTAACTAGTATTACTTTCCCAAAT/  
0 CTA CTGCTAGTTGCTAACAGGAAAGCTGAG  
0 TTACCATACTAACTAGTTATATATATACATT  
0 TAGCCTGCTAAATAGTTCGTGATCTTCCGAG  
0 TTACCCTTAG` tag g  
2 TTGTCTTTAG` long p  
2 CAGTGGGAGGGACGCTCAATTCATCTTATA/  
0 TCATCAGCGTGTTACAAGTGTACGCGAGAG/  
3 TTGTCATTAATTGCCATCATTGAGTTGAGCA  
0 TCGCCTTCAGTTGCCATCGGGTAAGGCTGGC/  
3 CTGTCATTAATTGCCATCATTGAGTTGGGCA  
0 TTGTCATTAGATGCTACGAAAGGGCACTCT/  
0 TTATCTTTAG` tag k  
0 TTACCATACTAACTAGTTATATTTATATTTT  
2 TTGTCGTTAATCGCCATCATTAAAGTTGGGCA  
0 TTGCCATTAGTTGCTACATTCAGTTGGACAC  
4 TCGCCATCTAGTTGCTAGCGGTTCGGCCGAG/  
0 TTGTCTTTAGTTGCTACGAAAGGGCACTCTA  
0 TCGTTCCATG` tag c  
3 0 TAACCTTCTAACTAGTATTACTATCCCAAAT/  
3 0 TTGTCATTAATTCCCATCATTGAGTTGGGCA  
3 0 TAACCTGCTAACTAGTATACTATCCCAAATA/  
3 0 TCCTCTTCAGTTGCCATCATTAAAGTTGGGAA  
0 2 TTGTCCCTAGTTGCCAGCGGTTCCGGCCAGG/  
0 0 TTGCCATTAGTTGCTACGTTTCAGTTGAGCAC  
0 0 TTGCCACTAG long o  
0 0 CTACGGTTAGTTGCCATCAGGTCATGCTGGC/  
0 0 TTGTCATTAG` long o  
0 0 TCGCTGCTAG long f  
0 0 CGAGAGGTTGGTTGAGGTTATTATTGAGGC  
0 0 CTGTCCATAGTTGCCAGCAATTCGGTTGGGC/  
0 0 TAGCCTACTAAATAGTTCGCCGACACCTCTG  
0 0 TAGCTTACTAAATAGTTCGCCGACACCTCTT/  
0 0 CGAGAGGGTGGTTGAGGTTATTATTGAGGC  
0 0 TTGTCGTTAACTGCCATCATTTGGTTGGGCA

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4	1	0 TTGTCATTAATTGCCATCATTGATTTGGGCA
5	0	0 TTGCCATTAGTTGCTTCATTCAGTTGGGCAC
6	0	0 TTGCCATTAGTTGCTACATTCAGCTGGGCAC
7		
8	0	0 TTGCCCTTAG` long g
9	0	0 CTCCTTATTAAGTAGTGTGGCTCGCGGCCAT
10		
11	1	1 TTGTCATTAATTGCCATCATTGAGTTGTGCA
12	0	0 TTGCCATTAGTTGCTACATTCAGTTAGGCAC
13	0	0 TTACTTTCTG1 long g
14	0	0 CAATCTGCTAAATAGTACCGTTCACAGGGG
15	0	0 TAACCCGCTAACTAGTATTACTATCCCAAAT
16		
17	0	0 CTGTTGCTAGTTACACGTGTCTAGCGATACT
18	0	0 TTATCCTTAG` long c
19	0	0 CCGTTGTTAGTTGCCATCGAGTCAAGTCGG
20	0	0 CTATTCTTAGTTGCCAGCATGTTATGGTGG
21		
22	0	0 TTA CTGTTAGTTGCTAACAGGAAAGCTGAG
23	0	0 TAACCTGCTAACTAGTGTACTATCCCAAAT
24	0	0 TTGTCGTTAATTGTCATCATTAAAGTTGGGCA
25	0	0 TTA CTGCTAGTTGCTAATAGGAAAGCTGAG
26	0	0 TTGCCTCTAGTTGCCACCATTAAAGTTGGGCA
27	0	0 CCACGTCCAGTTGCCAGCATTAGGTTGGGG
28	0	0 CTGTGTTTAGTTGCTAACATTAAAGTTGAGGA
29	0	0 TAACCTGCTA long g
30	0	0 CTGTCTTTAGTTGCCAGCCTTAAGTTGGGCA
31	0	0 TTGTCATTAATTGCCATCATTGAGTTGGTCA
32	0	0 TGATTTATTAATTAGTTGATCATAGATTTAA
33	0	0 CAGTTAATAAATAGGGGATATTATCTTTTAG
34	0	0 ATGCCATTAGTTGCTACATTCAGTTGAGCAC
35	0	0 TTGTCATCAATTGCCATCATTGAGTTGGGCA
36	0	0 TAACCTGCTAACTAGTATTACTACCCCAAAT
37	0	0 CTATTCTTAGTTGTCAGCATGTTATGGTGGG
38	0	0 CAGTGAGAGGGACGCAGTGATCATTGAAAC
39	0	0 TTACCTTTAG` long g
40	0	0 CAGTGGGAGGGACGCCCAATTCATCTCATA
41	0	0 CTGTGTCCTGTTGCCACCGAGATGAGAGTC
42	0	0 CTATTGCCAGTTACCATCATTGAGTTGGGA
43	0	0 CTGCCTTTAAATAGAGATAATTATAAGAAAT
44	0	0 TTGTCCCTAGTCGCCAGCGGTTTCGGCCGGG
45	0	0 TTGCCATTAGTTGCTACATTCAGTCGGGCAC
46		
47	0	0 CAGTGGGAGGGACGCCCAATTCATCTCATA
48	0	0 CTGTGTCCTGTTGCCACCGAGATGAGAGTC
49	0	0 CTATTGCCAGTTACCATCATTGAGTTGGGA
50	0	0 CTGCCTTTAAATAGAGATAATTATAAGAAAT
51	0	0 TTGTCCCTAGTCGCCAGCGGTTTCGGCCGGG
52	0	0 TTGCCATTAGTTGCTACATTCAGTCGGGCAC
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0 TTGTCATTAATTGCCATCATTGAGTCGGGCA  
0 CGACCTGCTAAATAGGACCGACAACCTCTCG  
0 TAGCCTACTAAATAGTTCGCCGAGACCTCTT  
2 TAACCTGCTAACTAGTATTACTATCCCAGAT,  
2 TAACCTGCTAACTAGCATTACTATCCCAAAT,  
2 TTGTCTTTAA1tag f  
0 CAGCCTACTAAATAGTTCGCCGACACCTCTT  
0 TCGCCGTTAG tag k  
0 TTGTCACTAATTGCTATCATTTGGTTGGGCA  
0 TCGCTACGTGTTATATGTGTACGTAGGACC  
0 TTACCTCTAGTTGCCAGCGAGTAAAGTCGGC  
0 TAGCCTACTAAATAGTACGCCGATCCTTAGT  
0 TCGTCTTTAG tag f  
0 CTGTCACTAG long g  
0 TCACTGTTAGTTGCCAACAGGTTTGGCTGGC  
0 TCGTCGTGTGTTACAAGTGTACACGAGAC  
0 CTATCCCTAG tag p  
0 TAACCTGCTA tag g  
0 CTGCCATCAGTTGCAACTTGCTTTGCAAGGC  
3 CTACGGTTAGTTGCCATCAGGTAAAGCTGGC  
3 TTGTCATTAATTGCATCATTGAGTTGGGCAC  
3 TGACCTACTAAATAGCTGGGTCAACAATTTG  
3 CAGTGGGAGGGACGCTCATCACATGAATAA  
3 TTAGTGCTAGTTGCTAACAGGGAAGCTGAG  
3 CTATCATTAGTTGCCAACGGGTAATGCCGGC  
0 TAGCCTACTAAATAGTTCGCCGGCACCTCTT  
0 TTGACATTAG tag o  
0 CTGACACTAGTTGCTAACATTAAGTTGAGG/  
0 TCATCTTCAGTTGCCAGCAGGTAGAGCTGGC  
0 CGGCCTGCTAAACAGTGCTCTGAACTCTTCC  
0 TTGTCCCTAG long g  
0 TTGTCATTAGTTGCCAGCATTGAGTTGGGCC  
0 TTGTCATTAGTTGCCAGCATTGAGCTGGGCA  
0 TTGTCACTAGTTGCAAGCATTAAAGTTGGGC/  
0 TTGTCGTTAATTGCCACATTTGGTTGGGCAC  
0 TTATCACTAG long g  
0 TCGTCCTCTGTTGCTAACAGGTCATGCTGAG  
0 TTGTCATTAGTTGCCAGCATTGAGTAGGGCA/



1		
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3		
4	0	0 TTGTCTTATG` long g
5	0	0 CTGTCATTAGTTGCCAGCATTTCAGTTGGGCA
6	0	0 CAGCCTGCTAAATAGTTATGTGAATTTTACT
7	0	0 TTGTCACTAGTTGCCATCATTTGGTTGGGCA
8	0	0 TCGTCCAATG long g
9	0	0 TAACCTGCTA long o
10	0	0 TTGTCGTTAATTGCCTTCATTTGGTTGGGCA
11	0	0 CTGCTTTCAGTTGCCACCGGGTCATGCCGAC
12	0	0 TTGCCATTAGTTGCTACATTCAGATGAGCAC
13	0	0 TTGCCATTATTTGCTACATTCAGTTGAGCAC`
14	0	1 TTGTCAATAATTGCCATCATTGAGTTGGGCA
15	0	1 TTGTCATTAATTGCCATCATTGAGTTGGGAA
16	0	0 TTGCCATTAATTGCTACATTCAGTTGAGCAC`
17	0	0 TAGCCTACTAAATAGATCGCCGACACCTCTT
18	0	0 TAGCCTACTGAATAGTTCGCCGACACCTCTT
19	0	0 TCGTCGCGTGTTATATGTGTACGCGAGAC(
20	0	0 CTATTTCTAG` tag f
21	0	0 TTACCGAGAGTTACCATCATTTCAGTTGGGG/
22	0	0 CTGTGTCTAGTTGCCAACGGGTCACGCCGGI
23	0	0 TCGTCCTATG` long c
24	0	0 TTGTCGTTAATTGACATCATTTAGTTGGGCA
25	0	0 CCGTGATTAGTTGCCAGCATTAAAGTTGGGC/
26	0	0 TTGCTTTCAGTTGCTACCGGGTCATGCCGAC
27	0	0 TTGCCCTTAG` tag p
28	0	0 TTGCCATTAGTGCTACATTCAGTTGGGCACT
29	0	0 TTGTCATTAATTGCCATCAATGAGTTGGGCA
30	0	0 TTGCATTAGTTGCTACATTCAGTTGGGCACT
31	0	0 TTGCCATTAGTTGCTACATTCAGTTGGGCAC
32	2	0 CAGTGGGAGGGACACTCAATTCATCATAAT(
33	2	0 TTACCAGCTAAATAGTGATTATTATGATTAT(
34	2	0 TAACCTGCTAACTAGTATTACTATCCCAAAT/
35	2	0 TTGTCGTTAGTTACCAGCATGTAATGGTGGC
36	2	0 CTGCCTTTAAATAGAGATGATTATATGAAA/
37	2	0 CTGTGTTTAGTTGCTAACAGGTCATGCTGAC
38	2	0 TAACCTGCTAGCTAGTATTACTATCCCAAAT/
39	2	0 TTGGTGGGGATGACGTCAAGTCCTCATGGC
40	2	0 CAGTGAGAGGGACGCTCAATTCATTTACT/
41	2	0 CGGTGGGAGGGACACTCAATTCATTGAAAG
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4 2 0 CTATCTTCAGTTGCCATCATTAGTTGGGCG  
5 2 0 TCATCCTTAGTTGCTACCAAGTTGCGGCTGGGC  
6 2 0 CTCCTTATTAAGTAGTGTGGCTCGCGGTCAT  
7 2 0 TTGTCGTTAATTGCTATCATTAAAGTTGGGCA  
8 2 0 CTTCTTATTAAGTAGTGTGGCTCGCGGCCAT  
9 2 0 TAACCTGCTAACTAGTATTACTATCACAAAT  
10 2 0 CAGTGGAGGGACGCTCAATTCATCTCATAA  
11 2 0 CTATTGCTAGTTGCAACCCTTTTGGGGCAC  
12 2 0 TTACCAGTTAAATAGTAATTATTTGATTTA  
13 0 0 TTGTCATTGATTGCCATCATTGAGTTGGGCA  
14 0 0 TTGCCATTAGTTGCTACATACAGTTGAGCAC  
15 0 0 TTGCCATTAGTTACTACATTCAGTTGGGCAC  
16 0 0 TTGCCATTAGTTGCTACAATCAGTTGGGCAC  
17 0 0 TAACCTGCTA tag g  
18 0 0 TTGTCTTCTG tag o  
19 0 0 TAACCTGCTA long p  
20 0 0 TTGTTGTTAATTGCTATTATTTGGTTGGGCA  
21 0 0 TCGCCTCTAG long f  
22 0 0 CGACTCGTTAACTAGTCCGGCGCAGCCTGC  
23 0 0 CATCACTAGTTGCCATCAGGTAACGCTGGG  
24 0 0 TTGACGTTAATTGCCATCATTAAAGTTGGGCA  
25 0 0 TTGTCGTTAATTGCCATCATTAAAGTTGGGCG  
26 0 0 CTGTGTCCTGTTGCCACCGGAACGCAAGTT  
27 0 0 TAGCCTACTAAATAGTTTCGCCGACGCCTCTT  
28 0 0 CTATCGTTAGTTGCTCACGGGTAATGCCGAC  
29 0 0 TTGTCGTTAATTGCCATCATTGTTGGGCT  
30 0 0 TCGTCACATAATAGAAGGCGTCATTGAATT  
31 0 0 TTGTCACTAGTTGCCGTCATTTGGTTGGGCA  
32 0 0 TAGCCTACTAAATAGTTTCGCCACACCTCTT  
33 0 0 TTGTCACTAGTTGCCAGCATTAGTTGGGCA  
34 0 0 TTGTCCTAGTTGCCATCAGTTTGGCTGGGC  
35 0 0 TTATCCTATGTTGCCAGCATTAGTTGGGCA  
36 0 0 TTGCCTCTAGTTGTTAGTGAGTTATGTTGGG  
37 0 0 CTGTTACTAGTTGCTAACATTAAGTTGAGGA  
38 0 0 TAGCCTACTAAATAGTTTCGCCAACACCTCTT  
39 0 0 TAACCTGCTAAATATGTCACCGGTAGACATC  
40 0 0 TTGTCATTAG long g  
41 0 0 TTGCCATTAGTTGCTACATTCAGTTGCACTC

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2		
3		
4	0	0 TTGCCATTAG` long c
5	0	0 CTGTTGTTAGTAGCCATCGAGTCAAGTCGGC
6	0	0 CTGCCTGCTA long f
7	0	0 CAGTAGGAGGGACGCTCAATCAATAGTCTT
8	0	0 TTGTCCCTAGTTACTAACGAGTCAAGTCGAG
9	0	0 TCACCTTATG` tag g
10	0	0 TCATTGCCAGTTACAAGTGTCTGGCGAGAC`
11	0	0 TTGTCGTTAATTGCCATCATTAAAGTTTGGCA/
12	0	0 TTGTCGTTAATTGCCATCATTAAAGTTGGCAC
13	0	0 TCATCCTCGGTTGCCATCGGGTTCGGCCGGC
14	0	0 TTGTCGTTAG` tag g
15	0	0 TCGTCGTTAG long c
16	0	0 CAGTGGGAGGGACGCATTGATCATTTTTCTT
17	0	0 TTGTCATTAAATTGGCATCATTGAGTTGGGCA
18	0	0 CAGTGGGAGGGACACTCTTTTCATCACGAT/
19	0	0 TTGTCGTTAATTGCCATCATTAAAGTTGGACA
20	0	0 TCCTCTTCAG` long p
21	0	0 CTGTGTGATGTTATAATTTCTTCACATACTGC
22	0	0 CAGTGGGAGGGACACTCCTTTCATCACAAAG
23	0	0 CTATCTTTAGTTGCCATCAGGTAATGCTGAG
24	0	0 TTAGTGCTAGTTGCTAACAGGAACGCTGAG/
25	0	0 CAGCCTGCTA tag p
26	0	0 CAGTGGGAGGGACTCTCAATTCATCTCATA/
27	0	0 CCGTTGTTAGTTGCCATTAGGTAATGCTGGC
28	0	0 CTGTTGATAGTTGCCATCGAGTCAAGTCGGC
29	0	0 TCGCTGTATGTTACATGTGTCATACAGGACC
30	0	0 TTGCCATTAGTTGCTACATTAGTTTGGCAC`
31	0	0 TTGTCCTTAG` long o
32	0	0 CTGTCGTCAGTTGCCAACGGGTAAAGCCGG
33	0	0 TAGCCTACTAAATAGTTCGCCGACACATCTT
34	0	0 TAGTCATTAGTTGCCAGCATTAGTTGGGCA/
35	0	0 CTATCTTTAG` tag g
36	0	0 TAGTCATTAG long c
37	0	0 CTTTTCTTAGTTGCCAGCATGTAATGGTGGC
38	0	0 TTGTCATTAGTTGCTACGAAATGGCACTCTA
39	0	0 CTATTCTTAG` long c
40	0	0 TAGCCTACCAAATAGTTCGCCGACACCTCTT
41	0	0 TTGTCATTAGTTGCCAGCATTCAATTGGGCA
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0 TTACCATACTAACTAGTTATATGTATACATC  
0 CCATGGCCAGTTACTCGTGTCTGGTCAGAC  
0 TTGTCACTATTGCCATCATTTGGTTGGGCAC  
0 TTGTCATTAATCGCCACATTGAGTTGGGCAC  
0 TGGTCTACTAACTAGTATTTATCACTTAGCA  
0 TAACCTGCTA tag f  
0 TTGTCATTAG long o  
0 CTGCTGCTAGTTACCATCATTTAGTTGGGGA  
0 TAGTCACTAATTGCCATCATTTGGTTGGGCA  
0 TCGCTTCTAG tag o  
0 TTGCATTTAGTTGCCAGCATTGAGTTGGGCA  
0 CCGTTGTTAG long o  
0 TAGCCTACTAAATAGTTTCGCCGTCACCTCTT  
0 TCATGTTTTGTTGCCAGCGAGTAAAGTCGGC  
0 TTGTCTTTAG long f  
0 TTGTCATTAATTGCTACCATTTAGTTGGACA  
0 CTATCAGTAG long f  
0 TTGTCCTTCGTTGCCATCATTAAAGTTGGGCA  
0 TTGTCATTAATTGCCATCACTGAGTTGGGCA  
0 CAGTGGGAGGGACGCTCAATCAATAGCCTT  
0 TTATTTTATATTGGACATACTTTTATTAGTAA  
0 TTGACATTAATTGCCATCATTTAGTTGGGCA  
0 TTGTCACTAATTGCCATCATTAAGTCGGGCA  
0 TCGCCGCGTGTTATACGTGTCACGCGGGAC  
0 CCATCTTTAGTTGCCATCAGGTTATGCTGGG  
0 TGTGTTAGTTGCCATCGAGTCAAGTCGGG  
0 CAACCAGCATCTACATGCCAGTTCCGTTTAA  
0 CTATTCTTAGTTGCCAGCATGTTATAGTGGG  
0 CTGCTTTCAGTCGCTACCGGGTCATGCCGAC  
0 TTACCAGCTAAATAGTGATTTTTATGACTTG  
0 CGGCTTATTAAATAGTCTAAAGTTCGCAGGC  
0 TCGTCGTCAGTTGCCACCATTAAAGTTGAGCA  
0 CTGCTTTCAGATGCTACCGGGTCATGCCGAC  
0 CAGTGGGAGGGACGCTTAATCAATAGTCTT  
0 TTA CTGCTAGTTGCTAACAGGAAAGCTGAA  
0 TCTTCCTTATTTGCTACGATTTTCGAGGACT  
0 CTGTCGTTAATTGCCATCATTTAGTTGGGCA  
0 TTGTCCTTATTTGCCAACAGGTTATGCTGGG

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4	0	0 TTGTCATTAATTGCAATCATTGAGTTGGGCA
5	0	0 CTATTCTTAGTTGCCAGCATGAAATGGTGGC
6	0	0 CTACTTTCAGTTGCTACCGGGTCATGCCGAG
7	0	0 TTACGTTATGTTGTTTAAAAATATTTGGTAAA
8	0	0 CAGTGGGAGGAACGCTCAATTCATCTCATA
9	0	0 TTAGACCCTAGTTGCCAGCGGTTCCGGCCGGG
10	0	0 CTGCGGCCAGTTAGAGCGTCACTGGCCGGA
11	0	0 TTGTCCCTAG` long f
12	0	0 CCGCCTGCTA long g
13	0	0 CCGCCTGCTAAATAGCGCAGCCTTGGCTCAT
14	0	0 TTACAGTGAGTTACCATCATTTAGTTGGGGA
15	0	0 TTACTGCTAGTTGCTAACAGGAAAGCTGTG
16	0	0 TTGTCCCTAGTTGCCAGCATTTCCGATGGGA
17	0	0 TTGTCATTAATTGCCATCATTTAGTTGGGTA
18	0	0 TTGTCCCTAGTTGCCAGCGGTTCCAGCCGGG
19	0	0 TTGTCATTAATGGCCATCATTGAGTTGGGCA
20	0	0 TTGTCCCTAG` long g
21	0	0 TTACCAGCTAAATAGTAATTATTAAGACTTG
22	0	0 TCGGTGTGCGTTACATGTGTGCGACACAAC
23	0	0 TTGTCCCTAG` tag f
24	0	0 TGTCGTTAATTGCCATCATTTAGTTGGGCAC
25	0	0 CAGTGGGAGGGACGCATCGGAAAGAGTTT
26	0	0 TAGTGGGAGGGACGCATTGGAAAGAGTTT
27	0	0 CTATCGCTAGTTGCCAGCGCGTAAAGGCCGG
28	0	0 TTGTCGTTAATTACCATCATTAAGTTGGGCA
29	0	0 TTACTGCTAGTTGCTAACAGGATAGCTGAG
30	0	0 CTACCGTTAG tag f
31	0	0 CAGTGGAGGGACACTCTTTTCATCACAAGA
32	0	0 CTGTCCTTTG` tag g
33	0	0 TCATCCTCAGTTACCATCGGGTTCCGGCCGGC
34	0	1 TTGTCATTAATTGCCATCATTGAGTTGGCCA
35	0	0 TTGACATTAGTTGCTACATTCAGTTGGGCAC
36	0	0 TTGTCATTATTTGCCATCATTCAGTTGGGCA
37	0	0 TTGTCATTAATTGCTATCATTCAGTTGGGCA
38	0	0 TTGTCCCTAGTTGCCAGCGGTTCCAGCCGGG
39	0	0 CCGCGGCCAGTTACTGGTGTCTGGCCGGAC
40	0	0 TTACCGCTAGTTGCTAACAGGAAAGCTGAG
41	0	0 TTTACTTTAATTATGTAAAAAATAATTTA
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0 TTACTGCTAGTTGCTAACAGGAAAGCTGAG,  
0 TCGTCCTGTGCTGCTAACCGAAAGGTGCAC`  
0 CTGTCGCTAGTTGCTAACGCGTAAAGGCCGA  
0 CTATTCTTAGTTGCCAGCATGTCATGGTGGC  
0 CAGTGGGAGGGACGCTCAATTAATCTCATA,  
0 TTACTGCTAGTTGCTACAGGAAAGCTGAGA,  
0 TTACCTTTAG` tag g  
0 TCGCCTCTAG` long f  
0 TTACCAGCTAAATAGTAATTTTTATGACTTG`  
0 TTATCCCTAG` long o  
0 CAGTGAGAGGGACGCTCGATTCATTTACAA,  
0 TTATCTTTAGTTGCCAGCATGTGATGGTGGC  
0 CTGTGATTAGTTGCCAGCGAGTCATGTCGGI  
0 TTGTCATTAATTGCTACCATAGTTGGGCACT  
0 CTA CTGCTAGTTGCTAACAGGAAAGCTGAG,  
0 TTACTGCTAGTTGCTAACTGGAAAGCTGAG/  
0 CTGTGATTTG` long g  
0 TTTACTTTAATTATGTAAAAAATAATTT/  
0 TTATCTTCTGTTACCAACGCGTAAAGGCGAG  
0 CTGCTTTCGGTTGCTACCGGGTCATGCCGAC  
0 TAACATGCAAACTAGCCGACGCGCTCTGC  
0 CAGTGGGAGGGACACTCAATTCATCTATAA`  
0 CTACCATTAGTTGCTAGCAGGTCATGCTGAC  
0 TTGTTCTAGTTGCCAGCGGTTCCGGCCGGG/  
0 TTGTCGCTAG tag g  
0 TTATCTTTAG` long f  
0 CTAGTATTATTTATTTTAAATTAATAAAAA  
0 CAGTGGGAGGGACGCTCATTTCATCTCATA/  
0 CTGGCATTAGTTGCTAACAGGTTTGGCTGAC  
0 TTATCCTTAG` tag k  
0 TCGGCTCCAGTTACACGATGTCTGGAGCAA/  
0 TAACATGCTAACTAGTATTACTATCCCAAAT,  
0 TTGTCCCTAG` tag g  
0 TTGTCATTAATTGCCATCATTGAGTTGGGCA  
0 CTATTGCCAGTTACCATCATTGAGTTAGGG/  
0 CTA CTCTTTAG` long k  
0 TCGTCTTCAGTTGCCATCGGGTAGGGCCGT  
0 TTGTCATTAGTTGCTACGATAGGGCACTCTA

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4	0	0 TAGCCTACTAATAGTTCGCCGACACCTCTTG
5	0	0 TAGCCTACTAAATAGTTTGCCGACACCTCTT
6	0	0 TTGCCATTAGTTGCCAACATGTAATGATGGC
7	0	0 ATGTCATTAATTGCCATCATTTAGTTGGGCA
8	0	0 TCGTCCTGTGTTGCTAACCGCAAGGTGCAC
9	0	0 TAGCCTGCTAAATAGTCCGTGATCTTCCAAG
10	0	0 TCGTCCTTAGTTGCTAACAGTTCAAGCTGAG
11	0	0 TAACCTACTA, long o
12	0	0 CAACTTGCTAACTAGTCGCACTAGTCTTCTA
13	0	0 CCATCCATAGTTGCCAGCGGGTAATGCCGG
14	0	0 TTATCGTTAATTGCCATCATTTAGTTGGGCA
15	0	0 TAGCCTACTAAATAGTTCGCCGACACCTTTT
16	0	0 TCGTCCTTAGTTGCCAGCGAGTAATGTCGGC
17	0	0 CTGCTCTCAGTTGCTACCGGGTCATGCCGAC
18	0	0 TCATTCTCTGTTGCTAACGCGTAATGGCGAG
19	0	0 TTGTCGTTAATTGCCATCATCAAGTTGGGCA
20	0	0 TCTTGTTGAGTTGCCAACAGGTAGTGCTGGC
21	0	0 TTGTCATTAGTCGCCAGCATTGAGTTGGGCA
22	0	0 TCGTCCTGTGTTGCTAACCGGAAAGGTGCAC
23	0	0 CTGCTTTCAGTTGCTACCGGGTCATGCCAAG
24	0	0 CAACTTGTTAACTAGTCCGGCGCAGCCTGCA
25	0	0 TTATCCTTAG, long g
26	0	0 TTGTCCTTGG, tag c
27	0	0 CTACCTCTAGTTGCCAGCGGTTTCGGCCGGG,
28	0	0 TAGCCTACTAAATAGTTCGCCGACACCTCTT
29	0	0 TCGTTCTATG, long g
30	0	0 TAGCCTGCTGAATAGTCCGTGATCTTCCGAG
31	0	0 TTGTCATTAATTGCCATCATTTAGTTGGGCA
32	0	0 TTGTCCCTGGTTGCCAGCATTTTGGATGGG,
33	0	0 CGAGAGGGTGTTGAGGTTATTAATGAGG,
34	0	0 CGAGAGGGTGTTGAGGTTATTATTGAAGC
35	0	0 TTGATCTTAG, long o
36	0	0 TCGCCTCCTGTTGCCAACAGATAATACTGGC
37	0	0 TTATTCTAATTTTATTGTTCTTTGAATTTGCT
38	0	0 TTGTTATTTGTTACCAACAGGTAAAGCTGGC
39	0	0 TTGCCATTAGTTGTTATGAAAGGGCACTCTA
40	0	0 CTGTCGTCAG tag p
41	0	0 CTGTCGTTAGTTGCTCGGCGAAAGCCAGTA
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0 ACGCCAACAC tag g  
0 TTGTCATTAG tag o  
0 TTGTGGTTAG tag g  
0 TTGTCATTAG long g  
0 TTGTCATTAGTTGCCAGCATCCAGTTGGGCA  
0 TCGTTCCATGATGCCAGCACGTAGTGGTGG  
0 CTGCTTTCAGTTGCTACCGGGTCATGCCGAC  
0 TCATCCCATG tag g  
0 TCGCATTATTTGCCGAGTAATGTCGGGAAC  
0 TCGTCTTTAG tag c  
0 CTGTCCGCAG long c  
0 CTGCTTCCAGTTGCTACCGGGTCATGCCGAC  
0 CGACTTGTTAACTAGTCCGGTGCAGCCTGC  
0 CTGTGGTTAGTTGCCAGCGAGTCAAGTCGG  
0 TCGTTCCATG long o  
0 TTGCCATTAA long c  
0 TAACCTACTAAATAGTTCGCCGACACCTCTT  
0 TAGCCTGCTAAATAGTCCGTGATCTTTCGAG  
0 TTATTGTTAG long g  
0 CTGCGACCAGTTGCACTTCTCTGGTCCGACC  
0 CTACCATTAGTTACCAACGGGTAAAGCCGG  
0 CTATTGTTAG long f  
0 CCGGTGGTAGTTACACGGTGTCTACCGCTAC  
0 CAGTTAATAAATAGGGGGTATAATCTTCTTA  
0 TTGCCCTTAG tag f  
0 TGGTCTACTAACTAGTATTTATCTTTTTTTTG  
0 TTGTCGTTGATTGCCATCATTTGGTTGGGCA  
0 TTGTCGTTAATTGCCATCATTTGGTTGGGCAC  
0 CTGCCTGCTAACTAGCGCGGGCTATCCCCTC  
0 TCGTCCTATG long o  
0 TTGTCACTAATTGCCATCATTTGGTTGGCAC  
0 TTGCCCTAG tag p  
0 TCGTTCATG tag g  
0 TAACCTGCTAAATAGTCAGGCCGGTTTTGGC  
0 CGACTTGTTAACTAGACCGGCGCAGCCTGC  
0 TTGTCACTAGTTGCCATCATTTGGTTGGGCA  
0 TTGTCATTAT tag g  
0 TTATCGTTAATTGCCATCATTTGGTTGGGCA



1		
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4	0	0 TCGTCCTTAG` tag g
5	0	0 TTGTCGTTAACTGCCATCATTAAGTTGGGCA
6	0	0 AACTTTTCAG` long g
7	0	0 TTGTCACTAATTGCCATCATTTGGTTGTGCA
8	0	0 TTGTTGTTAATTGCCATCATTTGGTTGGGCA
9	0	0 TTGTCATTAATTGCCATCATTTAGTTAGGCA
10	0	0 TTACCGTGAG long o
11	0	0 TTGTCATTAGTTGCCAGCATTTCAGTTGGCAC
12	0	0 ACGTCCCCAG long g
13	0	0 CGAGAGGGTGGTTGAGGTTATTATTGAGGC
14	0	0 CTATCGTTAGTTGCTCGGAGCAATCCTGTAC
15	0	0 TTGCCCTATG` long g
16	0	0 TCATCCTTAG` tag g
17	0	0 ACGCTGTTAGTTGCTAGCAGGTAAAGCTGA
18	0	0 TTATCGTTAGTTGCTCGGCGCAAGCCAGTAC
19	0	0 TCGTCCTGTGTTACTAACCGAAAGGTGCAC
20	0	0 TTGCCATTAA` tag g
21	0	0 TAGCCTGCTAAATAGTCCGTGATCTTCCGGC
22	0	0 TTAGCCCCCGTTACAAGTGTCTGGGGCGAC`
23	0	0 TTGCCATTAATTGCTATCATTTAGTTGGGCA
24	0	0 CTGTTGCTAG long f
25	0	0 TCGTGTCCAGTTGCCAGCAAGTAATGTTGGC
26	0	0 CTGTGTCTAG tag f
27	0	0 TTACTTTTAG` tag p
28	0	2 ATGTCATTAATTGCCATCATTTAGTTGGGCA
29	0	2 TAACCTGCTAACTAGTATTACTATTTCAAAT/
30	0	2 CTGCCAATAGTTGCCAGCGTTTAAAGACGG/
31	0	2 TAACCTGCTAACTAGTATTACTATCCAAGAT.
32	0	2 TTGTTATTAATTGCCATCCTTAAGTTGGGCA/
33	0	2 TAACCTGCTAACTAGTATTACTATCCCAAGT.
34	0	2 CTACCGCTAGTTGCTACAGTTAGGCTGAGC/
35	0	2 TCGCTGTATGTTACATGTGTCATACAGGACC
36	0	2 TTACCAGCTAAATAGTGATTGTTTGATTTAT/
37	0	2 TTGTCATTAATTGCCATCATTTAGTTGGGCAC
38	0	2 TAACCAGCTAACTAGTATTACTATCCCAAAT.
39	0	2 TTGTCATTAATTGCTATCATTTAGTTGGGCA/
40	0	2 CTATCCCATGTTGCATTTTCATGGGAGACTGC
41	0	2 TTGTCGTTAATCGCCATCATTTAGTTGGGCA
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0 2 TTGTCACTAGTTGCCATCATTTGGTTGGGCA  
0 2 TTTTCACTAGTTGCCATCATTTGGTTGGGCA/  
0 2 CAGTGGGAGGGACGCTCAATCAATAATCTT/  
0 2 CTGTTGTTAGTTGCCATCGAGTCAGGTCGGC/  
0 2 TAACCTGCTAACTAGTATTACTATACCAAAT/  
0 2 CAGTGTGAGGGACACTCTTTTCATCACAAG/  
0 2 AACCTGCTAACTAGTATTACTATCCCAAATA/  
0 2 TAACCTCCTAACTAGTATTACTATCCCAAAT/  
0 2 TTGTCCTTAG` long g  
0 2 TAACCTGCTATCTAGTATTACTATCCCAAAT/  
0 2 TTATCATTAG` long g  
0 2 TAACCTGCTACTAGTATTACTATCCCAAATA/  
0 2 TTGTCGTTAATTGCCATCATAAAGTTGGGCA  
0 2 TCGTTCCTTTGTTGCCAGCGATTAAAGTCGGC  
0 2 CAGCCTATTAAATAGCTATGCAGATTTGATT  
0 2 TTGACATTAATTGCCATCATTCAGTTGGGCA  
0 2 AAGCTGCCCAGTAGGAGCCGTAATTGCTT  
0 0 TTGCCATTAGTTGCTACATTCAGTTAAGCAC  
0 0 TTGTCATTAGTTGCTACGAAAGGGAAGCTCT/  
0 0 TTGTCGTTAG` long c  
0 0 ATGCCATTAGTTGCTACATTCAGTTGGGCAC  
0 0 TAGCCTGCTAAATAGTCCGTGATCTTCCGAG  
0 0 CCGTCACTAGTTGCCATCAGGTAACGCTGGC/  
0 0 TTATTGATAG` tag o  
0 0 TTGTCTCATG` long g  
0 0 TCATTTTTAGTTGCCAGCATTAAAGTTGGGCA  
0 0 TTGTCGTTAG` tag k  
0 0 TTGTCATTAGTTGACAGCATTAGTTGGGCA/  
0 0 TAACCTACTA` tag o  
0 0 GTCGGCTTTGGGCCGCATTAAAATCTACGG`  
0 0 CTATCTTTAGTTGCCATCAGGTATGCTGGGA  
0 0 TTACCGTGAGTTGCCATCATTCAGTTGGGG/  
0 0 CGACTTGTTAACTACTCCGGCGCAGCCTGCA/  
0 0 TTGTCCTTAG` tag c  
0 0 TCTTTTTTAATTTAAATTAAATAAATAAATTAA  
0 0 CTGTGATTAG` tag f  
0 0 CTACGATTAGTTGCCAACAGGTAAAGCTGG  
0 0 TTGCCCTTAGTTGCTACGCAAGAGCACTCTA

1			
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4	0	0 TTGTCCCTAG` tag	p
5	0	0 TTGTCCCTAG` long	g
6	0	0 CTGTCGCCAG tag	p
7	0	0 TCGTTCCATG` long	f
8	0	0 TTATCATTAG` tag	f
9	0	0 CTGTCCTTAG` tag	f
10	0	0 TTACCCTAAGTTGCCAGCATTTAGTTGGGCA	
11	0	0 TTGTCCCTAG` tag	c
12	0	0 TTGTCCCTAG` tag	g
13	0	0 TTGTCGTTAATTGCCATCATTTGGATGGGCA	
14	0	0 TTGTCATTAATTGCCATCATTTAGCTGGGCA	
15	0	0 CTGCGACTAG tag	g
16	0	0 TTGTCATTAG` long	o
17	0	0 CCATCTTCAGTTGCTACCAGGTTATGCTGGG	
18	0	0 TAGCCTGCTAAATAGTCCGTGATCTTCCGAG	
19	0	0 CAACCTGCTAAATAGGAAGTTTGATGGGGG	
20	0	0 TTGTCCCTAG` long	f
21	0	0 CTATCCTTAG` tag	g
22	0	0 TTATCTCTAGTTGCCATCAGGTTGGGCTGGG	
23	0	0 TTGTCATTAG` long	o
24	0	0 CGGCCTGCTAAATAGTGCTCGCCACTCCTCG	
25	0	0 CTGTCTTTAGTTGCCACCATTAAGTTGGGCA	
26	0	0 TTGTTATTAATTGCCATCATTAAGTTGGGCA	
27	0	0 CAGCCTACTAATAGTAATGCAAACCTTTACTA	
28	0	0 CTGTCATTAG` tag	o
29	0	0 TTGTCATTAGTTGCTACGAAAGGCCACTCTA	
30	0	0 TCGTCGTTAATTGCCATCATTTGGTTGGGCA	
31	0	0 TTGTCGTTAATTGCCATCAATTGGTTGGGCA	
32	0	0 TTGTCATTAGTTGCTAGCATTTCAGTTGGGCA	
33	0	0 TTGCCCTGTG` long	f
34	0	0 CAGCCTGCTAACTAGTCACAGGAATCGTCTC	
35	0	0 CTGTCTTTAGTTGCCACCAGGTAAAGCTGAC	
36	0	0 CTATGTTTAG` long	f
37	0	0 CGAGAGGGTGGTTGAGGTTATTATTGAGGC	
38	0	0 TTGCCATTAGTTGCTACATTTCAGTTAGCACTC	
39	0	0 TTGCCATTAGTTGCTACATTCTGTTGGGCAC	
40	0	0 TTGCCATTAGTTGCTACAATCAGTTGAGCAC	
41	0	0 TTGCCATTAGTTGCTACATACAGTTGGGCAC	
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0 TTGTCATTAG' tag f  
0 TTGTCATTAG' tag o  
0 TTGTCATTAATTGCCATCTTTGAGTTGGGCA  
0 TTGCCATTAGTTGCTACATTAGTTGAGCACT  
0 TTGCCTTTAGTTGCTACATTCAGTTGAGCAC  
1 0 TAACCTGCTAACTAGTATTACTATCCCAAAT  
1 0 TAACCTGCTAACTATTATTACTATCCCAAAT/  
0 0 TTGCCATTAGTTGCTACATCCAGTTGAGCAC  
0 0 TTTCCATTAGTTGCTACATTCAGTTGAGCAC  
0 0 TCGTGTTTAG' long c  
0 0 TTGCCATTAGTTAATACATTCAGTTGGGCAC  
0 0 TTGCCATTAGTTGCTACATTCAGTTGGGCAC  
0 0 TTGTCATTAATTGACATCATTGAGTTGGGCA  
0 0 TAGCCTACTAAATAGTTCTCCGACACCTCTT  
0 0 TAGCCTATTAAATAGTTCCGCCGACACCTCTT  
0 0 TAGCCTACTAAATAGTTCCGCCGACACCTCTT  
0 0 TTGCCGTTAGTTGCTACATTCAGTTGAGCAC  
0 0 TTGCCAATAGTTGCTACATTCAGTTGAGCAC  
0 0 TTTGCCATTAGTTGCTACATTCAGTTGGGCA  
0 0 TTCCATTAGTTGCTACATTCAGTTGGGCACT  
0 0 TAGCCTACTAAATAGTTCACCGACACCTCTT  
0 0 TTGTCATTAATGCCATCATTGAGTTGGGCA  
0 0 TTGTCATTAATTGCCATCATTGAGTTCGGCA  
0 0 TAACCTGCTAACTAGTATTACTATCCCAAAT  
0 0 TAACCTGCTAACTAATATTACTATCCCAAAT/  
0 0 TAACCTGCTAACTTGTATTACTATCCCAAAT/  
0 0 TTAGTGCTTGTGCTAACAGGAAAGCTGAG/  
0 0 TTGCCATTAG' long g  
0 0 TCACTGCTAGTTGCTAACAGGAAAGCTGAG  
0 0 TTGTCATTAATTGCCATGATTGAGTTGGGCA  
0 0 TTGTCATTAG' tag o  
0 0 TTGTCATTAGTTGCTACGAAAAGGCACTCTA  
0 0 TTGTCATTGG' long o  
0 0 TTGTCATTAGTTGCTACGAAAGTGCACTCTA  
0 1 TTGTCATTAATTGCGATCATTGAGTTGGGCA  
0 1 TAACCTGCTAACAAGTATTACTATCCCAAAT  
0 1 TAACCTGATAACTAGTATTACTATCCCAAAT  
0 1 TTGTCATTAATTGCCATCATTGCGTTGGGCA

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taxon_data	long	long_total	long_this	support	confidence
g	AAGTCCCGCA	12	12	789	0.95057034
g	AAGTCCCGCA	10	10	324	0.96296296
g	AAGTCCCGCA	12	12	194	1
AG	AATTCCGTTA	12	12		
g	AAGTCCCGCA	10	10	11244	0.98585912
GT	AATTCCGATA	6	6		
o	AAGTCCCGCA	12	12	2	1
g	AAGTCCCGCA	12	12	719	0.94019471
g	AAGTCCCGCA	12	12	32	1
g	AAGTCCCGCA	12	12	91	0.97802198
g	AAGTCCCGCA	12	12	387	0.96899225
g	AAGTCCCGCA	12	12	79	0.97468354
g	AAGTCCCGCA	12	12	274	0.8540146
g	AAGTCCCGCA	12	12	395	0.89620253
g	AAGTCCTATA	6	6	6	1
ATG					
f				881	0.99205448
g	AAGTCCCGCA	12	12	28	0.82142857
ATG	AATCCCGATA	6	6		
g	AAGTCCCGCA	12	12	116	0.95689655
g				8981	0.8558067
AA	AATTCCGCTA	12	12		
AT	AATTCCGTTA	6	6		
AAG	TATTCCGTTA	6	6		
GTG					
ATT	AATCCCGATA	6	6		
o	AAGTCCCGCA	12	12	64	1
g	AAGTCCCGCA	12	12	2	1
CTC	AAGTCCCTTA	12	12		
g	AAGTCCCGCA	6	6	43	0.95348837
f	AAGTCCCGCA	12	12	2	1
g	AAGTCCCGCA	8	8	3387	1
g	AAGTCCGCTA	6	6	2	1
TA	AAGTCCCTTA	8	8		
AA					
TGC	AAGTACGCTA	6	6		
f	AAGTCCCGCA	6	6	7	1

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2						
3						
4	AT	AATTCCGTTA	12	12		
5	g	AAGTCCCGCA	12	12	666	0.96996997
6	ACT	AAGTCCCGCA	6	6		
7						
8	ATG	AATTCCGTTA	12	12		
9	o	AAGTCCCGCA	10	10	27	1
10	ATG	AATCCCGATA	6	6		
11	f				34	0.97058824
12						
13	iATG	AATCCCGATA	6	6		
14	o	AAGTCCCGCA	12	12	5	1
15	ATG	AATCCCGATA	6	6		
16	CT	AAGTCCCGCA	6	6		
17						
18	g				250	0.88
19	GGA	AAGTCCCTTA	12	12		
20	g	AAGTCCCGCA	6	6	35	0.97142857
21	f	AAGTCCCGCA	6	6	4	1
22						
23	g				244	0.98360656
24	g				3	1
25	o	AAGTCCCGCA	7	7	3	1
26	g	AAGTCCCGCA	12	12	12177	0.98357559
27	g	AAGTCCCGCA	6	6	29	0.96551724
28	f	AAGTCCCGCA	11	11	43	0.93023256
29	g	AAGTCCCGCA	10	10	111	0.92792793
30	g	AAGTCCCGCA	6	6	15	0.93333333
31	iGG	AATTCCGTTA	6	6		
32	g	AAGTCCTGCA	4	4	194	1
33	AC	AATTCCGATA	10	10		
34	GT	AATTGTGATA	12	12		
35						
36	GATG					
37	g	AAGTCCCGCA	12	12	31	0.96774194
38	GGA	AAGTCCCGCA	7	7		
39	TTTC	AATCCCGATA	6	6		
40	CT	AAGTCCCGCA	6	6		
41	GC	AATTCCTTA	6	6		
42	g	AAGTCCCATA	6	6	3	1
43	p	AATTTGATA	12	12	16	1
44	f	AAGTCCGCTA	12	12	12	1
45	TGC	AAGTCCGAA	7	7		
46	o	AAGTCCCGCA	6	6	2	1
47						
48						
49						
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58						
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f	AAGTCCCGCA	6	6	5	1
CTC	AAGTCCTCTA	11	11		
g	AATTCCGATA	6	6	70	0.9
f	AAGTCCCGCA	12	12	4	1
g	AAGTCCCGCA	6	6	11	1
AA					
GA	AAGTCCTTTA	6	6		
g	AAGTCCTGCA	6	6	652	1
AC	AATTCCGTTA	5	5		
g	AATTCCGTTA	6	6	6	0.83333333
o	AAGTCCCGCA	12	12	29	1
g				230	0.86521739
g	AAGTCGCGCA	12	12	20	1
ACT	AAGTCCCGCA	6	6		
g	AAGTCCCGCA	7	6	1328	0.90737952
f				15	0.8
g	AATTCCGATA	6	6	4	1
f	AAGTCCCGCA	6	6	2	1
o	AAGTCCCGCA	6	6	2	1
g				59	0.83050847
TA	AAGTCCTTTA	12	12		
g	AAGTCCCGCA	9	9	167	0.83832335
AT	AATTCCGTTA	6	6		
TGA	AATCCCGATA	6	6		
AA	AAGTCCCGCA	12	12		
f	AAGTCCGCTA	12	12	14	1
f	AAGTCCCGCA	7	7	3	1
c	AAGTCCCGCA	12	12	2	1
o	AAGTCCCGCA	6	6	22	0.90909091
g	AAGTCCCGCA	6	6	509	0.92534381
CT	AAGTCCCGCA	6	6		
CTTT	AATCCCGATA	6	6		
AA	AAGTCCCGCA	10	10		
c	AAGTCCCTTA	12	12	17	1
o	AAGTCCCGCA	12	12	32	0.9375
CA	AAGTCCCGCA	6	6		
TCC	AATTCCGATA	9	9		
GCA	AAGTCCCGCA	7	7		



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2						
3						
4	gTC	AATTCCGATA	10	10		
5	gCA	AAGTCCCGCA	6	6		
6	CTTT					
7						
8	f	AAGTCCCGCA	12	12	2	1
9	f	AAGTTCCATA	6	6	2	1
10						
11	g	AAGTCCTTTA	12	12	2	1
12	g				16	0.875
13	g	AAGTCCCGCA	12	12	765	0.99084967
14						
15	CCG					
16	g	AAGTCCCGCA	12	12	578	0.85986159
17	g	AAGTCCCATA	6	6	43	1
18						
19	AAT					
20						
21	f				9	1
22	c	AAGTCCTTTA	11	11	4	1
23	g	AAGTCCCGCA	12	12	2	1
24	g	AAGTCCGGCA	6	6	41	0.97560976
25						
26	CTTT					
27	g	AATTCCGTTA	10	10	7	1
28	g	AAGTCCCGCA	9	9	919	0.8171926
29						
30	f				4	1
31	p	AATTCCGATA	6	6	3	1
32	g				920	0.84673913
33						
34	CCT	AATTCCGATA	7	7		
35	TAA	AATCCCGATA	6	6		
36						
37	f				24	1
38	ACT	AAGTCCCGCA	6	6		
39	ACT	AAGTCCCGCA	6	6		
40						
41	c	AAGTCCCGCA	12	12	5	1
42	TC	AATTCCGATA	10	10		
43	g	AAGTCCCGCA	12	12	294	0.98639456
44	CG	AATTCAGATA	6	6		
45						
46	g	AAGTCCGCTA	12	12	2	1
47	f	AAGTCCCGCA	11	11	3	1
48						
49	gGA	AAGTCCTCTA	6	6		
50						
51	g				300	0.98333333
52						
53	g	AAGTCCGGCA	12	12	277	0.94584838
54	g	AAGTCCCGCA	6	6	452	0.98230088
55	GAA	AAGTCCCTTA	6	6		
56						
57						
58						
59						
60						

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2						
3						
4	p	AAGTCCACTA	6	6	4	1
5	o	AAGTCCCGCA	5	5	91	0.97802198
6	TCT	AAGTCCCGCA	12	12		
7						
8	g				547	0.93235832
9	g				3087	0.81470684
10						
11	g	AAGTCCCGCA	11	11	33	0.81818182
12	f	AAGTCCCGCA	6	6	8	1
13						
14	TCT	AAGTCCCGCA	6	6		
15	o	AAGTCCCGCA	6	6	3	1
16	f	AAGTCCGCA	6	6	3	1
17	CT	AAGTCCCGCA	6	6		
18						
19	GCA	AAGTCCCGCA	6	6		
20						
21	g	AAGTCCCGCA	8	8	52	0.98076923
22	o	AAGTCCCGCA	6	6	13	1
23	f	AAGTCCCGCA	6	6	19	0.94736842
24						
25	TGC	AAGTCCGCA	7	7		
26	g	AAGTCCCGCA	10	10	10	0.9
27	TG	AAGTCCGATA	7	7		
28						
29	TA	AAGTCCCTTA	6	6		
30	g	AAGTCCCGCA	8	8	28	0.96428571
31						
32	GGC					
33	TGC	AAGTCCGCTA	12	12		
34	TC	AATTCCGATA	9	9		
35						
36	g	AAGTCCCGCA	10	10	10	1
37	f	AAGTCCCGCA	6	6	3	1
38						
39	AG	AATTCCGTTA	5	5		
40	GA					
41						
42	AT	AATTCCGATA	6	6		
43	g	AAGTCCCGCA	6	6	4	1
44	g				2152	0.96189591
45						
46	AC	AAGTCCCGCA	6	6		
47	o	AAGTCCCGCA	6	6	22	1
48						
49	GAA	AAGTCCAGCA	6	6		
50	ACT	AAGTCCCGCA	6	6		
51	GGA	AAGTCCCTTA	6	6		
52						
53	f	AAGTCCCGCA	12	12	3	1
54	f	AAGTCCCGCA	6	6	3	1
55						
56	g	AAGTCCCGCA	6	6	4	1
57						
58						
59						
60						

1						
2						
3						
4	AC					
5	g	AAGTCCGCTA	8	8	2	1
6	c	AAGTCCCGTA	6	6	6	1
7						
8	o	AAGTCCCGCA	6	6	67	0.94029851
9	CT	AAGTCCCGCA	12	12		
10	CGC	AAGTCCCGCA	12	12		
11						
12	TT	GATTCCGTCA	6	6		
13	GA	AAGTCCCGCA	6	6		
14						
15	TGT	AATTCCGATA	6	6		
16	GA	AAGTCCCGCA	6	6		
17						
18	c	TATTCCGTTA/	11	11	2	1
19	g				3958	0.91207681
20	f	AAGTCCTGCA	6	6	14	1
21						
22	AC	AATTCCTTTA/	11	11		
23	g	AAGTCCCGCA	10	10	108	0.88888889
24						
25	TC	AATTCCGATA	8	8		
26	CAC	AAGTCCCGCA	12	12		
27	TGC	AAGTCCACTA	6	6		
28						
29	f	AAGTCCCGCA	8	8	30	0.93333333
30	g	AAGTCCCGCA	11	11	44	1
31						
32	CGC	AAGTCCGCTA	7	7		
33	f	AAGTCCCGCA	6	6	3	1
34						
35	o	AAGTCCCGCA	6	6	2	1
36	g	AAGTTCCATA	6	6	31	1
37	f				7	0.85714286
38						
39	CT	AAGTCCCGCA	6	6		
40	ACT	AAGTCCCGCA	6	6		
41						
42	AA	AAGTCCCGCA	6	6		
43	f	AAGTCCCGCA	12	12	17	1
44	AT					
45						
46	g	AAGTCCCGCA	6	6	35	0.97142857
47	CT	AAGTCCCGCA	11	11		
48						
49	g	AAGTCCGGCA/	6	6	28	0.92857143
50	f	AAGTCCCGCA	7	7	57	0.92982456
51						
52	g				8	1
53	f	AAGTCCCGCA	6	6	2	1
54	f	AAGTCCCGCA	6	6	3	1
55						
56	ACT	AAGTCCCGCA	6	6		
57						
58						
59						
60						

3	TT	AATTCCGTTA	6	6		
4	CT	AAGTCCCGCA	6	6		
5	o	AAGTCCCGCA	6	6	86	0.87209302
6	g	AAGTCCCGCA	7	7	1975	0.98227848
7	g				605	0.95867769
8	TC	AATTCCGATA	8	8		
9	TTCC	TATTCCGATA	6	6		
10	f	AAGTCCCGCA	11	11	2	1
11	f				9	1
12	g	AAGTCCCGCA	6	6	61	0.8852459
13	g	AAGTCCCGCA	7	7	7	0.85714286
14	g				677	0.98966027
15	GAA	AAGTCCCGCA	6	6		
16	f	AAGTCCCGCA	11	11	12	0.91666667
17	g	AAGTCCCGCA	6	6	10	0.9
18	c	AAGTCCCGCA	6	6	76	0.96052632
19	f	AAGTCCCGCA	6	6	40	0.925
20	f				5	1
21	GA	AAGTCCCTTA	12	12		
22	ACT	AAGTCCCGCA	8	8		
23	TC	AATTCCGATA	9	9		
24	f				23	1
25	g	AAGTCCGCTA	12	11	14	1
26	GT	AATTCCGATA	6	6		
27	GG	AATTCCGTTA	6	6		
28	f	AAGTCCCGCA	6	6	4	1
29	f	AAGTCCCGCA	9	9	15	0.93333333
30	f	AAGTCCCGCA	8	8	7	1
31	g	AAGTCCCGCA	9	9	4	1
32	GCA	AAGTCCCTTA	6	6		
33	ACT	AAGTCCCGCA	6	6		
34	g	AAGTCCCGCA	11	10	381	0.8976378
35	c				177	0.84745763
36	GCA	AAGTCCCTTA	6	6		
37	GA	AAGTCCCTCA	6	6		
38	f	AAGTCCGAA	8	8	2	1
39	f	AAGTCCAGCA	6	6	2	1
40	f	AAGTCCCGCA	6	6	4	1

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2						
3						
4	CT	AAGTCCCGCA	9	9		
5	.TTA	GATTCCGTCA	6	6		
6	A					
7						
8	g	AAGTCCCGCA	6	6	234	0.98290598
9	CGC	AAGTCCGCTA	6	6		
10	f	AAGTCCGCA	12	12	16	1
11	f	AAGTCCCGCA	6	6	4	1
12	f	AAGTCCCGCA	6	6	28	0.85714286
13	f	AAGTGACGC	6	6		
14	g	AAGTCCCGCA	8	8	3895	0.84698331
15	CT	AAGTCCCGCA	6	6		
16	g	AAGTCCCGCA	6	6	19	0.89473684
17	g	AAGTCCCGTA	5	5	6800	0.98867647
18	g	AAGTCCCGCA	6	6		
19	g	AAGTCCCGTA	5	5		
20	GA	AAGTCCCGCA	12	12		
21	g	AAGTCCCGCA	11	11	935	0.99572193
22	TCC	AATTCCGATA	6	6		
23	g	AAGTCCCGCA	6	6	34	1
24	CA	AAGTCCCGCA	6	6		
25	CTC	AAGTCCCTTA	7	7		
26	g	AAGTCCCGCA	6	6	19	1
27	CTTT	AATTACGATA	6	6		
28	f	AAGTCCCGCA	6	6	9	1
29	f	AAGTCCCGCA	7	7	7	1
30	CA	AAGTCCCGCA	6	6		
31	p	AAGTCCACTA	6	6	2	1
32	AT	AATTCCGATA	5	5		
33	f	AAGTCCCGCA	10	10	5	1
34	o	AAGTCCCGCA	6	6	26	1
35	GA	AAGTCCCGTA	6	6		
36	g	AAGTCCATTA	6	6	9	0.88888889
37	g	AAGTCCCGCA	10	10	4693	0.99403367
38	f	AAGTCCCGCA	11	11	2	1
39	f	AAGTCCCGCA	6	6	11	0.90909091
40	g	AAGTCCCTTA	6	6	12	1
41	g	GATTCCGTCA	5	5	8	1
42	c				5	1
43	CT	AAGTCCCGCA	6	6		
44	CG	AATTCCGTTA	5	5		
45	f	AAGTCCCGCA	10	10	270	0.92222222
46						
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48						
49						
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TC	AATTCCGATA	8	8		
f				37	0.81081081
f	AAGTCCCGCA	6	6	3	1
GC	AAGTCCCGCA	9	9		
g	AAGTCCCGCA	10	10	7713	0.97212498
GAA	AAGTCCTATA	6	6		
g				756	0.99338624
g	AAGTCCCGCA	7	7	47	0.91489362
CTC					
o	AAGTCCCGCA	11	11	438	0.84018265
CA	AAGTCCTGCA	6	6		
g	AAGTCCCGCA	6	6	2	1
ACT	AAGTCCCGCA	6	6		
g	AAGTCCCGCA	6	6	29	0.89655172
GAA	AAGTCCCGCA	6	6		
f	AAGTCCCGCA	6	6	3	1
g				941	0.9946865
CTC	AAGTCCTCTA	6	6		
f	AAGTCCCGCA	6	6	17	1
AA	AAGTCCCGCA	6	6		
GCA	AAGTCCCGCA	6	6		
f	AAGTCCCGCA	12	12	7	0.85714286
o	AAGTCCCGCA	6	6	13	1
CT	AAGTCCCGCA	8	8		
CTTT	AATTACGATA	6	6		
g	AAGTCCCGCA	11	11	622	0.95176849
c				136	0.93382353
g	AAGTCCCGCA	6	6	161	0.93167702
ACT	AAGTCCCGCA	6	6		
g	AAGTCCTGCA	4	4	7440	0.93884409
f	AAGTCCCGCA	6	6	4	1
g	AAGTCCCGCA	6	6	30	1
f	AAGTCCCTTA	6	6	2	1
g				29	0.82758621
g	AAGTCCCTTA	6	6	132	0.97727273
f	AAGTCCCGCA	5	5	4	1
f	AAGTCCCGCA	5	5	3	1
GAA	AAGTCCCGCA	6	6		

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2						
3						
4	g	AAGTCCCGCA	5	5	5	1
5	g	AAGTCCCGCA	7	7	1630	0.98588957
6	\AT	AATTCCGATA	5	5		
7						
8	g				11	0.90909091
9	c	AAGTCCCGCA	6	6	8	1
10	GA	AATTGTGATA	9	9		
11						
12	iAT					
13	g	AAGTCCTTCA	6	6	8	1
14	g	AAGTCCCGCA	6	6	6	0.83333333
15						
16	.CT	AATTCCGATA	5	5		
17	f	AAGTCCCGCA	6	6	3	1
18						
19	g	AAGTCCCGCA	6	6	36	0.97222222
20	f	AAGTCCCGCA	6	6	130	0.95384615
21						
22	g	AAGTCCCGCA	6	6	5	1
23	\AT					
24						
25	TGC	AAGTCCGAA	6	6		
26	AA	AATTCCGATA	5	5		
27						
28	g	AAGTCGCGCA	10	10	61	1
29	IG					
30	p	AAGTCCCGCA	6	6	2	1
31						
32	g	AAGTCCCGCA	6	6	2	1
33	o	AAGTCCCGCA	6	6	2	1
34						
35	TC					
36	o	AAGTCCCGCA	5	5	10	0.9
37	\CT	AAGTCCCGCA	6	6		
38						
39	f	AAGTCCCGCA	11	11	6	1
40	GA	AAGTCCCTTA	8	8		
41						
42	g	AAGTCCCGCA	6	6	5	1
43	f				7	1
44						
45	GA	AAGTCCCGCA	6	6		
46	o	AAGTCCCGCA	6	6	7	0.85714286
47						
48	CTTT	AATTACGATA	5	5		
49	GA	AAGTCCCATA	6	6		
50	GA	AAGTCCCGCA	6	6		
51						
52	TC	AATTCCGATA	7	7		
53	GCC	AAGTCCCGCA	11	11		
54	GA	AAGTCCCGCA	6	6		
55						
56	\CT	AAGTCCCGCA	6	6		
57						
58						
59						
60						

GGA	AAGTCCTCTA	6	6		
g	AAGTCCCGCA	9	9	277	0.94945848
GA	AAGTCCCGCA	6	6		
g	AAGTCCAGCA	6	6	2	1
f	AAGTCCCATA	6	6	11	0.90909091
GAA	AAGTCCCATA	6	6		
CA					
p				5	0.8
CT	AATTCCGATA	6	6		
iT	CAGTCCTATA	6	6		
GA	AAGTCCCGCA	6	6		
f	AAGTCCCGCA	6	6	9	1
g	AAGTCCCGCA	6	6	2	1
f	AAGTCCGAAA	6	6	5	0.8
f				4	1
CA	AATTCCGTTA	5	5		
CA					
GAA					
CT	AAGTCCCGCA	6	6		
g	AAGTCCCGCA	6	6	193	0.82901554
g	AAGTCCCGCA	8	8	94	0.88297872
f				14	0.85714286
GGA	AAGTCCCTTA	6	6		
GA	AAGTCCTCTA	6	6		
TT	AAGTCCCGCA	9	9		
TGA					
g	AAGTCCCGCA	8	8	262	0.92748092
GGCG					
GA					
g	AAGTCCCGCA	6	6	12	1
igAC	AAGTCCCGCA	6	6		
TC	AAGTCCCGCA	6	6		
TGA					
CT	AAGTCCCGCA	5	5		
g				1060	0.99056604
f	AAGTCCCGCA	6	6	4	1
g	AAGTCCCGCA	6	6	53	0.9245283
o	AAGTCCCGCA	6	6	6	1



1						
2						
3						
4	g	AAGTCCCGCA	5	5	3	1
5	g				11	0.81818182
6	AC	AAGTCCCGCA	7	7		
7	ACT	AAGTCCCGCA	6	6		
8						
9	c	AAGTCCCGCA	10	10	29	0.96551724
10	GA	AAGTCCCGCA	6	6		
11						
12	g				838	0.9928401
13	c	AAGTCCCGCA	7	7	2	1
14						
15	g	AAGTCGCGCA	10	10	18	0.94444444
16	CA	AAGTCCCGCA	5	5		
17	GAG	TATTCCGTTA	6	6		
18						
19	TGC	AAGTACGCTA	5	5		
20						
21	g	AAGTCCCGCA	4	4	5	1
22	CT	AATTCCGATA	6	6		
23						
24	AC					
25	GA					
26	o	AAGTCCCGCA	5	5	5	0.8
27	p	AAGTCCCGCA	6	6	3	1
28						
29	AC	AATTCCTTTA	6	6		
30	g	AAGTCCCGCA	6	6	14	1
31					93	1
32	g					
33	TTC	GATTCCGTCA	5	5		
34	GA	AAGTCCTTTA	5	5		
35						
36	g	AAGTCCTATA	6	6	621	0.99194847
37	g				27	0.96296296
38						
39	GA	AAGTCCCGTA	6	6		
40	f	AAGTCCCGCA	7	7	2	1
41						
42	GGA	AAGTCCTCTA	6	6		
43	f	AAGTCCCGCA	6	6	53	0.88679245
44	f	AAGTCCCGCA	9	9	6	1
45						
46	g	AAGTCCCGCA	8	8	2	1
47	ITG	AAGTCCCGCA	6	6		
48						
49	f	AAGTCCCGCA	7	7	4	1
50	CT					
51						
52	TGC	AAGTCCGCTA	6	6		
53	CAA	GATTCCGTCA	5	5		
54						
55	g				211	0.98578199
56	f	AAGTCCCGCA	6	6	2	1
57						
58						
59						
60						

1							
2							
3							
4	g				14		1
5	f	AAGTCCCATA	6	6	14		1
6	GT	GATTCCGTTA	5	5			
7							
8	GCA						
9	g	AAGTCCCTTA	9	9	27	0.96296296	
10					19		1
11	g						
12	GGA	AAGTCCCGCA	6	6			
13	f	AAGTCCCGCA	6	6	3		1
14							
15	AA	AAGTCCCGCA	6	6			
16	GA	AATTCCTTTA	5	5			
17							
18	GGC						
19	f	AAGTCCCGCA	9	9	2		1
20	CT	AAGTCCCGCA	6	6			
21	CTG	AATTCCGATA	4	4			
22							
23	GAG						
24							
25	c	AAGTCCCTTA	5	5	243		1
26	AG						
27							
28	GGA	AAGTCCATTA	9	9			
29	TC	AAGTCCCGCA	6	6			
30	f	AAGTCGCTTA	6	6	107	0.85046729	
31							
32	c	AAGTCCAGCA	6	6	2		1
33	GCA	AAGTCCCGCA	10	10			
34							
35	p	AAGTACGCTA	7	7	11		1
36	f	AAGTCCCGCA	6	6	65	0.87692308	
37	CT	AAGTCCCGCA	5	5			
38							
39	GAT	AATTCCGATA	6	6			
40							
41	g				91	0.96703297	
42	c	AAGTCCCGCA	6	6	3		1
43	GCA	AAGTCCCGCA	6	6			
44	GCA	AAGTCCCGCA	5	5			
45							
46	AA	AAGTCCCGCA	6	6			
47	g	AAGTCCCGCA	6	6	210	0.99047619	
48					726	0.98209366	
49	o						
50	ACT	AAGTCCCGCA	6	6			
51							
52	g				54	0.98148148	
53	.CC	AAGTCCCGCA	10	10			
54	GAT						
55							
56	g	GATTCCGTCA	4	4	2		1
57							
58							
59							
60							

1						
2						
3						
4	AAC					
5	f				12	1
6	f	AATTCCGTTA	5	5	80	1
7						
8	GG	AATTCCGATA	6	6		
9	iCA	AAGTCCCGCA	6	6		
10	iCA					
11						
12	g				132	0.96212121
13	g	AATTCCGTTA	4	4	6	0.83333333
14						
15	g				2	1
16	GCA	AAGTCCCGCA	6	5		
17						
18	g	AAGTCCCGCA	6	6	2	1
19	g				3	1
20	f	AAGTCCCGCA	6	6	125	0.928
21						
22	GA	AAGTCCAGCA	5	5		
23						
24	g	AAGTCCTATA	5	5	24	1
25	f	AAGTCCCGCA	5	5	311	0.96463023
26	g	AAGTCCGGCA	5	5	130	0.99230769
27						
28	g				135	0.93333333
29	f	AAGTCCCGCA	5	5	3	1
30	f	AAGTCCCGCA	6	6	9	1
31						
32	f				13	1
33	GAA					
34						
35	o				27	0.88888889
36	g	AAGTCCCGCA	6	6	3	1
37	GGA	AAGTCCCTCA	5	5		
38						
39	g	AAGTCCCGCA	6	6	3	1
40	GC					
41						
42	iAAT					
43	CT	AAGTCCCGCA	8	8		
44						
45	GGA					
46	TC					
47	GGA	AAGTCCCGCA	6	6		
48						
49	GGA	AAGTCCAGCA	6	6		
50	CT	AAGTCCAGCA	6	6		
51						
52	g	AAGTCCCGCA	4	4	16	0.9375
53	iGGA	AAGTCCCGTA	7	7		
54						
55	TCA					
56	CT	AAGTCCCGCA	10	10		
57						
58						
59						
60						

1							
2							
3							
4	TA	AATTCCGATA	4	4			
5	g	AAGTCGCTAA	5	5	5		1
6	TTTT	AATTACGATA	6	6			
7	f	AAGTCCCGTA	4	4	4		1
8							
9	g				389	0.97686375	
10							
11	g				2		1
12	g	AAGTCCTATA	5	5	3		1
13	GGA	AAGTCCCGCA	6	6			
14	GCA	AAGTCCCGCA	7	7			
15							
16	g	AAGTCCCGCA	6	6	3		1
17	o	AAGTCCCGCA	6	6	2		1
18							
19	o				2		1
20							
21	GCA	AAGTCCCGCA	6	6			
22	g	AAGTCCCGCA	7	7	31		1
23	f	AAGTCCCGCA	5	4	3		1
24							
25	CAC	AAGTCCCGCA	2	2			
26	f	AAGTCCCGTA	4	4	28		1
27							
28	g	AAGTCCCGCA	4	4	12		1
29	g	AATTCCGTTA	3	3	26	0.84615385	
30	o	AATTCCGATA	6	6	2		1
31							
32	GCA	AAGTCCCGCA	4	4			
33	GCA	AAGTCCCGCA	6	6			
34							
35	.G						
36	g				130	0.95384615	
37	g				917	0.98146129	
38							
39	f				8		1
40	GGA	AAGTCCCGCA	5	5			
41							
42	g	AAGTCGCTTA	5	5	25		1
43	g	AATTCAGATA	2	2	15		1
44							
45	g				48	0.91666667	
46	TC	AAGTCCCGCA	6	6			
47	ICA	AAGTCCCGCA	4	4			
48							
49	GGA						
50	ACT	AAGTCCCGCA	5	5			
51							
52	g	AAGTCCCGCA	5	5	4		1
53	o				142	0.85915493	
54	T	AATTGCGTTA	7	6			
55							
56	g				48		1
57							
58							
59							
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2						
3						
4	ACT					
5	f				3	1
6	GCA	AAGTCCCGCA	5	5		
7	CG	AATTCCGATA	4	4		
8						
9	g	AATTGCGATA	4	4	19	0.84210526
10	GC					
11						
12	p	AATTTTCGATA	7	7	54	1
13	CTTT	AATTACGATA	5	5		
14						
15	p	AAGTCCCGCA	5	5	2	1
16	g				174	0.98850575
17	f	AAGTCCCGCA	6	6	26	1
18						
19	ACT	AAGTCCCGCA	4	4		
20						
21	g	AAGTCCCGTA	5	5	1075	0.93767442
22	g	AAGTCCCGCA	4	4	4636	0.97433132
23	o	AAGTCCCGCA	5	5	3	1
24						
25	TT	AAGTCCCGCA	6	6		
26	p	AAGTCCGCCA	5	5	15	1
27	g				2	1
28						
29	TC					
30	T	AACTCCGATA	4	4		
31						
32	c				39	1
33	A					
34	AG	AACTCCATTA	5	5		
35						
36	ACT	AAGTCCCGCA	6	6		
37	CT	AAGTCCCGCA	6	6		
38						
39	g	AAGTCCCGCA	5	5	2	1
40	o	AAGTCCCGCA	5	5	2	1
41						
42	g				30	1
43	CGC					
44						
45	g	AAGTCCCGCA	5	5	33	0.96969697
46	CT					
47						
48	g	AAGTCCCGCA	5	5	4	1
49	TC	AAGTCCCGCA	6	6		
50	GAA	AAGTCCCGTA	8	8		
51						
52	CTTT					
53	TC	AAGTCCCGCA	6	6		
54	AG	AATTCCGTTA	4	4		
55						
56	g				21	0.80952381
57						
58						
59						
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2							
3							
4	gCAC						
5	A						
6	g				453	0.81015453	
7	g				823	0.98420413	
8	g						
9	g	AAGTCCCGCA	5	5	2	1	
10	gAT	AATTCCGATA	6	5			
11	f	AAGTCCCGCA	7	7	3	1	
12	GGA	AAGTCCCGCA	6	6			
13	g	AAGTCCCGCA	6	6	203	0.97536946	
14	CT	AAGTCCCGCA	4	4			
15	g	AAGTCCCGCA	5	5	2	1	
16	g				697	0.84505022	
17	g	AAGTCCCGCA	5	5	74	0.85135135	
18	CGC						
19	o	AAGTCCCGCA	5	5	20	1	
20	gGA	AAGTCCCGCA	4	4			
21	f				7	1	
22	o				10	1	
23	gTA						
24	GC						
25	gGG	AAGTCCCATA	5	5			
26	o				6	0.83333333	
27	CT	AAGTCCCGCA	5	5			
28	f				72	0.86111111	
29	gGA	AAGTCCCGCA	6	6			
30	g	AAGTCCCGTA	6	6	2	1	
31	g				27	0.96296296	
32	g				348	0.92241379	
33	GA						
34	g	AAGTCCCGTA	6	6	11	1	
35	gAAT						
36	o	AAGTCCCGCA	5	5	12	1	
37	c	AAGTCCCGCA	6	6	18	0.88888889	
38	A	AACTCCATTA	4	4			
39	g	AAGTCCTTA	5	5	29	1	
40	f				2	1	
41	o				2	1	
42	CT	AAGTCCCGCA	5	5			
43							
44							
45							
46							
47							
48							
49							
50							
51							
52							
53							
54							
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57							
58							
59							
60							

1							
2							
3							
4	TC	AAGTCCCGCA	5	5			
5	f	AAGTCCCGCA	4	4	4		1
6	CT						
7							
8	ΓCA	AATTCCGATA	4	4			
9	.TT	AAGTCCCGCA	5	5			
10							
11	g	AAGTCCGGCA	5	5	21		1
12	f				4		1
13							
14	g	AAGTCCCGCA	5	5	4		1
15	f	AAGTCCCGCA	5	5	2		1
16	CT	AAGTCCCGCA	6	6			
17	TGC	AAGTCCGAA	6	6			
18							
19	g				157	0.99363057	
20							
21	g	AAGTCCCGCA	5	5	91		1
22	IGA	AATTCCGTTA	2	2			
23							
24	g	AAGTCCCGCA	4	4	68	0.98529412	
25	GAT	AATTCCGATA	4	4			
26	GGA	AAGTCCCATA	5	5			
27							
28	g				3		1
29	TGA						
30							
31	ΓTT						
32	g	AAGTCCCGCA	4	4	35	0.88571429	
33	g	AAGTCCCGCA	4	4	356	0.96629213	
34	GAA						
35							
36	TC	AAGTCCCGCA	6	6			
37							
38	g	AAGTCCCGCA	5	5	67	0.86567164	
39	g	AAGTCCCGCA	3	3	26		1
40	g	AAGTCCCGCA	4	4	5		1
41							
42	g	AAGTCCCGCA	5	5	4		1
43	ΓTA						
44							
45	TT	AATTCCGATA	4	4			
46	ΓGC	AAGTCCCGCA	4	4			
47							
48	g				2		1
49	f	AAGTCCCTTA	5	5	7		1
50	AG	AAGTCCGGTA	4	4			
51							
52	TT	AAGTCCCGCA	4	4			
53							
54	TCA						
55	CT	AAGTCCCGCA	4	4			
56	AG						
57							
58							
59							
60							

g				48	1
TGC	AAGTCCGAA	5	5		
f				602	1
g	AAGTCCCGCA	3	3	53	1
TT	AAGTCCCGCA	2	2		
g				15	0.93333333
g	AAGTCCCGCA	6	6	65	0.84615385
ACT	AAGTCCCGCA	5	5		
TC	AATTCCGATA	4	4		
f				18	0.94444444
g				91	1
g	AAGTCCCGCA	4	4	3	1
GACG					
f	AAGTCCCGCA	3	3	3	1
GAT					
A	AACTCCATTA	4	4		
AG	AATTCCGTTA	4	4		
ICA					
f	AAGTCCGCA	4	4	3	1
CTG					
p				2	1
GCA					
GC	AAGTCCCGCA	4	4		
IAA					
g	AAGTCCTCTA	5	5	5	1
p	AAGTCCCGCA	6	6	2	1
IGA	AAGTCCCGCA	3	3		
AAC	AAGTCCGCCA	5	5		
TA					
CT	AAGTCCCGCA	4	4		
CTC					
TA					
g	AAGTCCCGCA	4	4	103	0.96116505
IGA	AAGTCCCGCA	4	4		
g	AAGTCCCGCA	2	2	3031	0.99241175
f	AAGTCCCGCA	4	4	2	1
GGA	AAGTCCCATA	3	3		
f				3	1



1						
2						
3						
4	g				3	1
5	g				12	0.91666667
6	g				25	1
7	f				384	0.99479167
8						
9	TC	AAGTCCCGCA	6	6		
10	g	AAGTCCCGCA	4	4	57	0.96491228
11	AA					
12	g				15	1
13	g	AAGTCCCGCA	3	3	18	1
14	g				37	1
15	GA	AAGTCCCGCA	5	5		
16	TA					
17	g	AAGTCCCTTA	4	4	2	1
18	o				43	0.97674419
19	AG					
20	CT	AAGTCCCGCA	4	4		
21	f	AAGTCCCGCA	4	4	2	1
22	g				244	0.91803279
23	o	AAGTCCCTTA	4	4	3	1
24	ICA					
25	GGA					
26	AG					
27	ICA	AAGTCCCGCA	2	2		
28	AG	AATTCCGTTA	4	4		
29	GA					
30	f	AAGTCCCGCA	5	5	2	1
31	AAT	AATTCCGATA	4	4		
32	TC	AAGTCCCGCA	5	5		
33	g				8	0.875
34	g				88	1
35	f				5	1
36	GC					
37	f				13	1
38	ICT	AAGTCCCGCA	5	5		
39	f	AAGTCCCGCA	2	2	2	1
40	TC	AAGTCCCGCA	6	6		
41	IGA	AAGTCCCGCA	5	5		
42	ICT	AAGTCCCGCA	2	2		
43						
44						
45						
46						
47						
48						
49						
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51						
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57						
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p					25	1
g					40	0.85
ACT	AAGTCCGGCA	5	5			
CT	AAGTCCCGCA	5	4			
g	AAGTCCCGCA	3	3	10	1	
AA						
TT						
g				2854	0.90434478	
GC	AAGTACCCTA	3	3			
c	AAGTCCCGCA	5	5	9	1	
o	AAGTCCCGCA	4	4	6	0.83333333	
g	AAGTCCCGCA	5	5	2	1	
CT						
GG						
p	AAGTCCAGCA	2	2	3	1	
TC	AAGTCCCGCA	6	6			
GGA	AAGTCCCGCA	4	4			
GGA	AAGTCCCGTA	2	2			
f				6	1	
c	AAGTCCTATA	4	4	4	1	
TC	AAGTCCCGCA	5	5			
c	AAGTCCCATATA	2	2	9	1	
g	AAGTCCCGCA	4	4	2	1	
g	AAGTCCCGCA	4	4	6	1	
c				8	0.875	
CT	AAGTCCCGCA	5	5			
TA						
g				4	1	
g	AAGTCCCGCA	5	5	20	0.95	
o	AAGTCCCGCA	5	5	7	1	
CT	AAGTGACGCA	3	3			
CT	AAGTCCCGCA	5	5			
GG	AATTCCGTTA	2	2			
g				10	0.9	
c				261	0.96551724	
g	AAGTCCCGCA	4	4	6760	0.99571006	
GCA	AAGTCCCGCA	4	4			
g	AAGTCCCGCA	3	3	170	0.97647059	

1						
2						
3						
4	GG	AAGTCCCGCA	3	3		
5	.GC					
6	GGA					
7	GCC					
8	AG					
9	ACT	AAGTCCCGCA	3	3		
10	GAT					
11	f				4	1
12	CTC	AAGTCCTCTA	3	3		
13	o				9	1
14	CT	AAGTCCCGCA	3	3		
15	GCA					
16	g				30	1
17	AA					
18	CT					
19	o				45	0.91111111
20	g	AAGTCCCGTA	3	3	3	1
21	f	AAGTCCTCTA	4	4	2	1
22	CT	AAGTCCCGCA	4	4		
23	f	AAGTCCCGCA	3	3	10	1
24	CTC					
25	GGA	AAGTCCATTA	3	3		
26	AG					
27	g				7	1
28	CA	AAGTCCCGCA	3	3		
29	f	AAGTCCCGCA	4	4	9	1
30	AA	AAGTCCTTTA	1	1		
31	GCA					
32	g				39	0.97435897
33	GCA					
34	CT	AAGTCCCGCA	4	4		
35	g				725	0.91586207
36	GGA					
37	g	AAGTCCCGCA	3	3	3	1
38	G	AATTCCGATA	4	4		
39	TCG					
40	AG	AATTCCGTTA	4	4		
41	GGA					
42						
43						
44						
45						
46						
47						
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g				307	0.83387622
CG					
g				21	1
g	AAGTCCCGCA	2	2	2	1
AG					
g	AAGTCCTATA	4	4	8	1
k	AATTCCGATA	1	1	4	1
GT	AATTCCGTTA	3	3		
CT	AAGTCCCGCA	5	5		
TTA	AATTCCGATA	3	3		
g				3	1
g				50	0.98
g	AAGTCCCGCA	5	5	2	1
g				767	0.92959583
CT	AAGTCCCGCA	4	4		
f	AAGTCCCGCA	3	3	11	1
g				82	0.98780488
TC	AAGTCCCGCA	5	5		
g	AAGTCCCGCA	3	3	2435	0.97946612
G					
AG	AATTCCGTTA	2	2		
TC	AAGTCCCGCA	4	4		
GAC	AAGTCCCGCA	3	3		
TC					
TA					
CT					
AG					
f	AAGTGACGC	2	2	5	1
GCA	AAGTCCCGCA	3	3		
f				16	0.9375
p	AAGTCCGTCA	2	2	4	1
o				127	0.99212598
CT					
GC					
GAC					
TC	AAGTCCCGCA	4	4		
g	AAGTCCCGCA	3	3	20	1
CT					

1						
2						
3						
4	gAA					
5	g	AAGTCCCTTA	3	3	37	1
6	CT	AAGTCCCGCA	4	4		
7	CT	AAGTCCCGCA	4	4		
8						
9	TC					
10	GC					
11	GC					
12						
13	f				14	1
14						
15	GGA					
16	CT					
17						
18	gA	AACTCCATTA	2	2		
19	g				5956	0.99764943
20	g	AAGTCCCGCA	2	2	53	0.9245283
21	AT					
22						
23	g	AAGTCCGGCA	3	3	6	1
24	f				39	0.82051282
25						
26	G	AATTCCGATA	2	2		
27	g	AAGTCCCGCA	3	3	38	0.97368421
28	GT					
29						
30	CT	AAGTCCCGCA	4	4		
31	g	AAGTCCCGCA	3	3	2	1
32	AT					
33						
34	p				5	1
35	f				2	1
36						
37	CT					
38						
39	o				8	1
40	TC	AAGTCCCGCA	4	4		
41						
42	AG					
43	f	AAGTCCCGCA	2	2	32	0.9375
44	g				3	1
45	AG					
46						
47	gGA	AAGTCCCTTA	2	2		
48	g	AAGTCCCGTA	3	3	24	1
49	g	AAGTCCCGCA	2	2	3	1
50	GGA	AAGTCCCGCA	2	2		
51	GT					
52						
53	c	AAGTCCCCTA	3	3	6	1
54	TAT					
55						
56						
57						
58						
59						
60						

1						
2						
3	f	AAGTCCCGCA	3	3	5	1
4	TC	AAGTCCCGCA	4	4		
5	g	AAGTCCCGCA	3	3	6	1
6	CC	AAGTCCCGCA	3	3		
7	g	AATTGCGATA	2	2	9	1
8	g	AAGTCCCTTA	2	2	5	1
9	CT					
10	AG					
11	CT	AAGTCCCGCA	3	3		
12	f	AAGTCCCGCA	3	3	6	0.83333333
13	GT					
14	g	AAGTCCCGCA	3	3	8	1
15	TC	AAGTCCCGCA	3	3		
16	TC					
17	AG	AATTCCGTTA	2	2		
18	ACT	AAGTCCCGCA	2	2		
19	g	AAGTCCCGCA	2	2	12	0.91666667
20	TC	AAGTCCCGCA	4	4		
21	GGA	AAGTCCCTTA	3	3		
22	g				19	1
23	GGA					
24	AG	AATTCCGTTA	2	2		
25	TC	AAGTCCCGCA	4	4		
26	TC	AAGTCCCGCA	3	3		
27	AAC	AAGTCCCGCA	2	2		
28	GCA	AAGTCCCGCA	2	2		
29	GGA					
30	TC	AAGTCCCGCA	3	3		
31	TC	AAGTCCCGCA	3	3		
32	CAC	AAGTCCCGCA	2	2		
33	AG					
34	TC	AAGTCCCGCA	3	3		
35	TC	AAGTCCCGCA	3	3		
36	GC	AAGTCCCGCA	3	3		
37	g				39	1
38	CT	AAGTCCCGCA	5	5		
39	TC	AAGTCCCGCA	3	3		
40	g				7	1
41	f				3	1
42	AG	AATTCCGTTA	3	3		
43						
44						
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1						
2						
3						
4	AG					
5	gAA					
6	GGA					
7						
8	f	AAGTCCCGCA	2	2	9	0.88888889
9	g	AAGTCCCGCA	4	4	2	1
10	AG					
11	AG	AATTCCGTTA	2	2		
12	CT	AAGTCCCGCA	2	2		
13	TC	AAGTCCCGCA	4	4		
14	CT					
15	GGA	AAGTCCCTTA	2	2		
16	ACT	AAGTCCGGCA	2	2		
17	c				5	0.8
18	CCG	AAGTCCCGCA	2	2		
19	GAA	AAGTCCCGCA	3	3		
20	o				9	0.88888889
21	TC	AAGTCCCGCA	4	4		
22	AG					
23	gGA	AAGTCCCTTA	2	2		
24	g				1830	0.9704918
25	f	AAGTCCCGCA	3	3	76	0.92105263
26	CTGA	AATCCCGATA	2	2		
27	f				7	1
28	TT					
29	CAC	AAGTCCCGCA	2	2		
30	AG					
31	g				446	0.96188341
32	gGA	AAGTCCCGCA	2	2		
33	CT	AAGTCCCGCA	3	3		
34	GGA	AAGTCCCTCA	2	2		
35	c				3	1
36	TC	AAGTCCCGCA	4	4		
37	o	AAGTCCCGCA	3	3	62	0.80645161
38	AG	AATTCCGTTA	2	2		
39	GGA	AAGTCCCGCA	2	2		
40	CT	AAGTCCCGCA	3	3		
41	g	AAGTCCCGCA	1	1	4	1
42	f	AAGTCCCGCA	1	1	16	0.875
43						
44						
45						
46						
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48						
49						
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54						
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56						
57						
58						
59						
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f	AAGTCCCGCA	3	3	44	0.90909091
CT					
GGA					
G	AATTCCGATA	2	2		
g				22	1
GC					
f	AAGTCCCGCA	2	2	23	1
f				10	1
GAA	AAGTCCCGCA	2	2		
GAG					
AAC	AATTCCGATA	1	1		
GCA	AAGTCCCGCA	1	1		
g	AAGTCCCGCA	2	2	10	1
TC					
CT	AAGTCCCGCA	3	3		
g	AAGTCCCGTA	2	2	5	1
TC	AAGTCCCGCA	2	2		
TC	AAGTCCCGCA	3	3		
AG					
TC	AAGTCCCGCA	3	3		
TGC					
f	AAGTCCCGCA	2	2	8	1
g	AAGTCCCGCA	2	2	647	1
GGC					
AG					
GCA					
GAA	AAGTCCCTTA	2	2		
AG	AATTCCGTTA	2	2		
TGT					
f				17	1
CT	AAGTCCCGCA	3	3		
GGA					
o	AAGTCCCGCA	2	2	12	1
o	AAGTCCCGCA	2	2	9	1
p				5	1
g				16	1
TC	AAGTCCCGCA	3	3		
GA					



1							
2							
3							
4	GT						
5	CT	AAGTCCCGCA	2	2			
6	GTA						
7							
8	g	AAGTCCCGCA	2	2	4	1	
9	CT	AAGTCCCGCA	2	2			
10	f	AAGTCCCGCA	4	4	5	0.8	
11	AT	AATTCCGTTA	1	1			
12							
13	g				22	0.81818182	
14	f	AAGTCCCGCA	3	3	4	1	
15	CGAG	AATTCCGTTA	2	2			
16	TC	AAGTCCCGCA	2	2			
17	GT	AATTCCGATA	2	2			
18	CT	AAGTCCCGCA	2	2			
19							
20	CT	AAGTCCCGCA	2	2			
21	CT						
22	CT						
23	GG	AAGTCCCATA	2	2			
24	TC	AAGTCCCGCA	3	3			
25							
26	GCA						
27	f	AAGTCCCGTA	2	2	2	1	
28					7	0.85714286	
29	o						
30	f	AAGTCCCGCA	1	1	25	1	
31							
32	GAG						
33	CT	AAGTCCCGCA	1	1			
34	f	AAGTCCCGCA	2	2	114	0.97368421	
35							
36	CA						
37	AG						
38							
39	TC	AAGTCCCGCA	3	3			
40	TC	AAGTCCCGCA	4	4			
41	TC	AAGTCCCGCA	2	2			
42							
43	g				196	0.95918367	
44	CT	AAGTCCCGCA	2	2			
45							
46	g				30	0.83333333	
47	AG						
48							
49	CC	AAGTCCCGCA	2	2			
50	CT	AAGTCCCGCA	3	3			
51							
52	g	AAGTCCCGCA	2	2	2	1	
53	ATG	AATCCCGATA	2	2			
54	GTA	AAGTCCCTCA	2	2			
55							
56	AA						
57							
58							
59							
60							

AG						
CT	AAGTCCCGCA	2	2			
AG						
CT	AAGTCCCGCA	3	3			
g	AAGTCCCGTA	2	2	4		1
TT						
TT						
TC	AAGTCCCGCA	2	2			
ATTC	AATCCCGATA	1	1			
TTTT	AATCCCGATA	1	1			
GGC						
GCC						
CT	AAGTCCCGCA	1	1			
g	AAGTCCCGCA	1	1	31	0.96774194	
CT	AAGTCCCGCA	1	1			
g	AAGTCCCGCA	1	1	18	0.94444444	
g				9		1
o				4		1
CT	AAGTCCCGCA	2	2			
AC	AAGTCCCGCA	2	2			
TC	AAGTCCCGCA	4	4			
f				31		1
TTT	GATTCCGTCA	2	2			
AAC						
g				247	0.99595142	
f	AAGTCCCGCA	2	2	4		1
TC	AAGTCCCGCA	3	3			
g	AAGTCCCGCA	2	2	18	0.83333333	
g	AAGTCCCGCA	2	2	274	0.8649635	
f				25		0.8
f	AAGTCCCGCA	2	2	2		1
CA						
AT						
CT	AAGTCCCGCA	1	1			
g	AAGTCCCGTA	1	1	4		1
AAC	AAGTCCCGCA	1	1			
AA	AAGTCCCGCA	1	1			
GA						

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2						
3						
4	f	AAGTCCCGCA	2	2	8	0.875
5	g				5	1
6	AG	AATTCCGTTA	2	2		
7	AG					
8						
9	CAC	AAGTCCCGCA	1	1		
10	CG	AATTCCGATA	1	1		
11	AT	AATTCCGTTA	1	1		
12						
13	g				16	1
14	p	AAGTCCCGCA	2	2	6	0.83333333
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16	ATG					
17	CTG					
18						
19	CT					
20						
21	GCA	AAGTCCCGCA	2	2		
22	CT	AAGTCCCGCA	2	2		
23	AT	AAGTCCCGCA	1	1		
24	f	AAGTCCCGCA	1	1	86	1
25	T	AATTCCGATA	1	1		
26						
27	CT					
28						
29	TC	AAGTCCCGCA	2	2		
30	GCA	AAGTCCCGCA	1	1		
31	AT	AAGTCCCGCA	2	2		
32						
33	g				28	1
34	AG	AATTCCGTTA	1	1		
35	CT	AAGTCCCGCA	1	1		
36						
37	GT					
38						
39	CT	AAGTCCCGCA	1	1		
40	AAC	AAGTCCCGCA	2	2		
41	TC	AAGTCCCGCA	2	2		
42						
43	o	AAGTCCCGCA	3	3	5	1
44	GAA					
45						
46	g	AAGTCCCGCA	1	1	17	1
47	f	AAGTCCCGCA	1	1	16	1
48						
49	ATG					
50	GAC	AAGTCCCGCA	1	1		
51	TC					
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53	GT					
54	GAT					
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56	CT					
57						
58						
59						
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CT	AAGTCCCGCA	2	2		
TC	AAGTCCCGCA	2	2		
.TC	AAGTCCCGCA	2	2		
g	AAGTCCCGCA	1	1	5	1
'AG					
CT					
TC	AAGTCCCGCA	2	2		
g	AAGTCCCGCA	1	1	70	1
GGT	AAGTCCGATA	1	1		
AG					
'GC	AAGTCCCGCA	1	1		
g	AAGTCCCGCA	1	1	9	1
GAA	AAGTCCTATA	1	1		
iGG					
AAC	AAGTCCCGCA	1	1		
AG	AATTCCGTTA	1	1		
CT	AAGTCCCGCA	1	1		
AAC	AAGTCCCGCA	1	1		
.CT	AAGTCCCGCA	1	1		
ACT	AAGTCCCGCA	1	1		
\CT	AAGTCCCGCA	1	1		
g	AATTCCGTTA	1	1	121	0.99173554
.CT	AAGTCCCGCA	1	1		
CT	AAGTCCCGCA	1	1		
TT	GATTGTGATA	1	1		
iAT	AATTCCGATA	1	1		
.TC	AAGTCCCGCA	2	2		
.CT	AAGTCCCGCA	2	2		
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iGA					
GATG					
g	AAGTCCCGCA	1	1	10	1
ATG	AATCCCGATA	1	1		
TCG	AAGTCCCGCA	1	1		
\CT	AAGTCCCGCA	1	1		
TA	AATTCCGATA	1	1		
AAC	AAGTCCCGCA	1	1		
.TC	AAGTCCCGCA	2	2		

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3							
4	.CT						
5	TAG	AATTCCGTTA	1	1			
6	'GT						
7	AG						
8	AG						
9	AG						
10	g	AAGTCCCGCA	2	2	4	1	
11	GT						
12	o				2	1	
13	CT	AAGTCCCGCA	1	1			
14	CGC						
15	CGA						
16	CG						
17	g				7	1	
18	g	AAGTCCTGCA	1	1	80	0.95	
19	GCA	AAGTCCCGCA	1	1			
20	CGC						
21	g	AAGTCCCTTA	1	1	4	1	
22	g				9	1	
23	AC	AAGTCCTCTA	1	1			
24	GAA	AAGTCCTTTA	1	1			
25	TT	AAGTCCCGCA	1	1			
26	TT	AATTGCGATA	1	1			
27	TAA	AATCCCGATA	1	1			
28	AAC	AAGTCCCGCA	1	1			
29	GAA	AAGTCCCGCA	1	1			
30	GT						
31	f				6	1	
32	ACT	AAGTCCTGCA	1	1			
33	GCA	AAGTCCCGTA	1	1			
34	GG						
35	g	AAGTCCCGTA	1	1	16	0.8125	
36	CT	AAGTCCCGCA	1	1			
37	CT	AAGTCCCGCA	1	1			
38	CT	AAGTCCCGCA	1	1			
39	TT						
40	g	AAGTCCCGCA	1	1	6	0.83333333	
41	IAA						
42	CT	AAGTCCCGCA	1	1			
43							
44							
45							
46							
47							
48							
49							
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ACT					
AC					
.CC	AAGTCCCGCA	1	1		
g	AAGTCCCGCA	1	1	355	0.98309859
g	AATTGCGATA	1	1	26	0.80769231
CT	AAGTCCCGCA	1	1		
CA					
.TC	AAGTCCCGCA	2	2		
TC					
ACT					
.CT	AAGTCCCGCA	2	2		
TC	AAGTCCCGCA	1	1		
.GT	AATTCCGATA	1	1		
GT					
CAC					
f	AAGTCCCGCA	1	1	2	1
ACT	AAGTCCCGCA	1	1		
GAA					
f	AAGTCCCGCA	1	1	3	1
CT	AAGTCCCGCA	1	1		
ACT	AAGTCTCGCA	1	1		
CA	AAGTCCCGCA	1	1		
o				100	0.98
.CT	AAGTCCCGCA	2	2		
ACT					
CT					
.CC	AAGTCCCGCA	2	2		
GAA	AATCCCGATA	1	1		
CA					
AA					
GA	AAGTCCCGCA	1	1		
ATA					
GA					
AG					
CCT	AAGTCCCGCA	1	1		
ATG	AATCCCGATA	1	1		
ATG	AATCCCGATA	1	1		

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3						
4	CT	AAGTCCCGCA	1	1		
5	AC	AAGTCCCGCA	1	1		
6	AA					
7						
8	CT	AAGTCCCGCA	1	1		
9	AA					
10	AG	AATTCCGTTA	1	1		
11	TGA	AATCCCGATA	1	1		
12	TC	AAGTCCTCTA	1	1		
13	TC					
14	CT	AAGTCCCGCA	2	2		
15	TC	AAGTCCCGCA	2	2		
16	TC	AAGTCCCGCA	3	3		
17	TC	AAGTCCCGCA	2	2		
18	g	AATTCCGTTA	1	1	2	1
19	o				157	0.96178344
20	p	AATTCCGTTA	1	1	2	1
21	TT	AAGTCCCGCA	1	1		
22	g	AAGTCCCGCA	1	1	36	1
23	AAG	TATTCCGTTA	1	1		
24	AAC	AAGTCCCGCA	1	1		
25	CT	AAGTCCCGCA	1	1		
26	CT					
27	CG					
28	GT					
29	ATA	AAGTCCTCTA	1	1		
30	CT	AAGTCCCGCA	1	1		
31	AT					
32	CT	AAGTCCCGCA	1	1		
33	GT					
34	TT	AAGTCCCGCA	1	1		
35	AC					
36	CT	AAGTCCCGCA	1	1		
37	AA	AAGTCCCGTA	1	1		
38	CT					
39	GT	AATTCCGATA	1	1		
40	TG	AATTCCGTTA	1	1		
41	g	AAGTCCCGCA	1	1	569	0.82073814
42	TA	AAGTCCCGCA	2	2		
43						
44						
45						
46						
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48						
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59						
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o	AAGTCCCGCA	2	2	5	1
GAA	AAGTCCTATA	1	1		
g	AATTCCGTTA	1	1	2	1
ATT					
IGA	AAGTCCCTTA	1	1		
g	AAGTCCCGCA	1	1	567	1
TAC					
CT	AAGTCCCGCA	1	1		
TT					
GCA	AAGTCCCGCA	1	1		
g	AAGTCCCGCA	1	1	127	0.99212598
c	AAGTCCTGTA	1	1	10	1
TAA	AATCCCGATA	1	1		
ACT	AAGTCCCGCA	1	1		
ACC	AATCCCGATA	1	1		
CT	AAGTCCCGCA	1	1		
f	AAGTCCCGCA	1	1	3	1
CC	AAGTCCGGTA	1	1		
ATG	AATCCCGATA	1	1		
ICA	AAGTCCCGCA	1	1		
AAC	AAGTCCCGCA	1	1		
p				3	1
ATG	AATCCCGATA	1	1		
GCA	AAGTCCCGCA	1	1		
GAA	AAGTCCTATA	1	1		
IGA					
TC	AAGTCCCGCA	3	3		
o	AAGTCCCGTA	1	1	2	1
GCA	AAGTCCCGCA	1	1		
GT					
ACT	AAGTCCCGCA	1	1		
g				2	1
f	AAGTCCCGCA	1	1	3	1
IGA	AAGTCCCGCA	1	1		
.AT					
c	AAGTCCCGCA	1	1	5	0.8
GT					
ACT	AAGTCCCGCA	1	1		



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4	IG	AATTCCGATA	1	1		
5	IGC					
6	TT					
7						
8	TT	AAGTCCCGCA	1	1		
9	AC	AATTCCGATA	1	1		
10						
11	g				47	0.87234043
12	g	AAGTCCCGCA	1	1	9	0.88888889
13	CT	AAGTCCCGCA	1	1		
14	CT	AAGTCCCGCA	1	1		
15	CT	AAGTCCCGCA	1	1		
16	f				26	0.80769231
17	CT	AAGTCCCGCA	1	1		
18	o	AAGTCCCGCA	1	1	30	1
19	GT	AATTCCGATA	1	1		
20	GAA					
21	f	AAGTCCAGCA	1	1	3	1
22	CT					
23	g	AAGTCCCGCA	1	1	13	1
24	CT	AAGTCCCGCA	1	1		
25	CT					
26	CT	AAGTCCCGCA	1	1		
27	CT	AAGTCCCGCA	1	1		
28	CT	AAGTCCCGCA	1	1		
29	CT	AAGTCCCGCA	1	1		
30	ATT	AATCCCGATA	1	1		
31	CT	AATCCCGATA	1	1		
32	CT	AAGTCCCGCA	1	1		
33	CT	AAGTCCCGCA	1	1		
34	CT	AAGTCCCGCA	1	1		
35	CCG					
36	GA	AAGTCCCGCA	1	1		
37	AAC	AAGTCCCGCA	1	1		
38	GG	AATTGCGCTA	1	1		
39	GA					
40	CA					
41	TC	AATTCCGATA	1	1		
42	GAC	AATTCGATA	1	1		
43	CT					
44	CA					
45	ATT	AATCCCGATA	1	1		
46	AAC	AAGTCCCGCA	1	1		
47	CT					
48	CT	AAGTCCCGCA	1	1		
49	AA	AAGTCCCGCA	1	1		
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1							
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4	.CT	AAGTCCCGCA	1	1			
5	GA	AAGTCCCGCA	1	1			
6	CA	AAGTCCCGCA	1	1			
7	AT	CAGTCCAAAA	1	1			
8	ATG	AATCCCGATA	1	1			
9	AAC	AAGTCCCGCA	1	1			
10	CCG	AAGTCCCGCA	1	1			
11	f	AAGTCCCGCA	1	1	30		1
12	g	AATTCCGTTA	1	1	12	0.91666667	
13	CC						
14	CT						
15	AAC						
16	GC	AAGTCCCGCA	1	1			
17	CT	AAGTCCCGCA	1	1			
18	AAC						
19	CT	AAGTCCCGCA	1	1			
20	g	AAGTCCCGCA	1	1	24		1
21	TC						
22	GC	AAGTCCGAAA	1	1			
23	f				2		1
24	TT	AAGTCCCGCA	1	1			
25	TTTC	AATCCCGATA	1	1			
26	TTTC	AATCCCGATA	1	1			
27	GGA	AAGTCCCATA	1	1			
28	CT						
29	AAC	AAGTCCCGCA	1	1			
30	g	AAGTCCCATA	1	1	2		1
31	TGA	AATCCCGATA	1	1			
32	g				4168	0.98872361	
33	CA	AAGTCCCGCA	1	1			
34	CT	AAGTCCCGCA	2	2			
35	TC						
36	CT						
37	CT						
38	AAC	AAGTCCCGCA	1	1			
39	AGC	CAGTCCCGCA	1	1			
40	AAC	AAGTCCCGCA	1	1			
41	AA						
42							
43							
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2						
3						
4	ATC	AAGTCCCGCA	1	1		
5	TCT					
6	GGA					
7	GG					
8						
9	ATG	AATCCCGATA	1	1		
10	ACT	AAGTCCCGCA	1	1		
11						
12	g				18	1
13	f	AAGTCCCGCA	1	1	4	1
14	TT	AATTCCGATA	1	1		
15	o	AAGTCCCGCA	1	1	2	1
16						
17	ATG					
18	GA	AAGTCCCGCA	1	1		
19	GGA	AAGTCCCGCA	1	1		
20	TT	AAGTCCCGCA	1	1		
21	AAC	AAGTCCCGCA	1	1		
22	AAC	AAGTCCCGCA	1	1		
23	g	AAGTCCCGCA	1	1	2	1
24	AA	AATTCCCTTA	1	1		
25						
26	GA					
27	CA					
28	CCT	AATTCCGATA	1	1		
29	TGA	AATCCCGATA	1	1		
30	GG					
31	AAC	AAGTCCCGCA	1	1		
32						
33	g				2	1
34	f	AAGTCCCGCA	1	1	8	1
35	A	AATTCTTTA	1	1		
36	ATG	AATCCCGATA	1	1		
37	CA	AAGTCCCGCA	1	1		
38	f				5	1
39	CTG	AAGTCCTGTA	1	1		
40	AG	AATTCCGTTA	1	1		
41	g	AAGTCCCGCA	1	1		
42	AT	AAGTCCCGCA	1	1	24	0.95833333
43	CT	AAGTCCCGCA	1	1		
44						
45	p	AAGTCCCGCA	1	1	3	1
46	CA	AAGTCCCGCA	1	1		
47	AT					
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TC	AATTCCGATA	1	1		
GT	AATTCCGATA	1	1		
GA	AAGTCCCGCA	1	1		
CT					
TCG	AAGTCCCGCA	1	1		
AT	AATTCCGTTA	1	1		
AA	AAGTCCCGTA	1	1		
g	AATTGCGATA	1	1	291	1
AA					
GAA	AAGTCCCATA	1	1		
CT	AAGTCCCGCA	1	1		
GT					
GCA	AAGTCCCGCA	1	1		
GCA	AAGTCCCGCA	1	1		
AA					
CT	AAGTCCCGCA	1	1		
GGA	AAGTCCCGCA	1	1		
CT	AAGTCCCGCA	1	1		
TCC	AAGTCCCGCA	1	1		
GCA					
AAG	TATTCCGTTA	1	1		
g	AAGTCGCTAA	1	1	2	1
f	AAGTCCCGCA	1	1	4	1
AAC					
AT					
g	AAGTCCCGCA	1	1	3	1
AT	AATTCCGTTA	1	1		
CC	AAGTCCCGCA	1	1		
AAC	AAGTCCCGCA	1	1		
AATG	GATTCCGATA	1	1		
GTG					
g	AAGTCCCGCA	1	1	1916	0.99843424
GCA					
T	AACTTCTGTA	1	1		
GGA	AAGTCCCGCA	1	1		
AT	AAGTCCCGCA	1	1		
p	AAGTCCTCTA	1	1	2	1
CTT					

1							
2							
3						91	0.95604396
4	g						
5	g					11	1
6	g	AAGTCCCGCA	1	1		2	1
7	g	AAGTCCCGCA	1	1		2	1
8	g	AAGTCCCGCA	1	1			
9	ACT	AAGTCCCGCA	1	1			
10	GGA	AAGTCCCGCA	1	1			
11	GCG	AAGTCCCGCA	1	1			
12							
13	g					3	1
14	CTA	AAGTCCCGCA	1	1			
15							
16	o					5	0.8
17	o	AAGTCCCGCA	1	1		3	1
18	gCA	AAGTCCCGCA	1	1			
19	AAG	TATTCCGTTA	1	1			
20	GCA	AAGTCCCGTA	1	1			
21	g	AAGTCCCGCA	1	1		439	0.92027335
22	g	AAGTCCCGCA	1	1		18	0.94444444
23	GT						
24	iAT	AATTCCGTTA	1	1			
25	g	AAGTCCCGCA	1	1		4726	0.98011003
26	GCG						
27							
28	f	AAGTCTCGCA	1	1		3	1
29	CTG	AAGTCCTGTA	1	1			
30	AGA						
31	f					128	0.9765625
32	G						
33	.CT						
34	.TT	AAGTCCCGCA	1	1			
35	GCG	AATTCCGATA	1	1			
36	o	AAGTCCCGCA	1	1		4	1
37	TT						
38	o	AAGTCCCATA	1	1		3	1
39	g	AAGTCCCGCA	1	1		5	1
40	CTG	AATTCCGATA	1	1			
41	AAG	TATTCCGTTA	1	1			
42	.TT	AAGTCCCGCA	1	1			
43	g	AAGTCCCGCA	1	1		2	1
44	CT	AAGTCCCGCA	1	1			
45							
46							
47							
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53							
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55							
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57							
58							
59							
60							

g	AAGTCCCGCA	1	1	94	0.96808511
CT					
g	AAGTCCGGCA	1	1	7	0.85714286
CT	AAGTCCCGCA	1	1		
CT	AAGTCCCGCA	1	1		
CT					
o	AAGTCCCGCA	1	1	11	1
CTC	AAGTCCCGCA	1	1		
g	AAGTCCGGCA	1	1	202	1
GGGG					
CTC	AAGTCCTCTA	1	1		
g	AAGTCCCGCA	1	1	70	0.98571429
g	AAGTCCCGCA	1	1	5	0.8
GCA					
CTC					
CT					
g	AAGTCCCGCA	1	1	2	1
GAT	AATTCCGTTA	1	1		
TGC	AAGTCCACTA	1	1		
CT	AAGTCCCGCA	1	1		
f	AAGTCCCGCA	1	1	3	1
GGA	AAGTCCCGCA	1	1		
g				2	1
p	AAGTCCCGCA	1	1	7	1
CT	AAGTCCCGCA	1	1		
AG	AATTCCGTTA	1	1		
GGA					
AG					
CT	AAGTCCCGCA	1	1		
AG	AATTCCGTTA	1	1		
ACT	AAGTCCCGCA	1	1		
AC	AAGTCCGCTA	1	1		
CA					
TT	AAGTCCCGCA	1	1		
AG	AATTCCGTTA	1	1		
CT	AAGTCCCGCA	1	1		
CT	AAGTCGGGT	1	1		
CT	AAGTCCCGCA	1	1		

1							
2							
3							
4	.GT	AAGTCCCGCA	1	1			
5	CT	AAGTCCCGCA	1	1			
6	ATT	AATCCCGATA	1	1			
7	GAA	AAGTCCTATA	1	1			
8	AG	AATTCCGTTA	1	1			
9	ATG	AATCCCGATA	1	1			
10	GT						
11	AG	AATTCCGTTA	1	1			
12	g	AAGTCCCGTA	1	1	4		1
13	AG						
14	g	AAGTCCAGCA	1	1	12		1
15	GT						
16	CT	AAGTCCCGCA	1	1			
17	GAA						
18	AT						
19	CT						
20	TTG						
21	TC	AAGTCCCGCA	2	2			
22	AT						
23	g	AAGTCCCGCA	2	2	9		1
24	TC	AAGTCCCGCA	1	1			
25	GAA						
26	o				14		1
27	g	AAGTCCCGCA	1	1	670	0.96567164	
28	CT	AAGTCCCGCA	1	1			
29	o				16		1
30	CT	AAGTCCCGCA	1	1			
31	o				5		0.8
32	TAT	ACGTCCTTCA	1	1			
33	AC	AAGTCCCGCA	1	1			
34	CT	AAGTCCCGCA	1	1			
35	AG						
36	g				27	0.92592593	
37	A						
38	f	AAGTCCCGTA	1	1	17		1
39	GAA	AAGTCCTTTA	1	1			
40	GA	AAGTCCCATA	1	1			
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p	AAGTCCCTTA	1	1	21	0.80952381
g	AAGTCCCGTA	1	1	3	1
p	AAGTCCCGCA	1	1	3	1
g	AAGTCCCGCA	1	1	705	0.83262411
f				65	0.89230769
g				191	0.82722513
CT					
o	AAGTCCCGCA	1	1	2	1
g				19	0.89473684
CT	AAGTCCCGCA	1	1		
CT	AAGTCCCGCA	1	1		
g				2	1
g	AAGTCCCGCA	1	1	3	1
CA	AAGTCCCGCA	1	1		
AC					
AAA					
f	AAGTCCCTTA	1	1	40	1
g				21	0.9047619
CA	AAGTCCCGCA	1	1		
g	AAGTCCCGCA	1	1	3	1
GG	AATTCCGTTA	1	1		
CT	AAGTCGCGCA	1	1		
CT					
AA					
g				19	0.94736842
AT	AAGTCCCGCA	1	1		
CT					
CT	AAGTCCCGCA	1	1		
CT	AAGTCCCGCA	1	1		
f	AAGTCCCGCA	1	1	17	0.94117647
AA					
CA					
g	AAGTCCCGCA	1	1	63	1
GT					
CT	AAGTCCCGCA	1	1		
TC	AAGTCCCGCA	2	2		
TC	AAGTCCCGCA	1	1		
TC	AAGTCCCGCA	2	2		



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4	g				84	0.9047619
5	g				9	1
6	CT	AAGTCCCGCA	1	1		
7	CT	AAGTCCCGCA	1	1		
8	CT	AAGTCCCGCA	1	1		
9	TC	AAGTCCCGCA	1	1		
10	TG	AATTCCGTTA	1	1		
11	AG	AATTCCGTTA	1	1		
12	TC	AAGTCCCGCA	2	2		
13	TC	AAGTCCCGCA	1	1		
14	c	AAGTCCCGCA	1	1	498	0.99799197
15	TC					
16	CT					
17	CT	AAGTCCCGCA	1	1		
18	GT					
19	GT					
20	GA	AATTCCGATA	1	1		
21	TC	AAGTCCCGCA	1	1		
22	TC	AAGTCCCGCA	1	1		
23	CT	AAGTCCCGCA	1	1		
24	CT	AAGTCCCGCA	1	1		
25	GT					
26	CT	AAGTCCCGCA	1	1		
27	CT	AAGTCCCGCA	1	1		
28	GG					
29	AG	AATTCCGTTA	1	1		
30	AG					
31	AAC	AAGTCCCGCA	1	1		
32	g	AAGTCCCGCA	1	1	2	1
33	AAC					
34	CT					
35	g				10	1
36	AT	AAGTCCCGCA	1	1		
37	g	AAGTCCCGCA	1	1	7	1
38	AT	AAGTCCCGCA	1	1		
39	CT	AAGTCCCGCA	1	1		
40	AG					
41	AG					
42	CT					
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AG	AATTCCGTTA	1	1		
AG	AATTCCGTTA	1	1		
.TC	AAGTCCCGCA	1	1		
CT					
g	AAGTCCCGCA	1	1	3	1
f	AAGTCCCGCA	1	1	6	1
f	AAGTCCCGCA	1	1	10	1
g				3	1
g	AAGTCCCGCA	1	1	23	1
g	AAGTCCCGCA	1	1	15	1
TC					
TC	AAGTCCCGCA	1	1		
.TC	AAGTCCCGCA	1	1		
TG					
.TC					
.TC	AAGTCCCGCA	1	1		
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.TC	AAGTCCCGCA	1	1		
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TC	AAGTCCCGCA	1	1		
TC	AAGTCCCGCA	1	1		
TC	AAGTCCCGCA	1	1		
.TC					
f	AAGTCCCGCA	1	1	2	1
.TC	AAGTCCCGCA	1	1		
TC	AAGTCCCGCA	1	1		
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TC	AAGTCCCGCA	1	1		

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5	Bacteria	Proteobacteri	Betaproteobacteria			Comamonas
6	Bacteria	Proteobacteri	Betaproteobacteria			
7	Bacteria	Proteobacteri	Betaproteobacteria			
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10	Bacteria	Proteobacteri	Betaproteoba	Burkholderiales		
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13	Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
14	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
15	Bacteria	Proteobacteri	Betaproteobacteria			
16	Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
17	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	Zoogloea
18	Bacteria	Proteobacteri	Gammaproteobacteria			Candidatus Co
19	Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Gallionellaceae	
20	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	Thauera
21	Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriaceae	
22						
23	Bacteria	Proteobacteri	Betaproteobacteria			
24	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	Denitratisoma
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27	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	
28	Bacteria	Proteobacteri	Gammaproteobacteria	Xanthomonas	Xanthomonadaceae	
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32	Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
33	Bacteria	Proteobacteri	Betaproteoba	Nitrosomonas	Nitrosomonas	Nitrosomonas
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41	Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae	Candidatus Ac
42	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	Elev-16S-1166	
43	Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineae	Ornatilinea
44						
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46	Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17	
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55	Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17	
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Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
Bacteria	Proteobacteri Gammaproteobacteria
Bacteria	Bacteroidetes Cytophagia Cytophagales
Bacteria	Proteobacteri Deltaproteob Myxococcales
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophaga Ferruginibacte
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Defluviicoccus
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Bacteroidetes
Bacteria	Planctomycet Phycisphaera Phycisphaera Phycisphaera SM1A02
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Chlamydiae Chlamydiae Chlamydiales Parachlamydi Candidatus Pr
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillaceae
Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Thauera
Bacteria	Proteobacteri Deltaproteob Myxococcales Haliangiaceae Haliangium
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteriaceae
Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae
Bacteria	Bacteroidetes Bacteroidia Bacteroidales Rikenellaceae Blvii28 waste
Eukaryota	Metazoa
Bacteria	Chloroflexi Anaerolineae Anaerolineae Anaerolineaceae
Bacteria	Acidobacteria Holophagae Subgroup 7

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Bacteria	
Eukaryota	Basidiomycot Tremellomycet Tremellales Trichosporon; Trichosporon
Bacteria	Bacteroidetes Sphingobacte Sphingobacte env.OPS 17
Bacteria	Spirochaetae Spirochaetes Spirochaetale Spirochaetace Spirochaeta
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteriaceae
Eukaryota	Ciliophora Intramacronu Conthreep Oligohymeno Epistylis
Bacteria	Cyanobacteri; Melainabacte Obscuribacterales
Bacteria	Bacteroidetes Flavobacteriia Flavobacteria Flavobacteria Flavobacteriu
Bacteria	Verrucomicro Opitutae Opitutales Opitutaceae Opitutus
Bacteria	Proteobacteri Betaproteoba Methylophila Methylophilaceae
Bacteria	Chloroflexi Caldilineae Caldilineales Caldilineaceae
Eukaryota	Basidiomycot Tremellomycet Tremellales Trichosporon; Trichosporon
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Proteobacteri Deltaproteob Myxococcales
Bacteria	Bacteroidetes Sphingobacte Sphingobacteriales
Bacteria	Proteobacteri Gammaprote Order Incerta Family Incert; Marinicella
Bacteria	Chloroflexi Anaerolineae Anaerolineale Anaerolineaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 3 GOUTB8
Bacteria	Proteobacteria
Bacteria	Acidobacteria Acidobacteria Subgroup 17
Bacteria	Actinobacteri Actinobacteri Micrococcale; Micrococcaceae
Bacteria	Planctomycet OM190
Bacteria	Acidobacteria Acidobacteria Subgroup 4

Bacteria	Acidobacteria	Acidobacteria Subgroup 3	SJA-149
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteria NS9 marine group
Bacteria	Planctomycet	Phycisphaera	Phycisphaera SM1A02
Bacteria	Proteobacteria	Deltaproteob	Myxococcales Haliangiaceae Haliangium
Bacteria	Proteobacteria	Betaproteobacteria	
Bacteria	Proteobacteria	Betaproteoba	Burkholderia Oxalobacteria Massilia
Bacteria	Planctomycet	Planctomycet	Planctomycet Planctomycet Gemmata
Bacteria	Chloroflexi	Caldilineae	Caldilineales Caldilineaceae
Bacteria	Planctomycet	BD7-11	
Bacteria	Proteobacteria	Betaproteoba	Nitrosomona Nitrosomona Nitrosomonas
Bacteria	Actinobacteria	Actinobacteria	Micrococcales Microbacteriaceae
Eukaryota	Tubulinea	Arcellinida	Echinamoebida Echinamoeba
Bacteria	Firmicutes	Bacilli	Lactobacillale Lactobacillaceae Lactobacillus
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte env.OPS 17
Eukaryota	Metazoa		
Bacteria	Proteobacteria	Alphaproteobacteria	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale Anaerolineaceae
Bacteria	Chloroflexi	Ardenticatenia	
Bacteria	Proteobacteria	Alphaproteob	Rhizobiales Bradyrhizobia Bosea
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale Anaerolineaceae Ornatilinea
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte Chitinophagaceae
Bacteria	Proteobacteria	Betaproteobacteria	
Bacteria	Proteobacteria	Alphaproteob	Rhodobacter Rhodobacteraceae
Bacteria	Proteobacteria	Deltaproteobacteria	

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Bacteria	Candidate division OP11	
Bacteria	Acidobacteria	Acidobacteria Subgroup 4
Bacteria	Proteobacteri	Betaproteoba Burkholderiales
Bacteria	Actinobacteri	Actinobacteri Micrococcale Microbacteri Microbacteri
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Chitinophaga Niastella
Bacteria	Proteobacteri	Alphaproteob Rickettsiales AKIW1012
Bacteria	Elusimicrobia	Elusimicrobia MVP-88
Bacteria	Chloroflexi	Anaerolineae Anaerolineae Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteob Rhodospirillales Reyranela
Bacteria	Proteobacteri	Deltaproteob Myxococcales
Bacteria	Proteobacteri	Gammaprote Xanthomonas Xanthomonadaceae
Bacteria	Proteobacteri	Alphaproteob Caulobactera Hyphomonad Woodsholea
Bacteria	Actinobacteri	Actinobacteri Micrococcale Intrasporangi Tetrasphaera
Bacteria	Proteobacteri	Alphaproteob Rhizobiales
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Proteobacteri	Alphaproteob Rhodospirillal Rhodospirilla Defluviicoccus
Bacteria	Proteobacteri	Alphaproteob Rhizobiales
Bacteria	Proteobacteri	Deltaproteob Sva0485
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Proteobacteri	Alphaproteob Sphingomonadales
Bacteria	Proteobacteri	Deltaproteob Myxococcale Phaselicystid Phaselicystis

Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineae	Ornatilinea
Bacteria	Planctomycet	OM190			
Bacteria	Actinobacteri	Actinobacteri	PeM15		
Eukaryota	Cercozoa	Novel Clade	Gran-3		
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadaceae	
Bacteria	Chlorobi	Ignavibacteri	Ignavibacteri	BSV26	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149	
Bacteria	Proteobacteri	Alphaproteob	Caulobacteral	Hyphomonad	Woodsholea
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	SM2D12	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonadales		
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonac	Metallibacteri
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae	
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae	
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida	Neobodo
Bacteria	Acidobacteria			Holophagaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales		



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Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	NS9 marine group
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	Aquabacterium
Bacteria				Lactobacillus
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacteraceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales	
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales I Candidatus O
Bacteria	Cyanobacteri	Chloroplast		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	mle1-27
Bacteria				
Bacteria	Chloroflexi	Chloroflexia	Chloroflexale	Chloroflexale Candidatus Cl
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
Bacteria	Proteobacteri	Betaproteoba	Rhodocyclale	Rhodocyclaceae
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomonadaceae
Bacteria	Chloroflexi	Ardenticatenia		
Bacteria	Chloroflexi	Anaerolineae	Anaerolineale	Anaerolineaceae
Bacteria	Proteobacteri	Deltaproteob	Desulfuromor	GR-WP33-58
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae

Bacteria	Proteobacteri	Betaproteobacteria
Bacteria	Chloroflexi	Anaerolineae Anaerolineale Anaerolineaceae
Bacteria	Proteobacteri	Alphaproteob Caulobactera Caulobacteraceae
Bacteria	Proteobacteri	Betaproteoba Neisseriales Neisseriaceae
Bacteria	Proteobacteri	Alphaproteob Rhizobiales Bradyrhizobia Bradyrhizobiu
Bacteria	Proteobacteri	Betaproteoba Burkholderial Burkholderiac Chitinimonas
Bacteria	Proteobacteri	Gammaprote Pseudomona Pseudomona Pseudomonas
Bacteria	Proteobacteri	Alphaproteob Rhizobiales
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Chitinophaga Segetibacter
Bacteria	Proteobacteri	Deltaproteob Myxococcales Polyangiaceae Sorangium
Bacteria	Proteobacteri	Betaproteoba Nitrosomona Nitrosomonadaceae
Bacteria	Chlorobi	Chlorobia Chlorobiales OPB56
Bacteria	Chloroflexi	
Bacteria	Bacteroidetes	Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Acidobacteria	Acidobacteria Subgroup 4
Bacteria	Planctomycet	Phycisphaera Phycisphaera Phycisphaeraceae
Bacteria	Proteobacteri	Alphaproteob Rhizobiales
Bacteria	Chloroflexi	Anaerolineae Anaerolineale Anaerolineaceae
Bacteria	Acidobacteria	Holophagae Subgroup 10 ABS-19
Bacteria	Planctomycetes	Planctomycetaceae
Eukaryota	Euglenozoa	Kinetoplastea Metakinetopl Eubodonida Bodo
Bacteria	Verrucomicro	OPB35 soil group
Bacteria	Proteobacteri	Alphaproteob Rhizobiales

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5	Bacteria	Bacteroidetes	Sphingobacte env.OPS 17	
6	Bacteria	Bacteroidetes Sphingobacte	Sphingobacte Saprospiraceae	
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9	Bacteria	Proteobacteri Betaproteoba	Burkholderiales	
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11	Bacteria	Bacteroidetes Flavobacteriiz	Flavobacteria Flavobacteriaceae	
12	Bacteria	Proteobacteri Alphaproteob	Rhodospirillal Acetobacteraceae	
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16	Bacteria	Proteobacteri Betaproteoba	SC-I-84	
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19	Bacteria	Acidobacteria Holophagae	Holophagales Holophagacez Holophaga	
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22	Bacteria	Proteobacteri Alphaproteob	Rhizobiales	
23				
24	Bacteria	Bacteroidetes Cytophagia	Cytophagales Cytophagaceae	
25	Bacteria	Bacteroidetes Flavobacteriiz	Flavobacteria Flavobacteriaceae	
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29	Bacteria	Chloroflexi	Caldilineae	Caldilineales Caldilineaceae
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33	Bacteria	Proteobacteri Alphaproteob	Rhodospirillales	
34	Bacteria	Acidobacteria Acidobacteria	Subgroup 4	
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39	Bacteria	Proteobacteri Betaproteoba	Burkholderial Alcaligenacea Parasutterella	
40	Bacteria	Chloroflexi	KD4-96	
41	Bacteria	Actinobacteri	Actinobacteria	
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44	Bacteria	Bacteroidetes Flavobacteriiz	Flavobacteria Flavobacteria Cloacibacteriu	
45	Bacteria			
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50	Bacteria	Proteobacteri Alphaproteob	Rhodospirillales	Telmatospirill
51	Bacteria			Phycisphaera
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53	Bacteria	Acidobacteria Acidobacteria	Subgroup 3	
54	Bacteria	Proteobacteri Alphaproteob	Rhizobiales	
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Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Polyangiaceae	Byssovorax
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera	Brevundimon
Bacteria	Actinobacteri	Propionibacteriales			
Bacteria	Verrucomicro	OPB35 soil group			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga	Sediminibacte
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Hyphomonad	Hirschia
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Proteobacteri	Gammaprote	Xanthomonac	Xanthomonadales	Incertae
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Chloroflexi				
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonadae	Comamonas
Bacteria	Proteobacteri	Alphaproteob	DB1-14		
Bacteria	Cyanobacteri	Melainabacte	Obscuribacterales		
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae	Haliangium
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		

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Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydiaceae
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriia	NS9 marine group
Bacteria	Armatimonadetes			
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	NS11-12 marine group
Bacteria	Proteobacteria			Magnetococcaceae
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteria			
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	
Bacteria	Bacteroidetes		Sphingobacteriia	Saprospiraceae
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes
Bacteria	Actinobacteria	Actinobacteria		
Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylobacillaceae
Bacteria	Acidobacteria	Acidobacteria		

Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Sphingobacteriaceae	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomonadales		Nitrosomonas
Bacteria	Chloroflexi	TK10			
Eukaryota	Ascomycota	Sordariomycetes			
Bacteria	Chloroflexi	Ardenticatenia			
Bacteria	Verrucomicro	Opitutae	Opitutales	Opitutaceae	Opitutus
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera	Caulobacter
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales		
Bacteria	Candidate division	BRC1			
Bacteria	Actinobacteri	Acidimicrobi	Acidimicrobia	Acidimicrobia	CL500-29 mar
Bacteria					
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Gammaproteobacteria			
Bacteria					
Bacteria		Sphingobacte	Sphingobacte	NS11-12 marine group	
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	
Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagace	Geothrix
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	Verrucomicrobiaceae	
Bacteria	Proteobacteria				
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae	

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Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	NS9	marine group
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria					
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12	marine group
Bacteria					
Bacteria					
Bacteria					
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	AKAU3564	sediment group
Bacteria					
Bacteria	Chloroflexi				
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	MNG7	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Verrucomicro	OPB35	soil group		
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiracea	Nitrospira
Bacteria	Actinobacteria				
Bacteria	Bacteroidetes			Capnocytoph	
Eukaryota	Euglenozoa	Kinetoplastea	Metakinetopl	Neobodonida	Neobodo

Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	NS11-12 marine group
Eukaryota	Phragmoplast	Embryophyta		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Eukaryota	Ochrophyta	Chrysophyceae	Chromulinales	Poterioochro
Bacteria	Bacteroidetes			Reichenbachia
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prevotellaceae
Bacteria				Prevotella
Bacteria				Planctomycet
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriu
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteriaceae
Bacteria	Proteobacteri	Alphaproteobacteria		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirillaceae
Bacteria	Chlorobi	Chlorobia	Chlorobiales	SJA-28
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae
Bacteria	Proteobacteri	Deltaproteob	Sva0485	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteraceae
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob
				Pedomicrobiu



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Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Schlesneria
Bacteria	Proteobacteri	Gammaproteo	Legionellales	Legionellaceae	
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteriaceae	
Eukaryota	Gracilipodida				Filamoeba
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteria	Flavobacteriu
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Haliangiaceae	Haliangium
Bacteria	Proteobacteri	Alphaproteob	DB1-14		
Bacteria	Proteobacteri	Alphaproteobacteria			
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Hyphomonad	Woodsholea
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20	
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	DEV007	
Bacteria	Firmicutes	Bacilli	Lactobacillales		
Eukaryota	Tubulinea	Arcellinida	Echinamoebida		Vermamoeba
Eukaryota	Discosea	Flabellinia	Vannellida		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Bacteria	Proteobacteri	Gammaproteobacteria			
Bacteria					
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Planctomyces
Eukaryota	Heterolobose	Tetramitia			Naegleria
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Defluviimonas
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales	I Candidatus Ca
Bacteria	Proteobacteria				
Bacteria					

Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
Eukaryota	Ascomycota	Sordariomyce	Microascales	Microascaceae
Eukaryota	Metazoa			
Bacteria	Candidate division	BRC1		
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	I-10
Bacteria	Proteobacteri	Gammaproteobacteria	Chromatiaceae	
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderiac Burkholderia
Bacteria	Actinobacteri	Thermoleoph	Gaiellales	
Bacteria	Armatimonadetes			
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae Candidatus Rf
Bacteria				
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Rhodospirilla
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	Defluviicoccus
Bacteria	Actinobacteri	Actinobacteria		
Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiracea Nitrospira
Bacteria	Actinobacteri	Actinobacteria		
Bacteria	Proteobacteria			Bdellovibrio

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Bacteria	Proteobacteria
Bacteria	Proteobacteri Alphaproteob Sphingomona Sphingomona Sphingomona
Bacteria	Proteobacteri Deltaproteob Myxococcales Nannocystace Nannocystis
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Saprospiraceae
Bacteria	Proteobacteri Betaproteobacteria
Bacteria	Proteobacteri Alphaproteob Rhodospirillal Acetobacteria Stella
Bacteria	Proteobacteri Gammaproteobacteria
Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
Bacteria	Acidobacteria Acidobacteria Subgroup 6
Bacteria	
Bacteria	
Bacteria	Acidobacteria Acidobacteria Subgroup 17
Bacteria	Actinobacteri Acidimicrobii Acidimicrobiales
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Singulisphaera
Bacteria	Bacteroidetes Sphingobacte Sphingobacteriales
Bacteria	Proteobacteri Gammaproteobacteria
Bacteria	Proteobacteri Gammaprote Legionellales Coxiellaceae Aquicella
Bacteria	Acidobacteria Acidobacteria Subgroup 3
Bacteria	Verrucomicro OPB35 soil group
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Chloroflexi Anaerolineae Anaerolineale Anaerolineaceae
Bacteria	

Bacteria	Spirochaetae Spirochaetes Spirochaetales Spirochaetaceae
Bacteria	Actinobacteria Actinobacteria Micrococcales Microbacteriaceae
Bacteria	Bacteroidetes Sphingobacteriales Sphingobacteriales
Bacteria	Chloroflexi Chloroflexia Chloroflexales Roseiflexaceae Roseiflexus
Bacteria	Bacteroidetes Sphingobacteriales Sphingobacteriales env.OPS 17
Bacteria	Proteobacteria Gammaproteobacteria Pseudomonadales Pseudomonadales Pseudomonas
Bacteria	Proteobacteria Deltaproteobacteria Myxococcales Haliangiaceae Haliangium
Bacteria	Proteobacteria Alphaproteobacteria Sphingomonadales Sphingomonadales Sphingopyxis
Bacteria	Chlamydiae Chlamydiae Chlamydiales Parachlamydiaceae
Bacteria	Cyanobacteria Cyanobacteria Subsection I Family I Prochloron
Bacteria	Proteobacteria Gammaproteobacteria Xanthomonadales Xanthomonadaceae
Bacteria	Proteobacteria Betaproteobacteria Rhodocyclales Rhodocyclaceae Thauera
Bacteria	Proteobacteria Alphaproteobacteria Rickettsiales Rickettsiaceae Rickettsia
Bacteria	Proteobacteria Gammaproteobacteria Xanthomonadales Xanthomonadales Candidatus Cc
Bacteria	Proteobacteria Alphaproteobacteria Rhizobiales Hyphomicrobiales Rhodoplanes
Bacteria	Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes Gemmatimonadetes
Bacteria	Planctomycetes Planctomycetes Planctomycetes Planctomycetaceae

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Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrob	Devosia
Bacteria					
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Bradyrhizobiaceae	
Bacteria	Proteobacteri	Gamma	proteobacteria		
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga	Flavitalea
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria					
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrio
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophagaceae	
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Candidate division	BRC1			
Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Bacteria	SHA-109				
Bacteria	Proteobacteri	Alphaproteob	Caulobactera	Caulobactera	Caulobacter
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales		
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149	
Bacteria					

Bacteria	Planctomycet	Phycisphaera	Phycisphaera	Phycisphaera	SM1A02
Eukaryota	Ochrophyta	Chrysophyceae	Chromulinales		Poterioochro
Bacteria	Chloroflexi	Chloroflexia	Chloroflexales	Roseiflexacea	Roseiflexus
Bacteria	Chloroflexi	Anaerolineae	Anaerolineae	Anaerolineaceae	
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Singulisphaera
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirilla	Nisaea
Eukaryota	Ciliophora	Intramacronu	Conthreep	Oligohymeno	Tetrahymena
Bacteria					Planctomyces
Bacteria	Acidobacteria	Acidobacteria	Subgroup 6		
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Sphingomona	Sphingomona
Bacteria	Planctomycetes				
Bacteria	Firmicutes	Clostridia	Clostridiales	Ruminococcaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Pirellula
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	Cystobacteria	Anaeromyxob
Bacteria	Actinobacteri	Actinobacteria			
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae	
Bacteria	Chlorobi	Chlorobia	Chlorobiales	OPB56	

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5	Bacteria	Actinobacteri Actinobacteri Corynebacteriales
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9	Bacteria	Bacteroidetes Cytophagia Cytophagales Cytophagaceae Runella
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13	Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadaceae
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16	Bacteria	Chloroflexi TK10
17	Bacteria	Proteobacteria
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19	Bacteria	Proteobacteri Betaproteoba Burkholderial Comamonadae Comamonas
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23	Bacteria	Armatimonadetes
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29	Bacteria	Gemmatimon Gemmatimon Gemmatimon Gemmatimonadaceae
30	Bacteria	Planctomycet OM190
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33	Bacteria	Bacteroidetes BD2-2
34	Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirilla Defluviicoccus
35	Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Candidatus Al
36	Bacteria	Planctomycet OM190
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41	Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclaceae
42	Bacteria	Proteobacteri Betaproteoba Rhodocyclale Rhodocyclace Propionivibrio
43	Bacteria	Proteobacteri Betaproteoba TRA3-20
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50	Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae
51	Bacteria	Chloroflexi Ardentcatenia
52	Bacteria	Proteobacteri Gammaprote Pseudomona Moraxellaceae
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56	Bacteria	Proteobacteri Alphaproteob Rhodospirillal Rhodospirillal Reyranelia
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Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	TK34
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	
Bacteria	Bacteroidetes	Flavobacteri	Flavobacteria	Flavobacteriaceae
Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Isosphaera
Bacteria	Proteobacteri	Alphaproteob	Rhodospirill	Rhodospirillaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
Bacteria	Proteobacteri	Deltaproteob	Myxococcales	0319-6G20
Bacteria	Proteobacteri	Gammaproteobacteria		
Bacteria	Proteobacteri	Gammaprote	Alteromonad	Pseudoaltero
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	



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Bacteria	Proteobacteri	Alphaproteobacteria			
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Nocardiodac	Nocardioides
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Gemmata
Eukaryota					
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Parachlamydi	Neochlamydia
Eukaryota		Chlorophyceae			Desmodesmu
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonada	Comamonas
Bacteria	Firmicutes	Bacilli	Bacillales	Paenibacillac	Brevibacillus
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	KD3-93	
Bacteria	Actinobacteri	Actinobacteria			
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptostrepto	Incertae Sedis
Bacteria	Proteobacteri	Betaproteoba	Neisseriales	Neisseriaceae	
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirillaceae	
Bacteria	Candidate division	OD1			
Bacteria	Actinobacteri	Actinobacteria			
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales		

Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales	
Bacteria	Proteobacteri	Gammaprote	Pseudomonadales	
Bacteria	Thermotogae	Thermotogae	Thermotogae	Thermotogaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodobacteri	Rhodobacteri
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Alcaligenaceae
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Burkholderiac
Bacteria	Proteobacteri	Gammaprote	Xanthomonadales	Candidatus Cc
Eukaryota	Metazoa			
Bacteria	Proteobacteri	Deltaproteobacteria		
Bacteria	Proteobacteri	Alphaproteob	DB1-14	
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria			Anaerolineac	Anaerolinea
Bacteria	Proteobacteri	Gammaprote	Legionellales	Legionellaceae
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Saprospiraceae
Bacteria	Planctomycet	OM190		

Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae
Bacteria	Proteobacteria			
Eukaryota	Ascomycota	Saccharomycetes	Saccharomycetes	Metschnikowia Clavispora
Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerae	Phycisphaerae SM1A02
Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadaceae
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae Runella
Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriia	Chitinophagaceae
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	
Bacteria				
Bacteria				
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	
Bacteria				

Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	DA111	
Bacteria	Proteobacteri	Betaproteobacteria			Comamonas
Bacteria	Proteobacteri	TA18			
Bacteria	Planctomycet	Phycisphaerae			
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Methylobacte	Methylobacte
Bacteria	Actinobacteri	Acidimicrobi	Acidimicrobia	Sva0996	marine group
Bacteria					
Bacteria	Proteobacteri	Alphaproteob	Caulobacteral	Hyphomonad	Hyphomonas
Bacteria	Verrucomicro	OPB35	soil group		
Bacteria	Proteobacteri	Betaproteoba	TRA3-20		
Bacteria	Proteobacteri	Alphaproteob	Sphingomonadales		
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacteriaceae	

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Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	mitochondria
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet Isosphaera
Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimonadaceae
Bacteria				
Bacteria	Bacteroidetes			
Bacteria	Proteobacteri	Deltaproteob	Sh765B-TzT-29	
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Candidate division	OD1		
Bacteria	Proteobacteri	Alphaproteob	Rickettsiales	Rickettsiales I Candidatus Ca

Bacteria	Proteobacteri	Betaproteoba	Burkholderiales	
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillales	Defluviicoccus
Bacteria	Proteobacteri	Betaproteoba	Nitrosomona	Nitrosomonadaceae
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae
Bacteria	Planctomycet	Phycisphaera	CCM11a	
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	env.OPS 17
Bacteria	Actinobacteri	Actinobacteria		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal	Acetobacteraceae
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Intrasporangi
Bacteria	Bacteroidetes	Sphingobacte	Sphingobacte	Chitinophaga
				Ferruginibacte

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Bacteria	Proteobacteri	Gammaprote	Legionellales	Coxiellaceae	Coxiella
Bacteria	Proteobacteri	Deltaproteob	Desulfobacte	Desulfobulba	Desulfobulbus
Bacteria	Proteobacteri	Alphaproteob	Rhodospirilla	Rhodospirillaceae	
Eukaryota	Ochrophyta	Chrysophyceae	Ochromonadales		Paraphysomonas
Bacteria	Proteobacteri	Deltaproteob	Myxococcales		
Bacteria					
Bacteria	Proteobacteria				
Bacteria	Bacteroidetes	Sphingobacteria	Sphingobacteria	env.OPS 17	
Bacteria	Proteobacteri	Alphaproteob	Caulobacteriales	Caulobacteriales	Phenylobacterium
Bacteria	Proteobacteri	Alphaproteob	Sphingomonas	Sphingomonas	Sphingobium
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Bacteria	Acidobacteria	Acidobacteria		Elev-16S-1166	
Bacteria	Proteobacteria				

Bacteria Proteobacteri Alphaproteob Rickettsiales SM2D12  
Eukaryota Cercozoa Cercomonadidae Eocercomona

Bacteria Planctomycet Planctomycet Planctomycet Planctomycet Gemmata  
Bacteria Candidate division WS3

Bacteria

Bacteria Actinobacteri Actinobacteria

Bacteria Proteobacteri Betaproteoba TRA3-20

Bacteria Proteobacteri Betaproteoba Burkholderiales

Bacteria Proteobacteri Alphaproteob Rhodobacteri Rhodobacteraceae



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Bacteria	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimon	Gemmatimon
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Leptospiraceae	Leptospira
Bacteria	Proteobacteri	Gammaproteobacteria			
Eukaryota	Discosea	Longamoebia	Centramoebida		Acanthamoeb
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bdellovibrion	Bdellovibrion

Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacter	Syntrophaceae
Bacteria				
Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonas	Sphingomonadaceae
Bacteria	Bacteroidetes	Flavobacteriia	Flavobacterium	Flavobacterium Chryseobacterium
Bacteria	Proteobacteria			
Eukaryota	Ciliophora	Intramacronucleus	Conthreop	Oligohymenous Vorticella
Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	
Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcus	Methylococcus Methylocaldococcus
Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae Thauera

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Bacteria	Actinobacteri	Actinobacteri	Frankiales	Nakamurellac	Nakamurella
Bacteria	Actinobacteri	Actinobacteri	Propionibacte	Propionibacte	Propionibacte
Eukaryota	Ascomycota	Sordariomyce	Hypocreales		
Bacteria	Bacteroidetes	Flavobacteriiz	Flavobacteria	NS9	marine group
Bacteria	Actinobacteri	Actinobacteria			
Bacteria	Proteobacteria				

Eukaryota	Nucleariida	Nucleariidae	Nuclearia
Bacteria	Acidobacteria	Acidobacteria Subgroup 6	
Eukaryota	LKM74		
Bacteria	Proteobacteri	Alphaproteob	Rhodospirillal Acetobacteraceae
Bacteria	Proteobacteri	Betaproteoba	Neisseriales Neisseriaceae Neisseria

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Bacteria	Proteobacteri	Betaproteobacteria		
Eukaryota	Ochrophyta	Diatomea	Bacillariophyt	Bacillariophyceae
Bacteria	Spirochaetae	Spirochaetes	Spirochaetale	Leptospiraceae Leptospira
Bacteria	Firmicutes	Bacilli	Lactobacillale	Carnobacteriæ Dolosigranulu
Bacteria	Chloroflexi	Ardeentocatenia		
Bacteria	Proteobacteria			
Eukaryota	Phragmoplastophyta			
Bacteria	Proteobacteri	Gammaprote	NKB5	
Bacteria	Bacteroidetes			Wandonia
Bacteria	Proteobacteri	Betaproteobacteria		
Bacteria	Bacteroidetes	BD2-2		

Eukaryota	Basidiomycot Microbotryon Sporidiobolal Incertae Sedis
Bacteria	Proteobacteri Betaproteoba Burkholderiales
Bacteria	Proteobacteri Alphaproteob Rhizobiales
Bacteria	Cyanobacteri Melainabacte Obscuribacterales
Bacteria	Proteobacteri Deltaproteob Myxococcales 0319-6G20
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Chitinophagaceae

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Bacteria	Proteobacteri	Gammaprote	Thiotrichales	Thiotrichaceae	
Eukaryota	Ochrophyta	Chrysophyce	Ochromonadales		Ochromonas
Bacteria	Proteobacteri	Gammaprote	Xanthomonas	Xanthomonas	Candidatus Cc
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Rikenellaceae	
Bacteria	Proteobacteri	Gammaprote	Aeromonadal	Aeromonada	Aeromonas

Bacteria	Deinococcus-	Deinococci	Deinococcale	Deinococcace	Deinococcus
Bacteria	Proteobacteri	Alphaproteob	Rhizobiales	Hyphomicrobiaceae	
Bacteria	Proteobacteri	Gammaprote	HOC36		
Bacteria	Verrucomicro	Verrucomicro	Verrucomicro	Verrucomicro	Brevifollis
Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae	Simkania
Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	
Bacteria					
Bacteria	Proteobacteri	Gammaprote	Chromatiales	Chromatiaceae	Nitrosococcus
Bacteria					



Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycet	Schlesneria
Bacteria	Proteobacteri	Gammaproteobacteria			
Bacteria	Actinobacteri	Actinobacteria		Propionibacte	Propionificell
Bacteria	Firmicutes	Bacilli	Bacillales		
Bacteria	TM6				

Archaea	Euryarchaeot	Methanomicr	Methanomicr	Methanoregu	Methanolinea
Bacteria	Proteobacteri	Betaproteoba	Burkholderiales		
Bacteria	Firmicutes	Clostridia	Clostridiales	Eubacteriace	Acetobacteriu
Bacteria	Firmicutes	Bacilli	Lactobacillale	Lactobacillace	Lactobacillus
Bacteria	Armatimonad	Chthonomon	Chthonomon	Chthonomon	Chthonomon
Bacteria	Proteobacteri	Alphaproteobacteria			
Bacteria	Acidobacteria	Holophagae			
Bacteria	Actinobacteri	Actinobacteri	Micrococcales		
Bacteria	Proteobacteri	Betaproteobacteria			
Bacteria	Firmicutes	Bacilli	Lactobacillale	Enterococcac	Enterococcus
Bacteria	Proteobacteri	Deltaproteob	Bdellovibrion	Bacteriovoracaceae	
Bacteria	Proteobacteri	Gammaprote	Xanthomonad	Xanthomonadales	Incertae
Bacteria	Actinobacteri	Acidimicrobii	Acidimicrobiales		
Bacteria	Planctomycetes				
Bacteria	Actinobacteri	Actinobacteri	Micrococcale	Microbacteri	Microbacteriu
Bacteria	Proteobacteri	Betaproteoba	Burkholderial	Comamonad	Inhella

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Bacteria	Proteobacteri	Alphaproteob	Sphingomona	Erythrobacter	Altererythro
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Rhodobacter
Bacteria	Acidobacteria	Acidobacteria	Subgroup 4		
Bacteria	Proteobacteri	Alphaproteob	Rhodobacter	Rhodobacter	Paracoccus
Bacteria	Actinobacteri	Actinobacteri	Actinomyceta	Actinomyceta	Actinomyces
Bacteria	Bacteroidetes	Flavobacterii	Flavobacteria	Schleiferiaceae	Schleiferia
Bacteria	Proteobacteri	Betaproteoba	Methylophila	Methylophila	Methylotener
Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae	
Bacteria	Planctomycet	Planctomycet	Planctomycet	Planctomycetaceae	
Bacteria	SHA-109				

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30 Bacteria Proteobacteri Betaproteobacteria  
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36 Bacteria Acidobacteria Acidobacteria Subgroup 4  
37 Bacteria Actinobacteri Actinobacteri Corynebacter Mycobacteria Mycobacteriu  
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Bacteria	Proteobacteri Gammaprote Methylococcc Methylococcc Methylocaldu
Bacteria	Chloroflexi
Bacteria	Actinobacteri Actinobacteri Micrococcale Micrococcaceae
Bacteria	Firmicutes Clostridia Clostridiales Family XIII
Bacteria	Proteobacteri Gammaproteobacteria Xanthomonadaceae
Bacteria	Proteobacteri Gammaproteobacteria
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Planctomyces
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycet Singulisphaer
Bacteria	Proteobacteri Betaproteoba Burkholderiales
Bacteria	Planctomycet Planctomycet Planctomycet Planctomycetaceae
Bacteria	Bacteroidetes Cytophagia Cytophagales Flammeovirg Ekhidna
Bacteria	Proteobacteri Betaproteoba Burkholderiales
Bacteria	Proteobacteri Betaproteoba Burkholderiales
Bacteria	Acidobacteria Acidobacteria Subgroup 3 SJA-149
Bacteria	Bacteroidetes Sphingobacte Sphingobacte Sphingobacteriaceae

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonadaceae  
Bacteria Proteobacteri Betaproteoba Burkholderiales

Bacteria Cyanobacteri Chloroplast

Bacteria Proteobacteri Betaproteoba Burkholderial Comamonada Comamonas

Bacteria Proteobacteri Betaproteoba Burkholderiales

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Bacteria	Proteobacteri	Betaproteoba	Burkholderiales
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Bacteria	Proteobacteri	Betaproteoba	Burkholderiales

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	TAG	Unique Sequence	ConSlu1	ConSlu2	ConSlu3
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4	TAG 58	CATACTTGGTGTGAGCCATTCATTTGGTTCGTG	1067	1231	963
5	TAG 79	CAAACCTTGGTGTAGGCAGTTCAGTCTGTCTGTG	835	954	711
6	TAG 117	AACACTTGGTGTGGAGGGAGTTGACCCCTTCC	397	400	438
7	TAG 143	GGTGCTTGGTGTGCGGGGATCGACCCCTCCG	185	330	293
8	TAG 173	CATACTTGGTGTGGGCAGTTCATTCTGTCCGTG	166	232	223
9	TAG 137	CATACTTGGTGTGGGTGATTCAATTTATCCGTG	206	149	181
10	TAG 176	ATCGCTGGGTGTGGGGGGTTTTACTCCCCC	156	152	168
11	TAG 178	CATACTTGGTGTGAGTCCTTCATTGGATTCTGTG	120	212	134
12	TAG 180	CGGACTTGGTGTGGGCAGTTCAGTCTGTCTGTG	175	118	173
13	TAG 212	CACACTTGGTGTGAGCGATTCAATTCGTTTCGTG	105	207	151
14	TAG 243	CAAACCTTGGTGTGCGCCCTTCATTGGGTGCGTG	187	143	94
15	TAG 244	AATACTTGGTGTCTGGAGGTTTAATACTCCGGG	98	53	210
16	TAG 255	AACACTTGGTGTGGTGGGAGTTGACCCCTGCC	142	81	111
17	TAG 339	GGCACTTGATGTCGCGGGTTTTCTACCCCTGCG	46	99	66
18	TAG 292	GGAAGTAGATGTAGGGACCATTCCACGGTTTTCT	56	121	107
19	TAG 19	ATTACTCGTTGCTGGGAGGTAACATTCAGTGAC	3854	3204	4453
20	TAG 20	ATGACTCGATGTTGGCGATATACAGCCAGCGTC	3761	3492	3338
21	TAG 35	ATTACTCGACATACGCGATACACAGTGTGTGTC	1587	1640	2026
22	TAG 47	ATTACTCGACATACGCGATACACTGTGTGTGTC	1129	1770	2173
23	TAG 52	GATACTCGACATCAGCGATACACTGTTGGTGTGTC	1051	1037	1056
24	TAG 75	ATTACTCGCTGCTAGAGGGCAACTTTTAGTGGC	1082	363	870
25	TAG 30	ATTACTCGATGTGTGCGATACACGGCACGCGTC	768	663	804
26	TAG 92	TAAACTCGACATTAGCGATATACAGTTAGTGTC	578	527	632
27	TAG 90	GATACTCGACATACGCGATACACTGTGTGTGTC	569	403	424
28	TAG 115	GATACTCGACATTTGCGATACACTGTAAGTGTC	388	351	473
29	TAG 112	GATACTCGACATACGCGATATACTGTGTGTGTC	357	483	350
30	TAG 18	GATACTAGCTGTTGGGAGTAATTTAGTGCGTA	291	479	296
31	TAG 160	ATCACTAGATTTTGGTCGCAAGATCAGAGTCCA	186	448	227
32	TAG 158	ATTACTCGTTGCTGGGGAGCAATTTCCAGTGAC	198	344	250
33	TAG 56	ATTACTCGCTGCTGGGAGGTAACATTCAGTGGC	298	213	245
34	TAG 238	CTAACTCGTTTTTGGTATTTTCGGTATCAGAGAC	18	377	276
35	TAG 207	GATACTCGACATACGCGATACACAGTGTGTGTC	265	126	87
36	TAG 183	GATACTCGACATTTGCGATACACAGTAAGTGTC	178	112	184
37	TAG 224	ATCACTCGATGTTGGCGATACACTGTCAGCGTC	112	167	181
38	TAG 221	GATACTAGCTGTTTGGAGCAATCTGAGTGGCTA	232	100	119
39	TAG 232	ATTACTCGATGTGTGCGATACACTGTACGCGTC	133	174	104
40	TAG 336	CTAACTCGTTTTTGGGTTTTTCGGATTACAGAGAC	3	308	3
41	TAG 254	TAAACTCGACATTAGCGATATACTGTTAGTGTC	45	98	128
42	TAG 257	ATTACTCGTTCTCGGCGATATACGGTCGGGGAC	60	71	129
43	TAG 355	GATACTAGCTGTTTCGGAGCAATCTGAGTGGCTA	104	66	83
44	TAG 311	GATACTAGCTGTTGGGGGTAACATTCAGTGGCTA	83	85	69
45	TAG 29	CCGACTAGGGATCGGTCCACGTTATTTTTTGAC	658	10676	979
46	TAG 94	CCGACTAGGGATCGGTCCACGTTATTTTCTGAC	248	1988	475
47	TAG 68	CCAAGTAGGGATACGTGGACGTTTGTTCAAGA	1135	807	805
48	TAG 145	AATACTCGGTGTCGGGTGCGCAAGATTCGGCGC	355	302	277
49	TAG 41	TGAACCTGGCGTTGGTGGGTAAACTCCATCAG	1059	1470	1716
50	TAG 155	AGTACTAGGTGTAGGAGGAGTGAAATCCTTCTG	172	297	296
51	TAG 131	TGAACCTGGCGTCCGTGGCTTAAACACCATCGC	259	128	175
52	TAG 194	AGTACTAGGTGTGGGTGGAGTCAAACTATCCG	160	201	186
53	TAG 46	CCGACTCGGATTACAGATGAATATTAAGTTTCAT	120	2893	1188
54	TAG 3	CCGACTCGGATTACAGATGAATCAAAAAGTTTCAT	77	764	211
55	TAG 77	GATACTAGGCGTATCGGGTATCGACCCCTGATC	545	919	663
56	TAG 153	CTCATTAGGTATGGGGGGTATCGACCCCTCCC	60	433	223
57	TAG 128	GGTACTAGGCGTCTGGGGGGGAGCGACCCCTCC	297	312	310
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TAG 168	GGTACTAGGCGTCGGGGGGAGCGACCCTCCCC	185	319	186
TAG 159	GGCACTAGGTCCTTGGGGGAGCGACCCCGTGA	137	157	187
TAG 225	GGCACTAGGTCCTTGGGGGAGCGACCCCTTGA	131	159	121
TAG 342	GGTGCTAGGCGTCGGGGGGAGCGACCCCTTC	88	54	75
TAG 7	CCGACCAGGGATCGAGGACAGTCCCATGGTTG	2235	3346	3714
TAG 85	CCGACCAGCGATTGGGAGACGTTACATGGATG	859	324	577
TAG 28	CCGACTAGCGATCCGCCGGCGTGGTTTCGATG	3213	1640	3522
TAG 142	CCAAGTGTCTTTTAGATGCGGTTACTCATATGA	68	62	207
TAG 132	AGGACTAGGTATTGGCTCGCAAGAGTCGGTGCG	384	263	315
TAG 15	TACACTAGACTGGTGCGGTTTTGACGCCGTATC	248	450	472
TAG 140	AGAAGTAGGTAGTGGGTCCGACCTGGGCACAC	191	371	320
TAG 186	TGTGCTGGATCACGGCGGCTCTGACGCCGCTCG	141	223	232
TAG 192	TACATTGTATGGTGGGAATCTTGCAATTTCACT	6	457	53
TAG 264	TGTGCTGAATCACGGCAGCTCTGACGCTGTGCG	121	83	138
TAG 284	GGCACTGGGCAGGGGGGATACCTATGGTCCTC	46	114	94
TAG 164	GGCACTAGCTTGGGGTCTCCCTGTGTGATCCCC	85	66	84
TAG 261	GGCACTGGGTAGGGGGGCTCGCCGATGGGCTCC	57	62	90
TAG 2	TCAACTAGGTGTTGGGAGGGTTAAACCTTTTAG	52531	8590	19155
TAG 6	TCAACTGGTTGTTGGGAGGGTTTCTTCTCAGTA	5743	24589	27204
TAG 4	TCAACTAGTTGTTGCGGTGAGGAGACTCATTGAG	12757	11258	11724
TAG 11	CGAACTGGATGTTGGGCTCAACTTGGAGCTCAC	2991	5461	9262
TAG 8	TCAACTAGGTGTTGGGTGGGTAAAACCATTTAG	4968	4273	5434
TAG 23	CGAACTGGATGTTGGTCTCAACTCGGAGATCAC	2578	7279	4565
TAG 10	TCAACTAGTTGTGCGGATCTTAATAGATTTGGTA	3162	2244	4002
TAG 12	TCGACTAGTCGTTCCGGAGCAGCAATGCACTGAC	3190	1527	1643
TAG 55	TCTACTAGTTGTGCGGTCTTAATTGACTTGGTA	228	4008	1502
TAG 51	AGAAGTGGACGTTGGGAGGAATTCGCCTCTTAC	860	1551	1791
TAG 54	TCAACTAGTTGTGCGGTCTTATTGGGCTTGGTA	1306	765	1419
TAG 43	AGAAGTAGGTGTGCGTGGGTGTTGACCCCGCG	1083	727	971
TAG 95	TCGACTAGCCGTTGGAATCCTTGAGATTTTAGT	34	1780	855
TAG 81	CCAAGTAGTTGTTGGGGAAGGAGACTTCCTTAC	425	978	728
TAG 78	TCAACTAGTTGTGCGGCCTTAATAGGTTTGGTA	579	649	839
TAG 69	TCAACTGGTTGTTGGACGGCTTGCTGTTTCAGTA	859	495	594
TAG 73	AGAGCTAGTTGTGCGGCACGCATGCGTGTGCGGT	623	544	564
TAG 101	TCAACTGGTTGTTGGAGGGGTTTCTTTCAGTA	440	657	503
TAG 110	GGTGCTGGATGTGCGGGGGCTTGCCCTTCGGT	351	529	569
TAG 99	CGAACTAGGTGTTGGGGAAGGAGACTTCTTTAG	344	654	438
TAG 114	AATGCCAGTCGTCGGCAAGCATGCTTGTGCGGT	553	275	528
TAG 48	AGCACTAGACGTGCGGTGGGTGACCGTCCGGT	423	365	427
TAG 98	AATGCCAGCCGTTGGGGAGCTTGCTCTTCAGTC	387	246	565
TAG 105	AATGCCAGACGTGCGGCAGCATGCTGTTCCGGT	311	282	511
TAG 100	CGAACTGGATGTTGGGTGCAATTTGGCACGCA	162	304	599
TAG 134	AGTGCTAGTTGTGCGGCATGCATGCATGTCGGTC	146	467	404
TAG 32	AGCACTAGACGTGCGGGCGGGTGACCGTCCGGT	184	393	382
TAG 135	GGTGCTAGGTGTGCGGGGCTTTGACCCTCGCG	228	336	343
TAG 146	TCAACTAGTTGTGCGGTCTTATTAGATTTGGTA	254	254	341
TAG 161	TCAACTGGTTGTTGGGAATTCATTTTCTCAGTA	442	125	245
TAG 185	AGTGCTGGATGTGCGGAAGCCTAGCTTTTCGGT	112	270	201
TAG 230	TCAACTGGTTGTTGGGTTTTAATTAAGTCACTAGTA	167	194	198
TAG 196	AGTGCTAGGTGCTGCGGGTATTGACCCCTGCGT	180	195	162
TAG 172	GATGCTAGCCGTTGGACAGCTTGCTGTTTCAGTC	59	313	156
TAG 205	TGCGCTGGATGTTGGGTGACCTAGTCACTAGT	111	168	217
TAG 222	GGTGCTAGACGTTGGCGGGCTTGCTCGTCACTAGT	158	179	134
TAG 223	AATGCCAGCCGTTAGTGGGTTTACTCACTAGTG	69	258	114
TAG 250	TCGACTAGTTGTTGGGGAAGGAACTTCCTTAG	72	181	123

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	TAG 267	TCGACTGGTTGTTGGGGGTTTGACACTCTCAGT	141	104	125
	TAG 125	AATGCCAGACGTCGGCAAGCATGCTTGTCGGT	246	50	62
	TAG 1	TCAACTGGTTGTTGGGTCTTAAGTACTCAGTA	88	152	97
	TAG 286	TCGACTAGTTGTTTCGGAGCAGCAATGCACTGAC	106	110	105
	TAG 165	ATAACTAGCTGTCCGGGCACTTGGTGCTTGGG	95	86	129
	TAG 297	AGAGCTAGCCGTTGGAGGGTTTACCCTTCAGTC	53	135	114
	TAG 260	TCAACTAGTTGTTCGGGCTTAATAGGCTTGGTA	127	77	92
	TAG 327	GGTGCTAGGTGTTCGGGGCTTTGACCCCTGCG	22	150	97
	TAG 179	TCAACTAGTTGTTCGGATCTTAATAGGTTTGGTA	87	89	92
	TAG 281	CGAACTAGGTGTTGGGGAAGGAGACTTTCTTAG	54	108	98
	TAG 299	AGAAGTACGTTGGGAGGGTACAGCTCTCAG	55	113	88
	TAG 289	TCAACTGGTTGTTGGGGAAGGTAAGTCTCTAG	63	105	75
	TAG 343	ATGACTAGTTGTTGGAGGATTAATCCTTTAG	73	64	97
	TAG 322	TCAACTAGTTGTTCGGGGAAGCAATTCTTGGTA	77	83	66
	TAG 329	GAAGCTAGCCGTTGGCAAGTTTACTTGTTCGGTC	56	52	104
	TAG 320	GATGCTAGCCGTTGGCGAGCTTGCTCGTCAGTC	56	81	68
	TAG 369	GGTGCTAGATGTTGGGAGGCTTGCTTCTCGGT	46	83	76
	TAG 204	TATACTAGTTGTTGGTGGTTTCAACGCCATCAG	87	123	142
	TAG 5	CCGACTTGGGATTGGAGGCGTGCACCTTCCGC	28663	12547	13824
	TAG 14	CCAAGTAGGGATATGTGGACGTTTGTGTAAGA	5231	4613	4892
	TAG 22	CCGACTAGGGATGAGTGAACGTTGCATTATCGA	2077	4977	3605
	TAG 21	CGCACTAGACCGGTGCGGTTTGGACGCCGTAT	4337	2411	3358
	TAG 42	CTAACTCGTTTTTGGGGCGTAAGTTTCAGAGAC	833	6105	2336
	TAG 24	TCGACTAGGTGTTTCGGGAAGGAGACTTCTTGAC	1887	4012	3053
	TAG 39	CCGACCGGGGATGGGGAGAGGTAATACCTTAA	3038	1278	2023
	TAG 37	TATGCTAGACCGGTGCGGTTTGGACGCCGTATC	1496	2406	2261
	TAG 40	CCGACCAAGGATAAGAGGTCGTAATTATCTTGA	1542	1911	2381
	TAG 44	CTTACTCGACGTACGGCCCTGGCGGCTGTGCG	1330	1645	2094
	TAG 27	TCAACTAGTTGTTCGGGTCTGTTTAAAGATTGG	2280	1262	1034
	TAG 50	TACGCTAGATCGGTGCGGGTTTGACCCCGTATC	792	1879	1551
	TAG 59	TTCAGTGTGTTGCGGGTATTTATTTATCTGCA	900	700	1320
	TAG 71	AACACTAGATGTTACGGGTATTGACCCCTGTAG	544	1339	949
	TAG 67	CTGACTTGGTGTTCAGGTTTAAATCTTGGGG	1020	991	768
	TAG 74	TACGCTGAGTTAGAGCGGCTCTGACGCCGTTCC	712	903	911
	TAG 83	CCGACTTGGTGTTCGCCGTTTAAAGTCCGGGGC	664	735	1004
	TAG 88	TCAACTAGTTGTTGGATCCGTTTAAAGATTGG	1014	613	719
	TAG 61	CTGACTTGGTGCCCCCGGTTTAAAGTCCGGGGC	549	1325	359
	TAG 63	CCGACTAGGGATCGGTGGACGTTGCATAGCATC	13	2013	158
	TAG 89	CGCACTAGGTGACGGGACCTCTCACGGTCTCG	362	722	652
	TAG 133	CTAACTCGTTTTTGGGACGTAAGTTTCAGAGAC	135	1116	444
	TAG 97	TCAACTAGTTGTTGGATCCATTTAAAGATTAG	521	533	606
	TAG 93	CCGACCAGGGATTGGGAGACGTTAAATTTTATA	909	168	414
	TAG 104	CCGACCAGGGATCGGAGAGTGTTACATGGATG	373	523	590
	TAG 122	AGCACTAGGTGTTGGTCCCTTTGGGGCCAGTG	235	478	420
	TAG 76	TACGCTAGACTGGTGCGGTTTGAAGCCGTATC	397	349	379
	TAG 127	GCGACCGAGATTCAAGAAATGCCCAAGATGGC	206	564	260
	TAG 121	TCGACTGGGTGTTCGGCGATTAAAAACCGTCGG	213	435	333
	TAG 139	TACACTAGACCGGTGCGGTTTGGACGCCGTATC	213	369	275
	TAG 144	CCAACCAAAGATAAGAGGTTGTAAATACAAAA	305	135	367
	TAG 167	AACACTTGGTGTTCGGGAGTTGACCCCGGA	110	513	171
	TAG 154	ATCACTCGATGTGTGCGATACACAGCACGCGTC	204	302	235
	TAG 136	TCAACTAGTTGTTGGATCTTAATAGATTGGTA	171	144	407
	TAG 177	TCGACTAGGTGTTCGGCGCCTAAAAACCGTCGG	59	383	245
	TAG 174	CCGACCAAGGATCATGAGATGTTAAATATAAAT	373	12	211
	TAG 209	AATACTCGGTGTTGGTCCGCAAGGATCAGCGC	149	232	165

TAG 191	CCGACTTGGTGTCCCCGGTTTTAAGTCCGGGGG	116	201	199
TAG 226	AGAAGTAGGTATCGTGGGTGTTGACCCCCGCG	125	139	199
TAG 217	CTGACTAGGTGTCTGGCGATTAAAAACCGCCGG	71	236	149
TAG 228	GGTGCTGGATGTCTGGGGGGCTTGCCCCCTCGG	106	175	175
TAG 188	TTTACTTGCTGTTTCTGGGCAACTGGGAGTGGC	93	173	156
TAG 240	AATATTAATTGTCTGAATTTTCGGTAATTTAGTT	134	149	138
TAG 206	AATACTAGGCGTAGGGAGAGTCAAACTCTTCTG	71	235	111
TAG 227	TCAACTAGTTGTCTGGACCTTAATAGGTTTGGTA	89	156	157
TAG 241	TGCACTAGACTGGTGCGGTTTTGACGCCGTATC	114	124	155
TAG 251	CCGACTAGGGATCGGTGGATGTTTTATTGACG	186	68	107
TAG 252	TCAACTAGTTGTCTGGGCGCTTATTGGGCTTGGTA	91	78	165
TAG 275	CATACTAGATCCGGGAGACACTCATCGTAATCC	80	141	109
TAG 246	CCAACCAAAGATAAGAGGTTGTAAATATTATAA	106	68	155
TAG 266	TACGTTGAGTTAGAGCGGCTCTGACGCCGTTCC	86	120	123
TAG 276	TGCACTTGGCCTGGGAGGATTGACCCCTTCC	137	94	95
TAG 277	TCAACTAGTTGTCTGGACCTTATTGGGTTTGGTA	111	76	120
TAG 274	TCAACTAGCTGTCTGTAGATTAAAGTTTATAGG	142	71	81
TAG 248	TTTACTTGCTGTTTGGCTTTCGGGCGGAGTGGC	124	93	76
TAG 253	GGCACTAGCTTGGGGTCTCCCTGTGGGATCCC	68	125	100
TAG 269	TCAACTGGTTGTTGAGGGGGTTCCTCCTCAGTA	74	132	85
TAG 326	ATAACTCGCTGTTGGTGTTCATCAGTGGCT	153	39	76
TAG 319	CCGACTAGGGATTGGGAGGTTACTTACCTCTCA	102	89	69
TAG 234	CACACTAGGTTTTGGAGGATTCGACCCCTTCAG	76	93	83
TAG 293	GATGCTAGCCGTTGGGGGATACCCCTCAGTG	92	58	98
TAG 273	CACGCTTGATTACGACGGCTCTGACGCCGCCG	75	81	88
TAG 300	TACACTAGACCGGTGCGGCTCTGACGCCGTAT	53	93	79
TAG 402	TCAACTAGCCGTTGGGAGCTTTAAAGTTCTTAG	37	46	132
TAG 349	AATGCTAGTTGTCTAGTAAGTATACTTATTGGTG	53	94	66
TAG 312	ATGACTGGGTGTCTGGCGATTAAAAACCGTCGG	49	85	75
TAG 335	GGTGCTAGATGTCTGGGGAGCTTGCTCTTCGGT	68	73	67
TAG 268	ATTACTCGCTGCTGGGGGGCAACCTTCAGTGG	56	27	122
TAG 64	CACACTAGGTCTTGGCGGATTCGACCCCCCA	683	628	511
TAG 182	CACGTTTGCTGTGGGCGCAATCGACCGCGTCC	204	146	151
TAG 237	CACGTTTGCTGTAAAGAGGAATCGACCCCTTTG	144	117	133
TAG 263	CACGTTTGCTGTAAAGGAATCGACCCCTTTTG	112	102	120
TAG 239	CACACTAGGTCTTGGCGGATTCGACCCCA	56	66	113

	TrSlu1	TrSlu2	TrSlu3	Sum	LOG10(T1/C1)	LOG10(T2/C2)	LOG10(T3/C3)
1							
2							
3							
4		876	848	963	3261	-0.085660313	-0.161862201
5		587	525	714	2500	-0.153048374	-0.259389071
6		390	311	350	1235	-0.0077259	-0.109299602
7		286	280	229	808	0.189194305	-0.071355909
8		183	160	177	621	0.042343002	-0.161368002
9		161	134	181	536	-0.107041344	-0.04608147
10		307	183	206	476	0.294013777	0.080607502
11		127	171	122	466	0.024622475	-0.093339751
12		136	118	151	466	-0.10949914	0
13		124	126	118	463	0.072232386	-0.2155998
14		94	47	160	424	-0.298713753	-0.48323818
15		207	45	79	361	0.32474427	-0.071063356
16		95	99	134	334	-0.174564739	0.087150176
17		69	63	51	211	0.176091259	-0.196294645
18		61	93	59	284	0.037141808	-0.114302422
19	3616	2355	3647	11511	-0.027683289	-0.133701596	-0.086716932
20	2511	2249	2942	10591	-0.175456621	-0.19108478	-0.054843664
21	2024	1790	1921	5253	0.105633581	0.038009183	-0.023112076
22	1456	1265	831	5072	0.110467433	-0.145882741	-0.417458703
23	873	954	768	3144	-0.080588472	-0.036230382	-0.138302698
24	786	435	1140	2315	-0.138804715	0.078582632	0.117385599
25	500	507	583	2235	-0.186391216	-0.116505569	-0.139587494
26	501	319	413	1737	-0.062090113	-0.218019932	-0.184767027
27	414	328	547	1396	-0.138111925	-0.089431202	0.11062147
28	299	315	388	1212	-0.113160537	-0.046996563	-0.086029415
29	451	404	344	1190	0.101508326	-0.077565766	-0.007509602
30	231	417	242	1066	-0.100281009	-0.060199458	-0.087476345
31	191	203	123	861	0.011520423	-0.343781976	-0.266120746
32	195	253	126	792	-0.006630579	-0.133437921	-0.297569464
33	159	151	241	756	-0.27281914	-0.149402656	-0.007149042
34	3	24	2	671	-0.77815125	-1.196130108	-2.139879086
35	105	130	173	478	-0.402056575	0.013572807	0.298526851
36	89	90	137	474	-0.301029996	-0.094975513	-0.128097256
37	102	115	119	460	-0.040617851	-0.162018631	-0.182131613
38	106	84	176	451	-0.34018212	-0.075720714	0.169965706
39	105	88	81	411	-0.102662342	-0.296066576	-0.10854832
40	0	10	0	314	-0.477121255	-1.488550717	-0.477121255
41	105	189	73	271	0.367976785	0.285235728	-0.24388711
42	101	87	66	260	0.226170123	0.088260904	-0.291045775
43	13	34	32	253	-0.903089987	-0.288065018	-0.413928114
44	70	97	79	237	-0.073980052	0.057352809	0.058778001
45	70	1429	47	12313	-0.973127854	-0.873376336	-1.318684834
46	61	544	33	2711	-0.609121846	-0.56281748	-1.15817967
47	770	668	970	2747	-0.168505136	-0.082097072	0.080975854
48	206	209	221	934	-0.236361133	-0.159860657	-0.098087495
49	1825	2429	1570	4245	0.236366909	0.21811018	-0.038617631
50	201	250	244	765	0.067667611	-0.074816441	-0.083901885
51	433	458	343	562	0.223188132	0.553655508	0.292256071
52	141	160	211	547	-0.05490087	-0.099076075	0.054769511
53	1286	3542	162	4201	1.030059723	0.087900123	-0.865301426
54	293	702	50	1052	0.580376895	-0.036756246	-0.625312451
55	507	755	574	2127	-0.031388543	-0.08536856	-0.062601636
56	258	413	105	716	0.633468456	-0.020537845	-0.327115564
57	359	287	293	919	0.082337999	-0.036272697	-0.024494073
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261	186	144	690	0.149468779	-0.234277739	-0.111150452
267	127	110	481	0.289790694	-0.092095931	-0.230448921
143	122	106	411	0.038064742	-0.115037294	-0.057479505
66	32	56	217	-0.124938737	-0.227243782	-0.126873236
2822	2361	2529	9295	0.101279482	-0.15142995	-0.16689307
533	300	1001	1760	-0.207265955	-0.033423755	0.239258264
2687	1253	3333	8375	-0.077643059	-0.116892777	-0.023954038
113	62	125	337	0.220569531	0	-0.219060332
275	228	406	962	-0.144998531	-0.062020901	0.11021548
326	346	289	1170	0.118765919	-0.114136415	-0.213044156
283	326	164	882	0.170753068	-0.05615631	-0.29030613
181	179	138	596	0.108459462	-0.095451832	-0.225608898
48	360	8	516	0.903089987	-0.103613699	-0.821185883
102	63	119	342	-0.074185199	-0.119737543	-0.064332125
101	116	50	254	0.341563542	0.007553138	-0.274157849
114	69	88	235	0.127485926	0.019305155	0.020203386
47	56	70	209	-0.083776998	-0.044203662	-0.109144469
75167	71183	71594	80276	0.155611549	0.918383124	0.572594471
6862	9895	2696	57536	0.077311897	-0.395325068	-1.003912878
9881	10713	11809	35739	-0.110947656	-0.021550139	0.003137313
5503	3660	5435	17714	0.2647831	-0.173791091	-0.231505228
7349	6466	5886	14675	0.17004666	0.179902807	0.034700624
957	1398	1036	14422	-0.430370975	-0.716564548	-0.644081026
3073	2448	3307	9408	-0.012399305	0.037788561	-0.082842889
1469	1568	2677	6360	-0.336768887	0.011507021	0.212010808
92	840	24	5738	-0.39414702	-0.678648427	-1.796458691
1275	1296	1164	4202	0.171011734	-0.078006796	-0.187142606
1040	926	1279	3490	-0.098909838	0.082949552	-0.045111851
877	756	1037	2781	-0.091628863	0.016987385	0.028559526
36	552	20	2669	0.024823584	-0.508480925	-1.630936119
624	853	529	2131	0.16679566	-0.059389824	-0.138675707
669	680	621	2067	0.062747554	0.020264216	-0.130670361
1077	1129	1008	1948	0.098222539	0.358088743	0.229674087
481	496	335	1731	-0.11234297	-0.040117223	-0.226234297
372	484	515	1600	-0.072909737	-0.132720008	0.010239244
287	422	387	1449	-0.08742522	-0.098143221	-0.167401301
439	490	353	1436	0.105906078	-0.125381668	-0.093699405
385	210	338	1356	-0.157264402	-0.117113399	-0.193717222
264	270	360	1215	-0.204736441	-0.1309291	-0.074125374
526	218	382	1198	0.133274779	-0.052478613	-0.169985085
447	508	290	1104	0.157547134	0.255614604	-0.246022902
751	632	568	1065	0.666124922	0.317843495	-0.023078487
71	91	78	1017	-0.313094507	-0.710275488	-0.714286762
163	284	236	959	-0.052630219	-0.14107421	-0.20915136
275	237	260	907	0.081397847	-0.151590931	-0.120320772
252	257	258	849	-0.003433176	0.005099407	-0.121134673
209	105	228	812	-0.325275983	-0.075720714	-0.031231237
153	249	132	583	0.135473408	-0.035164417	-0.182622126
91	84	77	559	-0.263675079	-0.363522444	-0.410174465
124	157	161	537	-0.16185082	-0.094134959	-0.002689139
117	151	67	528	0.29733385	-0.31656739	-0.367049796
166	107	119	496	0.174785109	-0.195925504	-0.260912772
69	73	149	471	-0.359807996	-0.389530171	0.04608147
71	134	82	441	0.012409258	-0.284514908	-0.143090999
53	126	102	376	-0.133056627	-0.15730803	-0.08130494



1							
2							
3	94	66	84	370	-0.176091259	-0.197489404	-0.172630727
4	46	53	49	358	-0.728177275	0.025305865	-0.102195609
5	34	52	8	337	-0.413003755	-0.465840244	-1.083681747
6	38	86	80	321	-0.445522269	-0.106894234	-0.118099312
7	55	51	28	310	-0.237360916	-0.226928275	-0.663431679
8	69	64	32	302	0.114573221	-0.324153795	-0.551754873
9	119	86	136	296	-0.02825676	0.048007726	0.169751081
10	59	74	21	269	0.428429331	-0.306859539	-0.66455244
11	93	79	67	268	0.028963696	-0.051762915	-0.137713025
12	48	144	62	260	-0.051152522	0.124938737	-0.198834386
13	66	67	88	256	0.079181246	-0.227003641	0
14	78	68	86	243	0.092754053	-0.188680386	0.059437188
15	59	44	40	234	-0.092470848	-0.162727297	-0.384711743
16	74	38	85	226	-0.017259005	-0.339294496	0.10987499
17	46	40	54	212	-0.085430195	-0.113943352	-0.284639579
18	56	91	35	205	0	0.050556373	-0.288440868
19	20	69	49	205	-0.361727836	-0.080229002	-0.190617512
20	92	208	100	352	0.024268575	0.228158224	-0.152288344
21	8396	4115	9999	55034	-0.533249214	-0.484170058	-0.140677157
22	4655	3996	4708	14736	-0.050665035	-0.062357975	-0.016649994
23	2599	3196	2007	10659	0.097369783	-0.19236087	-0.254357897
24	2984	1971	3845	10106	-0.162390603	-0.087510586	0.058815652
25	113	275	13	9274	-0.867566558	-1.346352974	-2.254529486
26	2595	3771	2139	8952	0.138365462	-0.026904392	-0.15451602
27	1118	983	2561	6339	-0.434145966	-0.113977336	0.102413696
28	2202	1783	1467	6163	0.167885721	-0.13014428	-0.187870449
29	1678	1213	1332	5834	0.036707583	-0.197399886	-0.252255171
30	1349	1360	1613	5069	0.006160309	-0.082626994	-0.11334231
31	588	790	2170	4576	-0.588557521	-0.203432264	0.321939195
32	1237	1534	809	4222	0.193644518	-0.08810142	-0.282663276
33	1267	796	1132	2920	0.148534105	0.055815028	-0.066727504
34	845	1015	443	2832	0.191257809	-0.120314535	-0.330862486
35	739	692	1090	2779	-0.139955733	-0.15596756	0.152065278
36	701	746	684	2526	-0.006761976	-0.082948923	-0.124462275
37	715	571	683	2403	0.032137962	-0.109651231	-0.167313009
38	269	312	830	2346	-0.576285675	-0.29330588	0.062349202
39	341	506	554	2233	-0.206817965	-0.418065361	0.188415316
40	189	3582	7	2184	1.162518452	0.250281807	-1.353559047
41	465	627	403	1736	0.108744382	-0.061269657	-0.20894255
42	19	47	3	1695	-0.851580168	-1.375566337	-2.170261715
43	324	419	556	1660	-0.206292713	-0.104513186	-0.037397833
44	314	130	786	1491	-0.461634235	-0.111365929	0.278422205
45	415	470	397	1486	0.046339265	-0.046403831	-0.172061505
46	306	329	219	1133	0.114653564	-0.162231999	-0.282805176
47	343	255	321	1125	-0.063496387	-0.136285247	-0.072134178
48	304	344	115	1030	0.169006363	-0.214720661	-0.354275508
49	206	214	188	981	-0.014512383	-0.308075484	-0.248286384
50	255	279	227	857	0.078160577	-0.121422163	-0.083306837
51	301	125	343	807	-0.005733344	-0.033423755	-0.029371944
52	132	235	76	794	0.079181246	-0.339049503	-0.352182518
53	254	198	162	741	0.095203549	-0.183341753	-0.161552848
54	295	154	259	722	0.236825906	0.029158229	-0.196294645
55	146	217	120	687	0.393500844	-0.24673904	-0.309984838
56	170	2	492	596	-0.34125991	-0.77815125	0.367682647
57	123	170	94	546	-0.083281157	-0.135039064	-0.244356091
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157	199	167	516	0.131441663	-0.004342981	-0.076136605
124	96	97	463	-0.003488328	-0.160743567	-0.312081342
89	149	86	456	0.098131658	-0.199725735	-0.238687817
114	115	108	456	0.031598986	-0.182340208	-0.209614293
256	243	111	422	0.439757017	0.14756017	-0.14780162
116	114	67	421	-0.062646809	-0.116281417	-0.313804284
110	148	82	417	0.190134336	-0.200806147	-0.131509126
127	99	123	402	0.154413714	-0.197489404	-0.105994541
95	111	151	393	-0.079181246	-0.048098706	-0.011354751
139	52	123	361	-0.126498144	-0.116505569	0.060521334
120	96	69	334	0.120139854	0.09017663	-0.378634853
69	86	69	330	-0.064240896	-0.214720661	-0.198577407
104	70	131	329	-0.008272526	0.012589127	-0.073060403
75	87	50	329	-0.059437188	-0.139661993	-0.390935107
69	68	120	326	-0.297871476	-0.140618941	0.101457641
57	78	78	307	-0.289448123	0.01128101	-0.187086643
78	65	147	294	-0.260193742	-0.038344992	0.258832316
127	127	148	293	0.010382036	0.135320772	0.289448123
180	127	89	293	0.422763592	0.006893708	-0.050609993
95	87	94	291	0.108491886	-0.181054679	0.043708928
80	37	78	268	-0.281601444	-0.022862883	0.01128101
20	62	80	260	-0.707570176	-0.156998317	0.064240896
84	49	86	252	0.043465694	-0.278286869	0.015420359
79	55	124	248	-0.066160736	-0.023065304	0.102195609
76	75	83	244	0.005752329	-0.033423755	-0.02540458
58	42	68	225	0.039152124	-0.345233658	-0.065118179
18	6	0	215	-0.312929219	-0.884606581	#NUM!
68	54	32	213	0.108233043	-0.240734094	-0.314393957
80	89	66	209	0.212893907	0.019971081	-0.055517328
45	63	72	208	-0.179296399	-0.063982311	0.031257694
60	19	55	205	0.029963223	-0.152610163	-0.345997141
481	395	422	1822	-0.152275627	-0.201362548	-0.083108449
140	139	169	501	-0.163502132	-0.021338056	0.048909757
113	97	163	394	-0.105284049	-0.081414127	0.088335963
102	93	111	334	-0.040617851	-0.040117223	-0.033858267
54	82	72	235	-0.015794267	0.094269917	-0.195745947

1					
2					
3					
4	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	Elev-16S-1166
5	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	unknown
6	Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae
7	Bacteria	Acidobacteria	Holophagae	Subgroup 7	unknown
8	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	unknown
9	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	Elev-16S-1166
10	Bacteria	Acidobacteria	Acidobacteria	Subgroup 17	unknown
11	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	unknown
12	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	unknown
13	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	unknown
14	Bacteria	Acidobacteria	Acidobacteria	Subgroup 3	SJA-149
15	Bacteria	Acidobacteria	Acidobacteria	Subgroup 4	unknown
16	Bacteria	Acidobacteria	Holophagae	Holophagales	Holophagaceae
17	Bacteria	Acidobacteria	Subgroup 22	unknown	unknown
18	Bacteria	Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae
19	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	env.OPS 17
20	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
21	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
22	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
23	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
24	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	env.OPS 17
25	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae
26	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
27	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
28	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
29	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
30	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
31	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	NS9 marine group
32	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	env.OPS 17
33	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	env.OPS 17
34	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
35	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
36	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
37	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
38	Bacteria	Bacteroidetes	unknown	unknown	unknown
39	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
40	Bacteria	Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Chitinophagaceae
41	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae
42	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
43	Bacteria	Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae
44	Eukaryota	Basidiomycota	Tremellomycetes	Tremellales	Trichosporonaceae
45	Eukaryota	Basidiomycota	Tremellomycetes	Tremellales	unknown
46	Eukaryota	Cercozoa	Novel Clade Gran-3	unknown	unknown
47	Bacteria	Chlorobi	Ignavibacteria	Ignavibacteriales	BSV26
48	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae
49	Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
50	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae
51	Bacteria	Chloroflexi	Caldilineae	Caldilineales	Caldilineaceae
52	Eukaryota	Ciliophora	Intramacronucleata	Conthreep	Oligohymenophorea
53	Eukaryota	Ciliophora	Intramacronucleata	Conthreep	Oligohymenophorea
54	Bacteria	Cyanobacteria	Melainabacteria	Obscuribacterales	unknown
55	Bacteria	Elusimicrobia	Elusimicrobia	MVP-88	unknown
56	Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales	Gemmatimonadaceae
57					
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59					
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2				
3	Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales Gemmatimonadaceae
4	Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales Gemmatimonadaceae
5	Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales Gemmatimonadaceae
6	Bacteria	Gemmatimonadetes	Gemmatimonadetes	Gemmatimonadales Gemmatimonadaceae
7	Eukaryota	Gracilipodida	unknown	unknown unknown
8	Eukaryota	LKM74	unknown	unknown unknown
9	Eukaryota	Metazoa	unknown	unknown unknown
10	Eukaryota	Metazoa	unknown	unknown unknown
11	Bacteria	OC31	unknown	unknown unknown
12	Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales Phycisphaeraceae
13	Bacteria	Planctomycetes	Planctomycetacia	Planctomycetales Planctomycetaceae
14	Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales Phycisphaeraceae
15	Bacteria	Planctomycetes	BD7-11	unknown unknown
16	Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales Phycisphaeraceae
17	Bacteria	Planctomycetes	OM190	unknown unknown
18	Bacteria	Planctomycetes	OM190	unknown unknown
19	Bacteria	Planctomycetes	Planctomycetacia	Planctomycetales Planctomycetaceae
20	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales Rhodocyclaceae
21	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales Comamonadaceae
22	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales Rhodocyclaceae
23	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales Xanthomonadaceae
24	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales Rhodocyclaceae
25	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales Xanthomonadaceae
26	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales Nitrosomonadaceae
27	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales Rhodocyclaceae
28	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales Oxalobacteraceae
29	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales Xanthomonadaceae
30	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales Nitrosomonadaceae
31	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales unknown
32	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales Pseudomonadaceae
33	Bacteria	Proteobacteria	Betaproteobacteria	unknown unknown
34	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales Nitrosomonadaceae
35	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales Comamonadaceae
36	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacteriales Hyphomonadaceae
37	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales Comamonadaceae
38	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales Rhodospirillaceae
39	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales Rhodocyclaceae
40	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales Rhodobacteraceae
41	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales Xanthomonadales Incertae Sedi
42	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales unknown
43	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales Rhodobacteraceae
44	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales Xanthomonadaceae
45	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacteriales Caulobacteraceae
46	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales Xanthomonadales Incertae Sedi
47	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales unknown
48	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales Nitrosomonadaceae
49	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales Comamonadaceae
50	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales Rhodospirillaceae
51	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales Comamonadaceae
52	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales Haliangiaceae
53	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales unknown
54	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales Acetobacteraceae
55	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales Rhodospirillales Incertae Sedis
56	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales Bradyrhizobiaceae
57	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales Nitrosomonadaceae
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3	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae
4	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae
5	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae
6	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae
7	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae
8	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Hyphomicrobiaceae
9	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae
10	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales	unknown
11	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae
12	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae
13	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	unknown
14	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae
15	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae
16	Bacteria	Proteobacteria	Betaproteobacteria	Nitrosomonadales	Nitrosomonadaceae
17	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Phyllobacteriaceae
18	Bacteria	Proteobacteria	unknown	Rhizobiales	Hyphomicrobiaceae
19	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodospirillales	Rhodospirillaceae
20	Bacteria	Spirochaetae	Spirochaetes	Spirochaetales	Leptospiraceae
21	Eukaryota	unknown	unknown	unknown	unknown
22	Unclassified	unknown	unknown	unknown	unknown
23	Eukaryota	unknown	unknown	unknown	unknown
24	Bacteria	unknown	unknown	unknown	unknown
25	Unclassified	unknown	unknown	unknown	unknown
26	Bacteria	unknown	unknown	unknown	unknown
27	Eukaryota	unknown	unknown	unknown	unknown
28	Bacteria	unknown	unknown	unknown	unknown
29	Unclassified	unknown	unknown	unknown	unknown
30	Uncultured	unknown	unknown	unknown	unknown
31	Uncultured	unknown	unknown	unknown	unknown
32	Uncultured	unknown	unknown	unknown	unknown
33	Uncultured	unknown	unknown	unknown	unknown
34	Uncultured	unknown	unknown	unknown	unknown
35	Bacteria	Acidobacteria	unknown	unknown	unknown
36	Uncultured	unknown	unknown	unknown	unknown
37	Uncultured	unknown	unknown	unknown	unknown
38	Unclassified	unknown	unknown	unknown	unknown
39	Bacteria	Acidobacteria	unknown	unknown	unknown
40	Unclassified	unknown	unknown	unknown	unknown
41	Uncultured	unknown	unknown	unknown	unknown
42	Uncultured	unknown	unknown	unknown	unknown
43	Bacteria	unknown	unknown	unknown	unknown
44	Unclassified	unknown	unknown	unknown	unknown
45	Unclassified	unknown	unknown	unknown	unknown
46	Bacteria	Verrucomicrobia	unknown	unknown	unknown
47	Uncultured	unknown	unknown	unknown	unknown
48	Unclassified	unknown	unknown	unknown	unknown
49	Uncultured	unknown	unknown	unknown	unknown
50	Uncultured	unknown	unknown	unknown	unknown
51	Eukaryota	unknown	unknown	unknown	unknown
52	Unclassified	unknown	unknown	unknown	unknown
53	Uncultured	unknown	unknown	unknown	unknown
54	Unclassified	unknown	unknown	unknown	unknown
55	Uncultured	unknown	unknown	unknown	unknown
56	Eukaryota	unknown	unknown	unknown	unknown
57	unknown	unknown	unknown	unknown	unknown
58					
59					
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Uncultured unknown	unknown	unknown	unknown
Bacteria unknown	unknown	unknown	Myxococcales
Uncultured unknown	unknown	unknown	unknown
Bacteria unknown	unknown	unknown	Rhodospirillaceae
Bacteria unknown	unknown	unknown	Saprospiraceae
Unclassified unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Bacteria Proteobacteria	Betaproteobacteria	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Unclassified unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Uncultured unknown	unknown	unknown	unknown
Bacteria Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhodobiaceae
Uncultured unknown	unknown	unknown	unknown
Bacteria Verrucomicrobia	Opitutae	Opitales	Opitutaceae
Bacteria Verrucomicrobia	Verrucomicrobiae	Verrucomicrobiales	Verrucomicrobiaceae
Bacteria Verrucomicrobia	OPB35 soil group	unknown	unknown
Bacteria Verrucomicrobia	OPB35 soil group	unknown	unknown
Bacteria Verrucomicrobia	Opitutae	Opitales	Opitutaceae



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3		NCBI nr assignment
4	unknown	N.A.
5	unknown	N.A.
6	Geothrix	N.A.
7	unknown	N.A.
8	unknown	N.A.
9	unknown	N.A.
10	unknown	N.A.
11	unknown	N.A.
12	unknown	N.A.
13	unknown	N.A.
14	unknown	N.A.
15	unknown	N.A.
16	Holophaga	N.A.
17	unknown	N.A.
18	unknown	N.A.
19	unknown	N.A.
20	unknown	N.A.
21	unknown	N.A.
22	unknown	N.A.
23	unknown	N.A.
24	unknown	N.A.
25	unknown	N.A.
26	unknown	N.A.
27	unknown	N.A.
28	unknown	N.A.
29	unknown	N.A.
30	Flavobacterium	N.A.
31	unknown	N.A.
32	unknown	N.A.
33	unknown	N.A.
34	Cloacibacterium	N.A.
35	unknown	N.A.
36	unknown	N.A.
37	Flavobacterium	N.A.
38	unknown	N.A.
39	Chryseobacterium	N.A.
40	unknown	N.A.
41	Crocinitomix	N.A.
42	Flavobacterium	N.A.
43	Flavobacterium	N.A.
44	Trichosporon	N.A.
45	unknown	N.A.
46	unknown	N.A.
47	unknown	N.A.
48	Ornatilinea	N.A.
49	unknown	N.A.
50	unknown	N.A.
51	unknown	N.A.
52	unknown	N.A.
53	Carchesium	N.A.
54	unknown	N.A.
55	unknown	N.A.
56	unknown	N.A.

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2		
3	unknown	N.A.
4	unknown	N.A.
5	unknown	N.A.
6	unknown	N.A.
7	Filamoeba	N.A.
8	unknown	N.A.
9	unknown	N.A.
10	unknown	N.A.
11	unknown	N.A.
12	SM1A02	N.A.
13	Gemmata	N.A.
14	SM1A02	N.A.
15	unknown	N.A.
16	SM1A02	N.A.
17	unknown	N.A.
18	unknown	N.A.
19	unknown	N.A.
20	Candidatus Accumulibacter	N.A.
21	unknown	N.A.
22	Zoogloea	N.A.
23	Thermomonas	N.A.
24	unknown	N.A.
25	unknown	N.A.
26	Nitrosomonas	N.A.
27	Thauera	N.A.
28	unknown	N.A.
29	unknown	N.A.
30	Nitrosomonas	N.A.
31	unknown	N.A.
32	Pseudomonas	N.A.
33	unknown	N.A.
34	Nitrosomonas	N.A.
35	Aquabacterium	N.A.
36	Woodsholea	N.A.
37	Comamonas	N.A.
38	Defluviicoccus	N.A.
39	Denitratisoma	N.A.
40	unknown	N.A.
41	Candidatus Competibacter	N.A.
42	Bosea	N.A.
43	unknown	N.A.
44	Stenotrophomonas	N.A.
45	unknown	N.A.
46	Candidatus Competibacter	N.A.
47	unknown	N.A.
48	Nitrosomonas	N.A.
49	unknown	N.A.
50	Defluviicoccus	N.A.
51	unknown	N.A.
52	Haliangium	N.A.
53	unknown	N.A.
54	Reyranella	N.A.
55	Bradyrhizobium	N.A.
56	unknown	N.A.
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2		
3	unknown	N.A.
4	unknown	N.A.
5	unknown	N.A.
6	Thauera	N.A.
7	unknown	N.A.
8	Devosia	N.A.
9	Nitrosomonas	N.A.
10	unknown	N.A.
11	Nitrosomonas	N.A.
12	Sulfuritalea	N.A.
13	unknown	N.A.
14	unknown	N.A.
15	unknown	N.A.
16	unknown	N.A.
17	Mesorhizobium	N.A.
18	Rhodoplanes	N.A.
19	Defluviicoccus	N.A.
20	Turneriella	N.A.
21	Rattus	<i>Rattus</i> (Genus)
22	unknown	Unclassified
23	unknown	Eukaryota
24	unknown	Bacteria
25	unknown	Unclassified
26	unknown	Bacteria
27	unknown	Eukaryota
28	unknown	Bacteria
29	unknown	Unclassified
30	unknown	Uncultured Bacteria
31	unknown	Uncultured Bacteria
32	unknown	Uncultured Bacteria
33	unknown	Uncultured Bacteria
34	unknown	Uncultured Bacteria
35	unknown	Acidobacteria (Phylum)
36	unknown	Uncultured Bacteria
37	unknown	Uncultured Bacteria
38	unknown	Unclassified
39	unknown	Acidobacteria (Phylum)
40	unknown	Unclassified
41	unknown	Uncultured Bacteria
42	Endosymbiont of Nilaparva	Endosymbiont of Nilaparvata lugens
43	unknown	Bacteria
44	unknown	Unclassified
45	unknown	Unclassified
46	unknown	Verrucomicrobia (Phylum)
47	unknown	Uncultured Bacteria
48	unknown	Unclassified
49	unknown	Uncultured Bacteria
50	unknown	Uncultured Bacteria
51	Vexillifera	Vexillifera (Genus)
52	unknown	Unclassified
53	unknown	Uncultured Bacteria
54	unknown	Unclassified
55	unknown	Uncultured Bacteria
56	Mayorella	Mayorella (Genus)
57	unknown	unknown
58		
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3	unknown
4	unknown
5	unknown
6	unknown
7	unknown
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21	unknown
22	unknown
23	unknown
24	unknown
25	unknown
26	unknown
27	unknown
28	unknown
29	unknown
30	unknown
31	unknown
32	Parvibaculum
33	unknown
34	Opitutus
35	Prostheco bacter
36	unknown
37	unknown
38	Opitutus
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*Uncultured Bacteria*  
*Myxococcales (Order)*  
*Uncultured Bacteria*  
*Rhodospirillaceae (Order)*  
*Saprospiraceae (Order)*  
*Unclassified*  
*Unclassified*  
*Uncultured Bacteria*  
*Uncultured Bacteria*  
*Uncultured Fungus*  
*Uncultured Bacteria*  
*Unclassified*  
*Uncultured Eukaryote*  
*Uncultured Bacteria*  
*Unclassified*  
*Unclassified*  
*Uncultured Bacteria*  
*Unclassified*  
*Uncultured Bacteria*  
*Proteobacteria (Phylum)*  
*Unclassified*  
*Unclassified*  
*Uncultured Bacteria*  
*Unclassified*  
*Uncultured Bacteria*  
*Uncultured Bacteria*  
*Unclassified*  
*Uncultured Bacteria*  
*Uncultured Bacteria*  
*Parvibaculum (Genus)*  
*Uncultured Bacteria*

N.A.  
N.A.  
N.A.  
N.A.  
N.A.

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2							
3							
4	TAG	Unique Sequences	ConSlu1	ConSlu2	ConSlu3	TrSlu1	TrSlu2
5	TAG 26	ATGACTTGG	3899	3159	2125	2576	2250
6	TAG 58	CATACTTGG	135	129	163	88	100
7	TAG 137	CATACTTGG	163	70	102	135	69
8	TAG 178	CATACTTGG	84	49	64	44	32
9	TAG 180	CGGACTTGC	43	48	57	22	26
10	TAG 163	GGCGCTAGC	310	195	245	146	117
11	TAG 13	ATGACTCGA	8017	5653	2770	4514	3966
12	TAG 18	GATACTAGC	2041	3756	7517	1073	2241
13	TAG 25	ATGGCTGGA	2326	3602	3286	1724	2709
14	TAG 34	ATTACTCGA	4634	1789	540	2445	1169
15	TAG 36	ATCACTCGA	2981	2691	1018	1806	1632
16	TAG 30	ATTACTCGA	2666	2432	959	1717	1415
17	TAG 53	ATTACTCGA	1381	1531	1253	872	1192
18	TAG 49	ATCACTAGA	1442	1568	971	1663	1250
19	TAG 56	ATTACTCGC	891	1257	955	655	909
20	TAG 109	ATCACTCGA	617	564	295	313	334
21	TAG 52	GATACTCGA	407	457	144	218	290
22	TAG 141	GATACTCGA	462	308	181	207	204
23	TAG 20	ATGACTCGA	447	211	185	145	120
24	TAG 156	CTCACTCGA	231	230	363	100	166
25	TAG 170	TTTACTTGC	223	213	223	142	113
26	TAG 200	ATCACTCGT	212	135	188	144	175
27	TAG 90	GATACTCGA	229	161	97	186	135
28	TAG 35	ATTACTCGA	353	72	39	110	29
29	TAG 247	GATACTAGC	102	92	203	57	66
30	TAG 282	ATCACTCGA	96	62	93	34	61
31	TAG 92	TAAACTCGA	93	63	83	78	59
32	TAG 183	GATACTCGA	71	63	51	25	48
33	TAG 348	GATACTAGT	83	45	52	28	39
34	TAG 291	GATACTCGA	76	46	54	52	33
35	TAG 17	TATACTTGG	3455	4554	6254	1750	3224
36	TAG 171	TATGCTTGA	155	279	282	68	186
37	TAG 337	AATACTAGA	29	43	104	35	53
38	TAG 325	TATGCTTGG	70	37	40	47	28
39	TAG 57	TAAACTTGG	725	1163	1745	491	903
40	TAG 199	AATACTAGG	231	183	149	105	125
41	TAG 41	TGAACTTGG	77	93	125	69	63
42	TAG 328	AATACTAGG	114	86	85	48	57
43	TAG 345	AATACTAGG	75	45	50	58	51
44	TAG 3	CCGACTCGC	46896	46473	49311	108462	88309
45	TAG 301	GATACTAGA	100	109	126	55	51
46	TAG 77	GATACTAGC	74	53	131	41	49
47	TAG 210	GCCCCCATC	371	145	22	174	101
48	TAG 159	GGCACTAGC	170	95	30	74	52
49	TAG 7	CCGACCAGC	4976	5700	6662	2160	3081
50	TAG 85	CCGACCAGC	85	105	112	61	67
51	TAG 142	CCAAGTGTG	174	138	252	86	135
52	TAG 270	CCGACTAGC	155	82	163	39	37
53	TAG 296	CCGGTTAGC	56	121	185	35	24
54	TAG 15	TACACTAGA	4852	4989	3874	3351	3238
55	TAG 164	GGCACTAGC	176	155	169	130	103
56	TAG 388	AGCACTGGC	50	45	52	54	40
57	TAG 2	TCAACTAGG	38516	42438	46622	23021	36309
58	TAG 12	TCGACTAGT	4167	2451	3434	2803	2111
59							
60							

TAG 10	TCAACTAGT	3286	2850	3565	2287	2319
TAG 4	TCAACTAGT	2264	3300	3819	1893	2359
TAG 32	AGCACTAGA	3362	1649	1772	1475	1535
TAG 38	AATGCTAGA	2566	1966	1984	1181	1314
TAG 8	TCAACTAGG	2114	1946	1408	1405	1331
TAG 48	AGCACTAGA	1702	973	705	775	836
TAG 43	AGAACTAGC	522	830	1078	411	676
TAG 80	AGCACTAGA	746	665	944	436	509
TAG 87	AGTGCTAGA	1164	758	355	508	580
TAG 108	ATTGCTAGT	1023	531	119	374	277
TAG 106	AGCACTAGA	473	493	467	275	381
TAG 116	CGAACTGG	441	387	543	218	151
TAG 123	GATGCTGG	328	357	405	216	301
TAG 138	ATAACTAGC	465	344	280	198	140
TAG 73	AGAGCTAGT	383	488	154	258	232
TAG 129	AGTGCTAGA	275	301	417	225	290
TAG 125	AATGCCAGA	270	256	374	128	117
TAG 151	TGTGCTAGA	287	285	273	184	191
TAG 152	ATAACTAGC	397	257	93	258	133
TAG 98	AATGCCAGC	294	149	181	85	52
TAG 193	AATGCCAGT	234	171	205	88	104
TAG 236	AGAGCTAGC	210	158	191	45	70
TAG 208	AATGCTAGA	285	162	100	99	85
TAG 233	TCTACTAGT	107	271	120	21	113
TAG 165	ATAACTAGC	281	130	61	171	78
TAG 213	ATAACTAGC	248	182	41	150	117
TAG 189	CGAACTGG	91	79	289	72	58
TAG 229	TCAACTGGC	151	131	175	66	93
TAG 220	AGCACTAGA	175	128	129	142	93
TAG 259	AGTGCTAGT	201	118	100	101	71
TAG 201	AATGCCAGC	185	106	116	95	85
TAG 245	TCTACTAGT	118	162	107	34	174
TAG 54	TCAACTAGT	120	149	111	83	98
TAG 179	TCAACTAGT	115	117	120	57	86
TAG 256	GAAGCTAGC	125	103	96	28	42
TAG 285	GGTGCTAGC	112	150	61	45	72
TAG 308	AATGCCAGC	106	134	52	52	89
TAG 280	AGAACTAGA	90	85	111	67	51
TAG 235	TCGACTAGT	93	98	90	57	61
TAG 287	TGTGCTAGT	105	93	70	52	79
TAG 309	TGTGCTAGA	85	93	87	46	65
TAG 321	AATGCCAGC	87	55	112	57	39
TAG 105	AATGCCAGA	86	76	82	25	42
TAG 249	GATGCTAGC	131	46	56	63	31
TAG 317	GGTGCTAGC	79	56	95	49	55
TAG 172	GATGCTAGC	78	50	92	37	38
TAG 340	TTTACTTGC	68	77	59	47	45
TAG 134	AGTGCTAGT	73	82	47	137	50
TAG 353	TCAACTAGT	47	81	67	35	68
TAG 365	AGAGCTAGT	61	75	50	39	56
TAG 408	TGTGCTAGA	64	72	47	30	23
TAG 23	CGAACTGG	146	22	12	15	2
TAG 99	CGAACTAGC	33	40	93	21	41
TAG 415	TGTGCTAGC	58	39	59	16	27
TAG 9	TGCACTTGC	6979	8246	3924	5983	5618

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4	TAG 16	GATACTAGC	3097	4047	7988	1871	2854
5	TAG 31	ATTACTCGC	4267	2746	375	2725	2058
6	TAG 33	CTAACGATG	1664	2935	2312	1133	1851
7	TAG 27	TCAACTAGT	1597	1605	1676	850	1217
8	TAG 62	CTAACGATG	833	1520	1240	414	978
9	TAG 60	TCGACTAAG	1813	1102	604	812	836
10	TAG 65	ATTACTCGG	242	822	2039	148	633
11	TAG 70	CTAACGATG	755	1306	907	498	765
12	TAG 86	CTAACGATG	592	1105	735	370	558
13	TAG 84	CTAACGATG	554	1032	824	328	601
14	TAG 82	TTTACTTGC	728	833	643	570	666
15	TAG 91	ATCACTAGA	479	849	487	531	646
16	TAG 96	CATACTCGC	781	572	349	596	438
17	TAG 103	CTCACTTGC	393	445	849	205	340
18	TAG 102	CCGACTGGC	774	571	301	481	448
19	TAG 76	TACGCTAGA	700	635	232	458	424
20	TAG 61	CTGACTTGC	672	383	509	399	319
21	TAG 107	CTAACGATG	393	664	478	231	384
22	TAG 111	CTAACGATG	302	591	470	181	402
23	TAG 113	ATTACTAGA	328	626	291	287	515
24	TAG 119	TCGACCAGA	138	262	811	92	265
25	TAG 130	CCAGTTAGC	480	399	238	270	183
26	TAG 124	CCGACCAGC	309	325	421	185	256
27	TAG 126	CTAACGATG	249	433	369	177	255
28	TAG 120	AGAGCTAGC	181	467	386	153	262
29	TAG 66	CCGACTCAG	247	268	466	794	1061
30	TAG 147	AATGCCAGC	262	401	233	161	185
31	TAG 162	AGTGCTAGA	180	348	366	84	171
32	TAG 149	AGTACTAGC	230	199	430	203	193
33	TAG 148	GATGCTAGC	400	251	184	296	208
34	TAG 157	CATACTAGG	50	197	555	29	150
35	TAG 169	AGTGCTAGA	212	260	254	134	208
36	TAG 150	AGTGCTAGA	187	241	255	242	257
37	TAG 166	CCGACCAGC	248	194	233	143	110
38	TAG 40	CCGACCAAC	180	229	262	87	139
39	TAG 181	CGCACTAGC	283	197	175	128	140
40	TAG 184	CGCACTGGG	201	183	257	105	119
41	TAG 202	ACCCCCATC	134	200	258	41	124
42	TAG 175	CGCACTAGA	148	193	221	99	111
43	TAG 187	TATACTTGG	90	214	249	94	155
44	TAG 203	TGTGCTGGG	219	138	196	121	111
45	TAG 198	TCAACTAGT	185	184	135	97	147
46	TAG 214	AGTGCTAGT	189	127	152	95	89
47	TAG 197	TGCACTAGC	54	234	176	69	246
48	TAG 215	TACATTGTA	143	176	142	92	111
49	TAG 93	CCGACCAGC	122	123	205	58	83
50	TAG 219	AACACTCGA	204	112	133	182	85
51	TAG 216	CCAAC TAGA	148	165	128	110	131
52	TAG 231	CTTACTCGT	210	97	101	100	121
53	TAG 258	CCGACCAGT	143	193	67	80	86
54	TAG 242	CTAACGATG	98	186	116	50	113
55	TAG 272	AATGTAAAA	97	163	118	59	77
56	TAG 262	CGTGCTGGG	132	119	109	55	70
57	TAG 279	CACATTGGA	118	111	119	50	78
58	TAG 218	ACACCCATC	236	56	39	324	108
59							
60							

TAG 283	AGCACTAGA	158	71	83	70	70
TAG 190	CCGACCAGC	72	118	103	32	75
TAG 211	TTCCTAGT	50	86	150	46	58
TAG 302	CCGACCAGC	81	92	113	35	44
TAG 298	CCGACTCAG	63	70	150	36	43
TAG 271	TGCACTAGA	104	100	76	65	78
TAG 307	CAGACTCGC	101	93	71	58	55
TAG 316	CCGACCAGC	87	87	89	55	55
TAG 323	TATGCTTGG	101	66	92	51	56
TAG 303	CCGACCAGC	68	84	91	35	68
TAG 89	CGCACTAGC	77	91	70	54	64
TAG 305	TACACTGGA	93	83	58	63	61
TAG 310	GATGCTAGC	35	83	104	18	85
TAG 265	TCAACTGGC	22	81	118	101	129
TAG 304	AACACTTGG	80	80	61	41	69
TAG 330	CTAACTCGA	51	73	97	48	59
TAG 121	TCGACTGGC	54	67	92	50	53
TAG 358	CTTACTTGC	55	59	96	29	34
TAG 346	CCAGCTGG/	59	57	91	33	51
TAG 59	TTCCTAGT	79	93	29	54	71
TAG 368	TATGCTTGG	32	48	120	26	33
TAG 347	AGCACTGGC	83	52	61	73	51
TAG 356	GGCACTGG/	87	59	48	45	52
TAG 366	TGCACTAGC	80	57	54	31	43
TAG 370	GATACTAGC	95	44	39	63	27
TAG 364	TGTGCTAGT	58	63	56	45	49
TAG 377	AATGCTAGC	78	64	27	43	55
TAG 390	TAAACTTGG	40	54	71	15	33
TAG 344	TGCGCTAGA	63	67	28	53	37
TAG 387	ATTACTCGA	47	47	62	32	38
TAG 136	TCAACTAGT	55	56	36	43	45
TAG 234	CACACTAGC	32	55	57	26	29
TAG 64	CACACTAGC	431	498	559	334	390
TAG 118	CGCATTTGC	411	392	440	257	260
TAG 383	CACGCTTGC	65	55	45	54	34
TAG 239	CACACTAGC	50	40	64	30	56

TrSlu3	Sum	LOG10(T1/C1	LOG10(T2/C2	LOG10(T3/C3)		
1457	9183	-0.18000738	-0.14736711	-0.16389938	Bacteria	Acidobacteria
99	427	-0.1858511	-0.11058971	-0.21655241	Bacteria	Acidobacteria
64	335	-0.08185384	-0.00624895	-0.2024202	Bacteria	Acidobacteria
17	197	-0.28082661	-0.1850461	-0.57573105	Bacteria	Acidobacteria
27	148	-0.29104577	-0.26626789	-0.32451109	Bacteria	Acidobacteria
142	750	-0.32700884	-0.22184875	-0.23687774	Bacteria	Actinobacteria
1766	16440	-0.24945033	-0.15392628	-0.19548907	Bacteria	Bacteroidetes
4326	13314	-0.27924328	-0.22428373	-0.23995804	Bacteria	Bacteroidetes
2103	9214	-0.13007245	-0.1237347	-0.19382829	Bacteria	Bacteroidetes
315	6963	-0.27767717	-0.18479583	-0.23408321	Bacteria	Bacteroidetes
669	6690	-0.21764423	-0.21719354	-0.18232166	Bacteria	Bacteroidetes
617	6057	-0.19108985	-0.23520713	-0.19153344	Bacteria	Bacteroidetes
769	4165	-0.19967719	-0.10869894	-0.21202473	Bacteria	Bacteroidetes
480	3981	0.06192699	-0.09843605	-0.30597799	Bacteria	Bacteroidetes
645	3103	-0.1336364	-0.14077139	-0.17044366	Bacteria	Bacteroidetes
252	1476	-0.29474083	-0.22753264	-0.06842148	Bacteria	Bacteroidetes
137	1008	-0.27113792	-0.1975182	-0.02164192	Bacteria	Bacteroidetes
94	951	-0.34867163	-0.17892055	-0.28455072	Bacteria	Bacteroidetes
182	843	-0.48893952	-0.24510121	-0.00710034	Bacteria	Bacteroidetes
209	824	-0.36361198	-0.14161975	-0.23976034	Bacteria	Bacteroidetes
147	659	-0.19601652	-0.27530116	-0.18098753	Bacteria	Bacteroidetes
125	535	-0.16797337	0.11270428	-0.17724784	Bacteria	Bacteroidetes
58	487	-0.09032254	-0.07649211	-0.22334374	Bacteria	Bacteroidetes
20	464	-0.50638202	-0.3949345	-0.29003461	Bacteria	Bacteroidetes
124	397	-0.25272532	-0.14424389	-0.21407435	Bacteria	Bacteroidetes
130	251	-0.45079232	-0.00706185	0.1454604	Bacteria	Bacteroidetes
48	239	-0.07638835	-0.02848854	-0.23783686	Bacteria	Bacteroidetes
44	185	-0.45331834	-0.11809931	-0.0641175	Bacteria	Bacteroidetes
47	180	-0.47192006	-0.06214791	-0.04390549	Bacteria	Bacteroidetes
34	176	-0.16481025	-0.14424389	-0.20091484	Bacteria	Bacteroidetes
4570	14263	-0.29541	-0.14999799	-0.13624168	Bacteria	Chlamydiae
151	716	-0.35782279	-0.17609126	-0.27127216	Bacteria	Chlorobi
61	176	0.08167005	0.09080741	-0.2317035	Bacteria	Chlorobi
28	147	-0.17300018	-0.12104369	-0.15490196	Bacteria	Chlorobi
1066	3633	-0.16925651	-0.10989196	-0.21403823	Bacteria	Chloroflexi
112	563	-0.34242268	-0.16554108	-0.12396825	Bacteria	Chloroflexi
94	295	-0.04764163	-0.1691424	-0.12378216	Bacteria	Chloroflexi
30	285	-0.37566361	-0.1786236	-0.45229767	Bacteria	Chloroflexi
21	170	-0.11163327	0.05435766	-0.37675071	Bacteria	Chloroflexi
101682	142680	0.36414181	0.27880426	0.31430027	Eukaryota	Ciliophora
40	335	-0.25963731	-0.32985632	-0.49831055	Bacteria	Cyanobacteria
113	258	-0.25644786	-0.03407979	-0.06419285	Bacteria	Cyanobacteria
25	538	-0.32882466	-0.15704663	0.05551733	Eukaryota	Euglenozoa
19	295	-0.3612172	-0.26172026	-0.19836765	Bacteria	Gemmatimon
4152	17338	-0.36242662	-0.26718316	-0.20534728	Eukaryota	Gracilipodida
72	302	-0.14408909	-0.1951145	-0.19188553	Eukaryota	LKM74
157	564	-0.3060508	-0.00954532	-0.20550089	Eukaryota	Metazoa
47	400	-0.59926709	-0.34561213	-0.54008975	Eukaryota	Ochrophyta
19	362	-0.20411998	-0.70257413	-0.98841813	Eukaryota	Ochrophyta
2890	13715	-0.16074636	-0.18773666	-0.12726177	Bacteria	Planctomycet
76	500	-0.13156932	-0.17749447	-0.34707311	Bacteria	Planctomycet
27	147	0.03342376	-0.05115252	-0.28463958	Bacteria	Planctomycet
32669	127576	-0.22351699	-0.06774062	-0.15445506	Bacteria	Proteobacteria
2040	10052	-0.1722004	-0.06485508	-0.22617012	Bacteria	Proteobacteria



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2						
3	2429	9701	-0.15740139	-0.08954411	-0.16663202	Bacteria Proteobacteria
4	2669	9383	-0.07772581	-0.145786	-0.15560108	Bacteria Proteobacteria
5	1048	6783	-0.35780569	-0.03111228	-0.22810243	Bacteria Proteobacteria
6	1175	6516	-0.33700675	-0.17498815	-0.2275038	Bacteria Proteobacteria
7	1215	5468	-0.17742866	-0.16496478	-0.06402638	Bacteria Proteobacteria
8	659	3380	-0.34165785	-0.06590656	-0.0293037	Bacteria Proteobacteria
9	704	2430	-0.10382868	-0.0891314	-0.1850461	Bacteria Proteobacteria
10	671	2355	-0.23325234	-0.11610386	-0.14824947	Bacteria Proteobacteria
11	312	2277	-0.36008927	-0.11624121	-0.05607376	Bacteria Proteobacteria
12	103	1673	-0.43700403	-0.28261475	-0.06270974	Bacteria Proteobacteria
13	336	1433	-0.23552845	-0.11192194	-0.1429776	Bacteria Proteobacteria
14	279	1371	-0.3059821	-0.40873402	-0.28919563	Bacteria Proteobacteria
15	218	1090	-0.18142009	-0.07410172	-0.26899853	Bacteria Proteobacteria
16	166	1089	-0.37078776	-0.39043041	-0.22704994	Bacteria Proteobacteria
17	100	1025	-0.17157907	-0.32293184	-0.18752072	Bacteria Proteobacteria
18	290	993	-0.08715018	-0.0161685	-0.15773806	Bacteria Proteobacteria
19	256	900	-0.32415379	-0.3400541	-0.16463164	Bacteria Proteobacteria
20	144	845	-0.19306407	-0.17381149	-0.27780015	Bacteria Proteobacteria
21	64	747	-0.1871708	-0.28608148	-0.16230297	Bacteria Proteobacteria
22	56	624	-0.5389284	-0.45718292	-0.50949055	Bacteria Proteobacteria
23	90	610	-0.42473319	-0.21596277	-0.35751135	Bacteria Proteobacteria
24	55	559	-0.66900678	-0.35355905	-0.54067068	Bacteria Proteobacteria
25	89	547	-0.45920967	-0.28009609	-0.05060999	Bacteria Proteobacteria
26	36	498	-0.70716448	-0.37989085	-0.52287875	Bacteria Proteobacteria
27	49	472	-0.21571021	-0.22184875	-0.09513375	Bacteria Proteobacteria
28	24	471	-0.21836042	-0.19188553	-0.23257262	Bacteria Proteobacteria
29	242	459	-0.1017089	-0.1341991	-0.07708248	Bacteria Proteobacteria
30	130	457	-0.35943301	-0.14878835	-0.1290947	Bacteria Proteobacteria
31	115	432	-0.0907497	-0.13872702	-0.04989187	Bacteria Proteobacteria
32	22	419	-0.29887468	-0.22062366	-0.65757732	Bacteria Proteobacteria
33	80	407	-0.28944812	-0.09588694	-0.161368	Bacteria Proteobacteria
34	51	387	-0.54040309	0.03103423	-0.3218136	Bacteria Proteobacteria
35	85	380	-0.16010315	-0.18196019	-0.11590405	Bacteria Proteobacteria
36	93	352	-0.30482298	-0.13368741	-0.1106983	Bacteria Proteobacteria
37	33	324	-0.64975198	-0.38958793	-0.46375729	Bacteria Proteobacteria
38	52	323	-0.39600551	-0.31875876	-0.06932649	Bacteria Proteobacteria
39	38	292	-0.30930252	-0.17771479	-0.13621975	Bacteria Proteobacteria
40	100	286	-0.12816771	-0.22184875	-0.04532298	Bacteria Proteobacteria
41	78	281	-0.21260809	-0.20589624	-0.06214791	Bacteria Proteobacteria
42	64	268	-0.30518596	-0.07085586	-0.03891807	Bacteria Proteobacteria
43	54	265	-0.26666109	-0.15556959	-0.20712549	Bacteria Proteobacteria
44	49	254	-0.1836444	-0.14929808	-0.35902194	Bacteria Proteobacteria
45	28	244	-0.53655844	-0.2575643	-0.46665582	Bacteria Proteobacteria
46	57	233	-0.31793075	-0.17139614	0.00768683	Bacteria Proteobacteria
47	58	230	-0.20743101	-0.00782534	-0.21429561	Bacteria Proteobacteria
48	43	220	-0.32389288	-0.11918641	-0.33031937	Bacteria Proteobacteria
49	38	204	-0.16041105	-0.23327821	-0.19106842	Bacteria Proteobacteria
50	35	202	0.27339771	-0.21484385	-0.12802981	Bacteria Proteobacteria
51	47	195	-0.12802981	-0.07597611	-0.15397694	Bacteria Proteobacteria
52	32	186	-0.19426523	-0.12687324	-0.19382003	Bacteria Proteobacteria
53	32	183	-0.32905872	-0.49560466	-0.16694788	Bacteria Proteobacteria
54	5	180	-0.9882616	-1.04139269	-0.38021124	Bacteria Proteobacteria
55	62	166	-0.19629465	0.01072387	-0.17609126	Bacteria Proteobacteria
56	28	156	-0.55930801	-0.15970084	-0.32369398	Bacteria Proteobacteria
57	2750	19149	-0.0668742	-0.1666616	-0.1543963	Bacteria Spirochaetae



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2						
3	4754	15132	-0.21886742	-0.15167924	-0.22537888	Uncultured Bacteria unknown
4	264	7388	-0.19475614	-0.12525516	-0.15242734	Unclassified unknown
5	1651	6911	-0.16692341	-0.20020169	-0.14624076	Unclassified unknown
6	1250	4878	-0.27388599	-0.12018446	-0.127364	Uncultured Bacteria unknown
7	768	3593	-0.30364466	-0.19150473	-0.20806047	Unclassified unknown
8	537	3519	-0.34884177	-0.11997532	-0.05106265	Eukaryota Amoebozoa
9	1417	3103	-0.21355365	-0.11346811	-0.15804738	Uncultured Bacteria unknown
10	671	2968	-0.18071761	-0.23228174	-0.13088477	Unclassified unknown
11	481	2432	-0.20411998	-0.29672808	-0.18414226	Unclassified unknown
12	532	2410	-0.22763592	-0.23480523	-0.19001558	Unclassified unknown
13	450	2204	-0.10625652	-0.09717077	-0.15499846	Unclassified unknown
14	356	1815	0.04475901	-0.11867517	-0.13607896	Unclassified unknown
15	212	1702	-0.11740477	-0.11592192	-0.21648957	Unclassified unknown
16	612	1687	-0.28263869	-0.11688109	-0.14215627	Unclassified unknown
17	200	1646	-0.20659588	-0.10535809	-0.1775365	Unclassified unknown
18	143	1567	-0.18423256	-0.17540787	-0.21015195	Uncultured Bacteria unknown
19	289	1564	-0.22639638	-0.07940809	-0.24581994	Bacteria Acidobacteria
20	379	1535	-0.23078057	-0.23783686	-0.10078869	Unclassified unknown
21	352	1363	-0.22232837	-0.16736143	-0.12555519	Unclassified unknown
22	189	1245	-0.05799195	-0.0847671	-0.18743118	Bacteria Bacteroidetes
23	509	1211	-0.17609126	0.00494458	-0.20230307	Unclassified unknown
24	120	1117	-0.24987747	-0.33852181	-0.29739571	Eukaryota unknown
25	301	1055	-0.22278675	-0.1036434	-0.1457156	Unclassified unknown
26	229	1051	-0.14822608	-0.22994772	-0.20719088	Unclassified unknown
27	198	1034	-0.07298714	-0.25101559	-0.28992211	Bacteria unknown
28	1387	981	0.50712355	0.59758059	0.47369054	Unclassified unknown
29	146	896	-0.21147542	-0.33597264	-0.20300307	Bacteria unknown
30	169	894	-0.33099322	-0.30858313	-0.33559438	Bacteria unknown
31	221	859	-0.0542318	-0.01329577	-0.28907618	Uncultured Bacteria unknown
32	123	835	-0.13076828	-0.08161039	-0.17491271	Bacteria Chloroflexi
33	344	802	-0.23657201	-0.11837497	-0.20773454	Uncultured Bacteria unknown
34	174	726	-0.19923106	-0.09691001	-0.16428447	Uncultured Bacteria unknown
35	261	683	0.11197376	0.02791608	0.01010033	Unclassified unknown
36	138	675	-0.23911564	-0.24640904	-0.22747683	Unclassified unknown
37	164	671	-0.31575325	-0.21682068	-0.20345744	Unclassified unknown
38	108	655	-0.34457647	-0.14833819	-0.20961429	Uncultured Bacteria unknown
39	153	641	-0.28200676	-0.18690413	-0.22524169	Unclassified unknown
40	175	592	-0.51432094	-0.20760831	-0.16858166	Eukaryota unknown
41	143	562	-0.17462652	-0.24023433	-0.18905624	Uncultured Bacteria unknown
42	179	553	0.01888534	-0.14008208	-0.14334632	Uncultured Bacteria unknown
43	97	553	-0.25765874	-0.09455611	-0.30548434	Bacteria unknown
44	100	504	-0.28039999	-0.09750049	-0.13033377	Uncultured Bacteria unknown
45	74	468	-0.2987382	-0.15441371	-0.31261187	Uncultured Bacteria unknown
46	137	464	0.10645533	0.02171925	-0.1087921	Unclassified unknown
47	103	461	-0.19154821	-0.20018969	-0.13945112	Unclassified unknown
48	140	450	-0.32293184	-0.17082702	-0.16562583	Unclassified unknown
49	55	449	-0.04955878	-0.1197991	-0.38348895	Bacteria Bacteroidetes
50	92	441	-0.12886903	-0.10021265	-0.14342214	Unclassified unknown
51	67	408	-0.32221929	0.09601364	-0.17824657	Unclassified unknown
52	32	403	-0.25224605	-0.35105886	-0.32092482	Eukaryota unknown
53	100	400	-0.29225607	-0.2164345	-0.06445799	Unclassified unknown
54	79	378	-0.21591972	-0.32569688	-0.17425492	Unclassified unknown
55	67	360	-0.38021124	-0.23044892	-0.2113517	Uncultured Bacteria unknown
56	70	348	-0.372912	-0.15322838	-0.23044892	Unclassified unknown
57	31	331	0.13763301	0.28523573	-0.09970291	Eukaryota Euglenozoa

55	312	-0.35355905	-0.00616031	-0.1787154	Uncultured Bε unknown
76	293	-0.35218252	-0.19682074	-0.13202363	Unclassified unknown
112	286	-0.03621217	-0.17107046	-0.12687324	Uncultured Bε unknown
98	286	-0.36441697	-0.32033515	-0.06185237	Uncultured Bε unknown
80	283	-0.24303805	-0.21162958	-0.27300127	Uncultured Bε unknown
56	280	-0.20411998	-0.1079054	-0.13262557	Uncultured Bε unknown
65	265	-0.24089338	-0.22812026	-0.03834499	Uncultured Bε unknown
69	263	-0.19915656	-0.19915656	-0.11054092	Uncultured Eε unknown
49	259	-0.2967512	-0.07135591	-0.27359175	Bacteria Chlorobi
95	243	-0.28844087	-0.09177037	0.01868221	Unclassified unknown
35	238	-0.15409697	-0.15286142	-0.30103	Uncultured Bε unknown
47	234	-0.1691424	-0.13374826	-0.09133014	Uncultured Bε unknown
59	222	-0.28879554	0.01034083	-0.24618133	Uncultured Bε unknown
91	221	0.66189869	0.20210469	-0.11284061	Bacteria Proteobacteri
37	221	-0.29030613	-0.0642409	-0.21712811	Uncultured Bε unknown
67	221	-0.02632894	-0.09247085	-0.16069693	Bacteria Bacteroidetes
63	213	-0.03342376	-0.10179893	-0.16444728	Uncultured Bε unknown
72	210	-0.27796469	-0.23937309	-0.12493874	Uncultured Bε unknown
52	207	-0.25233807	-0.04830468	-0.24303805	Uncultured Bε unknown
23	201	-0.16523333	-0.1172246	-0.10067016	Uncultured Bε unknown
55	200	-0.09017663	-0.1627273	-0.33881856	Uncultured Bε unknown
37	196	-0.05575523	-0.00843317	-0.21712811	Uncultured Bε unknown
38	194	-0.28630674	-0.05484867	-0.10145764	Unclassified unknown
35	191	-0.41172829	-0.1224064	-0.18832572	Uncultured Bε unknown
30	178	-0.17838306	-0.21208891	-0.11394335	Unclassified unknown
22	177	-0.11021548	-0.10914447	-0.40576535	Bacteria Proteobacteri
18	169	-0.25862615	-0.06581728	-0.17609126	Uncultured Bε unknown
60	165	-0.42596873	-0.21387982	-0.0731071	Uncultured Bε unknown
20	158	-0.07506468	-0.25787308	-0.14612804	Unclassified unknown
34	156	-0.16694788	-0.09231426	-0.26091277	Uncultured Bε unknown
39	147	-0.10689423	-0.09497551	0.03476211	Unclassified unknown
58	144	-0.09017663	-0.27796469	0.00755314	Bacteria Verrucomicrol
350	1488	-0.1107308	-0.10616474	-0.20334376	Bacteria Verrucomicrol
253	1243	-0.2039087	-0.17831272	-0.24033216	Bacteria Verrucomicrol
37	165	-0.0805196	-0.20888377	-0.08501079	Bacteria Verrucomicrol
31	154	-0.22184875	0.14612804	-0.31481828	Bacteria Verrucomicrol

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3					NCBI nr assignment
4	Acidobacteria Subgroup 4	unknown	unknown		N.A.
5	Acidobacteria Subgroup 3	Elev-16S-116	unknown		N.A.
6	Acidobacteria Subgroup 3	Elev-16S-116	unknown		N.A.
7	Acidobacteria Subgroup 3	unknown	unknown		N.A.
8	Acidobacteria Subgroup 3	unknown	unknown		N.A.
9	Actinobacteria Micrococcales	unknown	unknown		N.A.
10	Cytophagia Cytophagales	Cytophagaceae	Chryseolinea		N.A.
11	Flavobacteriia Flavobacteriia	Flavobacteriia	Flavobacterium		N.A.
12	Bacteroidia Bacteroidales	Rikenellaceae	Blvii28 wastewater-sludge grou		N.A.
13	Cytophagia Cytophagales	Cytophagaceae	unknown		N.A.
14	Cytophagia Cytophagales	Cytophagaceae	unknown		N.A.
15	Cytophagia Cytophagales	Cytophagaceae	unknown		N.A.
16	Cytophagia Cytophagales	Cytophagaceae	unknown		N.A.
17	Flavobacteriia Flavobacteriia	NS9 marine g	unknown		N.A.
18	Sphingobacte Sphingobacte	env.OPS 17	unknown		N.A.
19	Flavobacteriia Flavobacteriia	NS9 marine g	unknown		N.A.
20	Sphingobacte Sphingobacte	Chitinophaga	unknown		N.A.
21	Sphingobacte Sphingobacte	Chitinophaga	Ferruginibacter		N.A.
22	Cytophagia Cytophagales	Cytophagaceae	unknown		N.A.
23	Sphingobacte Sphingobacte	Saprospiraceae	unknown		N.A.
24	Sphingobacte Sphingobacte	Saprospiraceae	unknown		N.A.
25	Flavobacteriia Flavobacteriia	NS9 marine g	unknown		N.A.
26	Sphingobacte Sphingobacte	Chitinophaga	unknown		N.A.
27	Sphingobacte Sphingobacte	Chitinophaga	unknown		N.A.
28	Flavobacteriia Flavobacteriia	Flavobacteriia	Flavobacterium		N.A.
29	Flavobacteriia Flavobacteriia	NS9 marine g	unknown		N.A.
30	Sphingobacte Sphingobacte	Chitinophaga	unknown		N.A.
31	Sphingobacte Sphingobacte	Chitinophaga	unknown		N.A.
32	Flavobacteriia Flavobacteriia	Flavobacteriia	Flavobacterium		N.A.
33	Sphingobacte Sphingobacte	Chitinophaga	unknown		N.A.
34	Chlamydiae Chlamydiales	Parachlamydi	Candidatus Protochlamydia		N.A.
35	Chlorobia Chlorobiales	OPB56	unknown		N.A.
36	Chlorobia Chlorobiales	SJA-28	unknown		N.A.
37	Chlorobia Chlorobiales	OPB56	unknown		N.A.
38	Anaerolineae Anaerolineae	Anaerolineaceae	unknown		N.A.
39	unknown unknown	unknown	unknown		N.A.
40	Anaerolineae Anaerolineae	Anaerolineaceae	Ornatilinea		N.A.
41	Caldilineae Caldilineales	Caldilineaceae	unknown		N.A.
42	Caldilineae Caldilineales	Caldilineaceae	unknown		N.A.
43	Intramacronu Conthreep	Oligohymenof	Carchesium		N.A.
44	Chloroplast unknown	unknown	unknown		N.A.
45	Melainabacteri Obscuribacteri	unknown	unknown		N.A.
46	Kinetoplastea Metakinetopla	Neobodonida	Neobodo		N.A.
47	Gemmatimon: Gemmatimon: Gemmatimon:	unknown			N.A.
48	unknown unknown	unknown	Filamoeba		N.A.
49	unknown unknown	unknown	unknown		N.A.
50	unknown unknown	unknown	unknown		N.A.
51	Chrysophyceae Chromulinales	unknown	unknown		N.A.
52	Diatomea Bacillariophyti	Bacillariophyc	Pinnularia		N.A.
53	Phycisphaera Phycisphaera	Phycisphaera	SM1A02		N.A.
54	OM190 unknown	unknown	unknown		N.A.
55	Planctomycet: Planctomycet: Planctomycet:	Planctomyces			N.A.
56	Betaproteoba: Rhodocyclace: Rhodocyclace	Candidatus Accumulibacter			N.A.
57	Betaproteoba: Rhodocyclace: Rhodocyclace	Thauera			N.A.
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Betaproteoba	Nitrosomonad	Nitrosomonad	Nitrosomonas	N.A.
Betaproteoba	Rhodocyclale	Rhodocyclace	Zoogloea	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Candidatus Competibacter	N.A.
Alphaproteob	Rhodospirillal	Rhodospirillac	unknown	N.A.
Betaproteoba	Rhodocyclale	Rhodocyclace	unknown	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Candidatus Competibacter	N.A.
Deltaproteoba	Myxococcales	unknown	unknown	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Candidatus Competibacter	N.A.
Deltaproteoba	Myxococcales	Haliangiaceae	Haliangium	N.A.
Alphaproteob	Caulobacteral	Caulobactera	Brevundimonas	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Candidatus Competibacter	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Aquimonas	N.A.
Alphaproteob	Rhodospirillal	CCU22	unknown	N.A.
Alphaproteob	Sphingomona	Sphingomona	unknown	N.A.
Alphaproteob	Caulobacteral	Hyphomonad	Woodsholea	N.A.
Alphaproteob	Rhodospirillal	JG37-AG-20	unknown	N.A.
Alphaproteob	Rhodobactera	Rhodobactera	unknown	N.A.
Alphaproteob	Rhodospirillal	I-10	unknown	N.A.
Alphaproteob	Sphingomona	unknown	unknown	N.A.
Alphaproteob	Rhizobiales	unknown	Bosea	N.A.
Alphaproteob	Rhodobactera	Rhodobactera	unknown	N.A.
Alphaproteob	Rhizobiales	Hyphomicrobi	Devosia	N.A.
Alphaproteob	Rhodospirillal	Rhodospirillac	Dongia	N.A.
Betaproteoba	Burkholderial	Oxalobactera	unknown	N.A.
Alphaproteob	Sphingomona	Sphingomona	unknown	N.A.
Alphaproteob	Sphingomona	Sphingomona	Zymomonas	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	unknown	N.A.
Betaproteoba	Hydrogenophi	Hydrogenophi	unknown	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Candidatus Competibacter	N.A.
Alphaproteob	Rhodospirillal	Rhodospirillac	unknown	N.A.
Alphaproteob	Rhizobiales	Xanthobacter	Labrys	N.A.
Betaproteoba	Burkholderial	Burkholderiac	Chitinimonas	N.A.
Betaproteoba	Nitrosomonad	Nitrosomonad	Nitrosomonas	N.A.
Betaproteoba	Nitrosomonad	Nitrosomonad	Nitrosomonas	N.A.
Alphaproteob	Rhizobiales	Phyllobacteria	unknown	N.A.
Alphaproteob	Rhizobiales	JG35-K1-AG5	unknown	N.A.
Alphaproteob	Rhizobiales	unknown	unknown	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	Plasticicumulans	N.A.
Betaproteoba	Nitrosomonad	Nitrosomonad	unknown	N.A.
Alphaproteob	DB1-14	unknown	unknown	N.A.
Alphaproteob	Rhodospirillal	B79	unknown	N.A.
Alphaproteob	Rhizobiales	F0723	unknown	N.A.
Alphaproteob	Rhodobactera	Rhodobactera	unknown	N.A.
Alphaproteob	Rhizobiales	Hyphomicrobi	unknown	N.A.
Deltaproteoba	Myxococcales	Phaselicystid	Phaselicystis	N.A.
Alphaproteob	Rhizobiales	unknown	unknown	N.A.
Betaproteoba	Neisseriales	Neisseriaceae	unknown	N.A.
Alphaproteob	Caulobacteral	Caulobactera	unknown	N.A.
Betaproteoba	Rhodocyclale	Rhodocyclace	unknown	N.A.
Alphaproteob	Caulobacteral	Hyphomonad	Hirschia	N.A.
Alphaproteob	Rhodospirillal	Rhodospirillac	Ferrovibrio	N.A.
Gammaprotec	Xanthomonad	Xanthomonad	unknown	N.A.
Betaproteoba	Rhodocyclale	Rhodocyclace	Denitratisoma	N.A.
Alphaproteob	DB1-14	unknown	unknown	N.A.
Spirochaetes	Spirochaetale	Spirochaetace	Spirochaeta	N.A.

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3					<i>Uncultured Bacterium</i>
4	unknown	unknown	unknown	unknown	<i>Unclassified</i>
5	unknown	unknown	unknown	unknown	<i>Unclassified</i>
6	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
7	unknown	unknown	unknown	unknown	<i>Unclassified</i>
8	Tubulinea	unknown	Euamoebida	Saccamoeba	<i>Saccamoeba (Genus)</i>
9	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
10	unknown	unknown	unknown	unknown	<i>Unclassified</i>
11	unknown	unknown	unknown	unknown	<i>Unclassified</i>
12	unknown	unknown	unknown	unknown	<i>Unclassified</i>
13	unknown	unknown	unknown	unknown	<i>Unclassified</i>
14	unknown	unknown	unknown	unknown	<i>Unclassified</i>
15	unknown	unknown	unknown	unknown	<i>Unclassified</i>
16	unknown	unknown	unknown	unknown	<i>Unclassified</i>
17	unknown	unknown	unknown	unknown	<i>Unclassified</i>
18	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
19	unknown	unknown	unknown	unknown	<i>Acidobacteria (Phylum)</i>
20	unknown	unknown	unknown	unknown	<i>Unclassified</i>
21	unknown	unknown	unknown	unknown	<i>Unclassified</i>
22	unknown	unknown	unknown	unknown	<i>Bacteroidetes (Phylum)</i>
23	unknown	unknown	unknown	unknown	<i>Unclassified</i>
24	unknown	unknown	unknown	Pinnularia	<i>Pinnularia (Genus)</i>
25	unknown	unknown	unknown	unknown	<i>Unclassified</i>
26	unknown	unknown	unknown	unknown	<i>Unclassified</i>
27	unknown	unknown	Cystobacterin	unknown	<i>Cystobacterineae (Family)</i>
28	unknown	unknown	unknown	unknown	<i>Unclassified</i>
29	unknown	unknown	unknown	unknown	<i>Bacteria</i>
30	unknown	unknown	unknown	Candidatus Lariskella	<i>Candidatus Lariskella</i>
31	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
32	unknown	unknown	unknown	unknown	<i>Chloroflexi (Phylum)</i>
33	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
34	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
35	unknown	unknown	unknown	unknown	<i>Unclassified</i>
36	unknown	unknown	unknown	unknown	<i>Unclassified</i>
37	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
38	unknown	unknown	unknown	unknown	<i>Unclassified</i>
39	unknown	unknown	unknown	Neobodo	<i>Neobodo (Genus)</i>
40	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
41	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
42	unknown	unknown	unknown	Acidocella	<i>Acidocella (Genus)</i>
43	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
44	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
45	unknown	unknown	unknown	unknown	<i>Unclassified</i>
46	unknown	unknown	unknown	unknown	<i>Unclassified</i>
47	unknown	unknown	unknown	unknown	<i>Unclassified</i>
48	Sphingobacte	Sphingobacte	unknown	unknown	<i>Sphingobacteriales (Order)</i>
49	unknown	unknown	unknown	unknown	<i>Unclassified</i>
50	unknown	unknown	unknown	unknown	<i>Unclassified</i>
51	unknown	unknown	unknown	unknown	<i>Eukaryota</i>
52	unknown	unknown	unknown	unknown	<i>Unclassified</i>
53	unknown	unknown	unknown	unknown	<i>Unclassified</i>
54	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
55	unknown	unknown	unknown	unknown	<i>Unclassified</i>
56	Kinetoplastida	Bodonidae	Bodo	unknown	<i>Bodo (Family)</i>
57					
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3	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
4	unknown	unknown	unknown	unknown	<i>Unclassified</i>
5	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
6	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
7	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
8	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
9	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
10	unknown	unknown	unknown	unknown	<i>Uncultured Eukaryote</i>
11	unknown	unknown	unknown	unknown	<i>Chlorobi (Phylum)</i>
12	unknown	unknown	unknown	unknown	<i>Unclassified</i>
13	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
14	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
15	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
16	Betaproteoba	Rhodocyclale	Rhodocyclace	Dechloromonas	<i>Dechloromonas (Genus)</i>
17	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
18	Sphingobacte	Sphingobacte	Saprospirace	unknown	<i>Saprospiraceae (Family)</i>
19	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
20	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
21	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
22	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
23	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
24	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
25	unknown	unknown	unknown	unknown	<i>Unclassified</i>
26	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
27	unknown	unknown	unknown	unknown	<i>Unclassified</i>
28	Alphaproteob	unknown	unknown	unknown	<i>Proteobacteria (Phylum)</i>
29	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
30	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
31	unknown	unknown	unknown	unknown	<i>Unclassified</i>
32	unknown	unknown	unknown	unknown	<i>Uncultured Bacterium</i>
33	unknown	unknown	unknown	unknown	<i>Unclassified</i>
34	Opitutae	Opitutaes	Opitutaceae	Opitutus	<i>Opitutus (Genus)</i>
35	Opitutae	Opitutaes	Opitutaceae	Opitutus	N.A.
36	OPB35 soil gr	unknown	unknown	unknown	N.A.
37	Verrucomicro	Verrucomicro	DEV007	unknown	N.A.
38	Opitutae	Opitutaes	Opitutaceae	Opitutus	N.A.
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