

Australian Oncology Nurses in the Genomic Era: Exploring Barriers and Enablers to Uptake of Genomic Innovations

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the degree of

Doctor of Philosophy

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Certificate of Original Authorship

I, Elle Elan, declare that this thesis is submitted in fulfilment of the requirements for the award of Doctor of Philosophy, in the Faculty of Health School of Nursing and Midwifery at the University of Technology Sydney.

This thesis is wholly my own work unless otherwise referenced or acknowledged. In addition, I certify that all information sources and literature used are indicated in the thesis.

This document has not been submitted for qualifications at any other academic institution.

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Elle Elan

Contents

Certificate of Original Authorship	ii
Contents	iii
List of Figures	vii
List of Tables	viii
Abstract	ix
Acknowledgements	xi
COVID-19 Impact Statement	xii
Key Terms	xiii
Chapter 1. Introduction.....	1
1.1 Introduction.....	1
1.2 Background – The genomic era: Foundations of genomic medicine	1
1.2.1 From genetics to genomics.....	1
1.2.2 The Human Genome Project as a catalyst for a new era	2
1.2.3 Technological advances and accessibility of genomics.....	3
1.2.4 Genomic applications to medicine and health	4
1.2.5 Global genomic medicine initiatives	7
1.2.6 Australian genomic medicine initiatives	10
1.2.7 Mainstreaming genomics.....	11
1.3 Genomics and cancer care.....	13
1.3.1 The global and national burden of cancer	14
1.3.2 Genomics across the cancer care continuum	14
1.4 The nursing workforce and the implementation of genomics in nursing practice.....	18
1.4.1 The need for a genomically capable workforce.....	18
1.4.2 Alignment with professional nursing standards and practice expectations.....	20
1.4.3 Oncology nursing and genomic practice	23
1.4.4 Competency frameworks for genomic nursing practice	24
1.5 Genomic literacy, knowledge, and attitudes	27
1.5.1 Assessment of genomic literacy	30
1.5.2 Evidence on nurses’ knowledge and attitudes towards genomics	30
1.6 Implementation, benchmarking and capacity building for genomic integration	32
1.7 Factors influencing genomic adoption	35
1.7.1 Barriers and enablers to genomic integration	36
1.8 Problem statement.....	39
1.9 Research question	40
1.10 Research aims and objectives.....	40
1.11 Significance of the study.....	41
1.12 Researcher positionality and reflexivity	42
1.13 Thesis structure	43
1.14 Conclusion	44
Chapter 2. Theoretical Framework.....	45
2.1 Introduction	45
2.2 Defining genomic innovations in the context of nursing	46
2.2.1 Genomics as an innovation	46
2.2.2 Innovation in nursing practice.....	46
2.3 Origins and evolution of the Diffusion of Innovations theory.....	48
2.3.1 Application to health and nursing	49
2.3.2 Theoretical foundations and elements	50
2.3.3 The innovation-decision process.....	53

2.4	Adopter categories	55
2.4.1	Attributes of innovations	56
2.4.2	Individual characteristics	58
2.4.3	Opinion leadership.....	64
2.4.4	Organisational characteristics.....	65
2.5	Limitations of DOI theory	66
2.6	Complementary theories	68
2.7	Application of DOI in the present study	70
2.8	Conclusion	70
Chapter 3 – Scoping Review		71
3.1	Preface.....	71
3.2	Cancer nurses’ knowledge and attitudes toward genetics/genomics: A scoping review	72
3.3	Chapter summary	114
Chapter 4 – Methods		115
4.1	Introduction.....	115
4.2	Research question, aims and objectives.....	115
4.2.1	Research questions	115
4.2.2	Aims	115
4.2.3	Objectives	115
4.3	Philosophical underpinnings	116
4.4	Methodology and sequencing.....	118
4.5	Data integration and triangulation.....	119
4.6	Phase 1 research	121
4.6.1	Method.....	121
4.6.2	Development of the survey instrument	122
4.6.3	Pilot.....	136
4.6.4	Sampling.....	136
4.6.5	Recruitment	137
4.6.6	Data collection procedure	138
4.6.7	Data analysis	138
4.7	Phase 2 qualitative research	144
4.7.1	Method.....	144
4.7.2	Development of interview guide	145
4.7.3	Validity	147
4.7.4	Sample.....	148
4.7.5	Recruitment	149
4.7.6	Procedure	149
4.7.7	Data analysis	151
4.8	Ethical considerations	160
4.8.1	Informed consent and participant autonomy	160
4.8.2	Minimising risk and managing potential distress	160
4.8.3	Confidentiality and risk of deductive disclosure	161
4.9	Data management and storage.....	162
4.10	Participant compensation	163
4.11	Conclusion	163
Chapter 5 – Quantitative Results.....		164
5.1	Introduction	164
5.1.1	Reiteration of research questions, aim and objective	164
5.1.2	Overview of analyses	165
5.2	Participant characteristics	165

5.3 Descriptive statistics: Aim 1	166
5.3.1 Perceived knowledge and awareness of genomics	166
5.3.2 Objective knowledge.....	169
5.3.3 Confidence	171
5.3.4 Attitudes.....	172
5.3.5 Engagement and adoption.....	174
5.3.6 Barriers and enablers.....	175
5.3.7 Cosmopolitaness and information-seeking behaviours.....	178
5.4 Aim 2: Distinguishing likely adopters from likely non-adopters.....	179
5.4.1 Inferential statistics	180
5.5 Summary of results	190
5.5.1 Oncology nurses' knowledge, engagement, and adoption of genomics in practice	190
5.5.2 Identifying individual characteristics associated with the uptake of genomics in nursing practice.....	191
5.6 Conclusion.....	192
Chapter 6 – Qualitative Results	193
6.1 Introduction	193
6.2 Participant characteristics.....	193
6.3 Findings	194
6.3.1 Domain 1: Attributes of the innovation	194
6.3.2 Domain 2: Education-related factors.....	198
6.3.3 Domain 3: Professional factors.....	204
6.3.4 Domain 4: Organisational factors	212
6.3.5 Domain 5: Individual factors	220
6.4 Conclusion.....	227
Chapter 7 – Discussion	228
7.1 Introduction	228
7.2 Integration of quantitative and qualitative findings	229
7.2.1 Oncology nurses' knowledge, engagement, and adoption of genomics in practice across Australia.....	230
7.2.2 Identifying individual characteristics associated with the uptake of genomics in nursing practice.....	233
7.2.3 Exploring perceived barriers and enablers to integrating genomics into oncology nursing practice.....	237
7.3 Theoretical interpretations.....	268
7.3.1 Relative advantage.....	271
7.3.2 Observability	271
7.3.3 Compatibility	272
7.3.4 Complexity.....	273
7.3.5 Trialability	274
7.3.6 Opinion leaders.....	275
7.3.7 Conceptual alignment with implementation frameworks.....	275
7.4 Limitations.....	276
7.4.1 Theoretical framework limitations	277
7.4.2 Sampling and generalisability	277
7.4.3 Context of data collection	278
7.4.4 Survey design and validation	279
7.4.5 Qualitative phase limitations	280

7.5 Contributions to knowledge	282
7.6 Recommendations	286
7.6.1 Education and awareness	287
7.6.2 Workforce development and role clarity	287
7.6.3 Organisation and leadership	288
7.6.4 Policy and system-level support	288
7.6.5 Integration with global implementation frameworks	289
7.7 Future research	290
7.8 Conclusion	291
References	295
Appendices	337
Appendix A: Checklist for Reporting Of Survey Studies (CROSS).....	337
Appendix B: REDCap Survey	340
Appendix C: Ethics Approval	356
Appendix D: Survey Email invitation	358
Appendix E: Social Media post	359
Appendix F: Semi-structured Interview Guide	360
Appendix G: Telephone Interview Participant Information Sheet	361
Appendix H: Thematic Table	0
Appendix I: Coding Journal Excerpt Entry	12
Appendix J: Distress Protocol	15
Appendix K: Incidental Disclosure and Victimisation Protocol.....	19

List of Figures

Figure 1.1. Cost per human genome sequenced from 2001 to 2022, illustrating a dramatic decline in sequencing costs relative to Moore’s Law.....	4
Figure 1.2. Genomic applications across the individual’s lifespan.....	5
Figure 1.3. Global national genomic medicine initiatives and approximate investment	8
Figure 1.4. Priorities from national genomics programs.....	9
Figure 1.5. Proportion of cancer cases that are sporadic, familial, or inherited.....	15
Figure 1.6. The future of precision oncology—a flowchart depicting the stages of the cancer care pathway	17
Figure 1.7. Conceptual model of relationships between competency, attitudes, confidence, and adoption	29
Figure 1.8. Global Genomics Nursing Alliance Roadmap for nurse leaders to implement genomics across nursing.....	34
Figure 2.1. S-curve diffusion.....	49
Figure 2.2. Innovation decision process	53
Figure 2.3. Relationship between types of adopters classified by innovativeness and their location on the adoption curve	55
Figure 3.1. PRISMA flow diagram.	81
Figure 3.2. Geographic distribution of included studies.	82
Figure 3.3. Methodological characteristics of included studies.	83
Figure 4.1. Searching for themes.	155
Figure 5.1. Participants’ responses to objective knowledge items on genomics-linked care and components of family history taking.....	170
Figure 5.2. Participants’ Likert-scale confidence ratings for family history taking and genomics-related clinical scenarios.....	172
Figure 5.3. Participants’ Likert-scale responses on cosmopolitanism and information-seeking behaviours.	179
Figure 5.4. Distribution of adopter score.	180
Figure 5.5. Distribution of personality scores in likely non-adopters and likely adopters. ...	183
Figure 5.6. Adopters’ and non-adopters’ responses to professional role expectations and influences across two clinical scenarios.....	190
Figure 6.1. Domain 1: Attributes of the innovation.	194
Figure 6.2. Domain 2: Education-related factors.	198
Figure 6.3. Domain 3: Professional factors.....	204
Figure 6.4. Domain 4: Organisational factors.....	212
Figure 6.5. Domain 5: Individual factors.	220
Figure 7.1. Barriers and enablers domains.....	238
Figure 7.2. Recommendations.....	286

List of Tables

Table 1.1. Genomic nursing practice mapped to standards and codes.....	21
Table 2.1. Early and late adopter characteristics.....	59
Table 3.1. Study surveys	84
Table 3.2. Terminology and knowledge assessed	87
Table B.1. PCC eligibility criteria.....	102
Table D1. Summary of studies included in scoping review.....	105
Table E.1. Correlates examined in studies reporting correlation analyses.....	113
Table 4.1. Survey adaptation.....	126
Table 4.2. Survey constructs	135
Table 4.3. Adoption scoring.....	140
Table 5.1. Descriptive information of participants	167
Table 5.2. Perceived knowledge and awareness	168
Table 5.3. Objective knowledge.....	170
Table 5.4. Confidence	171
Table 5.5. Attitudes	173
Table 5.6. Engagement and adoption	175
Table 5.7. Barriers and enablers.....	176
Table 5.8. Cosmopolitanness and information seeking behaviours.....	178
Table 5.9. Summary of components of the adopter score.....	179
Table 5.10. Demographics and work experience of participants	181
Table 5.11. Personality traits.....	184
Table 5.12. Stages of adoption, barriers and enablers.....	186
Table 5.13. Scenario questions.....	189
Table 7.1. Illustrative example of data integration.....	229
Table 7.2. Theoretical interpretations	269
Table 7.3. Contributions to knowledge	285

Abstract

Introduction

The integration of genomics into oncology has transformed cancer prevention, diagnosis, and treatment. Nurses are central to this transformation, yet their preparedness to adopt genomics into practice remains uncertain. International research consistently shows that while nurses recognise genomics as relevant, their knowledge, confidence, and engagement are limited. In Australia, evidence in this area is particularly scarce, especially within oncology nursing, where genomics holds essential clinical relevance. This study sought to advance understanding of how Australian oncology nurses engage with genomics, and the barriers and enablers influencing its adoption into practice.

Methods

A mixed-methods design was employed, incorporating a national online survey and interviews, complemented by a scoping review of the evidence on knowledge and attitudes to genetics/genomics. A survey assessed Australian oncology nurses' knowledge, engagement, and adoption of genomics in practice, and identified individual characteristics associated with the uptake of genomics in nursing practice ($n = 106$). Nine semi-structured interviews were conducted to explore perceived barriers and enablers to integrating genomics into oncology nursing practice.

Findings

The scoping review showed a fragmented, methodologically heterogeneous evidence base, lacking qualitative and oncology-specific research tools, and identified evidence gaps in the literature on oncology nurses' genomic knowledge and attitudes. Survey findings revealed a workforce receptive to genomics but constrained by limited knowledge, confidence, and exposure. While most nurses held positive attitudes and recognised genomics as relevant to their practice, few reported confidence in applying it clinically. Likely adopters were characterised by greater clinical experience, advanced practice and higher education, openness to experience, and opinion-leadership traits. Interviews identified a range of barriers and enablers grouped across five interrelated domains: attributes of the genomics innovation, education-related factors, professional factors, organisational factors, and individual factors.

Discussion and Conclusion

This study provides the first national evidence of how multilevel barriers and enablers shape Australian oncology nurses' engagement with genomics. Rogers' Diffusion of Innovations theory (2003) was used as an interpretive lens to guide interpretation and discussion. By identifying adopter characteristics and the contextual factors influencing uptake, it establishes an evidence base to guide education, leadership, and policy reform. In doing so, it offers empirically grounded direction for embedding genomics within nursing education, clinical governance, and organisational systems. The findings lay a foundation for national strategies that align with Australia's genomic medicine agenda and provide evidence of how to best support a confident, capable oncology nursing workforce that is prepared for the genomic era.

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This thesis does not exist in a vacuum, and so in many ways this section is both the hardest and most important to write. For a long time it seemed as though the day I would get to write these acknowledgements would never come, so it is with profound gratitude that I thank all those who helped me get here.

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Although “thank you” feels inadequate, this thesis was written in the shadow of illness and of war, and it is to those who carried me through both that I give thanks. To my family—Abba, Ima, and my boos, Eden and Carmi—who supported me, fed me, housed me, and whose love helped me pick up the pieces when everything fell apart. I would never have made it without you. Toda, ani ohevet otchem.

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COVID-19 Impact Statement

This PhD commenced as the first wave of the COVID-19 pandemic was subsiding, a time when it was hoped that the worst had passed. However, subsequent waves, prolonged lockdowns, and strict public-health restrictions had significant personal and professional impacts. The pandemic reshaped the health-care environment in which this research was situated. Nurses were experiencing extreme workload pressures, staff shortages, and profound fatigue, making research participation ethically and practically complex. Recruitment was particularly challenging during this period, and data collection was carefully adapted to minimise burden on participants and ensure safety for all involved. Although this period presented immense challenges, it also deepened my resilience and commitment to conducting research that honours the realities of nursing practice.

Key Terms

Adoption. In Diffusion of Innovations theory, adoption is defined as a decision to make full use of an innovation as the best course of action available (Rogers, 2003, p. 21). In this thesis, adoption refers to oncology nurses' engagement with genomic innovations as reflected in specific practice behaviours, including the collection and assessment of family history, awareness of genetic services and facilitation of referrals, provision of information and education to patients and families, and openness to the role of genomics in oncology care. These behaviours align with the Genetic Indicators of Adoption (Andrews et al., 2014b) used to derive the composite adoption score for this study (see Section 4.6.7.1).

Compatibility. In Diffusion of Innovations theory, compatibility refers to the degree to which an innovation is perceived as consistent with existing values, past experiences, and the needs of potential adopters. It is one of the five attributes of the innovation that influence adoption (Rogers, 2003, p. 15).

Complexity. In Diffusion of Innovations theory, complexity refers to the degree to which an innovation is perceived as difficult to understand or use. It is one of the five *attributes of the innovation* that influence adoption (Rogers, 2003, p. 16).

Cosmopolitaness. In Diffusion of Innovations theory, cosmopolitaness is defined as the degree to which an individual is oriented outside their immediate social system (Rogers, 2003, p. 290). Earlier adopters tend to be more cosmopolite than later adopters, reflecting a greater engagement with external information sources beyond routine local networks (Becker, 1970; Rogers, 2003).

Diffusion. In Diffusion of Innovations theory, diffusion is defined as the process in which an innovation is communicated through certain channels over time among the members of a social system (Rogers, 2003, p. 19).

DNA (Deoxyribonucleic Acid). Deoxyribonucleic acid (DNA) is the molecule that carries genetic information in all living organisms. It is composed of four chemical bases: adenine (A), cytosine (C), guanine (G), and thymine (T), that form sequences providing the instructions for cellular structure and function (Department of Health and Aged Care, 2017b).

Gene. A gene is a segment of DNA that contains the instructions for producing proteins or functional RNA molecules, which determine specific characteristics or functions in an

organism. Genes are the basic units of heredity and are arranged on chromosomes within the human genome (Department of Health and Aged Care, 2017b).

Genetics. Genetics refers to the study of heredity and the way in which specific traits or characteristics are passed from parents to offspring. In human health, it focuses on the structure and function of single genes and how variations or mutations in these genes can influence growth, development, and disease risk (Department of Health and Aged Care, 2017b).

Genomics. Genomics encompasses the study of the entire set of genes (the genome) and their interactions with each other and with environmental or non-genetic factors. It includes the analysis of multiple genes simultaneously and the use of technologies such as gene panels, whole exome sequencing, and whole genome sequencing to understand complex conditions. In contemporary health contexts, the term genomics is often used to encompass both genetic and genomic knowledge, reflecting the shift from a single-gene to a systems-based understanding of health and disease (Department of Health and Aged Care, 2017b).

Innovation. In Diffusion of Innovations theory, an innovation is defined as an idea, practice, or object that is perceived as new by the individual or other unit of adoption (Rogers, 2003, p. 12). The ‘newness’ of an innovation is determined by the perceptions of the potential adopter rather than by the objective age of the idea.

Mainstreaming. Mainstreaming genomics refers to the process of integrating genomics-informed healthcare as a routine part of clinical practice, enabling the broader health workforce—not just genetics specialists—to request tests, interpret results, and manage patients accordingly (Cancer Australia, 2025). Mainstream genetic testing represents a key component of this integration, involving the incorporation of genetic and genomic testing into routine clinical care where tests are ordered and managed by non-genetic specialists rather than clinical geneticists or genetic counsellors.

Observability. In Diffusion of Innovations theory, observability refers to the degree to which the results of an innovation are visible to others. It is one of the five attributes of the innovation that influence adoption (Rogers, 2003, p. 16).

Opinion Leadership. In Diffusion of Innovations theory, opinion leadership refers to the degree to which an individual is able to influence the attitudes or overt behaviour of others informally in a desired way with relative frequency (Rogers, 2003, p. 27).

Relative Advantage. In Diffusion of Innovations theory, relative advantage refers to the degree to which an innovation is perceived as better than the idea it supersedes. It is one of the five attributes of the innovation that influence adoption (Rogers, 2003, p. 15).

Social System. In Diffusion of Innovations theory, a social system is defined as a set of interrelated units that are engaged in joint problem solving to accomplish a common goal (Rogers, 2003, p. 23).

Trialability. In Diffusion of Innovations theory, trialability refers to the degree to which an innovation can be experimented with on a limited basis. It is one of the five attributes of the innovation that influence adoption (Rogers, 2003, p. 16).

Use of Genetics and Genomics in this thesis

While *genetics* and *genomics* are distinct yet interrelated constructs, the terms are often used interchangeably in clinical, health, and scholarly contexts. This thesis primarily adopts *genomics* as a broad, holistic term encompassing both genetic (single-gene) and genomic (multi-gene or whole-genome) concepts. This approach aligns with contemporary national and international policy usage, where *genomics* functions as an umbrella term reflecting the complexity of gene–environment interactions and systems-level perspectives on health.

It is recognised, however, that significant portion of the literature reviewed and several participants in this study used the term *genetics*. In such instances, the original terminology has been retained to maintain fidelity to the source material and participants' language. These references are nevertheless interpreted within the broader conceptual scope of *genomics*.

Chapter 1. Introduction

1.1 Introduction

This thesis examines how Australian oncology nurses engage with genomics and the factors influencing their adoption of genomic innovations in clinical practice. In the genomic era, nurses are increasingly expected to interpret and apply genetic and genomic information to deliver personalised cancer care. However, the extent to which nurses are equipped for this role depends on multiple interacting factors. Using data drawn from survey responses and interviews, this thesis examines the barriers and enablers to genomic adoption, including nurses' knowledge, attitudes, and the characteristics of nurse adopters. Understanding these factors is essential to preparing the workforce for, and supporting, the integration of genomics into routine cancer care.

This chapter introduces the background and contextual literature that frame the study, leading to an articulation of the problem statement and the overarching research aim, objectives, and questions. It then outlines the significance of the study and the researcher's positionality and reflexivity, before concluding with an overview of the structure of the thesis.

1.2 Background – The genomic era: Foundations of genomic medicine

This section outlines the foundations of genomic medicine and the global developments that have shaped its integration into healthcare. It first traces the shift from genetics to genomics and the landmark achievements of the Human Genome Project, before considering the technological advances that have expanded genomic accessibility and application. The discussion then turns to global and Australian initiatives that have advanced the implementation and mainstreaming of genomic medicine across health systems. Understanding this trajectory provides essential context for examining the factors influencing the uptake of genomics within oncology nursing practice.

1.2.1 *From genetics to genomics*

The journey from genetics to genomics began in the mid-nineteenth century with Augustinian monk Gregor Mendel's experiments on pea plants, which revealed the fundamental principles of heredity (Mendel, 1866). Although his work was only recognised posthumously, Mendel is now regarded as the father of modern genetics (Miko, 2008). His experiments established the

concept of discrete hereditary units—later termed *genes*—that determine how traits are transmitted from one generation to the next.

In the twentieth century, the focus of genetic research shifted from observable patterns of inheritance to the molecular mechanisms underpinning heredity. This transition was propelled by the pioneering work of British biochemist Rosalind Franklin, who first visualised the structure of deoxyribonucleic acid (DNA) using X-ray crystallography (Klug, 1968). Her findings provided critical evidence that enabled James Watson and Francis Crick to publish their groundbreaking 1953 paper ‘A Structure for Deoxyribose Nucleic Acid’, which described DNA as a double helix composed of two complementary strands of nucleotide pairs with a sugar–phosphate backbone (Watson & Crick, 1953). This discovery revolutionised biology by revealing how genetic information is stored, replicated, and transmitted at the molecular level, demonstrating how the DNA molecule directs heredity and undergoes mutation. It provided the foundation for modern molecular genetics and paved the way for the rapid advances in biological science that continue to this day.

As knowledge expanded, medical genetics developed into a clinical discipline focused on Mendelian disorders caused by identifiable changes in single genes or chromosomes, such as cystic fibrosis and Down syndrome (Khoury, 2003). The recognition that genetic variation could also occur across multiple genes and be influenced by environmental factors marked the beginning of a broader, more integrative understanding of human biology (Guttmacher & Collins, 2002). By the late twentieth century, this growing recognition culminated in an international effort to map the entire human genetic code—the *genome*—initiating what became known as the Human Genome Project (Guttmacher & Collins, 2003). This international initiative ultimately catalysed a shift toward large-scale, data-driven approaches to biological discovery, setting the foundation for contemporary genomics and its widespread clinical and research applications (Gibbs, 2020).

1.2.2 The Human Genome Project as a catalyst for a new era

The Human Genome Project (HGP), launched in 1990 and completed in 2003, marked a turning point in biomedical science. This international collaboration successfully sequenced the three billion base pairs of the human genome and identified more than 20,000 genes (Guttmacher & Collins, 2003). The project established the reference framework that underpins modern genomic research and clinical practice, sparking the transition into what is now referred to as the *Genomic Era*. Subsequent initiatives, such as the 1000 Genomes Project (1000 Genomes

Project Consortium, 2015) and the UK's 100,000 Genomes Project (Turnbull et al., 2018), extended this work by cataloguing population-level genomic variation and embedding whole-genome sequencing within clinical settings. Together, these efforts enhanced understanding of the molecular basis of disease and created new opportunities for diagnosis, prevention, and treatment (Carrasco-Ramiro et al., 2017). They also accelerated the development of sequencing technologies and data infrastructures that have made genomics increasingly accessible to researchers and clinicians, ushering in a period of rapid translation into healthcare practice and new expectations for healthcare professionals, including nurses, to engage with genomic practice.

1.2.3 Technological advances and accessibility of genomics

As scientific understanding has grown, so too has technological capacity. Advances in high-throughput techniques, particularly next-generation sequencing, along with complementary innovations in bioinformatics, data storage, and computational analysis platforms, have drastically reduced the time and cost associated with genome sequencing (Pareek et al., 2011). Whereas sequencing a human genome once cost over US\$100 million, it now sits closer to US\$100, enabling broad accessibility and adoption in clinical and research contexts (Pennisi, 2022; Singh, 2018). This reduction in cost has outpaced even Moore's Law—the observation that computational power tends to double approximately every two years while costs halve—illustrating the rapid acceleration of affordable genomic technologies (Muers, 2011) (see Figure 1.1). These developments have transformed genomics from a research-intensive pursuit into an increasingly routine component of clinical care that is increasingly accessible to health systems, researchers, and consumers alike (Birney et al., 2017; Stark, Dolman, et al., 2019). These technological and economic shifts have created unprecedented opportunities for integrating genomics across healthcare systems, setting the stage for the global and national initiatives described in the following sections.

[Production note: This figure is not included in this digital copy due to copyright restrictions.]

Figure 1.1. Cost per human genome sequenced from 2001 to 2022, illustrating a dramatic decline in sequencing costs relative to Moore’s Law. Source: National Human Genome Research Institute (2022), genome.gov/sequencingcosts

1.2.4 Genomic applications to medicine and health

Advances in understanding the role of genomic variants in human health and disease, together with technological innovations that enable their precise measurement and interpretation, have facilitated the integration of genomics into clinical research, practice, and care (Claussnitzer et al., 2020; Karczewski & Snyder, 2018). Genomic medicine now encompasses a broad and expanding range of applications, including disease risk assessment, diagnosis of rare and undiagnosed conditions, and the optimisation of drug safety and efficacy (Manolio et al., 2019). The application of genomics spans the entire healthcare continuum and is integrated into a growing number of healthcare domains, including but not limited to rare diseases, reproductive medicine, common diseases such as diabetes, hypercholesterolaemia, and cardiovascular disease, and cancer (Shendure et al., 2019). Genomic applications in healthcare extend across the human lifespan, encompassing preconception, preimplantation, prenatal, neonatal, paediatric, adult, and posthumous contexts (see Figure 1.2) (Bilkey et al., 2019; Calzone, Jenkins, Nicol, et al., 2013; Rehm, 2017). This life-course perspective demonstrates genomics’ expanding reach across clinical settings and underscores its growing relevance for all healthcare professionals, including nursing.

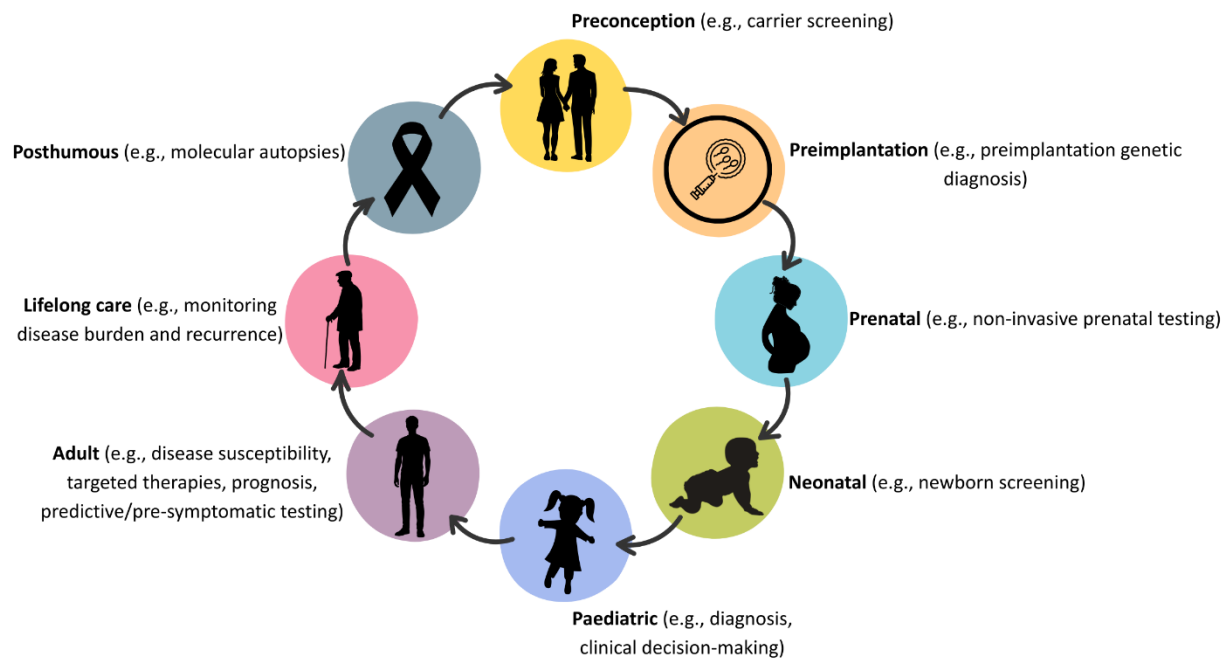


Figure 1.2. Genomic applications across the individual's lifespan. Adapted from Calzone, Jenkins, Nicol et al., (2013) and Rehm (2017).

Over the past two decades, clinical genetic testing has evolved from targeted, single-gene analysis to broader genomic approaches, including multi-gene panels, whole-exome sequencing, and whole-genome sequencing (Ishida et al., 2025). This shift from genetics to genomics has expanded diagnostic capabilities, increased diagnostic yield, and improved clinical management and patient outcomes (Claussnitzer et al., 2020; Lionel et al., 2018; Pritchard et al., 2022; Stavropoulos et al., 2016). These advances have laid the foundation for an era in which molecular data guide clinical decision-making and patient care. As genomic testing becomes increasingly accessible, its integration into mainstream healthcare continues to demonstrate substantial clinical utility and potential to improve health outcomes across diverse disease areas.

The integration of genomics into healthcare has transformed how disease is understood, diagnosed, and managed. Central to this transformation is the increasing use of genomic testing, which identifies genetic variation to inform risk prediction, diagnosis, and treatment. In oncology, for instance, identifying a pathogenic *BRCA* gene variant can guide treatment selection and determine eligibility for targeted therapies such as poly (ADP-ribose) polymerase (PARP) inhibitors (Hyman et al., 2017). Evidence also shows that universal genomic testing in cancer yields higher diagnostic rates than traditional guideline-based approaches (Samadder et al., 2021). As genomic testing becomes increasingly accessible, its

integration into mainstream healthcare continues to demonstrate substantial clinical utility and is expected to further enhance the precision, safety, and quality of patient care across diverse disease areas (Pritchard et al., 2022).

1.2.4.1 Precision Medicine

The emergence of this genomic era of medicine underpins the broader paradigm of *precision medicine*, which seeks to tailor prevention, diagnosis, and treatment strategies to an individual's genetic, environmental, and lifestyle factors (Ginsburg & Phillips, 2018). Advances in technologies such as DNA sequencing, proteomics, and computational power have enabled individualised therapies that account for genetic variations influencing disease risk, progression, and treatment response (Khan et al., 2025). Precision health extends this concept by integrating multi-omics data—such as proteomics, metabolomics, and microbiomics—with social, economic, cultural, and environmental determinants of health (Fu et al., 2020). Tailoring care to the individual genome allows for increased diagnostic accuracy, enhanced therapeutic efficacy, and improved management and treatment outcomes (Khan et al., 2025).

A central component of precision medicine is pharmacogenomics, which examines how genomic variation influences individual responses to medications, guiding drug selection and dosing to optimise efficacy and reduce toxicity (Dodson, 2017; Pirmohamed, 2023). Pharmacogenomics has been particularly influential in oncology, where treatment decisions increasingly rely on tumour and germline genomic information to identify therapeutic targets, anticipate adverse effects, and personalise both anticancer and supportive therapies (Akhoon, 2021). These approaches move cancer care away from a 'one-size-fits-all' model towards treatment strategies informed by patients' molecular and biological profiles.

The effective translation of precision medicine and pharmacogenomics into routine clinical care also depends on the capacity of the healthcare workforce to interpret, communicate, and apply genomic information across care settings, with nurses playing a key role in medication management, patient education, and care coordination (Dewell, Benzies, & Ginn, 2020; Fu et al., 2020). Realising the full potential of this paradigm therefore necessitates coordinated genomic health initiatives designed to support the systematic implementation of precision medicine across healthcare systems and practices.

1.2.5 Global genomic medicine initiatives

The transformative potential of genomics has prompted coordinated efforts worldwide to accelerate its integration into healthcare (Howley et al., 2025; Stark, Dolman, et al., 2019). The World Health Organization (WHO) has formally recognised genomics as a global health priority, establishing the WHO Science Division's Genomics Programme to support enhanced access to genomic knowledge and technologies for global health (WHO, n.d.; WHO, 2022). Recognising that no single country could address the scientific, ethical, and infrastructural challenges of genomics alone, governments and international consortia have launched large-scale initiatives to build capacity, share data, and ensure equitable access (Ginsburg, 2019; Howley et al., 2025). The implementation of genomic healthcare has since been recognised as a global responsibility, with at least 14 countries investing more than US\$4 billion to establish national genomic medicine initiatives (Stark, Dolman, et al., 2019). These large-scale efforts vary in focus, including rare diseases, cancer, population genomics, and pharmacogenomics, but collectively aim to integrate genomics into mainstream health systems.

More than 96 major genomics programs have now been launched globally, reflecting unprecedented investment in the implementation of genomic medicine (Howley et al., 2025). These efforts include some of the largest sequencing initiatives in history, such as the United States' *All of Us* research program, the European *1 + Million Genomes* initiative, and China's Precision Medicine Initiative, each aiming to sequence at least one million genomes to support evidence-based precision medicine (All of Us Research Program Investigators, 2019; Liu et al., 2020; Saunders et al., 2019). While national programs inevitably vary in scope, reflecting geographical, political, and cultural contexts, they converge on a shared recognition of genomics as central to the future of healthcare.

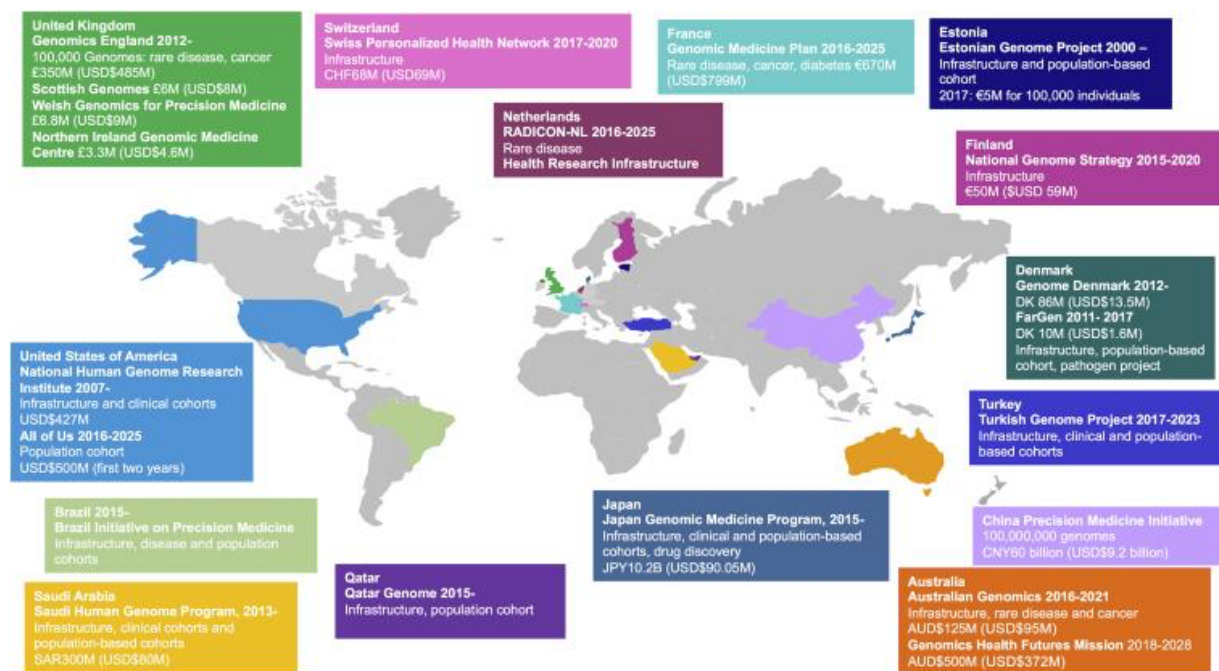


Figure 1.3. Global national genomic medicine initiatives and approximate investment. Source: Stark et al. (2019, p. 14).

A recent synthesis of international initiatives identified six common priorities across national genomics programs: participant involvement and public engagement; embedding ethical, legal, and social (ELSI) considerations into genomic medicine research; increasing diversity in genomic studies; creating virtuous cycles for implementation; developing innovative data infrastructure; and nimble prioritisation of funding and emerging technologies (Howley et al., 2025) (Figure 1.4). These priorities demonstrate not only the scale of global ambition but also a convergence of strategies aimed at building sustainable, equitable, and clinically integrated genomic medicine. This vision emphasises the importance of fostering international collaboration to advance genomic medicine. It advocates expanding efforts beyond national borders through participation in global initiatives such as the Global Alliance for Genomics and Health (GA4GH) and the Global Genomic Medicine Collaborative (G2MC), with the goal of accelerating the development and implementation of genomic medicine programmes worldwide (Birney et al., 2017; Ginsburg, 2019; Howley et al., 2025).



Figure 1.4. Priorities from national genomics programs. Source: Howley et al. (2025; graphical abstract).

However, despite this momentum, many initiatives acknowledge that workforce capability and clinical expertise remain key bottlenecks in realising the full potential of genomic medicine (Howley et al., 2025). These developments hold particular significance for nursing, given that nurses constitute the largest segment of the global health workforce and are often at the forefront of implementing new models of care. As precision health advances from the laboratory into routine clinical settings, nursing scholarship increasingly emphasises the need for all nurses to develop baseline genomic capability to support genuinely individualised care (Dewell, Benzies, & Ginn, 2020). This includes recognising the distinct contribution nurses can make to precision health through their patient-centred roles, their focus on the determinants of health, and their ability to identify practice gaps that require further evidence. Ensuring that nurses are equipped to translate genomic advances into practice is therefore essential to achieving the objectives of these global initiatives. Addressing this issue within the Australian context forms the central focus of this thesis.

1.2.6 Australian genomic medicine initiatives

Australia's health system operates within a federated structure in which responsibility for health care is shared between the Commonwealth, state, and territory governments. This arrangement creates a complex but interdependent network of services designed to meet population health needs (Australian Institute of Health and Welfare [AIHW], 2024a). In 2016, the Health Chief Executives Forum (formerly the Australian Health Ministers' Advisory Council) recognised the need for national coordination of genomic medicine, leading to the *National Health Genomics Policy Framework 2018–2021* (Department of Health and Aged Care, 2017a). This framework represented a shared intergovernmental commitment to embed genomics within the health system through collaboration, information sharing, and avoidance of duplication to improve health outcomes. Implementation activity paused during the COVID-19 pandemic, and the framework subsequently lapsed. While governments and stakeholders continued to advance genomic integration independently, the degree of coordination varied (Australasian Institute of Digital Health, 2022). In 2023, the Health Technology and Genomics Collaboration initiated a review to renew and update the framework, with a new *National Health Genomics Policy Framework and Implementation Plan 2026–2030* currently being drafted to guide future national efforts (Australian Genomics, n.d.). These evolving policy frameworks reflect an enduring national commitment to genomics and provide the foundation for Australia's substantial investments in this field.

Australia has made substantial and sustained investments to position itself as a global leader in integrating genomics into healthcare. Central to this ambition is the *Genomics Health Futures Mission* (GHFM), a AU\$500 million, ten-year initiative (2018–2028) funded under the Medical Research Future Fund (Department of Health and Aged Care, 2025b; Butler, 2022). The GHFM supports translational research to demonstrate how genomics can improve diagnosis, prevention, and treatment across the disease spectrum, signalling a long-term governmental commitment to precision medicine and population health (Department of Health and Aged Care, 2025b). Notably, the Australian Genomics Health Alliance, established in 2016 through an AU\$25 million National Health and Medical Research Council (NHMRC) grant, laid the groundwork for national collaboration and clinical translation by connecting more than 80 partner organisations and generating the evidence base to inform health policy (Stark, Boughtwood, et al., 2019). Building on this foundation, and to provide cohesive national leadership for the effective transition of genomics from research to clinical service delivery, on 1 July 2025 the Australian Government established Genomics Australia as a new statutory

authority within the Department of Health and Aged Care (Department of Health and Aged Care, 2025a). Genomics Australia oversees the *National Health Genomics Policy Framework and Implementation Plan (2026–2030)*, working with jurisdictions and key stakeholders to ensure equitable, culturally safe, and sustainable integration of genomics across the health system. Collectively, these initiatives represent one of the most significant national investments in precision health to date. However, the long-term success of these efforts depends on a genomically literate workforce capable of translating discovery into clinical benefit. Nurses, who constitute the largest segment of the Australian health workforce (AIHW, 2024b) and are central to patient education, consent, and care coordination, are therefore pivotal to ensuring that these investments achieve their intended impact. Without equivalent investment in nursing education and research, the benefits of Australia’s considerable financial and policy commitments risk being undermined by gaps in implementation and workforce readiness.

1.2.7 Mainstreaming genomics

Mainstreaming genomics refers to the process of integrating genomics-informed healthcare as a routine part of clinical practice, enabling the broader health workforce—not just genetics specialists—to request tests, interpret results, and manage patients accordingly (Cancer Australia, 2025). Mainstream genetic testing represents a key component of this integration, involving the incorporation of germline genetic and genomic testing into routine clinical care, with tests ordered and managed by non-genetic specialists rather than clinical geneticists or genetic counsellors (Cancer Australia, 2025). This model aims to improve timely access, reduce demand on overstretched genetic services, and embed genomics within standard care pathways (Berkman et al., 2025; George et al., 2016; Kentwell et al., 2017). In oncology, this shift has been particularly pronounced. Since November 2017, the Medicare Benefits Schedule (MBS) has supported mainstream genetic testing through item numbers for germline *BRCA1* and *BRCA2* testing. Eligible patients include those with breast or ovarian cancer who have a greater than 10% likelihood of carrying a pathogenic variant based on quantitative algorithms, or women with ovarian cancer who may benefit from targeted therapy such as PARP inhibitors if a *BRCA* variant is identified (Kirk et al., 2018; Young et al., 2024). Importantly, these tests can be ordered by non-genetic health professionals, signalling a deliberate policy move toward mainstreaming. Mainstreaming models therefore depend on the capacity of non-genetics healthcare professionals to engage with genomic testing, a need that has been increasingly highlighted as essential to meeting growing demand for genomic services (Campion et al., 2019; Nisselle et al., 2019; O’Shea et al., 2022).

Mainstreaming models have since been introduced across multiple tumour streams, including ovarian, breast, prostate, pancreatic, and endometrial cancers, supported by initiatives such as the Australian Genetic Testing Mainstreaming Collaborative and Australian Genomics (Young et al., 2024). This approach reduces reliance on specialised Familial Cancer Centres and clinical genetics services, which often experience long wait times and limited service capacity (Barlow-Stewart et al., 2016; Cancer Australia, 2025; Queensland Health, 2017). Evidence indicates that mainstreaming improves access to testing, reduces the interval between cancer diagnosis and receipt of genetic tests results, enhances continuity of care, and results in high patient decisional satisfaction (Berkman et al., 2025; Cancer Australia, 2024; Young et al., 2024).

National implementation efforts have included workforce training programs delivered through the Australian Genetic Testing Mainstreaming Collaborative Group (Gleeson et al., 2020) and continued expansion of mainstreaming across Australia (Beard et al., 2021; Stearnes et al., 2019). As testing indications and federally funded eligibility criteria broaden, increasingly large groups of cancer-affected individuals are expected to undergo genomic testing. This expansion places additional clinic-time pressures on oncologists, and several studies have suggested that nurses could play a critical role in addressing this gap through facilitating mainstreaming and providing nurse-assisted pathway to genomic testing (Scott et al., 2020; Young et al., 2024). This shift reflects broader recognition that mainstreaming genomic testing requires upskilling oncology clinicians outside traditional clinical genetics roles to support sustainable implementation (Rahman et al., 2022).

There is insufficient genetic counsellor capacity in Australia to meet this growing demand (Nisselle et al., 2019). To optimise efficiency and minimise burden on existing genetics services, increased access to genomic testing necessarily involves the delegation of responsibilities to clinicians not primarily trained in genetics (Cormack et al., 2024; Stark, Dolman, et al., 2019). Nurses are well placed to support the mainstreaming of genomics, as they are often the first point of patient contact and have expertise in education, advocacy, and care coordination (Wright et al., 2019). In settings where mainstream testing programs are implemented, nurses commonly facilitate key steps in the testing pathway, such as providing information, obtaining consent, and supporting patients through the testing process (Bokkers et al., 2022; Scott et al., 2020; Young et al., 2024). Recent findings indicate strong support for such nurse-led models, with clinicians identifying a nurse-assisted pathway as both useful and feasible, while patients expressed equal preference for nurses or medical specialists to offer genetic testing (Young et al., 2024). Consequently, nurses are increasingly exposed to genomics

in everyday oncology practice. This evolving role underscores the need for targeted education and competency development to ensure nurses are adequately prepared to participate in mainstream genomic care (Cormack et al., 2024; Wright et al., 2019).

1.3 Genomics and cancer care

The clinical impact of genomics is perhaps most advanced and visible in oncology, where genetic and genomic discoveries have rapidly translated into diagnostic, prognostic, and therapeutic advances. In oncology, genomics has become central to nearly every aspect of care, enabling risk stratification, tumour profiling, pharmacogenomic-guided therapies, and surveillance protocols for recurrence (Berger & Mardis, 2018; Krzyszczyk et al., 2018). As such, oncology provides a logical and meaningful context through which to examine genomic integration in healthcare and the nursing profession.

Aligned with the original, now-lapsed *National Health Genomics Policy Framework* (2018–2021), Cancer Australia recently published the *National Framework for Genomics in Cancer Control* (2025) to guide national policy and ensure equitable access to genomic medicine for all Australians affected by cancer. The framework outlines four strategic objectives spanning the cancer care continuum: (1) prevention and early detection, (2) diagnosis, treatment and clinical trials, (3) supportive care, and (4) awareness and education. Importantly, it recognises the need to build the capacity of the healthcare workforce, including nurses, to communicate clearly about genomic testing, future risk, and hereditary implications. Stakeholders emphasised improving genomic literacy and providing targeted education for nurses and other health professionals as critical to supporting patient understanding and informed decision-making. The framework also highlights the importance of developing genomics literacy and formal training pathways for Aboriginal and Torres Strait Islander nurses, liaison officers, and health practitioners so that their genomic qualifications are recognised within clinical skill sets. Although the framework acknowledges the need for workforce capacity building, explicit reference to nurses' broader roles in genomic care remains limited. This omission is particularly notable given the recognised potential for nurses to contribute to the implementation of genomic and precision health through care coordination, patient education, and interprofessional collaboration (Fu et al., 2020). As mainstream genomic testing becomes further embedded within oncology nursing workflows, the limited representation of nursing perspectives in national policy highlights a significant gap in implementation.

1.3.1 The global and national burden of cancer

Cancer remains one of the most significant public health challenges worldwide. In 2022, the WHO's International Agency for Research on Cancer reported an estimated 20 million new cancer cases and 9.7 million cancer deaths globally, with one in five people expected to develop cancer during their lifetime. By 2050, the global cancer burden is projected to rise to more than 35 million new cases annually—a 77% increase compared with 2022 (WHO, 2024). This growth reflects both population ageing and the increasing prevalence of cancer risk factors across diverse settings.

In Australia, cancer is a significant cause of disease burden and mortality, accounting for 17% of the total burden of disease and 32% of the fatal burden (Australian Institute of Health and Welfare, 2024). In 2023, an estimated 165,000 new cancer cases were diagnosed, more than 450 every day, and around 51,300 Australians died from cancer (AIHW, 2024). Although age-adjusted mortality rates have fallen by 25% since 2000, largely due to earlier detection and advances in treatment, cancer remains responsible for approximately three in every ten deaths in Australia in 2023 (AIHW, 2024). Importantly, disparities persist, with First Nations peoples experiencing age-standardised cancer incidence rates 12% higher than non-Indigenous Australians (AIHW, 2024). With new cases projected to rise to 204,000 annually by 2033, a total of about 1.9 million cases are expected to be diagnosed between 2024 and 2033. The demand for effective, equitable, and innovative cancer care strategies is therefore expected to intensify (AIHW, 2024). Given this growing and inequitable burden, oncology has become a central focus of precision medicine efforts, with genomics offering new opportunities to improve diagnosis, treatment, and prevention across populations.

1.3.2 Genomics across the cancer care continuum

At its core, cancer is a fundamentally genetic disease, arising from alterations in the structure or regulation of DNA. Whether these genetic mutations occur spontaneously, accumulate over time through environmental exposure, or are inherited, the role of genomics in cancer is both foundational and indisputable (Stratton et al., 2009). While not all cancers are hereditary, the mechanisms underlying carcinogenesis are invariably rooted in genomic instability and mutation (Garraway & Lander, 2013; Stratton et al., 2009).

A subset of cancers can be classified as *hereditary*, arising from inherited pathogenic variants, often in an autosomal dominant pattern wherein an individual has a 50% probability of

transmitting the variant to their offspring (Garber & Offit, 2005; Garutti et al., 2023). More than 200 hereditary cancer syndromes have been described, including well-known conditions such as hereditary breast and ovarian cancer syndrome and Lynch syndrome, and less common syndromes such as familial adenomatous polyposis and Li-Fraumeni syndrome (Nagy et al., 2004). As shown in Figure 1.5, these hereditary forms account for 5–10% of all cancers and are consistently observed across several malignancies, including breast, ovarian, colorectal, prostate, and pancreatic cancers.

In addition to clearly defined hereditary syndromes, a broader category known as *familial cancers* comprises approximately 15–20% of common cancers such as breast and colorectal cancer (Berliner & Fay, 2007). These familial patterns of disease may reflect unidentified genetic variants, gene–environment interactions, or shared lifestyle and environmental exposures within families. Unlike hereditary syndromes, familial cancers typically lack the hallmark features of Mendelian inheritance but may still confer an elevated cancer risk, particularly when a close relative has developed a site-specific malignancy. This recognition continues to drive genomic research aimed at identifying novel susceptibility genes and elucidating complex patterns of inheritance (Mavaddat et al., 2013; Mucci et al., 2016).

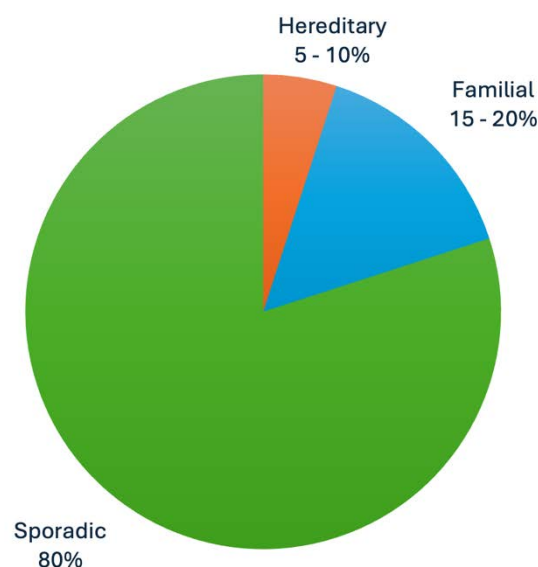


Figure 1.5. Proportion of cancer cases that are sporadic, familial, or inherited. Adapted from Nagy et al. (2004, p. 6446).

Advances in genomic medicine are now reshaping cancer care, with applications spanning prevention, screening, diagnosis, treatment, survivorship, and relapse management (Krzyszczuk et al., 2018; Pritchard et al., 2022). The convergence of next-generation sequencing and advanced computational analytics has transformed understanding of the

genomic mechanisms underpinning cancer development and progression, accelerating the clinical translation of genomic profiling in oncology (Berger & Mardis, 2018). Genomic analysis plays a central role in identifying inherited cancer syndromes (e.g., *BRCA1/2* mutations in breast and ovarian cancer, and mismatch repair variants in Lynch syndrome), informing individualised risk management and cascade testing for family members (Berger & Mardis, 2018).

Identification of pathogenic variants can directly guide treatment decisions, including eligibility for targeted therapies such as PARP inhibitors in *BRCA*-associated cancers, which have demonstrated improved outcomes in advanced disease (Hyman et al., 2017; Roy et al., 2023). Importantly, identifying such variants can also alert individuals to an elevated risk of developing another primary cancer, enabling informed decisions about preventive surgical or clinical management strategies. Beyond germline predisposition, somatic tumour profiling has become integral to precision oncology, enabling clinicians to characterise tumour-specific molecular features, guide targeted therapies, inform prognosis, and monitor treatment resistance or recurrence (Seed, 2021). As illustrated in Figure 1.6, genomic advances are poised to personalise every stage of the cancer care continuum—from diagnosis and treatment selection to prognosis, surveillance, and survivorship planning—marking a clear shift from population-based protocols to tailored approaches (Seed, 2021).

Universal genomic testing and cross-tumour genomic insights have further altered cancer classification and clinical trial design, yielding higher diagnostic rates than traditional guideline-based approaches (Samadder et al., 2021). Increasingly, multi-omics approaches integrating transcriptomic, epigenomic, proteomic, metabolomic, microbiome, and other data streams are deepening understanding of cancer biology and improving prognostic accuracy (Karczewski & Snyder, 2018). Pharmacogenomics exemplifies this shift toward individualised therapy by using genomic information to inform medication selection and dosing, thereby optimising efficacy and minimising toxicity (Pirmohamed, 2023; Wysocki & Seibert, 2019). Emerging tools such as circulating tumour DNA and liquid biopsy further extend the reach of precision oncology by enabling non-invasive disease monitoring and earlier detection of relapse (Cescon et al., 2020).

Importantly, the clinical implications of cancer genomics extend beyond treatment decisions. Survivorship care—including surveillance, psychosocial support, and reproductive health decision-making—is increasingly guided by genomic information, while families benefit from

opportunities for risk assessment and preventative interventions following the identification of hereditary cancer predisposition (Cancer Australia, 2025; Jacobs & Giarelli, 2004; Ruddy et al., 2016).

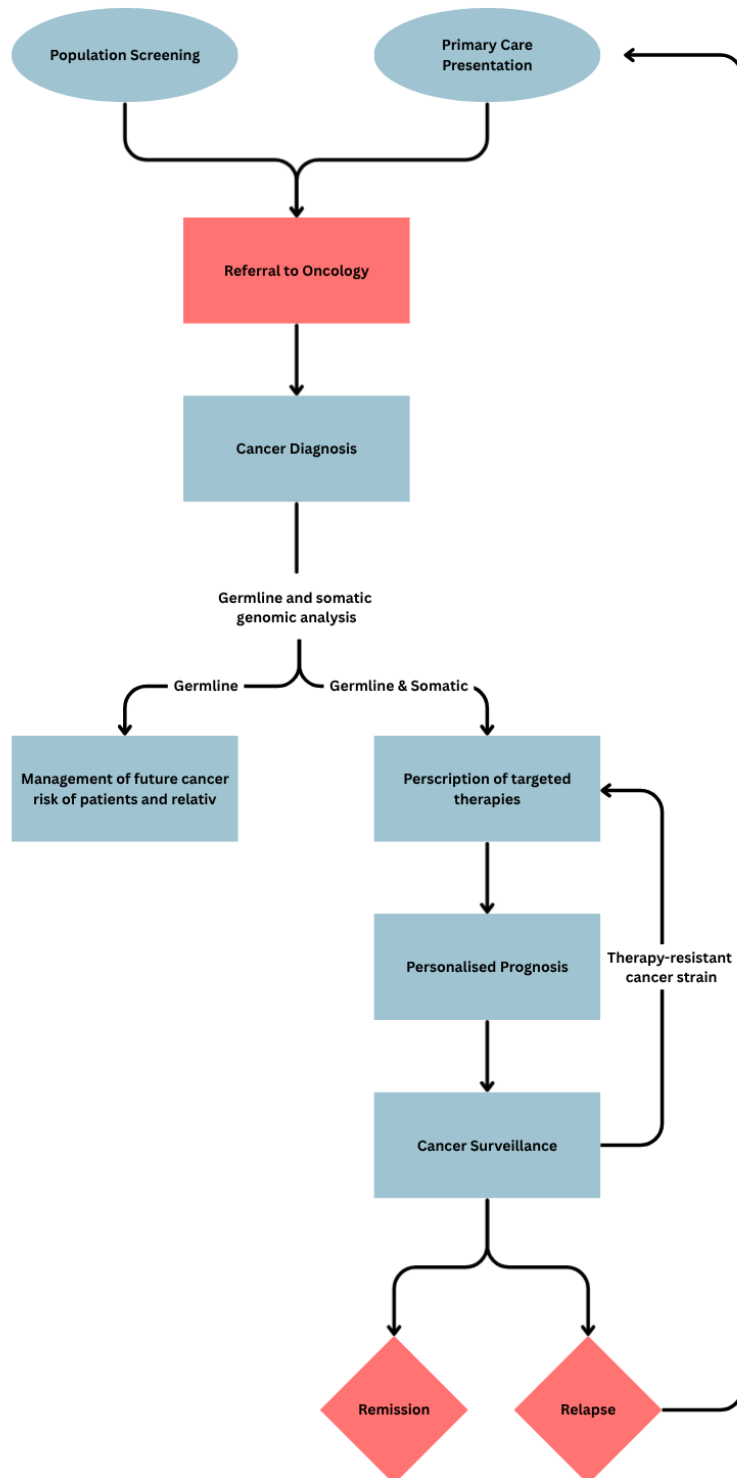


Figure 1.6. The future of precision oncology—a flowchart depicting the stages of the cancer care pathway. Blue boxes represent stages that will likely be personalised due to advances in genomic medicine over the next decade; red boxes represent other stages. Adapted from Seed (2021, p. 38).

1.4 The nursing workforce and the implementation of genomics in nursing practice

This section examines the role of the nursing workforce in the implementation of genomics into clinical practice. It outlines the growing need for a genomically capable workforce and considers the relevance of genomics to oncology nursing. It then explores how genomic practice aligns with professional nursing standards and the emergence of genomic nursing societies and advanced practice roles, before outlining key competency frameworks that define the knowledge, skills, and behaviours required for effective genomic practice. Understanding this context is essential to situating the current study and underpins its focus on the adoption of genomics within the oncology nursing workforce.

1.4.1 The need for a genomically capable workforce

Guttmacher and colleagues (2007) were among the first to describe the *genomic revolution* as one poised to reshape the future of healthcare, noting however that its clinical promise could only be realised with a workforce that is literate, capable, and competent in genomics. This observation remains highly relevant; all members of the health workforce require a level of genomic literacy that enables them to integrate genomics into interprofessional practice and adapt to rapidly advancing technologies (Guttmacher et al., 2007; Manolio et al., 2019; Tonkin et al., 2025). Developing such a workforce is therefore widely recognised as a prerequisite for the successful mainstreaming of genomics into healthcare systems worldwide (Lukhele et al., 2025; Stark, Dolman, et al., 2019). In the Australian context, there have been explicit calls to upskill non-genetics health professionals to support the mainstreaming of genomic medicine (O'Shea et al., 2022). While genetic specialists continue to play a vital role, the rapid growth in genomic testing—particularly in oncology—has exceeded the capacity of traditional clinical genetics services, necessitating greater involvement of healthcare providers outside specialist genetics in the delivery of genomic care (Campion et al., 2019; Nisselle et al., 2019; Rahman et al., 2022).

Within this new era of precision and genomic medicine, nurses occupy a central position in healthcare systems worldwide. As the largest professional group in the health workforce, with an estimated 29.8 million registered nurses globally (WHO, 2025), nurses are embedded across all sectors of care, from primary and community settings to highly specialised inpatient services. Their sustained, longitudinal engagement with patients and families across the care continuum positions nurses uniquely to provide ongoing support as individuals encounter and navigate genomic healthcare (Calzone et al., 2010; Calzone, Jenkins, Nicol, et al., 2013; Calzone & Badzek, 2025). Beyond their scale and reach, nurses play a critical role in translating scientific

innovation into ethically grounded, person-centred care. Precision health and genomics depend not only on technological advances, but on effective implementation through interprofessional collaboration, care coordination, and patient education—areas in which nurses have well-established expertise (Dewell, Benzies, & Ginn, 2020; Fu et al., 2020; Wright et al., 2019).

To remain current and practise safely amid the rapid integration of genomic science and emerging technologies, nurses at all levels of academic preparation, roles, and specialties must, at a minimum, possess foundational genomic literacy and competence (Calzone et al., 2024). Nurses require an understanding of genomic concepts to support key aspects of practice, including medication administration, patient advocacy for referral or targeted treatment, and patient education (Dewell et al., 2025). With appropriate genomic literacy (see Section 1.5), nurses can educate patients, facilitate referrals to genetic counselling services, contribute to the development of care pathways, engage in research activities, address ethical considerations related to genomics, and advocate for equitable policy initiatives (Limoges et al., 2022). Importantly, through established competencies in patient education and outreach, and the use of culturally and linguistically appropriate educational resources, nurses can play an important role in improving equitable access to genomic healthcare and addressing disparities (Katapodi et al., 2024). Indeed, integrating genomics into nursing practice has been articulated as a means of mitigating ethical, legal, and social risks, thereby supporting the provision of safe and effective patient care (Badzek et al., 2013). Accordingly, understanding nurses' genomic capability and preparedness is essential to determining how the nursing workforce can effectively respond to the demands of precision healthcare.

Organisations such as the WHO and the International Council of Nurses (ICN) have also affirmed the relevance of genomics to the nursing profession. The WHO (2022) emphasises the need to embed genomics into pre-qualification health education in all member states, while the ICN *Code of Ethics* highlights informed consent, privacy, and confidentiality as essential principles in managing genomic information (ICN, 2021). Additionally, the Sigma Theta Tau International Honor Society of Nursing identified genetic testing and research evaluating the implications of genetic advances as a priority for global nursing research and health equity (Sigma Theta Tau International, 2005). These international positions strengthen the argument that nursing engagement with genomics is not optional but essential, necessitating exploration of how nurses engage with and adopt genomics in practice and the enablers and barriers to doing so.

In the Australian context, the Australian College of Nursing (ACN) has articulated a congruent position through its 2020 statement *Nurses, Genomics and Clinical Practice* (ACN, 2020). It outlines a commitment to fostering a nursing workforce that is workplace-ready in the genomics era, supporting nurse leadership, and enhancing genomic literacy in practice. Together, these positions emphasise that genomic capability is integral to safe, person-centred, and evidence-based nursing care and lay the foundation for exploring how oncology nurses engage with genomic practice.

1.4.2 Alignment with professional nursing standards and practice expectations

The nurse–patient relationship is often characterised by high levels of trust, with patients and families relying on nurses for information and support during complex decision-making (Allande-Cussó et al., 2022). Relational and communicative nursing interventions foster patient engagement and an environment in which patients feel safe disclosing sensitive information (Crivelli et al., 2024), while nurses’ ongoing holistic presence and ability to translate complex concepts into accessible, patient-centred dialogue enhances understanding and empowerment (Grant et al., 2025). These relational competencies take on particular significance in genomics, where uncertainty and emotional complexity are common. Collectively, nurses’ capabilities in contextualising information, clarifying meaning, patient advocacy, interprofessional collaboration, and coordinating care align strongly with the demands of genomic healthcare (Moore et al., 2018).

Combined with nursing’s holistic approach to care, these capabilities position nurses to integrate genomics into practice and to lead efforts addressing genomic health disparities at clinical, policy, and systems levels (Fu et al., 2020; Katapodi et al., 2024). Core functions such as collecting and interpreting family history, explaining complex health information in accessible ways, advocating for patient preferences, and coordinating multidisciplinary care are all central to effective genomic practice (Calzone et al., 2024; Camak, 2016; Aiello, 2015).

In the Australian context, these responsibilities align directly with the expectations articulated in the Nursing and Midwifery Board of Australia (NMBA) *Registered Nurse Standards for Practice* (2016) and the *Code of Conduct for Nurses* (2018). For example, Standard 1 requires nurses to think critically and analyse practice, encompassing the evaluation of genomic information within personal and family histories. Standard 2 emphasises therapeutic and professional relationships, including the communication of sensitive risk information in culturally safe ways. Standard 3 highlights maintaining capability for practice, underlining the

need for ongoing professional learning to keep pace with rapidly advancing genomic technologies. Table 1.1 illustrates selected examples of how genomic nursing practice maps onto NMBA standards and the Code of Conduct. While not exhaustive, these examples demonstrate that genomic nursing is not a separate discipline but an extension of established professional expectations.

Table 1.1. Genomic nursing practice mapped to standards and codes

NMBA Standard / Code	Description	Example in Genomic Nursing Practice
Standard 1 – Thinks critically and analyses nursing practice (NMBA, 2016)	Applies critical thinking to inform and improve practice	Evaluating genomic test results in the context of personal and family history to guide appropriate care or referral
Standard 2 – Engages in therapeutic and professional relationships (NMBA, 2016)	Builds trust, communicates effectively, respects cultural safety	Explaining genetic risk and implications to patients and families in clear, sensitive, and culturally safe ways
Standard 3 – Maintains capability for practice (NMBA, 2016)	Undertakes ongoing professional development and self-care	Updating knowledge on emerging genomic technologies and evidence to ensure safe and current practice
Standard 4 – Comprehensively conducts assessments (NMBA, 2016)	Uses a systematic approach to assessment	Taking a detailed family health history to identify potential hereditary conditions
Standard 6 – Provides safe, appropriate, and responsive quality nursing practice (NMBA, 2016)	Delivers care that is evidence-based and meets the individual’s needs	Coordinating genetic testing and follow-up care tailored to the patient’s circumstances and values
Code of Conduct – Person-centred and ethical practice (NMBA, 2018)	Upholds respect, autonomy, confidentiality, and justice	Obtaining informed consent for genetic testing, ensuring privacy of genetic information, and discussing potential familial implications

In addition to professional standards, genomics amplifies ethical responsibilities already inherent in nursing practice. Issues of informed consent, confidentiality, equitable access, and the familial implications of genetic information are central to genomic care (Ascencio-Carbajal et al., 2021). Nurses are often the professionals who help patients navigate these complexities, ensuring decisions are informed, respectful, and contextually appropriate while navigating the cultural considerations of their patients (Badzek et al., 2013). Integration of genomics into nursing thus does not represent a departure from established roles and standards but, rather, their natural evolution into a new domain of practice. This professional alignment has also been reflected in the global formation of nursing societies and advanced practice roles dedicated to genomics.

1.4.2.1 Genomic nursing societies and associations

The growing recognition of genomics as a core component of nursing practice has prompted the formation of professional communities and societies dedicated to advancing the field. National societies for genetic and genomic nurses exist in the United Kingdom, United States, the Netherlands, Japan, Taiwan, and Brazil (Calzone et al., 2018b). These groups provide professional development, advocacy, and leadership to ensure that genomics is effectively integrated into nursing education and clinical practice.

At the international level, the International Society of Nurses in Genetics (ISONG), founded in 1988, has played a central role in fostering the scientific and professional growth of nurses in human genetics and genomics worldwide (ISONG, n.d.). Subsequently, the Global Genomics Nursing Alliance (G2NA) was established to promote the integration of genomics into everyday nursing practice, with an emphasis on education, policy engagement, and workforce collaboration (Calzone, Kirk, et al., 2018b). Additionally, the Omics Nursing and Science Education Network (ONSEN) was developed recently to provide an interdisciplinary resource platform supporting the integration of omics concepts into nursing education and research. ONSSEN stress the importance of nurses understanding the genomic basis of disease and its associated symptoms, reinforcing the need for genomics literacy across both research and clinical domains (Tully et al., 2020). Together, these organisations illustrate the profession's commitment to building genomic nursing capacity globally. Notably, while Australian nurses contribute to these international communities, there is currently no equivalent national organisation dedicated to genetic or genomic nursing.

1.4.2.2 Genomic advanced practice roles

In parallel with the establishment of professional societies, several countries have introduced specialist advanced practice nursing roles in genetics and genomics to meet the growing demand for genomic healthcare (Barr et al., 2018; Dragojlovic et al., 2020; International Society of Nurses in Genetics & American Nurses Association, 2007). These developments reflect the increasing professionalisation of genomic nursing and underscore the leadership potential of nurses in shaping precision healthcare. In the Australian context, however, little is known about nurses working in genetics or genomics. The available literature does not describe the size of this workforce, the types of roles nurses occupy, or the scope of their practice, making it difficult to ascertain how genomic nursing is currently configured nationally. Unlike some international jurisdictions, Australia has no formally defined specialist roles or recognised

career pathways in genomic nursing, and nursing bodies have not articulated a coordinated agenda for developing such positions. This contrasts with the NMBA's definition of advanced nursing practice, which emphasises complex decision-making, autonomous practice, and leadership across clinical, educational, and systems levels (NMBA, 2019). These attributes position advanced practice nurses at the intersection of clinical expertise and workforce development, suggesting they may be well placed to facilitate genomic integration through both direct patient care and organisational change.

While Australian nurses may participate in international collaborations and benefit from global initiatives, the absence of formalised national structures or policy support represents a critical workforce development gap. Addressing this gap will be essential to ensure Australia's nursing workforce is equipped for the genomic era and capable of contributing to the implementation of precision medicine across health systems. To achieve this, professional societies and advanced practice roles must be supported by clearly defined genomic competency frameworks that articulate the knowledge, skills, and attitudes required for safe and effective practice. The following section situates these issues within the context of oncology nursing practice, before examining the competency frameworks that underpin the development of a genomically capable nursing workforce.

1.4.3 Oncology nursing and genomic practice

Oncology nurses provide continuous care across the cancer trajectory, offering repeated opportunities to explain genomic information, facilitate testing, support decision-making, and coordinate referrals to genetics services (Jenkins, 2011; Limoges, Puddester, Gretchev, et al., 2024; Rahman et al., 2022; Young et al., 2020). Oncology nurses are increasingly expected to develop competencies in areas such as family history taking, pedigree construction, identifying hereditary risk indicators, facilitating referral to genetics services, engaging in interdisciplinary collaboration, and supporting patients through the ethical and cultural considerations associated with genomic information (Dickman et al., 2025; Hoxhaj et al., 2022). As genomics becomes further mainstreamed, non-genetic clinicians, including oncology nurses, are also assuming greater responsibility for elements of pre-test counselling, consent, and test coordination, embedding genomics more deeply into routine cancer care (Bokkers et al., 2022; Scott et al., 2020). The expanding use of precision therapies similarly extends nursing responsibilities, from assisting patients on targeted regimens and managing toxicities to interpreting pharmacogenomic information and providing education about the meaning of genomic or omic

tests (Fu et al., 2020; Lebet et al., 2019). Beyond bedside care, they contribute to research, education, and policy by supporting genomic clinical trials, advancing patient literacy, advocating for equitable access, and addressing health disparities (Katapodi et al., 2024; Limoges, Chiu, et al., 2024; Vorderstrasse et al., 2014; Young et al., 2020). These activities demonstrate how genomics is no longer confined to specialist teams but is embedded in everyday oncology nursing practice. Genomic literacy (see 1.5) is therefore essential, enabling nurses to translate complex information into language that is understandable and meaningful for patients and families (Mahon, 2024), while reducing potential errors and improving care quality (Friend et al., 2021).

Collectively, these contributions position oncology nurses as active agents in the translation of genomics into practice, rather than passive recipients of the genomic era. However, fulfilling this role requires contemporary knowledge, communication skills, and confidence in applying genomic information (Rahman et al., 2022). The competencies required to support this capability are discussed in Section 1.4.4. Importantly, these competencies align closely with the foundational standards and expectations that guide professional nursing practice, thus linking the integration of genomics into nursing directly with the core values, communication skills, and ethical commitments outlined in the following section.

1.4.4 Competency frameworks for genomic nursing practice

To practise safely and effectively in this genomic era, nurses require clearly defined genomic competencies which encompass the knowledge and skills necessary to provide ethical, person-centred, and evidence-based genomic care (Calzone et al., 2024; Jenkins & Calzone, 2007). In a systematic scoping review, Thomas et al. (2023) found that global clinical integration of genomics remains limited, largely due to a healthcare workforce lacking genomic competency. The review identified minimal literature addressing genomic nursing competencies and emphasised that substantial work is needed to build genomic nursing capacity. The authors concluded that establishing core competencies is a critical component of workforce development, providing a foundation to guide nursing education, training, and standards of care. This evidence reinforces the importance of competency frameworks as a mechanism for advancing workforce readiness and integrating genomics into practice.

Given the wide-ranging application of genomics in healthcare, genomic competence is required of nurses across all educational levels, professional roles, and clinical specialties. This encompasses nurse educators preparing future practitioners, nurse leaders and managers

overseeing the workforce, nurse researchers, those contributing to policy development, and nurses providing direct patient care. Recognition of this universal requirement for genomic knowledge, skills, and attitudes underpinned efforts to define a set of minimum genetics and genomics competencies applicable to the nursing profession as a whole (Calzone et al., 2024).

These expectations have been formalised in several national frameworks, which have become a central mechanism for standardising genomic nursing practice globally. The United States led this work with the *Essential Nursing Competencies and Curricula Guidelines for Genetics and Genomics*, first reported in 2006, refined in 2009 with outcome indicators, and most recently updated in 2024 to encompass whole-genome and somatic applications (Calzone et al., 2024; Consensus Panel on Genetic/Genomic Nursing Competencies, 2006, 2009; Jenkins & Calzone, 2007). The American Nurses Association (ANA) now recognises genomics as a central science for nursing, with competencies organised across four domains: assessment, care planning, interprofessional collaboration, and evaluation (Calzone et al., 2024). Internationally, the United Kingdom produced its first competency framework in 2003 (Kirk, 2004), subsequently revised to align with the *NHS Genomic Competency Framework for Nurses and Midwives* (NHS, 2023); Europe extended this work to multiple health professions (Skirton et al., 2010); and Japan developed national genomic nursing competencies through expert consensus (Murakami et al., 2020). At the global level, G2NA is developing minimum international genomic competencies applicable across nursing roles and education levels (Tonkin et al., 2025).

Genomic nursing competencies broadly centre on assessment, risk identification, referral, and the provision of patient education, care, and support. Achieving these competencies requires all nurses, regardless of role or practice setting, to possess foundational knowledge of genomics and its relevance across healthcare disciplines and levels of practice (Calzone et al., 2024; Calzone & Badzek, 2025). Core expectations include the ability to undertake a genomically informed assessment, such as collecting and interpreting a three-generation family history; recognising indicators of hereditary risk; facilitating timely referral for further genetic evaluation; and effectively addressing patient and family advocacy needs (Calzone et al., 2024; Camak, 2016). In addition to technical skills, genomic competence requires relational capabilities. This includes demonstrating in practice the importance of tailoring genomic information and services to individuals based on culture, religion, knowledge level, health literacy, and preferred language when communicating about genomic testing, results, and

referral pathways (Calzone et al., 2024). Together, these skills and attributes constitute the minimum standard for genomic practice across all nursing roles and clinical contexts.

Within oncology, genomic competence assumes heightened importance due to the expanding role of genomics in precision cancer care. In the context of precision health, nurses are increasingly expected to incorporate genomic competencies into the delivery of personalised care (Dewell et al., 2020). For oncology nurses, understanding genomics is therefore critical to reducing potential clinical errors, enhancing patient comprehension, and supporting the delivery of high-quality, evidence-based care (Friend et al., 2021; Mahon, 2017). Pharmacogenomics represents a particularly salient area of competency within oncology, given the increasing use of targeted therapies and genomically informed treatment selection. Knowledge in pharmacogenomics has been identified as an essential nursing competency (Cheek, 2015) and is positioned alongside broader genomic understanding as necessary for safe medication management and effective patient education in oncology settings (Cheek et al., 2015; Germany & Kueber, 2023).

Despite international efforts to develop broad genomic competency frameworks for nurses (Calzone et al., 2024; NHS, 2023), there remains a scarcity of frameworks specifically tailored to oncology nursing practice (Dickman et al., 2025). One international systematic review and modified Delphi study identified core cancer-genomics competencies for non-genetic healthcare professionals, including nurses, and organised these competencies across domains of knowledge, attitudes, and practical abilities (Hoxhaj et al., 2022). This work emphasised foundational genomic understanding, psychosocial awareness, and practical skills such as eliciting multigenerational family histories, constructing pedigrees, and supporting patients' access to screening and genetic services (Hoxhaj et al., 2022). Dickman et al. (2025) mapped existing genomic nursing competency frameworks directly to oncology practice through a crosswalk approach, demonstrating how general genomic competencies translate into oncology-specific activities such as participating in nurse-led clinics, supporting patients through biomarker testing, educating patients on cancer-specific concepts (e.g., differences between somatic and germline testing), and coordinating long-term follow-up and family communication of risk. Together with the cancer-genomics competencies identified by Hoxhaj et al. (2022), this work demonstrates that relevant genomic competencies for oncology practice have been articulated at a conceptual level. However, the existence of competency statements alone does not indicate whether oncology nurses possess the foundational genomic knowledge, confidence, and engagement required to enact these competencies consistently in clinical

practice. Understanding whether, and to what extent, oncology nurses currently hold these foundational attributes is therefore critical to supporting the effective integration of genomics into precision cancer care

Collectively, these initiatives underscore the centrality of competencies in workforce development, curriculum design, and the delivery of safe, equitable genomic healthcare (Thomas et al., 2023). Despite substantial international progress, Australia has not yet established a national genomic nursing competency framework, leaving the profession without a consistent mechanism to guide education, practice, or policy. Addressing this gap is critical to preparing Australia's nursing workforce for the integration of genomics into routine care and ensuring alignment with evolving global standards.

Underlying all genomic competency frameworks is the fundamental requirement that nurses possess sufficient genomic literacy, knowledge, and attitudes on which such competencies are built. In contexts where oncology-specific frameworks remain limited or absent, insight into nurses' baseline genomic literacy, confidence, and engagement becomes particularly important, as these foundational elements underpin the capacity to adopt, enact, and sustain genomic practice irrespective of formal competency standards. The following section therefore examines these foundational dimensions in greater depth.

1.5 Genomic literacy, knowledge, and attitudes

The call for genomic nursing competencies established in Section 1.4.4 stemmed from the recognised need for nurses to possess the genomic knowledge, skills, and attitudes required to deliver safe, person-centred, and evidence-based care (Calzone et al., 2024; Jenkins & Calzone, 2007). Central to this expectation is genomic literacy, defined as the knowledge, skills, and attitudes needed to appropriately apply genomic information in clinical practice (Calzone et al., 2014; Hurle et al., 2013). Genomic literacy is now widely recognised as fundamental to the delivery of high-quality, person-centred nursing care, extending beyond scientific understanding to include the ability to communicate complex genomic concepts, support informed decision-making, and navigate the ethical and sociocultural dimensions of genomic care (Calzone et al., 2024).

Maintaining genomic literacy is essential as ongoing scientific and technological advances continue to reshape healthcare. To remain current amid the rapid integration of genomics into clinical practice, nurses must possess a baseline level of genomic knowledge and competency

(Calzone et al., 2024). Genomic understanding underpins key aspects of nursing practice, including medication administration, patient advocacy for referral or targeted treatment, and patient education (Dewell et al., 2025). A nursing workforce with genomic literacy enables the effective integration of genomics into routine clinical practice, facilitates access to appropriate resources for patients and families, and supports broader professional contributions, including patient education, referral to genetic counselling services, research participation, addressing ethical issues associated with genomics, and advocacy for equitable public policy (Dewell et al., 2024; Limoges et al., 2022). Conversely, substantial evidence indicates that inadequate genomic literacy can contribute to adverse events in clinical practice (Friend et al., 2021).

These considerations are particularly relevant in oncology, where nurses increasingly engage with genomic information across screening, treatment, and survivorship care. Oncology nurses cannot accurately apply genomic knowledge in practice without foundational genomic literacy, and limitations in this area have implications for the safe and effective delivery of care (Friend et al., 2021). This is especially important given the central role oncology nurses play in translating complex genomic information into forms that are comprehensible and meaningful for patients and families (Mahon et al., 2024).

Within this context, pharmacogenomics represents a particularly visible and clinically embedded application of genomics in oncology. As targeted therapies and genomically informed treatment selection become more common, oncology nurses are increasingly required to engage with pharmacogenomic information in routine practice. To apply pharmacogenomics appropriately, nurses require a clear understanding of pharmacogenomic principles, including how DNA specimens are collected, how test results are interpreted, and how to educate patients about the lifelong implications of pharmacogenomic findings (Germany & Kueber, 2023).

As a measurable construct, genomic literacy is often examined through nurses' *knowledge* and *attitudes*, which together provide critical insight into workforce readiness for genomic integration. Definitions of these constructs are grounded in Calzone et al.'s (2012; 2013) seminal work, which drew on Rogers' (2003) *Diffusion of Innovations* (DOI) theory (discussed further in Chapter 2). Within this framework, *knowledge* refers to awareness and understanding of genomics and its clinical application, whereas *attitudes* capture nurses' perceptions of genomics' value and receptivity and relevance to practice, shaping their willingness to engage with it.

Closely related constructs include *confidence*—the degree of certainty nurses feel in applying genomics—and *preparedness*, their perceived readiness to integrate it into care. These factors are interdependent: greater knowledge tends to foster more positive attitudes and higher confidence, whereas deficits in these domains undermine preparedness and uptake. These interdependencies are also noted by Plavskin et al. (2019), who proposed a conceptual model positioning nurses' genomic competency and knowledge as antecedents to attitudes and receptivity, which subsequently influence adoption (Figure 1.7). Confidence mediates this relationship by shaping nurses' perceived ability and willingness to apply genomics in practice. The model further highlights the pervasive role of social systems, which exert both direct and indirect influence across all variables. Collectively, these relationships suggest that knowledge acquisition initiates a sequential process of attitude formation, confidence building, and eventual behavioural uptake—a dynamic that informs the conceptual basis of the present study. Given these relationships, examining nurses' genomic knowledge and attitudes is critical to understanding workforce readiness and the factors that influence adoption. The following section examines the evidence on nurses' genomic knowledge and attitudes to contextualise these constructs within current practice.

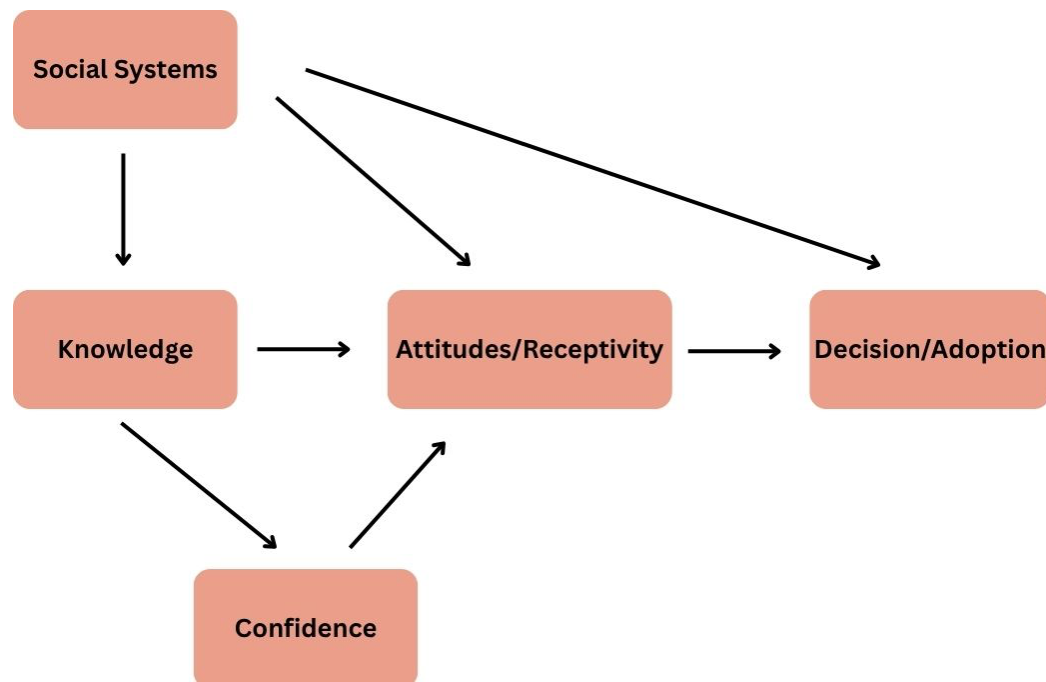


Figure 1.7. Conceptual model of relationships between competency, attitudes, confidence, and adoption. Adapted from Plavskin et al. (2019).

1.5.1 Assessment of genomic literacy

Recognising the importance of nurses' genomic knowledge and competency, there are only two validated instruments currently available to assess nurses' genomic knowledge and competency: the Genomic Nursing Concept Inventory (GNCI), which measures conceptual understanding of key genomic principles, and the Genetics & Genomics in Nursing Practice Survey (GGNPS), which evaluates nurses' genomic knowledge, attitudes, and practice behaviours (Ward et al., 2014). The GNCI focuses on theoretical genomic knowledge and is most appropriate for assessing students or academic faculty. The GGNPS centres on applied nursing practice and is particularly suited to evaluating practising nurses. However, it was developed for general nursing populations within the United States and includes content areas that may be less directly aligned with oncology-specific genomic contexts (e.g., chronic disease management such as diabetes) or with features of the Australian health system. While adapted versions have recently been developed in Canada and China (Limoges, Puddester, Pike, et al., 2024; Zhao et al., 2022), published evidence regarding cross-cultural applicability, comparability, and established face validity for oncology nursing populations or for use within the Australian healthcare context remains limited. This absence underscores the rationale for the scoping review presented in Chapter 3 and informed the decision to adapt an existing survey instrument for the present study to enable the exploration of oncology-specific genomic knowledge, attitudes, and adoption behaviours.

1.5.2 Evidence on nurses' knowledge and attitudes towards genomics

Building on the conceptual foundations outlined in the previous section, internationally, evidence consistently indicates that nurses' genomic knowledge and confidence remain limited despite increasing recognition of genomics' relevance to practice. Early synthesis by Skirton, O'Connor, and Humphreys (2012) demonstrated that nurses lacked sufficient knowledge and skills to meet core genetic and genomic competencies. A subsequent systematic review by Wright et al. (2018), conducted to update this evidence, identified 12 new studies and confirmed that nurses continued to demonstrate poor genomic knowledge and competency, even though most acknowledged genomics as important to their role.

More recent reviews indicate that this gap has persisted over the past decade. A systematic scoping review of literature published between 2012 and 2022 found that nurses continue to hold misconceptions and inaccuracies in their understanding of genomics, which in turn limits integration into clinical practice (Thomas et al., 2023). Similarly, a recent scoping review by

Dante et al. (2025) revealed widespread low levels of genomic literacy among clinical nurses, students, and faculty, encompassing deficits across knowledge, competency, practical application, and confidence.

In Australia, research into nurses' genomic knowledge, attitudes, and preparedness remains limited but is gradually emerging. The first large-scale national assessment by Wright et al. (2019) found that registered nurses and midwives demonstrated low genomic literacy, with mean scores on the GNCI falling below established thresholds. Although most participants (80.5% of RNs and 97.2% of midwives) acknowledged genomics as relevant to their practice, more than 80% rated their knowledge as inadequate—mirroring international trends where nurses recognise genomics as important yet feel underprepared to apply it in care.

Focusing specifically on oncology, Wright et al. (2020) conducted the first qualitative exploration of Australian oncology nurses' genomic engagement through interviews at a large regional hospital in Queensland. Three themes were identified: adequacy of knowledge, relevance of knowledge, and application in practice. Participants described their understanding as 'poor' or 'average', with most limiting their interpretation of genomics to targeted therapies and family-history taking. While they valued its relevance, few could articulate how genomics informed daily clinical decision-making, underscoring a persistent theory–practice gap. The study's regional single-site design, however, highlights the need for broader national research capturing the diversity of oncology nursing contexts. Recent investigations have begun to evaluate the impact of educational interventions. Alexander et al. (2024) reported significant short-term improvements in nurses' and midwives' confidence across multiple genomic domains following participation in national workshops, yet found that ongoing self-reported learning needs remained. Similarly, Saleh et al. (2019) found that while Australian nurses, midwives, and allied health professionals expressed strong interest in genomics education, they lacked clarity about credible resources and prioritised learning in genetic fundamentals, recognition of hereditary conditions, and the psychosocial dimensions of testing.

Collectively, Australian evidence depicts a workforce that values genomics but remains underprepared to integrate it confidently into routine care. Existing studies are limited by small or localised samples and variable methodologies, leaving no consistent national picture of nurses' genomic knowledge, attitudes, and readiness. Addressing these gaps is critical to building a genomically capable nursing workforce and provides the rationale for the present study, which examines these issues within the context of Australian oncology nursing.

1.5.2.1 Oncology nurses' genomic knowledge and attitudes

As established, while oncology nurses occupy pivotal positions across the cancer care continuum, their ability to deliver genomically informed care depends not only on competency frameworks but also on their knowledge and attitudes toward genomics in practice. However, the existing literature examining these domains is limited and methodologically inconsistent. Although several reviews have examined genomic literacy, education needs, and competency development among general nursing populations (Cao et al., 2025; Dante et al., 2025; Thomas et al., 2023; Wright et al., 2018), none have specifically focused on oncology nurses' genomic knowledge and attitudes. This represents a critical gap, as oncology nurses practise within a genomically intensive specialty and routinely care for patients whose treatment and prognosis are directly informed by genomic information. Understanding their baseline knowledge and attitudes is therefore essential to inform education, research, and policy development. Yet the available evidence remains fragmented, with studies varying in conceptual focus, sample characteristics, and measurement approaches, often relying on unvalidated instruments. These inconsistencies not only hinder comparative assessment of preparedness and the development of targeted strategies for workforce capacity-building but also make it difficult to identify clear evidence gaps to inform future research design.

To address these limitations, the scoping review presented in Chapter 3 mapped global evidence on oncology nurses' genomic knowledge and attitudes to establish the current state of literature, identify critical gaps, and inform subsequent phases of this thesis. Moreover, knowledge and attitudes should not be viewed merely as educational outcomes but as key determinants of innovation adoption. As conceptualised within Rogers' Diffusion of Innovations framework, knowledge forms the foundation for attitude formation, which in turn influences adoption decisions (Rogers, 2003). This theoretical framing is explored further in the following chapter (Chapter 2). Building on this understanding, the next section considers how these competencies and behavioural determinants are operationalised through implementation strategies, benchmarking initiatives, and capacity-building efforts that support genomic integration across health systems.

1.6 Implementation, benchmarking and capacity building for genomic integration

Building on the preceding discussion of genomic competencies and the behavioural determinants of adoption, it is necessary to consider how these elements are operationalised through implementation strategies, benchmarking initiatives, and capacity-building efforts that

support genomic integration across health systems. Having established the competencies required for genomic nursing, the next challenge concerns how these competencies are implemented and sustained across practice, education, and policy. Internationally, this implementation agenda has been progressed through the G2NA, which developed a roadmap for accelerating genomics integration in nursing (Figure 1.8; Tonkin et al., 2020b). Drawing on the Consolidated Framework for Implementation Research (CFIR) (Damschroder et al., 2009), the roadmap outlines an evidence-informed process for planning, engaging stakeholders, executing, and evaluating genomic implementation, with ongoing reflection and evaluation embedded throughout. It emphasises identifying barriers and facilitators as a crucial part of the implementation process, and highlights the importance of leadership, collaboration, and accessible resources to enable sustainable genomic integration.

To operationalise the roadmap, G2NA developed the Assessment of Strategic Integration of Genomics across Nursing (ASIGN) maturity matrix. ASIGN identifies six critical success factors underpinning genomic implementation and enables organisations and systems to evaluate their level of genomic integration over time. Together, the roadmap and ASIGN represent a coordinated international approach to embedding genomics within nursing, providing a model for capacity building and strategic implementation.

Alongside these structural approaches, implementation science recognises that the success of such frameworks depends not only on structural and policy factors but on individual adoption. Drawing on Rogers' DOI theory, Leach et al. (2016) applied behavioural-change theory to propose that identifying and supporting early nurse adopters is a key strategy for accelerating genomic integration. Their work posits that successful implementation relies on individuals who both adopt innovations and influence others, reinforcing adoption as a social and behavioural process rather than a purely educational one. Relatedly, Andrews et al. (2014a, 2014b) empirically examined the characteristics of nurse adopters, identifying that opinion leadership, openness to experience, and communication networks can shape how innovations diffuse through professional groups. These studies position adopters as critical change agents capable of catalysing broader genomic uptake within nursing practice.

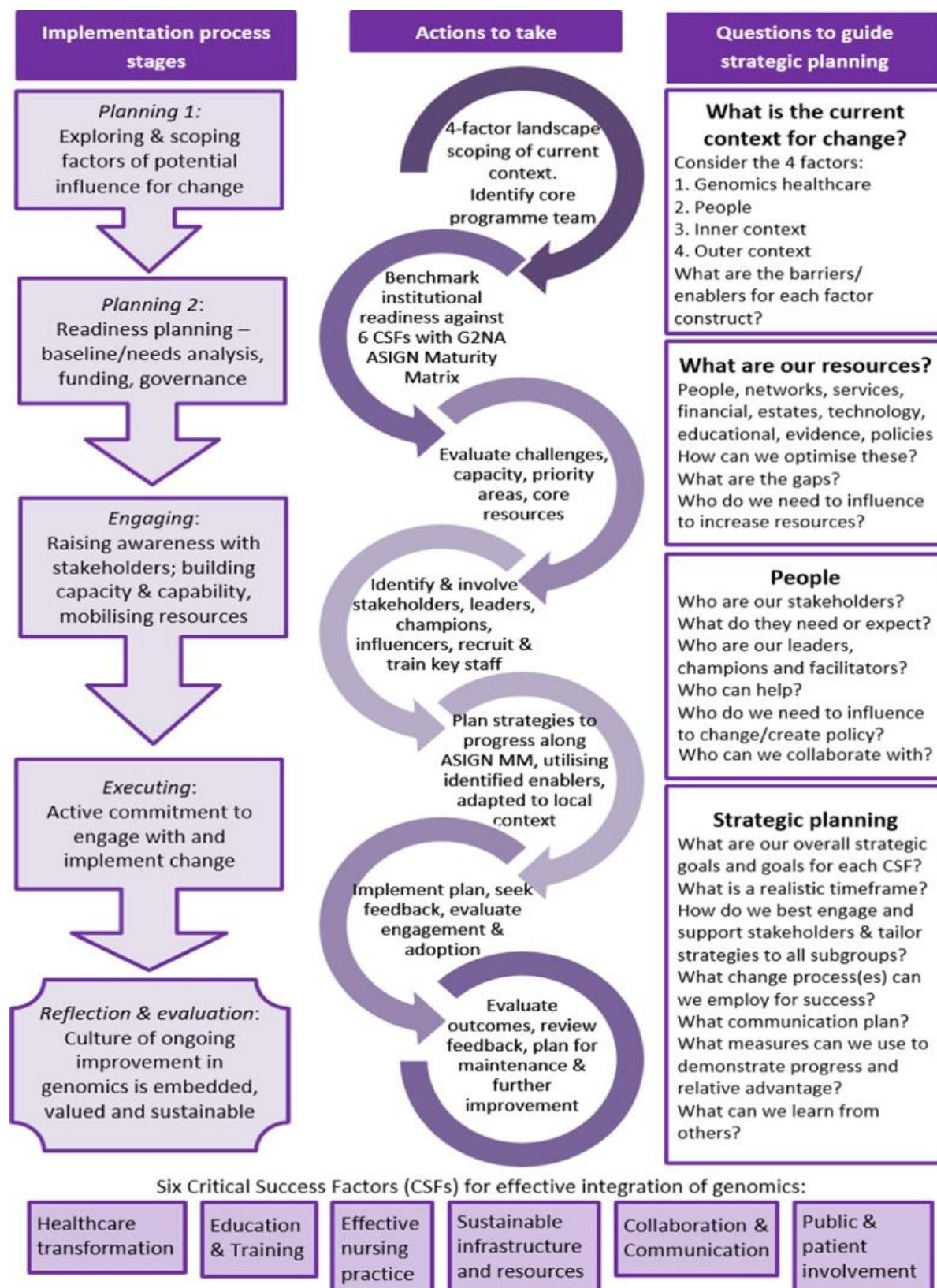


Figure 1.8. Global Genomics Nursing Alliance Roadmap for nurse leaders to implement genomics across nursing. Source: Tonkin et al. (2020b, p. 335).

Despite this international effort, these implementation mechanisms have not been applied or established within the Australian nursing context. While genomics has advanced rapidly within medicine and allied health, there remains no consistent process for assessing national nursing preparedness or identifying workforce-specific implementation barriers. This gap is particularly salient in oncology, where genomic mainstreaming is advancing most rapidly but nursing readiness remains underexplored. Understanding these contextual barriers and enablers is therefore essential to inform how such global frameworks might be adapted to the Australian context in future. Addressing this implementation gap also requires attention to the individual and behavioural factors that influence adoption.

Given the pace at which clinical genomic applications continue to emerge, implementation research is needed to determine how best to ensure their prompt adoption, systematic scale-up, and sustained integration into routine care to improve patient outcomes (Manolio et al., 2019; Roberts et al., 2017). Collectively, this body of work highlights that integrating genomics into nursing is not solely a matter of defining competencies but also of understanding how innovation diffuses through the workforce. Sustainable implementation requires identifying and engaging nurse adopters who can influence and support others during the diffusion process, while simultaneously addressing the contextual barriers and enablers that shape engagement.

In reviewing this literature, it became evident that key determinants of genomic integration, namely the individual characteristics of adopters and the organisational, educational, and systemic factors that support or constrain uptake, have scarcely been examined in the Australian nursing context. These insights informed the development of the present study's aims and objectives, which seek to address this evidence gap by investigating how Australian oncology nurses engage with genomics, who is adopting it, and what factors influence its uptake.

1.7 Factors influencing genomic adoption

The successful adoption of genomics into nursing practice depends on a range of interrelated influences that shape whether and how new approaches are adopted. These influences extend beyond individual knowledge and competence to include organisational, educational, and system-level conditions that can enable or constrain change (Nilsen, 2020). This section provides a brief overview of these factors and introduces the barriers and enablers that have been identified in the literature as key determinants of genomic adoption in nursing.

1.7.1 Barriers and enablers to genomic integration

A core function of implementation research is the systematic identification of factors that influence whether an innovation is adopted, implemented, and sustained in practice. Nilsen (2020) describes these as *determinants*, encompassing barriers and enablers operating across individual, organisational, and system levels. Identifying these determinants is essential not only for understanding the conditions under which innovations are used, but also for selecting and tailoring implementation strategies to address barriers, enhance facilitators, and support real-world practice change (Nilsen, 2020). Understanding these determinants is therefore critical for examining how nurses engage with genomics, as they shape the conditions under which genomic knowledge, competencies, and behaviours translate into clinical practice.

Substantial evidence underscores the importance of systematically assessing barriers and enablers associated with the innovation itself, the potential adopters, and the broader health practice environment (Bach-Mortensen & Verboom, 2020; Handley et al., 2016; Kirchner et al., 2020; Lewis et al., 2018). Such assessments are critical for identifying factors that may impede or facilitate uptake (Graham & Logan, 2004; Harrison & Graham, 2021). The insights gained from this process inform the selection and tailoring of implementation strategies to address identified barriers and strengthen existing supports for knowledge translation into practice (Grimshaw et al., 2012). Assessment of the practice environment for possible barriers and facilitators is essential, especially when the potential adopters are nurses, who deliver the majority of direct patient care and often implement evidence-based changes at the point of care (Estabrooks, 2003; Harrison & Graham, 2021; Squires et al., 2021). In the context of genomics, this aligns with calls to assess existing levels of genomic integration, identify barriers, and gauge readiness to inform collaborative global efforts to increase nursing capacity for genomic practice (Calzone, Kirk, et al., 2018b; Tonkin et al., 2020b).

Globally, the literature demonstrates that challenges to genomic integration in nursing are multifaceted, reflecting limitations in education, infrastructure, leadership, and workforce preparedness. In their global survey of nursing leaders across 18 countries, Calzone et al., (2018b) identified critical barriers including limited access to point-of-care educational materials and decision support, a lack of genomic expertise, and insufficient opportunities for training. Education-specific challenges included inadequate curriculum time, a shortage of qualified educators, and the absence of competency assessment requirements for practice. At a systems level, the absence of national leadership, limited professional recognition of nursing's

role in genomics, and competing health priorities further constrained integration efforts. The most urgent priority areas for action were raising awareness, strengthening education, and ensuring resources to support nursing engagement with genomics. They also emphasised the establishment of national and international collaborations and openness to innovative training approaches to accelerate integration (Calzone et al., 2018b).

Subsequent analyses confirm that these structural issues persist, as Tonkin et al. (2020) reported the most significant obstacles continue to involve inadequate leadership, a lack of agreed standards for training, and limited access to education and resources. More recently, Tonkin et al. (2025) identified four major roadblocks impeding genomic integration: the deprioritisation of genomics within health systems; a shortage of nurse educators capable of teaching genomics; the rapid pace of genomic discovery outstripping workforce readiness; and insufficient recognition by nursing leadership and credentialing bodies. Relatedly, Thomas et al. (2023) concluded in their review that the global integration of genomics remains limited, primarily because of a workforce lacking genomic competence and that limited knowledge, communication skills, and confidence among clinicians posed barriers to supporting patients' genomic decision-making.

Empirical studies provide further evidence of the barriers and enablers shaping nurses' engagement with genomics. Hines-Dowell et al. (2024) found that paediatric oncology nurses identified time constraints, limited educational materials, lack of understanding and confidence, and uncertainty regarding scope of practice as significant barriers to genomic utilisation. White et al. (2020), in a scoping review including nurses and physicians in secondary and tertiary care, reported similar obstacles—limited genetics knowledge, low confidence in initiating genomic discussions, inadequate resources and guidelines, and concerns about patient discrimination and psychological harm. Facilitators included positive attitudes toward genetics and a willingness to engage in genomic education when opportunities were available. In a recent Canadian study, Chiu et al. (2024) examined oncology nurses' perspectives on the policy needs and action drivers shaping genomics-informed oncology nursing education and practice, identifying key factors that enabled or constrained progress, including the need for nursing policy infrastructure and strong leadership and advocacy across practice, organisational, and systems levels. From a developing-country perspective, Abad and Sur (2022) highlighted systemic barriers such as the absence of competency standards, insufficient educational preparation, lack of a professional genomic nursing organisation, and workload pressures, underscoring the influence of structural and contextual factors on implementation capacity.

Together, these findings illustrate the persistent structural and workforce barriers that shape nurses' engagement with genomics globally and highlight the importance of investigating how such barriers and enablers are experienced within the Australian oncology nursing context.

1.7.1.1 Barriers and Enablers to Genomic Integration in the Australian context

Within Australia, research on barriers and enablers to genomic adoption remains limited, and the available evidence is fragmented across disciplines and settings. At a broader health system level, commentators have noted that, despite rapid advances in genomic and precision medicine and increasing public investment, the uptake of genomics into routine care remains 'far from equitable or routine' in Australia (O'Shea et al., 2022). They highlight persistent challenges including variable preparedness among non-genetics clinicians, an insufficient genetics workforce, and difficulties embedding genomic innovations into existing models of care, and argue that implementation science-based health care research is urgently needed to support the mainstreaming of genomics and precision medicine nationally. While this analysis is not specific to nursing, it underscores a wider imperative to understand the contextual factors that shape how different clinical workforces, including nurses, are positioned to engage with genomics.

Some work has examined barriers and enablers to organisational adoption of genomics in Australia (Best et al., 2021). From an education-provider perspective, between 2016 and 2017 the Australian Genomic Health Alliance (Janinski et al., 2018) interviewed education providers about the training needs of non-genomic health professionals (including nurses), identifying barriers related to education and curriculum design and learner attributes such as confidence, perceived relevance, and time. Potential enablers included targeted education, adequate funding, and collaboration with genomic specialists. Efforts have also been made to examine perceived barriers and enablers among broad groups of Australian allied health professionals, including nurses and midwives (Saleh et al., 2019), who reported a lack of Australian education programs, difficulty finding relevance, and limited access to training opportunities.

To date, the only nursing-specific evidence on perceived barriers and enablers is offered by Wright et al. (2020), who explored the experiences of oncology nurses in a regional Queensland hospital. Participants described barriers such as lack of personal time, financial constraints, and limited workplace flexibility to pursue further genomic education. While this work provides valuable insight, it is limited to a single site in a non-metropolitan hospital and cannot capture the diversity of oncology nursing contexts across Australia. As a result, there is still little

empirical understanding of how Australian nurses more broadly—and oncology nurses in particular—perceive and navigate genomic integration in their day-to-day practice.

Without a clear understanding of the barriers and enablers that nurses themselves encounter, national and organisational efforts to advance genomic integration risk overlooking the realities of frontline clinical practice. In the context of broader calls for implementation-focused research in genomic and precision medicine in Australia (O’Shea et al., 2022), this thesis addresses a key knowledge gap by examining how Australian oncology nurses perceive and engage with genomics, and what influences their readiness and ability to integrate it into care. This understanding is essential to inform locally relevant, scalable strategies for building genomic capacity within Australia’s nursing workforce.

1.8 Problem statement

The integration of genomics into oncology has transformed cancer care, with applications spanning prevention and screening to diagnosis, treatment, survivorship, and relapse management. Nurses are central to delivering this care, yet their capacity to adopt and integrate genomics remains uncertain. International research demonstrates that while nurses consistently recognise the importance of genomics, their knowledge is often limited, and adoption into practice is hindered by multiple barriers.

In Australia, the evidence base is scarce. Only a small number of studies have examined nurses’ genomic knowledge and attitudes (Alexander et al., 2024; Schluter, 2023; Wright et al., 2019, 2020). Focusing specifically on oncology nurses, Chapter 3 presents a scoping review that maps the available evidence and highlights the limited number of Australian studies in this area. This limited evidence base constrains the ability of educators, professional bodies, and policymakers to design strategies that support oncology nurses’ engagement with genomics. Without an engaged workforce prepared to adopt genomic innovations, Australia risks undermining its substantial national investment in genomic medicine.

Established implementation guidance for genomic nursing emphasises the importance of identifying barriers and enablers during early, pre-implementation assessment (Tonkin et al., 2020b). In addition, global evaluations highlight the need to assess existing genomic integration and associated challenges or barriers to gauge readiness within the nursing workforce (Calzone, Kirk, et al., 2018b). However, to date no studies have specifically evaluated the barriers and enablers experienced by nurses in Australia, leaving a critical gap in understanding how to

facilitate adoption at the level of practice. Furthermore, while international research acknowledges the importance of identifying and supporting early adopters as a strategy for accelerating diffusion (Andrews et al., 2014b; Leach et al., 2016), little is known about the extent of genomic adoption among Australian oncology nurses or the characteristics of those leading this change. Understanding who is adopting genomics, and the attributes associated with adoption, is essential to informing targeted strategies that can engage and influence nurses across the wider workforce.

1.9 Research question

To address these gaps, this study aims to answer the following research question:

How do oncology nurses in Australia engage with genomics, and what individual characteristics and perceived barriers or enablers influence its adoption into practice?

1.10 Research aims and objectives

The intention of this work is to inform workforce development, education, and implementation strategies that support the effective integration of genomics into Australian nursing practice and facilitate the transition of the nursing workforce into the genomic era.

Aims

1. To assess oncology nurses' knowledge, engagement, and adoption of genomics in practice across Australia.
2. To identify individual characteristics associated with the uptake of genomics in nursing practice.
3. To explore perceived barriers and enablers to integrating genomics into oncology nursing practice.

Objectives

1. To scope and critically examine existing research on oncology nurses' knowledge and attitudes towards genetics and genomics (scoping review – supports Aim 1).
2. To assess levels of genomic knowledge, engagement, and adoption among Australian oncology nurses, and explore associations with individual, professional, and demographic characteristics (quantitative survey – supports Aims 1 & 2).

3. To explore perceived barriers and enablers to genomic uptake in oncology nursing across diverse clinical roles and healthcare contexts (qualitative interviews – supports Aim 3).

1.11 Significance of the study

The significance of this study lies in its original contribution to understanding how genomics is being integrated into nursing practice, with a particular focus on the oncology workforce in Australia. Despite genomics being central to contemporary healthcare, evidence on nurses' genomic knowledge, engagement, and adoption remains limited, with a notable scarcity of Australian empirical research. Addressing this gap, the study provides the first nation-wide examination of how Australian oncology nurses are engaging with genomics and identifies the factors that shape their adoption of genomic practice.

Building on international research that has highlighted the role of early nurse adopters in accelerating genomic integration (Andrews et al., 2014a, 2014b; Leach et al., 2016), this study applies Rogers' Diffusion of Innovations theory (2003) to the Australian oncology nursing context for the first time. By examining how demographic, professional, and personality characteristics relate to adoption, it extends existing evidence and provides new insight into how diffusion processes operate within Australian nursing practice, informing strategies to engage and support nurses in adopting genomic innovations.

This study is also significant in capturing nurses' perspectives on the perceived barriers and enablers to integrating genomics into oncology nursing practice—an area that remains largely unexplored in Australia. These qualitative insights complement the examination of adoption by illuminating how nurses themselves understand and experience the factors that facilitate or hinder their engagement with genomics. In doing so, the study contributes contextually grounded evidence to guide educational, professional, and organisational strategies that support the integration of genomics into nursing care.

Finally, this study contributes to the international dialogue on genomic nursing by providing empirical evidence from the Australian context, where formal genomic nursing roles and competency frameworks remain in their infancy. Situating Australian oncology nursing within the global landscape enables benchmarking, collaboration, and shared learning, ensuring that Australian nurses are equipped to participate fully in the genomic era and to lead the translation of genomic innovation into person-centred cancer care.

Having established the scholarly and practical significance of this research, the following section outlines the researcher's positionality and reflexivity, acknowledging the perspectives and experiences that have shaped the development and interpretation of this work. This account situates the researcher within the study context and demonstrates how these influences were critically considered throughout the research process. As this section discusses the researcher's own experiences, the first-person voice is used to convey reflexive insight.

1.12 Researcher positionality and reflexivity

I am a registered nurse, a nurse academic, and an educator with training as a qualified genetic counsellor. Since becoming a registered nurse, I have had the privilege of working across a range of healthcare settings, including hospitals, community, not-for-profit, and academic research environments. A personal experience with genetic healthcare inspired me to pursue a Master's degree in genetic counselling, where my dissertation research evaluated a community genetic carrier screening program with a focus on educational outcomes. After completing my training, I worked as a genetic counsellor specialising in neurogenetics, contributing to large-scale NHMRC- and internationally funded research within a leading neurogenetics group.

Despite enjoying this work and gaining valuable clinical and research skills, I found myself increasingly pulled back to nursing—not just as a profession, but as a core part of my identity. While working in genetics, I often felt the need to choose between my 'nursing hat' and my 'genetic counselling hat'. Yet I believed strongly that the two could, and should, coexist. My PhD emerged from that space of professional tension and possibility.

In 2019, I stepped away from genetic counselling to focus solely on nursing education and research. Since then, I have developed a passion for teaching and learning and have had the opportunity to develop innovative education initiatives, lecturing in both nursing and genomics across undergraduate and postgraduate programs.

The knowledge and experience I gained as a genetic counsellor provided essential tools that have enriched my nursing practice, skills such as therapeutic communication, psychosocial insight, clinical reasoning, and an understanding of ethical, legal, and social considerations. I began to see these not as exclusive to genetic counselling, but as valuable assets within a broader nursing toolkit. This perspective motivated me to explore how nurses might be supported to expand their own professional toolboxes in the context of genomic healthcare.

Although I am not an oncology nurse, I selected this specialty for its high genomic relevance: oncology nurses routinely care for patients whose treatment is shaped by genomic information. I positioned myself to participants as a nurse and educator researching nursing practice, and while I am an outsider to oncology specifically, I remain an insider to the broader Australian nursing community.

Throughout the study, I remained reflexive and aware of my dual professional background and the potential biases it might bring, particularly the assumption that genomics has a place in nursing. I took active steps to mitigate these influences through regular supervision, reflective journaling, and a careful thematic analysis process that prioritised participants' voices over my own expectations. While my research is motivated by a vision of positive change in the nursing workforce, that vision is grounded in empirical inquiry and critical reflection; the aim is not to impose, but to understand and represent the lived realities of nurses navigating the evolving landscape of the genomic era.

1.13 Thesis structure

This thesis is presented in seven chapters.

Chapter 1—Introduction. This chapter has established the background and context for the study, outlined the research problem, aim, objectives, and questions, and articulated the significance, positionality, and reflexive stance of the researcher. It concludes with an overview of the thesis structure.

Chapter 2—Theoretical framework. This chapter introduces Rogers' Diffusion of Innovations (DOI) theory as the interpretive lens for the thesis. It defines key constructs, explains mechanisms of diffusion in health professions, and justifies how DOI theory informs the study's components and interpretation.

Chapter 3—Scoping review: Oncology nurses' knowledge and attitudes. This chapter is presented in manuscript format, as it has been prepared for submission to a peer-reviewed journal. It maps the scope of international evidence on oncology nurses' genomic knowledge and attitudes, identifies existing gaps, and informs the design and focus of the empirical phases of the study.

Chapter 4—Methods. This chapter details the philosophical underpinnings of the study and its mixed-methods design, describing the rationale, methodology, sampling, data collection

instruments, and analytic procedures for both the quantitative and qualitative phases. Considerations of rigour, ethics, and researcher reflexivity are also addressed.

Chapter 5—Quantitative findings (Survey). This chapter reports national survey results on oncology nurses' genomic knowledge, engagement, and adoption, examines associations with individual, professional, and demographic characteristics, and provides descriptive and inferential analyses relevant to Aims 1 & 2.

Chapter 6—Qualitative findings (Interviews). This chapter presents thematic analysis of semi-structured interviews with oncology nurses, exploring perceived barriers and enablers to genomic integration, offering analysis relevant to aim 3, and contextual depth to the survey findings.

Chapter 7—Discussion and conclusions. This chapter integrates quantitative and qualitative results, interpreting findings through the DOI lens and the broader literature. It articulates implications for education, workforce development, implementation, and policy; outlines study limitations; proposes recommendations and future research; and concludes the thesis.

1.14 Conclusion

This chapter has outlined the background and context for the study and positioned the research within the fields of oncology nursing and genomics. It described the research problem, aims, objectives, and questions, and articulated the study's significance, alongside the researcher's positionality and reflexive approach. The next chapter presents the theoretical framework that informed this thesis and was applied as a lens to interpret and contextualise the findings.

Chapter 2. Theoretical Framework

2.1 Introduction

A strong theoretical framework, foundational to doctoral research, shapes how the research problem is understood, how data are interpreted, and how findings are positioned within broader scholarly conversations (Grant & Osanloo, 2014). Eisenhart (1991, p. 205) defines a theoretical framework as ‘a structure that guides research by relying on a formal theory... constructed by using an established, coherent explanation of certain phenomena and relationships’. Grounding the study in such a framework ensures that key concepts are well-defined, logically connected, and appropriate to the phenomenon under investigation, while also aligning the research with a clear philosophical, epistemological, and analytical orientation (Grant & Osanloo, 2014).

This chapter presents the theoretical framework underpinning the current study, which investigates the uptake of genomics in Australian oncology nursing practice. Given the study’s focus on understanding how new clinical practices are perceived, adopted, and integrated into existing roles and systems, the Diffusion of Innovations (DOI) theory (Rogers, 2003) was selected as the guiding theoretical lens. DOI theory has been widely applied to examine how innovations spread through social systems and is particularly relevant to the healthcare context, where adoption processes are shaped by a complex interplay of individual, professional, and organisational factors. In the present study, the DOI theory did not underpin every aspect of the research design but was primarily applied as an interpretive lens. This approach aligns with the study’s pragmatic worldview, which emphasises methodological flexibility and the instrumental use of theory to generate practical understanding (see Section 4.3). While certain concepts from the theory informed the development of the research aims, particularly those related to recognising adopters and their characteristics, and contributed to the formulation of some interview questions, the framework was deliberately not used to guide data analysis. Rather, it was employed to interpret and contextualise the findings, offering a coherent theoretical basis for explaining observed patterns and relationships within the discussion chapter (see Section 7.6).

The chapter begins by defining innovation in the context of nursing and explaining why genomics qualifies as an innovation within this framework. It then outlines the origins and evolution of DOI theory and presents its key constructs, including the innovation-decision process, adopter categories, and attributes of innovations. Individual, social, and organisational

influences on adoption are also examined. The chapter then reviews the application of DOI theory in health and nursing research, before detailing how the theory informed the design and interpretation of this mixed-methods study. Finally, the limitations of DOI theory are discussed, along with a brief overview of complementary theoretical perspectives that may enrich future research.

2.2 Defining genomic innovations in the context of nursing

2.2.1 Genomics as an innovation

The adoption of innovations in healthcare is essential to improving care delivery, patient outcomes, and professional practice. Understanding how innovations are perceived and integrated into nursing contexts requires conceptual clarity about what constitutes an innovation. According to Rogers (2003), an innovation is defined as ‘an idea, practice, or object that is perceived as new by the individual or other unit of adoption’ (p. 12). Genomics meets this definition both conceptually and in practice. While molecular scientists have studied genetics and genomics extensively for decades, and the Human Genome Project was completed in 2003, the translation of this knowledge into routine clinical practice, particularly in nursing, remains relatively new, uneven, and evolving (Calzone, Kirk, et al., 2018b; Thomas et al., 2023; Wright et al., 2020).

Nurses are increasingly expected to engage with genomic information in patient education, risk assessment, and care planning, yet many have had limited exposure or training in this domain (Calzone, Kirk, et al., 2018b; McLaughlin et al., 2024). As such, genomics is still widely perceived as a novel and emerging field within the nursing profession, positioning it clearly as an innovation in Rogers’ terms. Importantly, the field itself continues to expand, with ongoing discoveries in gene–environment interactions, molecular diagnostics, and targeted therapies. In oncology, for example, tumour profiling, pharmacogenomics, and precision treatments are introducing knowledge and clinical responsibilities that many nurses are encountering for the first time. Thus, despite its scientific maturity, genomics continues to function as a novel and evolving domain in nursing practice, aligning with Rogers’ criteria for an innovation.

2.2.2 Innovation in nursing practice

Innovation stands as a driving force behind societal progress and is increasingly vital to the advancement of healthcare. Within the nursing profession, innovations such as artificial intelligence, mobile health applications, and big data analytics have introduced new paradigms

for patient care, while simultaneously presenting complex clinical, ethical, and technological challenges. Nurses are central to these developments, acting as both implementers and drivers of innovation across diverse care settings (Ronquillo et al., 2021; Topaz & Pruinelli, 2017).

There is growing recognition of the tangible impacts of nurse-led innovation. Empirical studies have demonstrated that nurses can directly enhance patient outcomes and care quality through innovations in workflow, the development of new tools, medication administration processes, and the integration of information technology to reduce medical errors (Hughes, 2006). During the COVID-19 pandemic, for example, nurses spearheaded innovations including digital tools for remote patient monitoring and the creation of novel protective equipment (Ziegler et al., 2024). These efforts reduced response times and improved safety for both patients and staff (Harrington, 2020). More broadly, nurse-led initiatives such as home-based care models, community health outreach, and continuity of care programs for vulnerable populations have contributed to improved access and equity in healthcare delivery (Institute of Medicine, 2011; Seifert, 2016).

In oncology, innovation is particularly critical. Rising cancer incidence and increasingly complex treatment modalities have expanded the scope and intensity of oncology nursing practice. Innovative nursing approaches are necessary not only to manage complex clinical pathways but also to support patients through significant psychosocial, physical, and existential challenges. Innovations in oncology nursing can improve patient safety, enhance treatment experiences, and ultimately elevate the quality of life for people affected by cancer (Fasola et al., 2021; Wujcik, 2016).

Despite the evident value of innovation in nursing, however, the pace at which new practices and technologies are adopted into routine care often lags behind the emergence of new evidence. This delay, commonly referred to as the *theory-to-practice gap*, has been widely documented in the literature and remains a persistent challenge for implementation efforts in nursing and other health professions (Curtis et al., 2017). Slow or inconsistent adoption of evidence-based practice can adversely impact care quality, safety, and patient outcomes (Hanberg & Brown, 2006). Understanding this gap is therefore essential for examining how genomic innovations are adopted in nursing practice.

To understand and address this gap, various theoretical models have been employed to examine the processes through which innovations are adopted, diffused, and sustained in practice. Among these, the Diffusion of Innovations theory, developed by Everett Rogers, provides a

widely accepted conceptual framework that has been applied across healthcare disciplines, including nursing. The DOI theory offers a structured approach to understanding how innovations spread across social systems or organisations, and how individual, organisational, and systemic factors influence the pace and extent of adoption (Rogers, 2003). This framework underpins the present study and informs its exploration of genomic innovation in Australian oncology nursing.

2.3 Origins and evolution of the Diffusion of Innovations theory

The DOI theory offers a conceptual model for understanding how new ideas, practices, or technologies spread within and across social systems (Rogers, 2003). Its intellectual lineage can be traced to early European sociology. Gabriel Tarde (1903) was among the first to observe the now-familiar ‘S-shaped’ patterns of adoption and to propose the importance of opinion leadership as a driver of social change. Georg Simmel (1908) extended this foundation by highlighting the structuring influence of interpersonal networks on individual behaviour. Together, these insights established an enduring premise: that system-level dynamics interact with individual decision-making to shape the diffusion of innovation.

In the American context, diffusion research was crystallised through Ryan and Gross’s (1943) seminal study of hybrid seed corn adoption among Iowa farmers. Their findings not only confirmed the S-shaped adoption curve (Figure 2.1) but also demonstrated the pivotal role of interpersonal communication and opinion leaders in adoption decisions. Building on this and subsequent work, Rogers synthesised empirical findings into a comprehensive framework in the first edition of *Diffusion of Innovations* (1962), which he refined across four later editions, culminating in the 2003 version. Across these editions, Rogers integrated concepts of innovation attributes, individual characteristics, communication channels, time, and social systems, creating one of the most influential theories of social change. Over subsequent decades, diffusion research expanded well beyond rural sociology into education, communication studies, organisational theory, and public health, becoming a widely applied framework for analysing adoption processes, including in health and nursing (Strang & Soule, 1998).

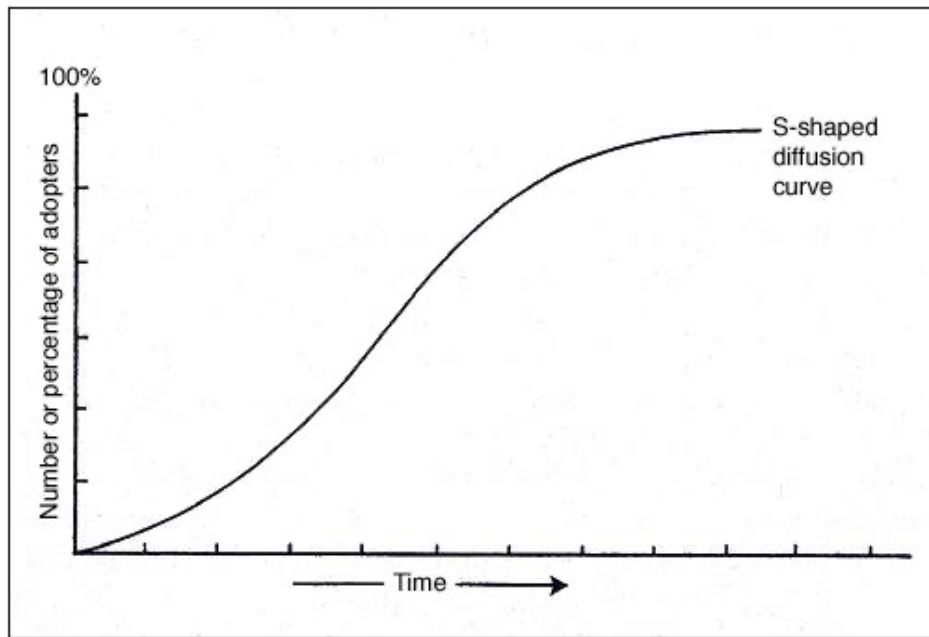


Figure 2.1. S-curve diffusion. Adapted from Rogers (2003, p. 272).

2.3.1 Application to health and nursing

Diffusion theory has been extensively applied in healthcare to explain the spread of clinical practices, organisational reforms, and evidence-based interventions (Balas & Chapman, 2018; Cain & Mittman, 2002; Glanz et al., 2008; Greenhalgh et al., 2004; Iqbal & Zahidie, 2022). Carole A. Estabrooks has written prolifically on DOI theory as a core framework for understanding how nursing research is translated into practice, moving beyond linear ‘barriers models’ to acknowledge the fundamentally social and interactive nature of knowledge uptake (Estabrooks, 1999, 2009; Estabrooks et al., 2003, 2006, 2011). Indeed, within nursing specifically, DOI theory has been applied to a wide range of innovations, from midwifery continuity-of-care models to the implementation of clinical guidelines, emerging technologies, and the integration of genomics into practice (Andrews et al., 2014b; Cummins et al., 2018; Hadorn et al., 2016; Lee, 2004; Nezamdoust et al., 2022). Importantly, while not comprehensive, several key studies from the USA (Calzone et al., 2012; Calzone, Jenkins, Culp, et al., 2013; Dodson, 2014; Horner et al., 2004, 2004; Jenkins et al., 2015; Jenkins & Calzone, 2007), Canada (Dewell, Benzies, Ginn, et al., 2020; Dewell et al., 2021; Limoges et al., 2022; Puddester et al., 2023), the UK (Andrews et al., 2014b, 2014a; Leach et al., 2016), and China (Wang et al., 2023) demonstrate the prominence of DOI as a theoretical lens in genomic nursing research, reflecting its utility in framing both the challenges and opportunities of adoption in this emerging field. These applications highlight the framework’s capacity to illuminate the

interplay between individual adopter characteristics, peer and opinion leader influence, and social system conditions in shaping the uptake of new genomic knowledge. Such breadth of application underscores DOI theory's relevance for examining how Australian oncology nurses engage with genomics, and how barriers and enablers influence adoption processes within complex clinical and professional contexts.

2.3.2 Theoretical foundations and elements

Rogers (2003) identified four essential elements of the diffusion process: the innovation itself, communication channels, time, and the social system. These elements interact dynamically to determine the speed and extent of adoption. Taken together, they provide a foundation for understanding how new practices are introduced, discussed, and integrated within professional communities such as nursing.

2.3.2.1 Innovation

An innovation is defined as 'an idea, practice, or object that is perceived as new by an individual or unit of adoption' (Rogers, 2003, p. 12). Importantly, 'newness' is determined not by the objective age of the idea but by the perceptions of the potential adopter. Rogers further identified five perceived attributes of innovations—relative advantage, compatibility, complexity, trialability, and observability—as critical determinants of adoption rates. These attributes are explored in greater detail in Section 2.4.1.

2.3.2.2 Communication channels

Communication channels refer to the means by which information about an innovation is transmitted from one individual to another (Rogers, 2003, p. 36). Rogers distinguished between mass media and interpersonal channels, each of which plays a distinct role at different stages of diffusion.

- **Mass media channels** (e.g., television, print, internet, and professional education materials) are particularly effective in creating broad awareness of an innovation. They are most influential in the early stages of diffusion, especially the *knowledge stage*, at which individuals are first exposed to new ideas (see Section 2.3.3). Genomics, for instance, has entered public discourse through mass media coverage of the Human Genome Project (Costa, 2003), television programs such as *CSI: Crime Scene Investigation* (Ley et al., 2012), and widespread references to genomic concepts during

the COVID-19 pandemic (Park et al., 2024). Such exposure contributes to general awareness, even when clinical application remains limited.

- **Interpersonal channels**, in contrast, are most influential during the *persuasion stage*, when individuals begin to form attitudes about an innovation. While mass media may create awareness of an innovation, interpersonal influence through social networks is the dominant mechanism for diffusion (Greenhalgh et al., 2004). Communication through colleagues, peers, or opinion leaders carries the added weight of trust, social reinforcement, and contextual relevance. This dynamic is particularly salient in healthcare, where adoption decisions are shaped not only by formal education or guidelines but also by trusted colleagues and local champions (Ominyi & Alabi, 2025). Nurses, for example, may be more receptive to integrating genomics when information is modelled and shared by peers working in similar clinical contexts. Such exchanges may reduce uncertainty and build confidence in uptake (Rigtering et al., 2023).

The two-step flow model of communication (Lazarsfeld et al., 1944), central to DOI theory, emphasises that mass communication influence is often filtered through interpersonal communication and opinion leaders (discussed further in Section 2.4.3), who then shape and transmit information to others within their social networks (Rogers, 2003, p. 304). In nursing contexts, this interplay between formal education and interpersonal influence underscores the importance of tailored communication strategies for genomic adoption.

2.3.2.3 Time

Time is a central dimension in DOI theory, evident in three areas:

1. The innovation-decision process, through which individuals move from first knowledge of an innovation to adoption or rejection.
2. The innovativeness of individuals or units, reflecting how early or late they adopt relative to others.
3. The rate of adoption within a system, typically represented by the characteristic S-shaped adoption curve. (Rogers, 2003; Ryan & Gross, 1943)

Time thus allows the diffusion process to be understood not as a one-time event but as a dynamic trajectory unfolding across individuals and groups. In nursing practice, the adoption

of genomics illustrates this temporal dimension: some clinicians act as early adopters, while others require sustained exposure and reinforcement over time before integration occurs.

2.3.2.4 Social system

The social system refers to ‘a set of interrelated units that are engaged in joint problem-solving to accomplish a common goal’ (Rogers, 2003, p. 23). Innovations do not diffuse in a vacuum; they are adopted (or rejected) within specific social systems whose structure, norms, and interpersonal dynamics directly influence the diffusion process. As such, the adoption of innovations by individuals is powerfully influenced by the structure and quality of their social networks (Greenhalgh et al., 2004).

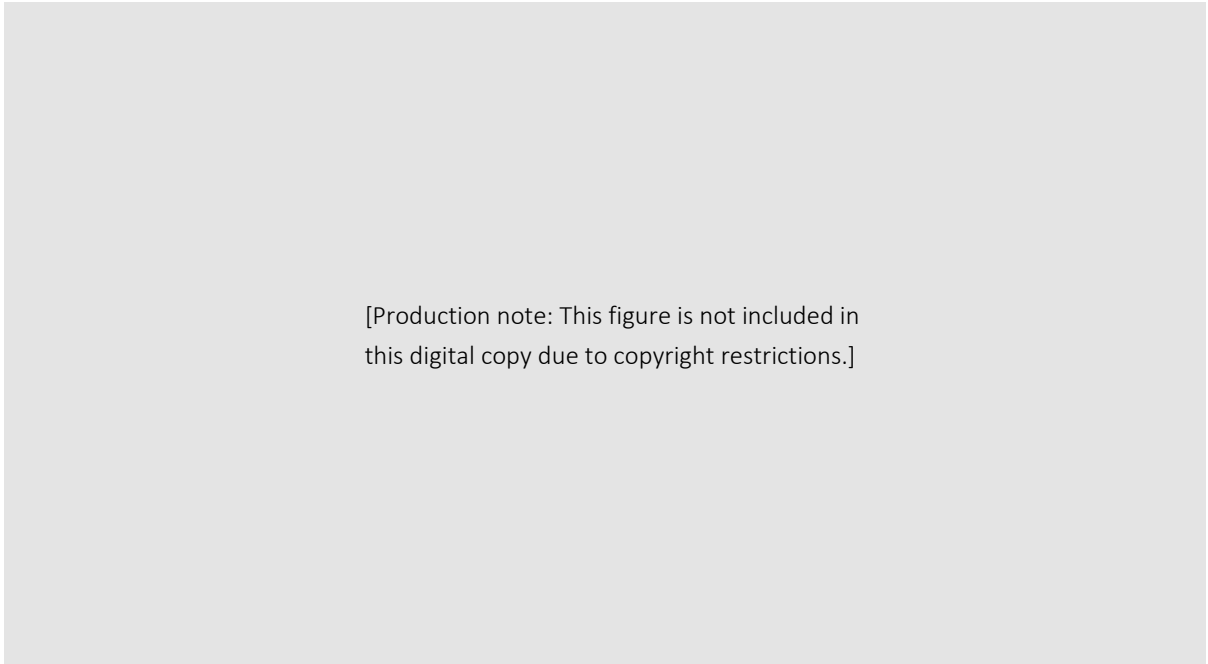
Rogers posits that interpersonal relationships, particularly trust, communication frequency, and perceived authority, strongly affect uptake. Individuals are embedded within networks of peers and organisations that provide information, normative pressure, and reinforcement. Systems characterised by high collaboration and open communication tend to diffuse innovations more rapidly, while rigid hierarchies or low trust may impede change.

In healthcare, the influence of social systems is particularly pronounced, as organisational culture, professional hierarchies, and leadership all shape whether an innovation is adopted, resisted, or re-invented (Cain & Mittman, 2002; Greenhalgh et al., 2004; Wong et al., 2023). DOI theory also highlights the role of opinion leaders, individuals whose expertise, accessibility, and social standing grant them disproportionate influence over peers’ adoption decisions (Rogers, 2003, p. 27). Their role in shaping diffusion within professional networks will be discussed further in Section 2.4.3.

By foregrounding these four foundational elements—innovation, communication channels, time, and social system—DOI theory provides a comprehensive framework for understanding how diffusion occurs within professional communities. These elements interact to determine not only whether an innovation spreads, but also how quickly and under what conditions. Building on this foundation, the next section examines the innovation-decision process, the sequential stages through which individuals progress when deciding whether to adopt a new practice.

2.3.3 The innovation-decision process

According to DOI theory, individuals typically move through five sequential stages when encountering a new idea: knowledge, persuasion, decision, implementation, and confirmation (Figure 2.2). This model, known as the *innovation-decision process*, describes how individuals come to understand, evaluate, and ultimately adopt or reject an innovation.



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Figure 2.2. Innovation decision process. Source: Rogers (2003. p. 170).

In the *knowledge* stage, an individual becomes aware of the innovation and begins to seek information about what it is, how it works, and why it may be useful. During *persuasion*, the individual forms a positive or negative attitude toward the innovation. As Rogers observed, however, a favourable attitude does not necessarily guarantee adoption. The *decision stage* involves making a choice to adopt or reject the innovation. If adoption occurs, the individual moves into *implementation*, where the innovation is put into practical use. Finally, in the *confirmation* stage, the individual seeks reinforcement for their decision and may continue, adapt, or discontinue use of the innovation based on subsequent experiences or feedback.

This process is influenced by multiple interrelated factors. At the knowledge and persuasion stages, individual characteristics (e.g., socioeconomic status, personality traits, communication behaviours), innovation attributes (e.g., relative advantage, compatibility, complexity, trialability, observability), and contextual conditions within the social system all play important roles in shaping whether an innovation is ultimately adopted or rejected. For instance, in the

early stages, traits such as prior experience, communication behaviours, or cosmopolitanism—the degree to which an individual is oriented outside their immediate social system (Rogers, 2003, p. 290)—may influence receptivity to new ideas. In the later stages, the perceived characteristics of the innovation itself, such as whether it offers a clear advantage, fits existing values, or appears manageable in complexity, become more prominent in shaping the adoption decision, with the exchange of innovation-related information among peers lying ‘at the heart’ of this diffusion process (Rogers, 2003, p. 233).

Importantly, Rogers (2003) posits that at the persuasion stage in the innovation-decision process, the individual forms a favourable or unfavourable attitude towards the innovation. Rogers defines attitudes as a ‘relatively enduring organisation of an individual’s beliefs about an object that predisposes his or her actions’ (p. 174). In essence, Rogers clarifies that at the knowledge stage the individual is primarily relying on a cognitive process (*knowing*), but that the main type of thinking at the persuasion stage is affective (*feeling*). Knowledge acquisition therefore precedes attitude formation; until an individual knows about a new idea, they cannot begin to form an attitude toward it. This dynamic underpinning adoption is crucial, as the relationship between knowledge and attitudes and innovation adoption is also central to the model proposed by Plavskin et al. (2019) in which nurses’ genomic competency and knowledge underpin attitudes and receptivity, which in turn drive adoption, with confidence acting as a mediating factor (see Figure 1.6, discussed in Chapter 1.5).

Indeed, this framework is particularly useful for conceptualising the decision-making processes underpinning the adoption of genomic innovations in nursing. It highlights that adoption is not a simple binary outcome (adopt/reject) but, rather, a dynamic process shaped by interactions between the innovation, the individual, and the wider organisational and social environment. Importantly, this framework also provides a lens for identifying the barriers and enablers that influence progression through the different stages. For instance, limited genomic knowledge may constrain progress at the knowledge stage, whereas organisational support or strong peer influence may act as enablers during persuasion and implementation. Positioning DOI theory as the guiding theoretical lens therefore allows this study to illuminate the factors that facilitate or impede the integration of genomics into nursing practice.

While the innovation-decision process explains *how* adoption unfolds over time, it does not account for *who* adopts innovations at different points in this trajectory. Rogers addressed this through his categorisation of adopter types, which helps to explain the distribution of uptake

across social systems. The following section outlines these adopter categories and their relevance to understanding the diffusion of genomics in nursing practice.

2.4 Adopter categories

A central concept within DOI theory is the categorisation of adopters according to the relative timing of their adoption. Rogers (2003) identified five adopter categories, *innovators*, *early adopters*, *early majority*, *late majority*, and *laggards*, which are distributed along a bell-shaped curve representing the frequency of adoption over time (Figure 2.3). When plotted cumulatively, these distributions form the characteristic S-shaped diffusion curve (Ryan & Gross, 1943; Rogers, 2003) (see 2.3).

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Figure 2.3. Relationship between types of adopters classified by innovativeness and their location on the adoption curve. Source: Rogers (2003, p. 281).

- **Innovators (2.5%)** are venturesome and willing to take risks, often the first to experiment with new ideas.
- **Early adopters (13.5%)** are often respected opinion leaders who, while more judicious, are still receptive to change and play a crucial role in influencing others.
- **Early majority (34%)** adopt just before the average person, typically engaging in careful deliberation before making decisions.
- **Late majority (34%)** are more sceptical and cautious, usually adopting only once a critical mass has done so.
- **Laggards (16%)** are the most resistant to change, typically adopting only when innovations become mainstream or unavoidable.

These categories underscore that adoption does not occur simultaneously across a social system; instead, individuals differ in their readiness, risk tolerance, and susceptibility to influence. In professional contexts such as nursing, these differences are particularly significant, as the adoption of complex and rapidly evolving innovations like genomics often depends on the willingness of early adopters and opinion leaders to champion change (Gottlieb & Gottlieb, 2017; Leach et al., 2016; Santos et al., 2022).

However, it is important to note that while adopter categories have been widely cited in diffusion research, they can be misused as explanatory variables. The adoption of innovations by individuals is powerfully influenced by the structure and quality of their social networks; as Greenhalgh et al.'s (2004) seminal work discusses, such adopter labels are often oversimplified and value-laden, and may obscure the more nuanced psychological and social factors that underpin adoption. For example, individual characteristics, including openness to experience, cosmopolitanism, or perceived influence over others, may provide richer insight into adoption behaviours than broad categorical labels. These traits, and their relevance to understanding the uptake of genomics among oncology nurses, will be examined in detail in Section 2.4.2. Therefore, highlighting variation in adoption timing and the influence of adopter traits, this concept provides an important bridge to the next dimension of DOI theory: the attributes of the innovation itself, which strongly shape adoption decisions across all categories of adopters.

2.4.1 Attributes of innovations

According to Rogers (2003), the rate of adoption is strongly influenced by how potential adopters perceive an innovation. Five perceived attributes—*relative advantage*, *compatibility*, *complexity*, *trialability*, and *observability*—account for a substantial proportion of the variance in adoption rates across settings. These characteristics shape how individuals evaluate an innovation and their attitudes towards it, thereby influencing their willingness to adopt it.

- **Relative advantage** refers to the degree to which an innovation is perceived as superior to the idea or practice it replaces. The clearer an innovation's advantage in effectiveness or cost-effectiveness, the greater its likelihood of adoption and integration into practice (Greenhalgh et al., 2004; Rogers, 2003). In oncology nursing, genomics may be seen as offering clear clinical advantages by enabling personalised care, refining risk assessment, or guiding targeted therapies. Rogers (2003) posits that when perceived benefits are evident, adoption is accelerated.

- **Compatibility** is the extent to which an innovation aligns with the values, experiences, and needs of potential adopters (Rogers, 2003). Subsequent diffusion research in healthcare demonstrates that innovations perceived as compatible with adopters' professional values, organisational norms, and established ways of working are more readily adopted and more successfully assimilated into practice (Greenhalgh et al., 2004). DOI theory thus suggests that nurses may be more likely to adopt genomics if it resonates with core nursing values, such as holistic, patient-centred care, or if it integrates smoothly into existing workflows and practice frameworks. Conversely, if genomics appears misaligned with professional identity or daily responsibilities, adoption may be slowed.
- **Complexity** refers to the degree to which an innovation is perceived as difficult to understand or implement. Complexity is negatively correlated with the rate of adoption, as innovations viewed as highly technical or burdensome are less likely to diffuse rapidly (Greenhalgh et al., 2004; Rogers, 2003). Genomics may be perceived as scientifically dense and conceptually challenging (Calzone et al., 2010; Dewell et al., 2021), which may deter engagement among nurses without prior training or confidence in this domain.
- **Trialability** reflects the degree to which an innovation can be experimented with on a limited basis before full integration. The ability to trial an innovation in a limited way increases the likelihood that users will adopt and embed it into practice (Greenhalgh et al., 2004; Rogers, 2003). Opportunities for nurses to engage with genomics through short-term placements, pilot programs, simulations, or structured training may enhance trialability, reducing uncertainty and building confidence (Dwyer et al., 2025; Greenhalgh et al., 2004).
- **Observability** refers to the visibility of an innovation's results. In healthcare, observable outcomes, such as improved patient outcomes, streamlined workflows, or enhanced treatment precision, can reinforce the perceived value of an innovation and motivate adoption (Greenhalgh et al., 2004). Where results are less visible, clinicians may hesitate to adopt, particularly if doing so carries reputational or professional risks (Greenhalgh et al., 2004; Hayes et al., 2015; Lee, 2004).

These attributes highlight that adoption is shaped not only by system-level conditions or individual readiness, but also by how the innovation itself is perceived in practice. In oncology

nursing, perceived benefits, alignment with existing practice, and visibility of genomic outcomes may act as powerful enablers, while perceived complexity may serve as a barrier.

Yet innovation attributes alone cannot fully explain adoption. Rogers also emphasised the importance of individual characteristics, such as sociodemographic and personality traits, which may influence patterns of genomic uptake. These characteristics are therefore directly relevant to the present study, which examines how nurses' perceptions of genomic innovation and their individual attributes influence the likelihood of adoption within Australian oncology settings. The next section elaborates on these individual characteristics in more detail.

2.4.2 Individual characteristics

In addition to categorising adopters by the timing of adoption, Rogers (2003) identified a range of individual characteristics that are associated with a person's likelihood of adopting an innovation. These traits collectively reflect an individual's level of *innovativeness*, defined as the degree to which someone is relatively early in adopting new ideas compared to others in their social system (Rogers, 2003, p. 22). Adoption is therefore not a uniform process but is shaped by the interaction of personal, social, and contextual factors.

Rogers and subsequent diffusion studies provide generalisations about the distinctive attributes of each adopter category. He identified three primary domains that distinguish earlier from later adopters (see Table 2.1):

- **socioeconomic status** (e.g., higher levels of education and higher social status);
- **personality variables** (e.g., greater empathy, rationality, and openness to new experiences); and
- **communication behaviour** (e.g., broader social participation and cosmopolitanness).

Table 2.1. Early and late adopter characteristics (Rogers, 2003)

Early Adopters	Late Adopters
Socioeconomic Characteristics	Socioeconomic Characteristics
More years of formal education More literate Have higher social status Greater degree of upward social mobility Likely to work in larger organisations	Fewer years of formal education Less literate Lower social status Lower degree of social mobility Likely to work in smaller organisations
*Early adopters are no different from later adopters in age	
Personality Variables	Personality Variables
Greater empathy Less dogmatic Greater ability to deal with abstractions Greater rationality More intelligent More favourable attitude towards change Better able to cope with uncertainty and risk More favourable attitude toward science Less fatalistic Have higher aspirations	Less empathy More likely to have a closed belief system Less able to deal with abstractions Less able to use rationality Less intelligent Less favourable attitude toward change Less able to cope with uncertainty and risk Less inclined towards science More fatalistic Has fewer aspiration
Communication Behaviours	Communication Behaviours
Have more social participation More highly inter-connected More cosmopolite Greater exposure to mass media Greater exposure to inter-personal communication More actively seek information about innovations Have greater knowledge of innovation Have higher degree of opinion leadership	Less social participation Less inter-connected Less oriented outside their social system Less exposure to mass media Less exposure to inter-personal communication Less active in seeking information about innovations Less knowledge of innovation Lesser degree of opinion leadership

2.4.2.1 Socioeconomic and demographic factors

Rogers (2003) identified socioeconomic and demographic factors (table 2.1) as key influences on an individual's likelihood of adopting innovations. Variables such as social status, educational attainment, and practice setting may shape how individuals progress through the knowledge and persuasion stages of the innovation-decision process. For example, individuals with prior exposure to an innovation, or related technologies, may experience reduced uncertainty and greater receptivity to adoption. Thus, nurses working in urban or well-resourced practice environments may be advantaged by greater access to information, professional support, and institutional infrastructure, compared to colleagues in more resource-limited contexts. Notably, Rogers initially characterised early adopters as younger in the first edition of *Diffusion of Innovations* (1962). In later editions, however, he reported that empirical findings on age were inconsistent and concluded that early and later adopters do not differ systematically in this regard (Rogers, 2003).

Several nursing studies support that demographic and professional variables including age, educational background, and years of clinical experience, may influence adoption, although findings are not always consistent (Bourgault et al., 2014; Hilz, 2000; Mohammadi et al., 2018; van der Weide & Smits, 2004). Higher levels of formal education have frequently been associated with greater receptivity to evidence-based innovations, reflecting stronger information-seeking skills and more recent exposure to advanced training (Bourgault et al., 2014; Mohammadi et al., 2018). In contrast, some studies report that longer tenure in the same role may potentially hinder adoption, as established routines and workplace norms may reduce willingness to alter practice (Dooks, 2001; Hilz, 2000; Mohammadi et al., 2018; Sarıköse & Türkmen, 2020; van der Weide & Smits, 2004).

These findings indicate that demographic factors such as education and professional experience may shape adoption behaviours, but their influence is neither uniform nor deterministic. Contextual factors, such as access to resources, organisational expectations, and opportunities for professional development, may mediate their impact (Greenhalgh et al., 2004; Ominyi et al., 2025). In the context of this doctoral study, examining sociodemographic characteristics provides a useful starting point for understanding variation in genomic uptake among oncology nurses. However, Rogers (2003) also emphasised that adoption is influenced by less tangible individual attributes, including personality traits and communication behaviours.

2.4.2.2 Personality traits

Rogers (2003) identified a set of personality variables (Table 2.1) that differentiate earlier adopters from later adopters, reflecting their underlying attitudes, values, and approaches to novelty. Earlier adopters were generally described as more empathetic, rational, and able to deal with abstractions, with a greater capacity to cope with uncertainty and change. They also tended to hold more favourable attitudes toward science, scored higher on intelligence measures, and aspired to greater personal and professional goals compared with later adopters. In contrast, later adopters were often more dogmatic, less comfortable with risk, and more likely to rely on established routines and beliefs.

These distinctions highlight Rogers' argument that adoption of innovations is influenced not only by external conditions or structural opportunities but also by psychological dispositions that shape how individuals perceive and respond to innovation. Traits such as empathy and rationality may enable earlier adopters to interpret innovations in more flexible and constructive ways, while openness to change and lower fatalism reduce the perceived risks of engaging with

the unfamiliar. However, these personality variables should not be viewed as deterministic. Later research has cautioned against treating adopter categories or trait lists as explanatory variables in themselves, noting that the effects of personality are often mediated by contextual and social factors (Greenhalgh et al., 2004).

2.4.5.2.1 Openness to experience

While Rogers (2003) emphasised traits such as rationality, empathy, and openness to change as distinguishing earlier from later adopters, subsequent scholarship has sought to refine and operationalise these personality dimensions using broader psychological frameworks. One of the most influential is the ‘Big Five’ factor model of personality (McCrae & John, 1992), which describes five core personality traits: openness to experience, conscientiousness, extraversion, agreeableness, and neuroticism. Within this model, *openness to experience* is particularly relevant to innovation adoption. In their seminal work, Costa and McCrae conceptualise openness to experience as a defining dimension of personality, encompassing intellectual curiosity, broad interests, liberal views, adventurous tendencies, and a need for variety. They argue that ‘Openness to Experience is an apt label, because it suggests a preference for the new and different in many different aspects of life’ (McCrae, 1993, 1994; McCrae & Costa, 1985). Individuals with a high degree of openness can be described as creative, imaginative, curious, and untraditional (George & Zhou, 2001; McCrae & Costa, 1985), often with a strong appreciation for ideas, art, and aesthetics (McCrae & John, 1992). In contrast, individuals low in openness tend to be more conventional, narrower in interests, unadventurous, and analytical in their orientation (McCrae & Costa, 1987). These distinctions align closely with Rogers’ depiction of early adopters as venturesome and receptive to new ideas, suggesting that openness to experience provides a meaningful extension of the personality variables underpinning innovativeness in DOI theory.

More broadly, extensive research has consistently demonstrated that openness to experience is positively related to creativity and innovativeness (Ali, 2019), with individuals high in openness more likely to engage in innovative behaviours (Batey & Furnham, 2006; Hammond et al., 2011; Patterson & Zibarras, 2017). Openness to experience has also been associated with health-promoting behaviours and preventive healthcare utilisation, such as influenza vaccination (Iwasa et al., 2009; Nolan et al., 2019; Pandhi et al., 2016). This body of evidence suggests that openness to experience not only predicts general innovativeness but may also

influence adoption of health-related innovations, providing a foundation for studies that have explicitly combined DOI theory and openness to examine healthcare adoption.

Indeed, openness to experience and DOI theory have been used as complementary models in studies of health innovation adoption. This includes recent work on COVID-19 vaccination (Mo et al., 2021) and, of particular relevance to the present doctoral study, Andrews et al.'s (2014b) study which found a significant association between openness and nurses' adoption of genomics. These findings highlight the utility of openness to experience as a complementary construct to DOI in nursing research, offering insight into the personal characteristics that may shape adoption of complex innovations such as genomics.

Importantly, openness to experience has also been linked to opinion leadership in diffusion processes. McCrae (1996) and Andrews et al. (2014a) noted that open individuals are more likely to seek out diverse information sources, adopt novel practices earlier, and influence peers through role-modelling behaviours. This theoretical connection underpinned the inclusion of an openness measure in Andrews and colleagues' survey, which informed the design of the present study. While not part of Rogers' original DOI theory, openness to experience represents a meaningful operationalisation of the personality variables associated with early adoption and opinion leadership. Therefore, in this thesis, it is examined as one potential factor influencing the uptake of genomics in oncology nursing.

2.4.2.3 Communication behaviours

In addition to socioeconomic and personality variables, Rogers (2003) identified communication behaviours as a key domain distinguishing earlier from later adopters. These behaviours reflect the ways individuals seek, exchange, and process information about new ideas, and they strongly influence the likelihood and speed of adoption. Earlier adopters tend to engage in greater social participation, higher interconnectedness, stronger cosmopolitanism, and broader exposure to both mass media and interpersonal communication channels. They are also more likely to actively seek information about innovations and develop greater knowledge of new practices. In contrast, later adopters or non-adopters tend to rely more heavily on local and familiar networks, drawing primarily on narrower and more traditional channels of communication. This pattern can reduce their exposure to diverse information sources and slow the diffusion of new ideas.

A central construct in this domain is cosmopolitanism, which Rogers defined as ‘as the degree to which an individual is oriented outside their immediate social system’ (2003, p. 290), observing that earlier adopters are consistently more cosmopolite than later adopters. Innovators, for example, tend to maintain interpersonal networks beyond their local setting, travel widely, and engage with activities that extend beyond the boundaries of their immediate workplace or community. In healthcare, cosmopolite professionals are more likely to draw on external sources of information, such as professional journals, conferences, and interdisciplinary collaborations, which can reduce uncertainty and expose them to innovations earlier in the diffusion process. These behaviours often involve a deliberate element of information-seeking, where individuals actively pursue knowledge from both formal and informal sources rather than relying on routine or local custom (Becker, 1970; Bourgault et al., 2014; Rogers, 2003).

Empirical studies in nursing support this association between cosmopolite behaviours and adoption. Conference attendance has repeatedly been linked to higher levels of research utilisation (Adams & Barron, 2009; Amicucci et al., 2022; Rodgers, 2000), while regular engagement with scholarly journals has been shown to correlate with increased adoption of research findings (Leasure et al., 2008; Milner et al., 2006; Rodgers, 2000; Sortedahl, 2012). Systematic reviews likewise report that attending education sessions or research events enhances nurses’ likelihood of integrating new knowledge into practice (Squires et al., 2011). More recently, internet use has extended the scope of cosmopolite behaviours, functioning both as a mass medium and a form of interpersonal communication. Studies have found that online resources, specialty websites, and professional listservs are positively associated with evidence-based practice among nurses (Demery Varin et al., 2019; Doran et al., 2010; García-Expósito et al., 2025; Hew & Hara, 2008).

The relevance of cosmopolitanism to this doctoral research is reflected in its inclusion as a measured variable. Building on Andrews et al. (2014b), the present survey incorporated an item adapted from Adams and Barron (2010) to assess nurses’ cosmopolitanism and information-seeking behaviours (see question #14, Appendix B). This addition was intended to capture a dimension of early adopter behaviour that is particularly pertinent in a rapidly evolving field such as genomics, where engagement with external sources of knowledge may play a critical role in shaping uptake.

While cosmopolitanism and information-seeking capture how individuals access and engage with knowledge, these behaviours also enhance their potential to influence peers within their networks. This dynamic is central to Rogers' concept of opinion leadership, which is discussed in the following section.

2.4.3 Opinion leadership

Within the broader social system, opinion leaders play a pivotal role in shaping the adoption and spread of innovation. Rogers (2003) defined opinion leaders as individuals who are respected, knowledgeable, and viewed as credible by their peers, enabling them to exert informal yet significant influence over others' attitudes and behaviours. Crucially, their authority does not stem from formal hierarchy but from perceived expertise, accessibility, and alignment with group norms. Opinion leaders are particularly influential during the persuasion and decision stages of the innovation-decision process, where peers often look to them for reassurance, guidance, and practical endorsement of new practices.

In healthcare, opinion leaders may include senior clinicians, nurse educators, clinical champions, or respected peers whose credibility derives from clinical judgement and experiential knowledge rather than positional authority (Locock et al., 2001). Their influence is typically exercised through interpersonal communication, such as mentoring, modelling behaviours, or informal discussions, rather than through formal directives. By leveraging trust, reducing uncertainty and demonstrating feasibility in everyday contexts, opinion leaders help translate abstract innovations into workable practices (Flodgren et al., 2019; Valente & Pumpuang, 2007; Verkaik et al., 2011).

Scholars have employed diverse strategies to identify opinion leaders, including peer nomination (Kelly et al., 1991), sociometric mapping of networks (Valente & Pumpuang, 2007), and structured scales (King & Summers, 1970; Lomas et al., 1991). Grimshaw et al., (2006) advanced this work by developing a pragmatic set of survey items to assess opinion leadership in scientific contexts. Building on this, Andrews et al. (2014b, 2014a) adapted four of Grimshaw's items for nursing and used them to measure opinion leadership in genomic adoption. They also incorporated the 10-item Personality Strength (PS) scale (Noelle-Neumann, 1983, 1985; Weimann et al., 2007) to assess perceived influence over others, reflecting the idea that self-perceptions of influence are an important dimension of informal leadership. In the present doctoral study, both of these measures were retained, allowing

continuity with Andrews' work while situating opinion leadership and perceived influence in the context of Australian oncology nursing and genomic innovation.

In nursing, opinion leaders have been recognised as critical drivers of innovation adoption. Research has shown their value in promoting evidence-based practice, guideline implementation, and organisational change (Arsenault Knudsen et al., 2024; Borbas et al., 2000; Flodgren et al., 2019). In the context of genomics, oncology nurses who engage with genomic knowledge may act as early adopters and informal champions, modelling integration of genomics into care and encouraging peers to follow. Indeed, opinion leadership has been explored as a key strategy in genomic nursing scholarship (Andrews et al., 2014a; Leach et al., 2016). By shaping both personal adoption and peer engagement, opinion leaders may bridge the gap between knowledge and collective practice. This highlights the importance of situating individual-level factors within the wider organisational and system context, which is examined in the following section.

2.4.4 Organisational characteristics

Just as innovations diffuse through individuals and social systems, they also spread within and between organisations (Rogers, 2003). Organisational adoption, however, is often more complex than individual adoption due to hierarchical decision-making, formalised routines, and the need for coordinated action across multiple departments. In healthcare, these complexities are particularly prominent, as adoption decisions are frequently shaped by institutional policies, leadership priorities, and resource constraints (Ghodeswar & Vaidyanathan, 2007; Marjanovic et al., 2020; Rye & Kimberly, 2007).

Rogers (2003) identified several organisational characteristics that influence an institution's capacity for innovation. *Centralisation* refers to the degree to which decision-making authority is concentrated in the hands of a few individuals. While centralised organisations can sometimes accelerate adoption if leaders strongly endorse an innovation, excessive centralisation may reduce flexibility and limit grassroots engagement. *Complexity*, in contrast, reflects the extent of specialised expertise within the organisation. More complex organisations, particularly those with a strong knowledge base and interdisciplinary expertise, are often better equipped to adopt sophisticated innovations such as genomics.

Formalisation describes the reliance on written rules, procedures, and standardised roles. Moderate levels of formalisation can support adoption by embedding new practices into

workflows, but excessive rigidity can hinder responsiveness to change. *Interconnectedness* refers to the strength of interpersonal and interdepartmental networks within the organisation. High levels of collaboration and communication enable innovations to diffuse more quickly across departments and teams. Finally, *organisational slack* describes the availability of surplus resources, such as funding, staff time, or training capacity, that can be allocated toward experimentation and implementation. Slack resources often make the difference between theoretical readiness and practical adoption (Greenhalgh et al., 2004).

Diffusion research in the healthcare context illustrates the importance of these characteristics. For example, studies of evidence-based practice adoption have highlighted how leadership endorsement, interprofessional collaboration, and investment in staff development can accelerate implementation, whereas resource constraints and rigid hierarchies often slow diffusion (Alodhialah, 2025; Melnyk et al., 2021; Ominyi et al., 2025; Ominyi & Alabi, 2025; Weng et al., 2015). In nursing specifically, organisational commitment to training, mentorship, and innovation culture has been shown to increase the uptake of new clinical practices and technologies (Clavijo-Chamorro et al., 2021; Furtado et al., 2024).

Although this doctoral study centres on individual-level factors influencing the adoption of genomics, it recognises the critical contextual role that organisational characteristics play in enabling or constraining innovation uptake. Factors such as access to workforce training, support for professional development, leadership endorsement, and the integration of genomics into clinical protocols, may significantly influence whether nurses feel supported and empowered to engage with genomic innovations in their practice. In the context of Australian oncology nursing, organisational engagement with genomics is in its infancy, and there is limited literature describing how institutions support or prioritise genomic integration. This emerging state of organisational readiness partly informed the study's decision to focus on individual adopters; however, it is acknowledged that institutional contexts shape the broader conditions under which diffusion occurs.

2.5 Limitations of DOI theory

While Rogers' DOI theory has been widely applied across diverse disciplines, including healthcare and nursing, it is not without limitations. One of the most frequently cited critiques is that it tends to portray diffusion as a relatively linear and predictable process, moving sequentially from knowledge to persuasion, decision, implementation, and confirmation (Rogers, 2003). In practice, adoption is often non-linear, recursive, and shaped by feedback

loops, interruptions, and external pressures. This means that the model may oversimplify the complex realities of innovation uptake, particularly in healthcare settings where decision-making involves multiple actors, competing priorities, and systemic constraints.

A further limitation lies in the tendency of DOI theory to privilege individual-level explanations of adoption. While Rogers acknowledged the influence of social systems and organisational characteristics, the theory has often been criticised for underplaying broader structural, political, and cultural determinants of change (Rogers, 2003). This is especially significant in healthcare, where adoption frequently requires coordinated, team-based action and is heavily shaped by institutional resources, leadership support, and policy environments. By focusing heavily on the characteristics of individual adopters, DOI theory risks overlooking the wider system-level barriers that constrain change, such as inequities in workforce training or differential access to professional development opportunities.

The categorisation of adopters into groups such as innovators, early adopters, and laggards has also been subject to critique. These labels, while descriptively useful, have been criticised as overly simplistic and value-laden, with terms like ‘laggards’ carrying pejorative connotations that fail to recognise the legitimate contextual reasons some individuals delay adoption (Rogers, 2003; Greenhalgh et al., 2004). Moreover, treating adopter categories as explanatory variables risks reifying them, when in fact adoption behaviours may be better explained through nuanced combinations of individual, interpersonal, and organisational factors.

Scholars have also highlighted a number of inherent biases within the theory. A key concern is its tendency toward a *pro-innovation bias*—the assumption that adoption is inherently desirable and that all members of a system should ultimately adopt an innovation (Rogers, 2003). This perspective risks overlooking the possibility that innovations may be resisted, re-invented, or even rejected for legitimate contextual reasons. As a result, diffusion research has historically focused more on cases of successful adoption than on failures or non-adoption, limiting insights into counter-diffusion processes. A second concern is the *individual-blame bias*, whereby responsibility for failed adoption is attributed to the characteristics of individuals rather than to wider system-level factors (Rogers, 2003). This orientation can obscure important structural influences, such as organisational constraints, resource limitations, or policy barriers, that significantly shape adoption trajectories. In the case of genomics in oncology nursing, for example, insufficient institutional support, lack of training opportunities, or restrictive clinical policies may be as influential as individual attitudes in shaping uptake.

Finally, DOI theory has been critiqued for offering more descriptive than explanatory insights. While it identifies *how* innovations diffuse, it provides less guidance on *how to intervene* to accelerate or support adoption (Iqbal & Zahidie, 2022). This limitation has led to calls for integration with other behavioural or implementation science frameworks that explicitly address mechanisms of change and intervention design.

Despite these limitations, DOI theory remains a valuable framework for conceptualising the uptake of innovations in nursing. Its enduring strength lies in its ability to illuminate the interplay between individual characteristics, interpersonal influence, and perceptions of the innovation itself. For the purposes of this doctoral study, DOI theory provides a well-established and empirically supported lens for identifying the individual-level barriers and enablers that shape nurses' engagement with genomics. At the same time, it is acknowledged that adoption is influenced by wider organisational and systemic factors that are not fully captured by DOI theory alone.

2.6 Complementary theories

Although DOI theory provides a valuable framework for understanding the spread of new ideas and practices, a range of complementary theories and models have been developed which may address some of its limitations. These frameworks often extend beyond the individual level to account for the multilevel and contextual factors influencing implementation, particularly within complex healthcare systems. Among these, the Consolidated Framework for Implementation Research (CFIR), the Theoretical Domains Framework (TDF), and the Theory of Planned Behaviour (TPB) have been especially influential in health services and behavioural research (Sales et al., 2022; Williams & Beidas, 2019) and were considered in the initial design of the study.

CFIR offers a comprehensive typology for examining implementation processes, integrating constructs from multiple theories to identify the contextual determinants that facilitate or hinder adoption (Damschroder et al., 2009). It comprises five major domains: intervention characteristics, outer setting, inner setting, characteristics of individuals, and the implementation process. By systematically mapping barriers and enablers across these domains, CFIR provides a structured means for intervention design and evaluation, particularly in organisational and policy-driven implementation contexts. The Global Genomics Nursing Alliance (G2NA) adopted CFIR to guide the development of its Roadmap and ASIGN Maturity Matrix for accelerating the global integration of genomics into nursing (see Section 1.6)

(Tonkin et al., 2020b, 2020a). These models highlight CFIR's utility in assessing system-level readiness and guiding implementation strategies across health services.

However, while CFIR offers valuable insights across a broad set of domains, it has been critiqued for lacking sufficient depth in individual-level constructs, with overlaps identified between domains and limited attention to personal characteristics that may shape adoption (Damschroder et al., 2022; Varsi et al., 2015). As such, its broad organisational scope was less directly aligned with the present study's focus on individual-level adoption behaviours and perceived barriers and enablers to genomic uptake. This doctoral research sought to explore how individual characteristics and perceived barriers and enablers influence nurses' engagement with genomics, rather than to evaluate implementation processes or organisational readiness. DOI theory was therefore considered a more conceptually congruent framework, offering a well-established theoretical basis for examining diffusion at the individual and interpersonal levels.

In nursing and genomics research, behaviour change theories have played an important role in informing implementation studies (Leach et al., 2016). Both TPB (Ajzen, 1991, 2011) and TDF (Atkins et al., 2017) are widely used for understanding and changing behaviour, but each has notable limitations that affect their application and effectiveness.

The TPB provides a structured, predictive model of individual behaviour that emphasises behavioural intention as the main driver of action (Ajzen, 1991, 2011). However, its focus on rational and deliberate decision-making can understate the influence of habit, emotion, and contextual or structural constraints, including socioeconomic and organisational factors. While the TPB incorporates subjective norms as a form of social influence, it offers limited explanation of the broader social and organisational mechanisms shaping professional practice (Sniehotta et al., 2014).

The TDF, developed to synthesise multiple psychological theories into a single diagnostic framework, excels at identifying and categorising specific behavioural determinants and is frequently used to diagnose implementation challenges in healthcare (Atkins et al., 2017). Nevertheless, it remains largely centred on individual-level cognitive and motivational processes. The framework does not address the characteristics of the innovation itself or the influence of social networks on adoption, nor does it capture the interpersonal, organisational, and temporal dynamics through which new practices diffuse across professional systems.

In contrast, DOI theory provides an integrative model that connects individual decision-making with the broader social system in which adoption occurs. As such, DOI theory offers a more comprehensive theoretical basis for addressing this doctoral study's aims and objectives, allowing exploration of both the personal characteristics that shape adoption and the relational contexts that influence the spread and uptake of genomic innovations within oncology nursing practice.

2.7 Application of DOI in the present study

Although the limitations of DOI theory highlight the importance of considering complementary perspectives, the theory remains central to this doctoral research. DOI provided the theoretical scaffolding for both phases of the study: it informed the design of the original instrument (Andrews et al., 2014b) adapted for the Phase 1 survey and guided the framing of the Phase 2 interview schedule, while also shaping the interpretation of findings across the thesis. This ensured continuity with prior genomic nursing research, particularly Andrews et al. (2014b), while extending its application to the Australian oncology nursing context.

The influence of DOI theory is also evident in the constructs examined in the following scoping review. As Rogers (2003) emphasised, knowledge forms the foundation of the innovation-decision process, shaping attitudes that ultimately influence adoption. Subsequent genomic nursing scholarship has extended these relationships (Calzone et al., 2012, 2014; Plavskin et al., 2019). Plavskin et al. (2019), drawing on DOI theory, proposed a model in which nurses' genomic competency and knowledge underpin attitudes and receptivity, which in turn drive adoption, with confidence acting as a mediating factor (see Figure 1.6). This model illustrates that adoption is not a singular event but, rather, a sequential process influenced by individual and social factors that shape readiness for change.

2.8 Conclusion

This chapter has outlined Rogers' Diffusion of Innovations theory as the theoretical lens guiding this study, explaining its key constructs and their relevance to understanding the adoption of genomics in nursing practice. Building on this theoretical foundation, the next chapter presents a scoping review of oncology nurses' knowledge and attitudes toward genetics and genomics. By situating these constructs within DOI and the broader genomic nursing literature, the review maps current evidence, identifies conceptual and methodological gaps, and establishes the foundation for the empirical phases of this study.

Chapter 3 – Scoping Review

3.1 Preface

Building on the theoretical discussion of how knowledge and attitudes shape the adoption of innovations such as genomics, this chapter presents a scoping review addressing Objective 1 of the thesis: to scope and critically examine existing research on oncology nurses' knowledge and attitudes toward genetics and genomics. The review provides a broad overview of the current evidence base and identifies areas where conceptual and methodological gaps remain. A protocol for this review was prospectively registered and made publicly available on the Open Science Framework (OSF).

The manuscript presented in this chapter has been prepared in manuscript format for submission to a peer-reviewed academic journal.

3.2 Cancer nurses' knowledge and attitudes toward genetics/genomics: A scoping review

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CRedit authorship contribution statement

Elle Elan: Conceptualisation, Methodology, Formal analysis, Investigation, Data Curation, Writing – Original Draft, Visualisation, Project administration. **Jane Maguire:** Conceptualisation, Methodology, Validation, Writing – Review & Editing, Supervision. **Deborah Debono:** Conceptualisation, Methodology, Validation, Writing – Review & Editing, Supervision. **Kris Rogers:** Writing – Review & Editing, Supervision.

Abstract

Background: Genomics is increasingly embedded across the cancer care continuum, placing new demands on nursing practice. Oncology nurses play pivotal roles in implementing genomic innovations, yet their ability to do so depends on their knowledge of and attitudes to genomics. Understanding these factors is essential to ensure preparedness for genomically informed oncology care.

Objective: This scoping review aims to systematically map the scope, characteristics, and extent of existing evidence on cancer nurses' knowledge and attitudes toward genetics and/or genomics.

Methods: A scoping review was conducted using an a-priori developed protocol following Joanna Briggs Institute methodology and PRISMA-ScR reporting guidelines. MEDLINE, Embase, CINAHL, PsycINFO, and Scopus were searched in June 2025 for peer-reviewed studies published in English from 2003 onward using terms related to oncology nurses' knowledge of and attitudes to genetics/genomics.

Results: A total of 799 records were screened, and 21 studies were included. Most were quantitative (76.2%) and conducted in high-income countries, predominantly North America (47.6%). Research was dominated by cross-sectional surveys, with few qualitative or mixed-methods designs. Knowledge and attitudes were defined inconsistently, and only a small number of studies assessed both perceived and objective knowledge. Considerable variability in study design, terminology, and measurement tools limited comparability, with most instruments being researcher-developed or adapted without validation. Oncology-specific instruments were notably scarce, and few studies examined emerging areas such as precision medicine or pharmacogenomics.

Conclusions: This review highlights a fragmented and methodologically heterogeneous evidence base on oncology nurses' genomic knowledge and attitudes. The scarcity of validated, oncology-specific instruments and limited qualitative inquiry constrain understanding of nurses' preparedness for genomics. Strengthening methodological rigour, tool development, and contextually grounded research will be essential to inform education, workforce development, and the effective integration of genomics into oncology nursing practice.

Registration: Protocol registered (4 June 2025) on the open Science Framework (doi.org/10.17605/OSF.IO/G6DAP)

Keywords

Attitudes, Knowledge, Genetics, Genomics, Oncology Nursing

Highlights

What is already known

- Genomics is integral to cancer care, and oncology nurses play key roles in its clinical implementation.
- Genomic literacy—knowledge, skills, and attitudes—is essential for safe, person-centred oncology nursing.
- The scope and extent of research on oncology nurses’ genomic knowledge and attitudes remains unclear.

What this paper adds

- This review maps the international evidence on oncology nurses’ genomic knowledge and attitudes, clarifying the breadth and focus of existing research in this area.
- It identifies a heterogeneous evidence base, including limited qualitative inquiry and a lack of validated, oncology-specific instruments.
- It outlines priority areas for future research, including methodological rigour, instrument development, and contextually grounded investigation.

Background

The completion of the Human Genome Project in 2003 marked the beginning of the genomic era, accelerating discoveries that have reshaped contemporary models of healthcare (Guttmacher and Collins, 2003). Genomics, now recognised by the World Health Organization as a global health priority, is defined as the study of the complete set of genes (genome) and the ways they interact with each other and the environment (World Health Organization, 2022). These advances underpin the broader paradigm of precision medicine, which seeks to tailor prevention, diagnosis, and treatment to individual genetic, environmental, and lifestyle factors (Ginsburg and Phillips, 2018). This shift from population-based protocols towards more individualised approaches reflects a fundamental change in modern healthcare delivery.

The clinical impact of genomics is particularly advanced in oncology. Cancer is fundamentally a genetic disease driven by alterations in DNA structure or regulation, whether spontaneous, environmentally acquired, or inherited (Garraway and Lander, 2013; Stratton et al., 2009). Consequently, genomics now informs nearly every aspect of cancer care, including risk stratification, tumour profiling, targeted therapy selection, pharmacogenomic-guided treatment optimisation, and recurrence surveillance (Berger and Mardis, 2018; Krzyszczyk et al., 2018). Across the cancer care continuum, germline testing identifies inherited cancer syndromes and guides cascade testing, while somatic profiling directs targeted therapies, informs prognosis, and supports monitoring for resistance and recurrence (Seed, 2021). Established treatments such as PARP inhibitors for *BRCA1/2*-related cancers, EGFR tyrosine kinase inhibitors in lung cancer, and immune checkpoint inhibitors for mismatch repair deficiency highlight the precision enabled by genomic discovery (Hyman et al., 2017). Pharmacogenomics, the study of genomic factors that influence how individuals respond to medications, helps guide treatment selection and dosing to reduce toxicity and optimise efficacy, reinforcing the centrality of genomic information in personalised cancer care (Pirmohamed, 2023). Genomic information also increasingly shapes survivorship care, psychosocial support, reproductive decision-making, and long-term surveillance (Cancer Australia, 2025; Jacobs and Giarelli, 2004; Ruddy et al., 2016). Collectively, these advances highlight oncology as a genomically intensive specialty.

The promise of genomic medicine, however, depends not only on scientific progress but on a workforce equipped to apply these discoveries in everyday practice. While genetic specialists remain essential to delivering genomic services, educating the broader healthcare workforce is necessary to meet rising demand and support the integration of genomics into mainstream care

(Campion et al., 2019). Nurses, who constitute the largest segment of the global health workforce (World Health Organization, 2025), may play a central role in translating innovation into ethically grounded, safe, patient-centred care (Dewell et al., 2020; Fu et al., 2020). Although genomics is relevant across many nursing specialties, it holds particular importance in oncology, where nurses often serve as a key conduit through which genomic information is communicated and integrated into routine care. Their sustained engagement across the cancer trajectory provides opportunities to explain genomic concepts, facilitate genetic testing, support informed decision-making, and coordinate referrals to genetics services (Jenkins, 2011; Rahman et al., 2022).

Oncology nurses must incorporate genomics into their practice to provide competent, evidence-based care and potentially improve patient health outcomes (Aiello, 2015). Indeed, nurses are increasingly expected to develop competencies in areas such as family history taking, pedigree construction, identifying hereditary risk indicators, facilitating referral to genetics services, engaging in interdisciplinary collaboration, and supporting patients through the ethical and cultural considerations associated with genomic information (Dickman et al., 2025; Hoxhaj et al., 2022). As genomics continues to be mainstreamed, non-genetic clinicians, including oncology nurses, are also assuming greater responsibility for elements of pre-test counselling, consent, and test coordination (Bokkers et al., 2022; Scott et al., 2020). The expanding use of precision therapies similarly extends nursing responsibilities, from assisting patients on targeted regimens and managing toxicities to interpreting pharmacogenomic information and providing education about the meaning of genomic or omic tests (Fu et al., 2020; Lebet et al., 2019). Beyond bedside care, they contribute to research, education, and policy by supporting genomic clinical trials, advancing patient literacy, advocating for equitable access, and addressing health disparities (Katapodi et al., 2024; Limoges et al., 2024; Vorderstrasse et al., 2014; Young et al., 2020). Collectively, these contributions position oncology nurses as active agents in the translation of genomics into practice, rather than passive adjuncts to genomic treatment. However, their ability to perform this role depends on their baseline knowledge and attitudes towards genomics.

Genomic literacy, defined as the knowledge, skills, and attitudes required to apply genomic information in care, is now recognised as foundational to safe, person-centred, and evidence-based practice (Calzone et al., 2024; Hurle et al., 2013). It encompasses not only scientific understanding but also the ability to communicate complex concepts, support decision-making, and navigate ethical and sociocultural implications (Calzone et al., 2024). Oncology nurses

cannot accurately apply genomic knowledge in practice without foundational genomic literacy, and limitations in this area have implications for the safe and effective delivery of care (Friend et al., 2021). This is especially important for oncology nurses as they translate complex information in a way that is understandable for patients and families (Mahon et al., 2024). Despite international efforts to develop competency frameworks and capacity-building tools (Calzone et al., 2024; NHS England, 2023; Tonkin et al., 2020a, 2020b), uptake remains uneven. Studies consistently report that nurses may be underprepared to engage with genomics, citing gaps in knowledge, confidence, and access to training opportunities (Dante et al., 2025; Thomas et al., 2023). These concerns highlight ongoing gaps between genomic innovation and workforce capability and underscore the need to understand baseline preparedness within the oncology nursing workforce.

Other reviews have examined genomic literacy, competency development, and educational needs among general nurses (Cao et al., 2025; Thomas et al., 2023; Wright et al., 2018), and a recent scoping review by Dante et al. (2025) took a broader approach by including nurses, nursing students, and academics. Rahman et al. (2022) also conducted a scoping review within the oncology context; however, their focus was on identifying the genetic and genomic learning needs required for the adoption of genomics in clinical care, and the review included both oncology nurses and oncologists. Despite these valuable contributions, no review has focused specifically on oncology nurses' knowledge and attitudes. This represents a critical gap, as oncology nurses work in a genomically intensive specialty and routinely encounter patients for whom genomic information directly shapes care. Understanding their baseline knowledge and attitudes is therefore essential to informing education, research, and policy.

Aims and review questions

This scoping review aims to systematically map the scope, characteristics, and extent of existing evidence on cancer nurses' knowledge and attitudes toward genetics and/or genomics. The review is guided by the following research question:

'What is the scope of existing evidence regarding cancer nurses' knowledge and attitudes toward genetics and/or genomics?'

Key Concepts

In this review, key concepts are informed by Rogers' Diffusion of Innovations theory (Rogers, 2003) and the broader genomic nursing literature (Calzone et al., 2014, 2013, 2012; Plavskin et

al., 2019). Within this body of work, several interrelated constructs are central to understanding professional readiness.

Knowledge is typically defined as both awareness of genetics and genomics and understanding of their application in clinical practice. Attitudes refer to nurses' perceptions of the value and relevance of genomics to their work, which in turn shape their willingness to engage with genomic content. Closely related constructs frequently reported in the literature include confidence—describing the degree of certainty nurses feel in their ability to apply genomics in practice—and preparedness, reflecting their perceived readiness to integrate genomics into care.

Although often treated as discrete outcomes in empirical studies, we view these constructs as interdependent. Greater knowledge may foster positive attitudes and confidence, while knowledge deficits can undermine preparedness and limit adoption. This interconnectedness aligns with Diffusion of Innovations theory, which positions knowledge as the foundation for attitude formation, with this subsequently influencing adoption decisions (Rogers, 2003).

Methods

Study design

This scoping review was conducted in accordance with the Joanna Briggs Institute (JBI) methodology for scoping reviews (Peters et al., 2020) and is reported in line with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) checklist (Tricco et al., 2018). The completed PRISMA-ScR checklist is included in Appendix A (Supplemental Materials).

A protocol for this review was developed a priori and registered (4 June 2025) on the Open Science Framework (OSF): <https://doi.org/10.17605/OSF.IO/G6DAP>

Eligibility criteria

Eligibility criteria were structured using the PCC (Population, Concept, Context) framework, consistent with the JBI methodology (Peters et al., 2020). An outline of how inclusion and exclusion criteria were operationalised across PCC domains is available in Table B.1 (Supplemental Materials).

The 'Concept' was interpreted broadly to include studies on 'knowledge' or 'attitudes,' as well as related constructs such as awareness, understanding, beliefs, perceptions, confidence,

readiness, and preparedness, reflecting both formal indexing terms and keyword variations commonly used in health-related knowledge and attitude reviews (Hann et al., 2017; Shaqiqi et al., 2022).

Criteria were defined a priori, with minor refinements during full-text screening to ensure consistency. Clarifications were documented and agreed upon by the review team. Interventional studies were eligible only when baseline (pre-intervention) measures of knowledge and/or attitudes were reported, ensuring data reflected cancer nurses' existing knowledge/attitudes rather than intervention effects. Studies without separate baseline data were excluded.

Information sources and search strategy

A comprehensive search strategy was designed using the PCC framework and developed in consultation with a university health librarian. An initial limited search of MEDLINE and CINAHL identified relevant articles and associated keywords and indexing terms, which informed database-specific search strategies. A small set of known studies acted as benchmark references to validate the sensitivity of the final strategy.

Searches were conducted across five databases: MEDLINE (Ovid), Embase (Elsevier), CINAHL (EBSCO), PsycINFO (Ovid), and Scopus (Elsevier), chosen for their coverage of nursing, health, psychological, and interdisciplinary research. Strategies were refined iteratively and adapted for each database using controlled vocabulary and free-text keywords. The final search was run on 4 June 2025, limited to English-language studies from 2003 onwards. Reference lists of included studies were screened manually to identify eligible literature. Full search strategies are provided in Appendix C (Supplemental Materials).

Selection of sources of evidence

All search results were imported into Covidence systematic review software (Veritas Health Innovation, Melbourne, Australia, available at www.covidence.org), which automatically identified and removed duplicates. A single reviewer manually reviewed the deduplication list to ensure accuracy.

A pilot screening of a small sample of studies was conducted independently by two reviewers (EE, JM) to ensure consistency in applying eligibility criteria, with minor clarifications made based on this process.

After calibration, two reviewers independently screened all titles and abstracts, blinded to each other's decisions. Potentially relevant studies were retrieved in full and assessed independently by two reviewers. The lead author (EE) screened all records at both stages, with a second reviewer (JM or DD) screening each record in duplicate. A third reviewer adjudicated unresolved discrepancies.

Full-text screening decisions and exclusion reasons were documented in Covidence and are summarised in the PRISMA flow diagram (Figure 3.1). No automation or artificial intelligence tools were used.

Data charting process

A customised data extraction tool was developed in Covidence, aligned with the PCC framework and tailored to the review objectives.

A pilot charting exercise on a small sample of studies assessed the tool's clarity and usability, leading to iterative revisions.

During full data charting, one reviewer (EE) completed primary extraction, and a second reviewer (JM) independently verified all entries, with discrepancies resolved through discussion or adjudication by a third reviewer (DD).

Synthesis of results

A descriptive and narrative synthesis was undertaken to map the scope, characteristics, and key concepts of included studies. Data were summarised using summary tables and visual representations, including charts and graphs where appropriate. Following JBI guidance, no critical appraisal or risk of bias assessment was conducted (Peters et al., 2020), as scoping reviews aim to map existing evidence rather than assess methodological quality. No formal synthesis or statistical comparison was undertaken.

Because study designs, outcome measures, and data collection instruments varied widely, direct comparisons across studies were not feasible. Findings were summarised using the interpretations reported by the original study authors (e.g., knowledge described as 'limited' or 'moderate'; attitudes as 'positive').

Results

Selection of sources of evidence

The initial search, along with manual reference list screening, identified a total of 799 records.

After removing 385 duplicates, 414 unique records were screened by title and abstract. Of these, 54 full-text articles were retrieved and assessed for eligibility. Following full-text review, 21 studies met the inclusion criteria and were included in the final review.

The review process is summarised in the PRISMA flow diagram (Figure 3.1), which outlines the number of records identified, screened, excluded, and included, as well as the reasons for exclusion.

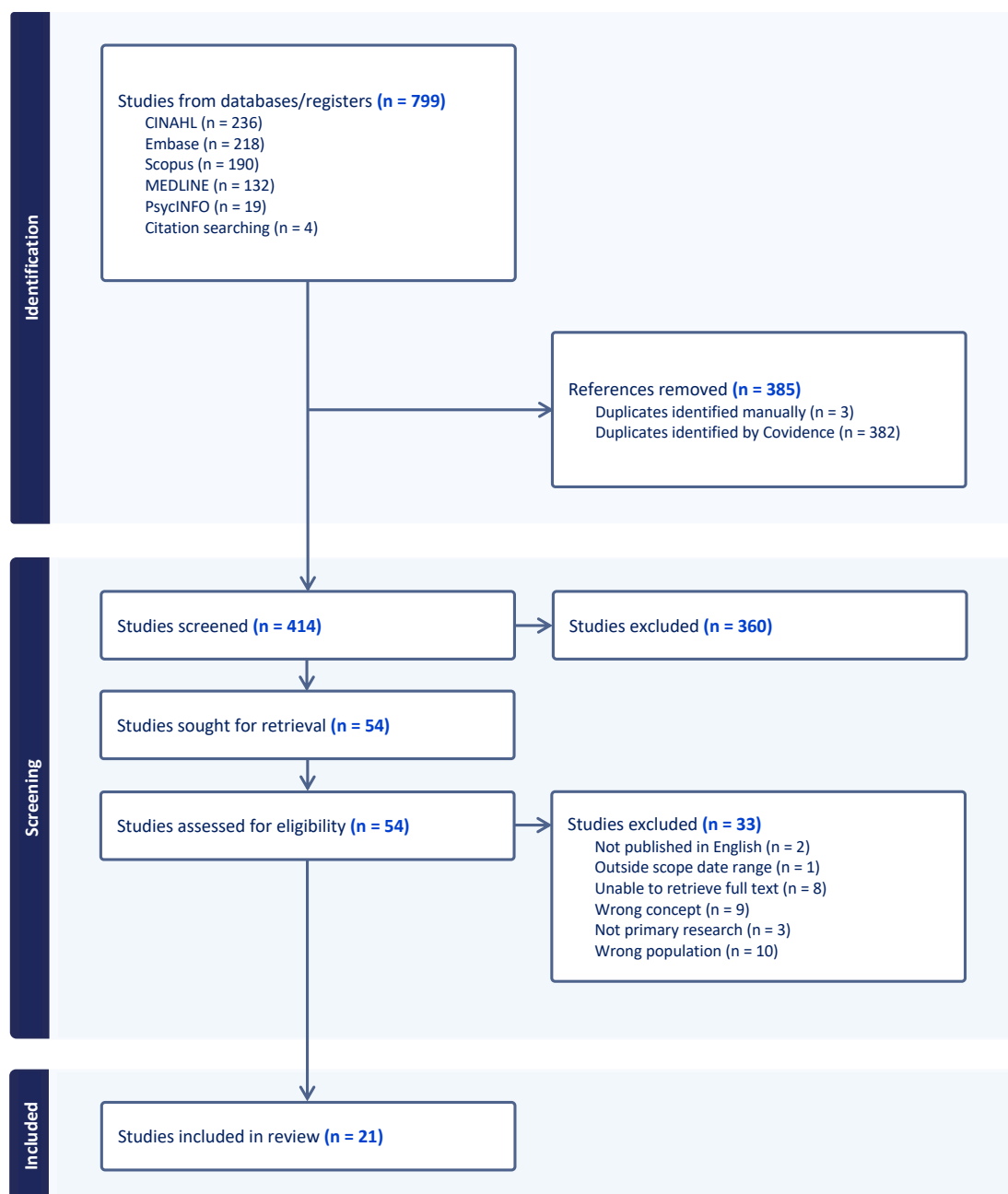


Figure 3.1. PRISMA flow diagram.

Characteristics of the included studies

A summary of extracted data is provided in Table D.1 (Supplemental Materials). The included studies spanned ten countries (Figure 3.2), although they were disproportionately concentrated in North America, where almost half of the studies (10/21, 47.6%) were conducted. Specifically, eight studies originated from the United States (Dodson, 2018, 2017, 2015, 2014; Fee-Schroeder and Nelson, 2019; Hines-Dowell et al., 2024; Lester et al., 2014; Quinn et al., 2014), and two from Canada (Gonthier et al., 2018; Hébert et al., 2022). The United Kingdom (Cuthill et al., 2025; Metcalfe et al., 2010), Turkey (Kocatepe et al., 2022; Seven et al., 2017), and China (Liu et al., 2011; Zhao et al., 2022) each contributed two studies. One study was conducted across both Australia and New Zealand (Aotearoa) (Burcher et al., 2013). The remaining four studies were conducted in Japan (Matsumoto et al., 2023), Malaysia (Liu et al., 2021), Brazil (Dornelles Prolla et al., 2015), and Australia (Wright et al., 2020). Based on World Bank income classifications at the time of publication, fifteen studies (71.4%) were conducted in high-income countries, and six (28.6%) in upper-middle-income countries (Dornelles Prolla et al., 2015; Kocatepe et al., 2022; Liu et al., 2021, 2011; Seven et al., 2017; World Bank, 2025; Zhao et al., 2022).

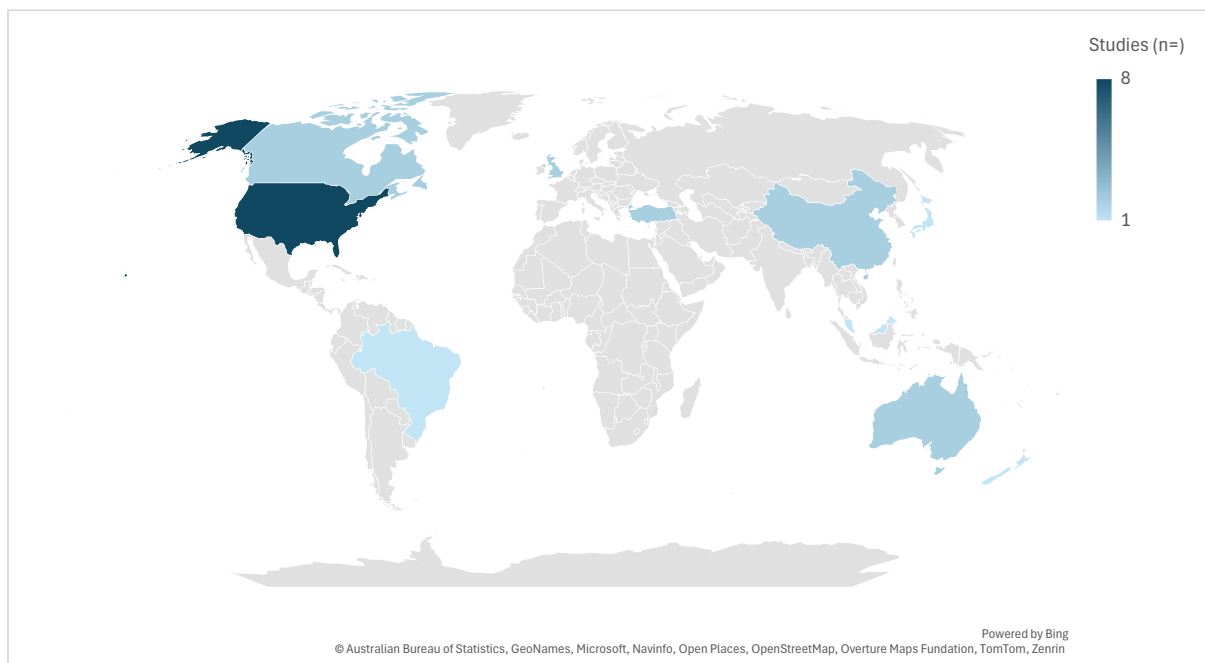


Figure 3.2. Geographic distribution of included studies.

The included studies were published between 2010 and 2025. While most (15/21; 71.4%) were published in the last decade, the annual publication pattern was inconsistent, with some years having no publications and a maximum of three studies published in any given year.

Fifteen (71.4%) studies included samples comprising exclusively oncology nurses, or used closely related terms such as *cancer nurses*, *chemotherapy nurses*, or *nurses working with cancer patients* (Cuthill et al., 2025; Dodson, 2018, 2017, 2015, 2014; Dornelles Prolla et al., 2015; Fee-Schroeder and Nelson, 2019; Hébert et al., 2022; Kocatepe et al., 2022; Lester et al., 2014; Matsumoto et al., 2023; Metcalfe et al., 2010; Quinn et al., 2014; Seven et al., 2017; Wright et al., 2020). Six (28.6%) studies involved mixed professional populations, including both oncology nurses and other groups such as physicians or non-cancer/general nurses (Burcher et al., 2013; Gonthier et al., 2018; Hines-Dowell et al., 2024; Liu et al., 2021, 2011; Zhao et al., 2022). These studies were included only if findings specific to oncology nurses were disaggregated or separately analysed, consistent with the eligibility criteria. Notably, only one study (4.8%) reported on a sample of paediatric oncology nurses (Hines-Dowell et al., 2024). Two studies (9.5%) focused on palliative care nurses, with both explicitly identifying cancer care as a focus in these studies (Gonthier et al., 2018; Metcalfe et al., 2010).

Sample sizes across the included studies ranged from nine to 1166 participants, based on 20 unique samples. One study (Dodson, 2015) was a secondary analysis of data reported in Dodson (2014) and is therefore excluded from this count.

In relation to methodology (Figure 3.3), the vast majority of studies (16/21, 76.1%) employed quantitative methods (Burcher et al., 2013; Cuthill et al., 2025; Dodson, 2018, 2014; Dornelles Prolla et al., 2015; Fee-Schroeder and Nelson, 2019; Gonthier et al., 2018; Hébert et al., 2022; Kocatepe et al., 2022; Lester et al., 2014; Liu et al., 2021, 2011; Matsumoto et al., 2023; Quinn et al., 2014; Seven et al., 2017; Zhao et al., 2022), while three studies (14.3%) used qualitative approaches (Dodson, 2017, 2015; Wright et al., 2020), and two (9.5%) included mixed-methods designs (Hines-Dowell et al., 2024; Metcalfe et al., 2010). In terms of study design, most were non-interventional (19/21, 90.5%), while two studies (9.5%) utilised pre-/post-test designs (Dodson, 2018; Fee-Schroeder and Nelson, 2019). As specified in the eligibility criteria, interventional studies were included only if they reported baseline measures of knowledge and/or attitudes.

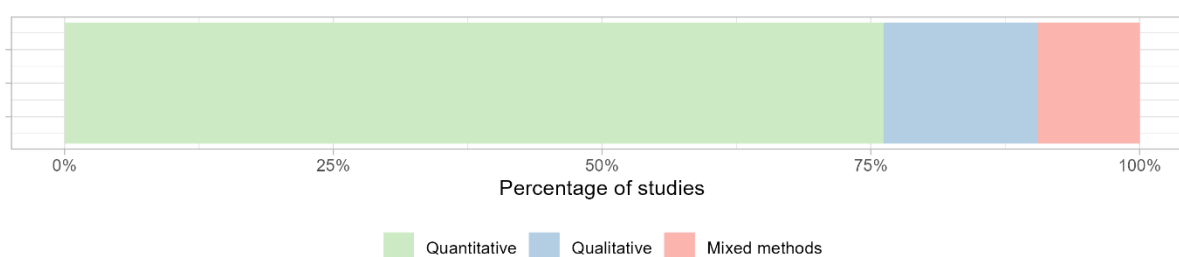


Figure 3.3. Methodological characteristics of included studies (n=21).

As per Table 3.1, of the 20 studies that employed survey-based data collection, 11 (55%) utilised researcher-developed instruments (Burcher et al., 2013; Dodson, 2017, 2015; Dornelles Prolla et al., 2015; Gonthier et al., 2018; Hébert et al., 2022; Kocatepe et al., 2022; Lester et al., 2014; Liu et al., 2011; Matsumoto et al., 2023; Seven et al., 2017), while three additional surveys (15%) were also researcher-developed but drew on existing sources by modelling their instruments on previously published tools or incorporating adapted scales or questions (Cuthill et al., 2025; Hines-Dowell et al., 2024; Liu et al., 2021). Five studies (25%) employed adapted versions of previously published instruments (Dodson, 2018, 2014; Metcalfe et al., 2010; Quinn et al., 2014; Zhao et al., 2022), and only one study (5%) used a fully established validated survey (the Genetics & Genomics in Nursing Practice Survey, GGNPS) (Fee-Schroeder and Nelson, 2019).

With respect to validation, 12 studies (60%) reported partial validation procedures, most commonly expert review, pilot testing, or internal reliability testing (Cronbach's α) (Burcher et al., 2013; Cuthill et al., 2025; Dodson, 2018, 2014; Gonthier et al., 2018; Hébert et al., 2022; Hines-Dowell et al., 2024; Kocatepe et al., 2022; Lester et al., 2014; Liu et al., 2021; Metcalfe et al., 2010; Zhao et al., 2022). Seven studies (35%) reported no validation evidence (Dodson, 2017, 2015; Dornelles Prolla et al., 2015; Liu et al., 2011; Matsumoto et al., 2023; Quinn et al., 2014; Seven et al., 2017), and only one study (5%) used a fully validated instrument without adaptation (Fee-Schroeder and Nelson, 2019). Notably, in cases where surveys were adapted from existing tools, the original sources were not always validated, and re-validation of the modified instruments was rarely conducted. An exception was the Chinese adaptation of the GGNPS (GGNPS-CV), for which content validity testing and internal consistency were reported (Zhao et al., 2022).

Table 3.1. Study surveys (n=20)

Study	Survey & Origin	Validation
Burcher et al. (2013)	Researcher-developed	Partial—Developed with expert panel; piloted with 5 professionals; ‘internal reliability’ (Cronbach's α) reported; no further validation
Cuthill et al. (2025)	Researcher-developed survey (modelled on Health Education England 2021 genomics in practice survey)	Partial—Based on HEE 2021 survey (itself adapted from AGHA). Trialled with small cancer nursing team. No psychometric statistics reported in this or source surveys.

Study	Survey & Origin	Validation
Dodson (2014)	Modified Knowledge & Attitude Questionnaire (Roederer 2012) and Nursing Practice Questionnaire (Brett 1987)	Partial—Both instruments adapted for oncology context. Internal consistency reported (Cronbach's $\alpha = 0.64$ – 0.68 for knowledge, $\alpha = 0.59$ for practice); no further psychometric testing reported.
Dodson (2015)	Open-ended item from Dodson (2014) survey	N/A
Dodson (2017)	Researcher-developed	No—No pilot, expert input, or psychometric validation reported
Dodson (2018)	Modified KAQ-PGx (from Roederer et al., 2012)	Partial—KAQ-PGx adapted with removal of subscales and addition of knowledge questions; piloted with oncology nurse panel; internal consistency reported for knowledge scale ($\alpha = 0.81$); no other psychometric testing reported
Dornelles Prolla et al. (2015)	Researcher-developed	No—No pilot, expert input, or psychometric validation reported
Fee-Schroeder and Nelson (2019)	Established Genomic Nursing Concept Inventory (GNCI, 13 items); Genetic/Genomic Nursing Practice Survey (GGNPS)	Yes—Both GNCI and GGNPS are validated instruments. GNCI used in shortened 13-item form
Gonthier et al. (2018)	Researcher-developed	Partial—Developed by research team using literature, ASCO curriculum, and prior studies; reviewed by cancer genetics experts; pretested with health professionals for understanding; no psychometric statistics reported.
Hébert et al. (2022)	Researcher-developed	Partial—Based on prior studies; pre-tested for face validity; authors note reliability and validity uncertain. No psychometric statistics reported
Hines-Dowell et al. (2024)	Researcher-developed survey (with 4 adapted items from Johnson et al., 2019)	Partial—Adapted 4 items from survey for parents (Johnson et al., 2019); piloted with 10 genomics-proficient professionals; revisions made for clarity and usability; no psychometric statistics reported.
Kocatepe et al. (2022)	Researcher-developed	Partial—Developed using National Nursing Core Curriculum; reviewed by 10 experts across nursing, molecular biology, and medical biology; finalized based on expert feedback; no psychometric testing reported.

Study	Survey & Origin	Validation
Lester et al. (2014)	Researcher-developed	Partial—One genetic risk question included; instrument developed via literature review and expert panel; content validity assessed (CVI = 0.89 then 1.00); no other psychometric testing reported.
Liu et al. (2021)	Researcher-developed (knowledge scale adapted from National Health Interview Survey (NHIS))	Partial—Knowledge scale adapted from NHIS; internal consistency reported ($\alpha = 0.78$). Attitude scale developed from literature and reviewed by expert panel; no additional psychometric testing reported.
Liu et al. (2011)	Researcher-developed	No—No pilot testing, expert input, or psychometric validation reported
Matsumoto et al. (2023)	Researcher-developed	No—No pilot testing, expert input, or psychometric validation reported
Metcalfe et al. (2010)	Adapted survey (originally validated by Werrett et al., 2001; Metcalfe et al., 2008)	Partial—Adapted from validated instrument; original $\alpha > 0.80$ with >400 nurses. Modified for hospice setting and piloted locally; no psychometric testing reported for adapted version.
Quinn et al. (2014)	Modified consumer survey on PGD (from Kalfoglou et al., 2004)	No—Adapted from non-validated patient/consumer survey. No psychometric validation reported for original or modified versions
Seven et al. (2017)	Researcher-developed	No—Developed by authors (experts in genetics and oncology nursing) and informed by literature. No pilot testing or psychometric statistics reported
Zhao et al. (2022)	GGNPS-CV (Chinese adaptation of GGNPS)	Partial—Cross-cultural adaptation of GGNPS using AAOS (2002) guidelines; content validity tested (S-CVI = 0.94); internal consistency reported ($\alpha = 0.867$); pilot tested with 30 nurses.

Genetics/Genomics Terminology

The terms genetics, genomics and hereditary/familial cancer were used heterogeneously in the studies (see Table 3.2). In describing the knowledge and attitude focus of these studies, 12 used genetics (Burcher et al., 2013; Dornelles Prolla et al., 2015; Gonthier et al., 2018; Hébert et al., 2022; Kocatepe et al., 2022; Lester et al., 2014; Liu et al., 2021, 2011; Matsumoto et al., 2023; Metcalfe et al., 2010; Quinn et al., 2014; Seven et al., 2017), six used genomics (Cuthill et al., 2025; Dodson, 2018, 2017, 2015; Hines-Dowell et al., 2024; Wright et al., 2020), and three used a combination of both genetics and genomics (Dodson, 2014; Fee-Schroeder and Nelson, 2019; Zhao et al., 2022).

Concept Focus

Knowledge

The majority (18/21, 85.7%) of studies focused on knowledge variables (see Table 3.2). Of these, 38.9% (7/18) assessed objective knowledge (Dodson, 2018; Dornelles Prolla et al., 2015; Gonthier et al., 2018; Hines-Dowell et al., 2024; Kocatepe et al., 2022; Liu et al., 2021; Seven et al., 2017), 38.9% (7/18) assessed perceived knowledge (Cuthill et al., 2025; Lester et al., 2014; Liu et al., 2011; Matsumoto et al., 2023; Metcalfe et al., 2010; Quinn et al., 2014; Wright et al., 2020), and 22.2% (4/18) assessed both (Dodson, 2014; Fee-Schroeder and Nelson, 2019; Hébert et al., 2022; Zhao et al., 2022).

Table 3.2. Terminology and knowledge assessed (n=21)

Study	Terminology			Knowledge assessed		
	Genomics	Genetics	Both	Objective	Perceived	Both
Burcher et al. (2013)		×		N/A	N/A	N/A
Cuthill et al. (2025)	×				×	
Dodson (2014)			×			×
Dodson (2015)	×			N/A	N/A	N/A
Dodson (2017)	×			N/A	N/A	N/A
Dodson (2018)	×			×		
Dornelles Prolla et al. (2015)		×		×		
Fee-Schroeder and Nelson (2019)			×			×
Gonthier et al. (2018)		×		×		
Hébert et al. (2022)		×				×
Hines-Dowell et al. (2024)	×			×		
Kocatepe et al. (2022)		×		×		
Lester et al. (2014)		×			×	
Liu et al. (2021)		×		×		
Liu et al. (2011)		×			×	
Matsumoto et al. (2023)		×			×	
Metcalfe et al. (2010)		×			×	
Quinn et al. (2014)		×			×	
Seven et al. (2017)		×		×		
Wright et al. (2020)	×				×	
Zhao et al. (2022)			×			×

Several studies focused on broad genetics and genomics knowledge (Cuthill et al., 2025; Fee-Schroeder and Nelson, 2019; Hines-Dowell et al., 2024; Kocatepe et al., 2022; Seven et al., 2017; Zhao et al., 2022), while four focused specifically on knowledge of cancer genetics or hereditary cancer syndromes, such as hereditary breast and ovarian cancer (Dornelles Prolla et al., 2015; Gonthier et al., 2018; Hébert et al., 2022; Matsumoto et al., 2023). Two studies focused on pharmacogenomics knowledge (Dodson, 2018, 2014) and four examined

knowledge related to genetics and genomics in practice and care activities (Cuthill et al., 2025; Metcalfe et al., 2010; Seven et al., 2017; Wright et al., 2020).

Knowledge relating to family history, including inheritance patterns as well as the collection and interpretation of family history, was reported in four studies (Fee-Schroeder and Nelson, 2019; Gonthier et al., 2018; Hébert et al., 2022; Matsumoto et al., 2023). Several studies assessed knowledge of genetic risk factors (Dornelles Prolla et al., 2015; Gonthier et al., 2018; Seven et al., 2017) or perceived knowledge to discuss these with patients and families (Lester et al., 2014). Knowledge of genetic testing was examined in four studies, including awareness of available tests, interpretation of results, and the impact of testing on clinical decision-making (Hébert et al., 2022; Hines-Dowell et al., 2024; Liu et al., 2021; Zhao et al., 2022). Three studies assessed knowledge of genetic counselling—either understanding its purpose or knowledge of services and referral pathways (Dornelles Prolla et al., 2015; Gonthier et al., 2018; Quinn et al., 2014). Finally, two studies focused on specialised genetic interventions, such as pre-implantation genetic diagnosis (PGD) (Quinn et al., 2014) and gene therapy (Liu et al., 2011).

Overall, seven studies reported that nurses' knowledge was limited, lacking, or poor, or identified a 'knowledge deficit' (Cuthill et al., 2025; Dodson, 2018, 2014; Hébert et al., 2022; Lester et al., 2014; Matsumoto et al., 2023; Quinn et al., 2014; Wright et al., 2020). Conversely, three studies described knowledge as 'moderate' (Kocatepe et al., 2022; Seven et al., 2017; Zhao et al., 2022) and one study reported that most nurses had adequate moderate-to-high knowledge (Liu et al., 2021).

Attitudes

Attitudes were explicitly measured in ten (47.6%) of the studies (Burcher et al., 2013; Dodson, 2017, 2015, 2014; Fee-Schroeder and Nelson, 2019; Hébert et al., 2022; Liu et al., 2021, 2011; Matsumoto et al., 2023; Zhao et al., 2022). However, attitudinal constructs (e.g., perceived importance, interest in education, etc) were reported in several other studies, even when not defined by authors as 'attitudes' (Cuthill et al., 2025; Dornelles Prolla et al., 2015; Gonthier et al., 2018; Hines-Dowell et al., 2024; Kocatepe et al., 2022; Metcalfe et al., 2010; Quinn et al., 2014; Seven et al., 2017; Wright et al., 2020).

Attitude studies

Of the ten studies explicitly measuring attitudes, three focused on pharmacogenomics (Dodson, 2017, 2015, 2014). Dodson (2014) examined attitudes toward pharmacogenomic testing in

general and oncology contexts, reporting on trust, fears and concerns (e.g., unauthorised access, discrimination, and family impact), and perceptions of need for pharmacogenomics alongside the difficulty of understanding the field. This study also noted nurses' views that they should educate patients and that pharmacogenomics could help reduce adverse events. Dodson (2015) described nurses' thoughts and concerns regarding pharmacogenomics, including Ethical, Legal, and Social Implications (ELSI) themes such as rising insurance costs and the disparities between insured and uninsured patients. Dodson (2017) updated themes from the 2015 study, expanding on perspectives that had emerged since the earlier work.

Two studies addressed cancer genetics (Hébert et al., 2022; Matsumoto et al., 2023). Matsumoto et al. (2023) reported on attitudes about learning and education related to hereditary breast and ovarian cancer. Hébert et al. (2022) examined nurses' perceived roles and professional duties in oncogenetics, including serving as someone to whom patients can talk, providing referrals to resources, empowering families, understanding the ethical implications of genetic testing, raising genetic testing with patients and families, and incorporating family history into practice. This study also reported interest in further education, including interest in learning about ELSI issues.

Two studies focused on genetics and genomics concepts, including both general and cancer-specific contexts (Fee-Schroeder and Nelson, 2019; Zhao et al., 2022). Fee-Schroeder and Nelson (2019) reported on the perceived importance of nurses' understanding of genetics and genomics. Zhao et al. (2022) examined attitudes and receptivity toward genomics, including the perceived importance of being educated, perceived advantages of integrating genomics into practice (e.g., informing treatment decisions), perceived disadvantages (e.g., the need to 're-tool' professionally, risk of insurance discrimination), and intention to pursue further learning.

Two studies examined genetic testing (Burcher et al., 2013; Liu et al., 2021). Burcher et al. (2013) explored treatment-focused genetic testing (TFGT), including its perceived usefulness and value, impact on treatment decision-making, attitudes toward future use, and preferences for timing and the preferred professional to offer testing. Liu et al. (2021) reported on general objective attitudes regarding *BRCA1/2* testing. Finally, one study focused on gene therapy (Liu et al., 2011), reporting perceptions of its safety and nurses' willingness to accept it.

Studies including attitudinal variables

Nine additional studies reported attitudinal constructs, although these were not explicitly labelled as 'attitudes'. Several of these related to education, including interest in education or

learning (Dornelles Prolla et al., 2015; Gonthier et al., 2018; Wright et al., 2020), willingness to pursue further education (Seven et al., 2017), and desire or need for education (Cuthill et al., 2025; Hines-Dowell et al., 2024; Metcalfe et al., 2010).

Other studies examined perceptions of relevance and application to practice, including views on the relevance of genomics to nursing and overall preparedness to use genomics in practice (Cuthill et al., 2025; Kocatepe et al., 2022; Metcalfe et al., 2010; Wright et al., 2020). In addition, studies reported on role clarity and professional responsibilities, such as patient advocacy, educating patients and families, taking family history, making referrals, and explaining genomic concepts (Cuthill et al., 2025; Hines-Dowell et al., 2024; Wright et al., 2020).

Some attitudinal constructs reported in these studies also addressed ELSI issues. One study assessed nurses' awareness of their own personal values that may affect care, consideration of social, cultural, legal, and financial issues in genomic practice, and support for patient autonomy and informed decision-making (Kocatepe et al., 2022). Another examined acceptability and concerns regarding PGD, including affordability, misuse, social and religious concerns, and perceptions of 'playing god' (Quinn et al., 2014).

Four studies described 'positive attitudes' (Burcher et al., 2013; Dodson, 2015, 2014; Liu et al., 2021), whereas the remaining studies did not provide descriptive characterisations of attitudes.

Confidence

Nurses' confidence in relation to genomics was reported in eight studies across several domains (Cuthill et al., 2025; Fee-Schroeder and Nelson, 2019; Gonthier et al., 2018; Hébert et al., 2022; Hines-Dowell et al., 2024; Metcalfe et al., 2010; Quinn et al., 2014; Zhao et al., 2022). Some studies examined confidence in genomic knowledge and understanding (Fee-Schroeder and Nelson, 2019; Hines-Dowell et al., 2024; Quinn et al., 2014). Others assessed confidence in applying genomics in practice, including discussing genomics with patients and families, providing education, and addressing questions or concerns (Cuthill et al., 2025; Gonthier et al., 2018; Hébert et al., 2022; Hines-Dowell et al., 2024; Metcalfe et al., 2010; Zhao et al., 2022). Confidence in collecting or recognising significant family history was also assessed (Gonthier et al., 2018; Hébert et al., 2022; Metcalfe et al., 2010; Zhao et al., 2022). Other studies examined confidence in requesting or facilitating referrals to genetic services (Metcalfe et al., 2010; Zhao et al., 2022). In terms of ELSI issues, one study specifically assessed confidence in psychosocial genetics-related activities such as confidentiality, informed choice, and respect for patient

autonomy (Metcalf et al., 2010). Confidence regarding the requirements for patient consent to genomic testing was also reported (Cuthill et al., 2025). Finally, several studies reported on confidence related to genetic testing, encompassing a broad range of activities such as explaining risks and benefits, selecting appropriate tests, communicating results, and accessing information about available tests (Cuthill et al., 2025; Metcalf et al., 2010; Zhao et al., 2022).

Overall, while the specific domains varied, several studies explicitly reported that confidence was low among their nursing samples (Cuthill et al., 2025; Gonthier et al., 2018; Hébert et al., 2022; Metcalf et al., 2010).

Correlates of knowledge and attitudes

In addition to describing levels of knowledge, attitudes, and confidence, ten studies also conducted correlation analyses (see Table E.1, Supplemental Materials). These examined associations with knowledge/attitude variable, sociodemographic factors such as age, gender, education level, and years of experience, as well as professional characteristics including cancer specialty and prior genetic training (Cuthill et al., 2025; Dodson, 2018, 2014; Dornelles Prolla et al., 2015; Kocatepe et al., 2022; Liu et al., 2021, 2011; Metcalf et al., 2010; Quinn et al., 2014; Seven et al., 2017).

Discussion

This scoping review mapped the international literature examining oncology nurses' knowledge and attitudes toward genetics and genomics. Twenty-one studies conducted across ten countries revealed a limited, fragmented and heterogeneous evidence base. Research in this area has been concentrated in high-income settings, with few studies from low- and middle-income countries. Most investigations employed quantitative cross-sectional survey designs, with comparatively few qualitative or mixed-methods approaches capable of capturing the contextual and experiential dimensions of genomic practice.

The concepts and outcomes assessed varied considerably. Knowledge and attitudes were defined and measured inconsistently across studies, with related constructs such as confidence, preparedness, and perceived relevance examined to differing extents. Inconsistent use of genomic terminology, including conflation of 'genetics' and 'genomics', further contributed to conceptual variability, despite calls for accurate terminology as essential for safe practice (Friend et al., 2021; Mahon, 2024). Furthermore, ELSI concepts and precision medicine constructs such as pharmacogenomics were seldom explored. Methodological diversity was

also evident in the instruments employed, as most were researcher-developed or adapted ad hoc, and only a small number demonstrated evidence of psychometric validation.

The findings of this review align with broader scoping reviews of genomic nursing research, which have consistently highlighted a fragmented and heterogeneous evidence base. Thomas et al. (2023) reported that much of the published nursing literature on genomics concentrates on knowledge, attitudes, and beliefs, yet remains geographically and methodologically uneven, with the majority of studies originating from high-income countries such as the United States. Similarly, Dante et al., (2025) described genomic literacy research as limited, heterogeneous, and dominated by quantitative designs, noting the scarcity of evidence from low- and middle-income contexts. As their review included nurses, nursing students, and academics and was not specific to oncology nursing, these conclusions speak to the broader developmental stage of the field, where conceptual and methodological diversity impedes direct comparison across studies and limits the generalisability of findings to varied healthcare systems.

Most studies identified in this review employed quantitative cross-sectional designs, with only a small number adopting qualitative ($n = 3$) or mixed-methods ($n = 2$) approaches. This narrow methodological range limits understanding of the contextual and experiential factors shaping oncology nurses' genomic knowledge and attitudes. Quantitative surveys are valuable for identifying trends, yet they offer limited insight into the underlying reasons—the 'why'—for these patterns. In contrast, qualitative and mixed-methods approaches can illuminate how nurses interpret and experience genomics in practice. Mixed-methods research, which integrates quantitative and qualitative data to provide a more comprehensive understanding of complex phenomena (Creswell and Plano Clark, 2018; Teddlie and Tashakkori, 2009), has proven particularly valuable in health and nursing contexts where behaviours and decisions are highly contextual (Halcomb and Hickman, 2015; Wasti et al., 2022). The absence of lived-experience perspectives in this literature constrains understanding of how nurses' knowledge and attitudes are formed, reinforced, or challenged within real-world clinical environments. Greater methodological diversity is therefore essential to capture the nuances of nurses' engagement with genomics beyond what can be quantified.

Although genomics is now integral to precision oncology, relatively few studies have examined oncology nurses' knowledge and attitudes toward genomic precision or personalised medicine, including pharmacogenomics and genomically guided therapies. This gap is notable given that knowledge in pharmacogenomics has been identified as an essential oncology nursing

competency (Cheek et al., 2015), and that oncology nurses are well positioned to play leadership roles in implementing pharmacogenomics in routine clinical practice. To do so effectively, nurses must understand how DNA is collected and tested, how to interpret genomic test results, and how to educate patients about the implications of these results (Germany and Kueber, 2023). Strengthening this evidence base is essential to ensure that oncology nurses are adequately prepared to participate in precision medicine delivery and to translate emerging genomic advances into equitable patient care.

Across the included studies, knowledge and attitudes were conceptualised and measured inconsistently. Of the 18 survey-based studies assessing knowledge, seven examined objective knowledge, seven assessed perceived knowledge, and four incorporated both approaches. As highlighted in previous reviews, many studies rely primarily on self-reported or perceived knowledge rather than direct assessment, which may inflate estimates of competence and obscure actual preparedness (Wright et al., 2018). Using both perceived and objective measures may provide a more balanced understanding, capturing not only factual knowledge but also nurses' confidence and self-awareness in applying genomics to practice.

Considerable variability was also evident in the instruments used to assess these constructs. Most studies employed researcher-developed or adapted tools, often created ad hoc for single investigations without evidence of validation. This mirrors broader findings in genomic nursing research, where genomic literacy is frequently measured using non-standardised instruments (Thomas et al., 2023; Dante et al., 2025). Only one study utilised a fully validated survey, the GGNPS, which is a psychometrically robust instrument developed for general nursing populations (Plavskin et al., 2019). However, its emphasis on common diseases (e.g., diabetes) and USA-specific competencies may limit its applicability to oncology and to differing international contexts. The absence of validated, context-appropriate instruments constrains comparability across studies and underscores the need for further tool development and cross-cultural adaptation, aligning with Thomas et al.'s (2023) call for future research that is responsive to the needs of diverse patients, communities, and populations nurses serve.

Gaps and Future Directions

Despite growing recognition of genomics as a critical component of cancer care, the evidence base on oncology nurses' knowledge and attitudes remains methodologically and conceptually underdeveloped. Few studies have explored these domains in the context of precision or personalised medicine, particularly pharmacogenomics, despite their increasing relevance to

cancer treatment and nursing practice. This is particularly concerning given that oncology nurses work in one of the most genomically intensive areas of clinical practice, where genomic information directly informs diagnosis, treatment, and patient education. Future research should prioritise greater methodological diversity, including qualitative and mixed-methods designs capable of capturing the experiential and contextual dimensions of genomic practice.

Measurement approaches also require strengthening, as most existing instruments have been researcher-developed or adapted ad hoc, with limited oncology-specific focus or cross-cultural applicability. Advancing this field will require tools that are not only psychometrically sound but also theory-informed, contextually grounded, and transparent in their development. Instruments that assess both perceived and objective knowledge may yield a more comprehensive understanding of nurses' preparedness, providing the evidence base needed to inform education, workforce development, and implementation strategies that support readiness for the genomic era. Moreover, the dominance of research from high-income countries highlights the need for studies in low- and middle-income settings to ensure global representativeness and equity in genomic nursing capacity building.

Limitations

This review has several limitations. First, articles were excluded if they did not disaggregate findings for cancer nurses, or if fewer than 70% of participants were cancer nurses. While this ensured that the evidence reflected the oncology nursing workforce specifically, it may have led to the omission of potentially relevant perspectives. Nursing students were also excluded, and interventional studies were only included where baseline knowledge or attitudes were reported, limiting the scope of educational evidence captured. Second, only peer-reviewed studies published in English were considered and grey literature was not searched. These decisions may have introduced language and publication bias, and potentially excluded insights from non-English-speaking contexts. Finally, in line with scoping review methodology, the quality of included studies was not appraised. Combined with the methodological variability of the evidence base, this may constrain the interpretability and transferability of findings.

Conclusions

This scoping review provides the first review of international evidence on oncology nurses' knowledge and attitudes toward genetics and genomics. The findings reveal a fragmented and heterogeneous field characterised by methodological variability, limited qualitative inquiry, and a lack of validated, oncology-specific instruments. Despite widespread recognition of genomics

as central to cancer care, evidence of nurses' preparedness remains limited. Addressing these gaps through methodologically rigorous, contextually grounded, and theoretically informed research is essential to strengthen nursing workforce readiness for the genomic era.

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Appendix. A: Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) Checklist

SECTION	ITEM	PRISMA-ScR CHECKLIST ITEM	REPORTED ON PAGE #
TITLE			
Title	1	Identify the report as a scoping review.	72
ABSTRACT			
Structured summary	2	Provide a structured summary that includes (as applicable): background, objectives, eligibility criteria, sources of evidence, charting methods, results, and conclusions that relate to the review questions and objectives.	73
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known. Explain why the review questions/objectives lend themselves to a scoping review approach.	75-77
Objectives	4	Provide an explicit statement of the questions and objectives being addressed with reference to their key elements (e.g., population or participants, concepts, and context) or other relevant key elements used to conceptualize the review questions and/or objectives.	77
METHODS			
Protocol and registration	5	Indicate whether a review protocol exists; state if and where it can be accessed (e.g., a Web address); and if available, provide registration information, including the registration number.	78
Eligibility criteria	6	Specify characteristics of the sources of evidence used as eligibility criteria (e.g., years considered, language, and publication status), and provide a rationale.	78-79
Information sources	7	Describe all information sources in the search (e.g., databases with dates of coverage and contact with authors to identify additional sources), as well as the date the most recent search was executed.	79
Search	8	Present the full electronic search strategy for at least 1 database, including any limits used, such that it could be repeated.	Appendix C (Supplemental Materials)
Selection of sources of evidence	9	State the process for selecting sources of evidence (i.e., screening and eligibility) included in the scoping review.	79-80
Data charting process	10	Describe the methods of charting data from the included sources of evidence (e.g., calibrated forms or forms that have been tested by the team before their use, and whether data charting was done independently or in duplicate) and any processes for obtaining and confirming data from investigators.	80
Data items	11	List and define all variables for which data were sought and any assumptions and simplifications made.	80
Critical appraisal of individual sources of evidence	12	If done, provide a rationale for conducting a critical appraisal of included sources of evidence; describe the methods used and how this information was used in any data synthesis (if appropriate).	N/A
Synthesis of results	13	Describe the methods of handling and summarizing the data that were charted.	80
RESULTS			
Selection of sources of evidence	14	Give numbers of sources of evidence screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally using a flow diagram.	80-81

SECTION	ITEM	PRISMA-ScR CHECKLIST ITEM	REPORTED ON PAGE #
Characteristics of sources of evidence	15	For each source of evidence, present characteristics for which data were charted and provide the citations.	82-86 & Table D.1 (Supplemental Materials)
Critical appraisal within sources of evidence	16	If done, present data on critical appraisal of included sources of evidence (see item 12).	N/A
Results of individual sources of evidence	17	For each included source of evidence, present the relevant data that were charted that relate to the review questions and objectives.	D.1 (Supplemental Materials)
Synthesis of results	18	Summarize and/or present the charting results as they relate to the review questions and objectives.	87-91
DISCUSSION			
Summary of evidence	19	Summarize the main results (including an overview of concepts, themes, and types of evidence available), link to the review questions and objectives, and consider the relevance to key groups.	91-94
Limitations	20	Discuss the limitations of the scoping review process.	94
Conclusions	21	Provide a general interpretation of the results with respect to the review questions and objectives, as well as potential implications and/or next steps.	94-95
FUNDING			
Funding	22	Describe sources of funding for the included sources of evidence, as well as sources of funding for the scoping review. Describe the role of the funders of the scoping review.	72

Source: Tricco AC, Lillie E, Zarin W, O'Brien KK, Colquhoun H, Levac D, et al. PRISMA Extension for Scoping Reviews (PRISMA-ScR): checklist and explanation. *Ann Intern Med*. 2018;169:467–473. doi: [10.7326/M18-0850](https://doi.org/10.7326/M18-0850).

Table B.1. PCC eligibility criteria

PCC Element	Inclusion Criteria	Exclusion Criteria
Population	— Oncology/cancer nurses, including registered nurses, advanced practice (non-genetic/genomic) nurses, and clinical nurse educators — Mixed nurse populations where $\geq 70\%$ were oncology nurses, or where oncology-specific data were reported separately — Registered nurses practising oncology nursing	— General or non-cancer-specific nursing populations — General or mixed nursing populations without disaggregated oncology-nursing reporting or sub-analyses — Nursing students (pre-registration) or non-practicing nurses
Concept	— Studies reporting on nurses' baseline knowledge and/or attitudes toward genetics and/or genomics — Included related constructs such as understanding, awareness, confidence, perceptions, beliefs, readiness, interest, and preparedness	— Studies not reporting outcomes related to knowledge, attitudes, or related constructs (e.g., studies focused solely on clinical outcomes, intervention effectiveness, without reporting baseline knowledge or attitudinal variables) toward genetics and/or genomics
Context	— Working across the clinical cancer care continuum in adult or paediatric settings — Studies conducted in clinical cancer care settings (e.g., inpatient, outpatient, community, or tertiary care environments), or involving nurses actively working in these contexts	— Studies focused solely on educational settings, simulations, or pre-licensure training environments involving non-practicing nurses or nursing students (pre-registration)
Other criteria	— Published from 2003 onward (post-Human Genome Project era) — Peer-reviewed, primary research studies (quantitative, qualitative, or mixed-methods) — Full-text available in English	— Reviews, commentaries, editorials, theoretical papers, conference abstracts, grey literature, or unpublished-theses/dissertations — Non-English publications — Published before 2003 — Not available as full text

C: Search Strategies

MEDLINE (Ovid):

1. Oncology Nursing/ OR oncology nurs*.mp.
2. cancer nurs*.mp.
3. genetic*.mp. OR Genetics/ OR Genetics, Medical/ OR Human Genetics/ OR exp Genetic Testing/
4. Genomics/
5. genom*.mp. OR Genome/
6. Knowledge/ OR Health Knowledge, Attitudes, Practice/ OR knowledge.mp.
7. Attitude/ OR Attitude of Health Personnel/ OR attitude*.mp.
8. (awareness OR understanding OR belief* OR perception* OR confiden* OR readiness OR prepared*).mp.
9. 1 OR 2
10. 3 OR 4 OR 5
11. 6 OR 7 OR 8
12. 9 AND 10 AND 11
13. limit 12 to yr="2003 -Current"

EMBASE (Elsevier):

1. exp oncology nursing/ OR oncology nurs*.mp.
2. oncology nurse/ OR cancer nurs*.mp.
3. genetic*.mp. OR exp genetics/ OR exp genetic screening/
4. genom*.mp. OR exp genome/
5. exp knowledge/ OR knowledge.mp.
6. exp nurse attitude/ OR attitude*.mp.
7. (awareness OR understanding OR belief* OR perception* OR confiden* OR readiness OR prepared*).mp.
8. 1 OR 2
9. 3 OR 4
10. 5 OR 6 OR 7
11. 8 AND 9 AND 10
12. limit 11 to yr="2003 -Current"

PsychINFO (Ovid):

1. oncology nurs*.mp.
2. cancer nurs*.mp.
3. genetic*.mp. OR exp genetics/ OR exp Genetic Testing/
4. exp Genomics/
5. genom*.mp. OR exp genome/
6. exp "knowledge (general)"/ OR knowledge.mp.
7. exp Attitudes/ OR exp Health Personnel Attitudes/ OR attitude*.mp.
8. (awareness OR understanding OR belief* OR perception* OR confiden* OR readiness OR prepared*).mp. [mp=title, abstract, heading word, table of contents, key concepts, original title, tests & measures, MeSH word]
9. 1 OR 2
10. 3 OR 4 OR 5
11. 6 OR 7 OR 8
12. 9 AND 10 AND 11
13. limit 12 to yr="2003 -Current"

Scopus (Elsevier):

(TITLE-ABS-KEY("oncology nurs*" OR "cancer nurs*") AND TITLE-ABS-KEY(genetic* OR genom*) AND TITLE-ABS-KEY(knowledge OR attitude* OR "awareness" OR "understanding" OR "belief*" OR "perception*" OR "confiden*" OR "readiness" OR "prepared*")) AND PUBYEAR > 2002 AND PUBYEAR < 2026

CINAHL (EBSCO):

S1: (MH "Oncology Nursing+")

S2: (MH "Oncology Nurses+")

S3: (MH "Oncology Nurse Practitioners")

S4: oncology nurs*

S5: cancer nurs*

S6: genetic*

S7: (MH "Genetics+")

S8: genom*

S9: (MH "Knowledge+")

S10: knowledge

S11: (MH "Attitude") OR (MH "Attitude of Health Personnel") OR (MH "Nurse Attitudes")

S12: attitude*

S13: awareness OR understanding OR belief* OR perception* OR confiden* OR readiness OR prepared*

S14: S1 OR S2 OR S3 OR S4 OR S5

S15: S6 OR S7 OR S8

S16: S9 OR S10 OR S11 OR S12 OR S13

S17: S14 AND S15 AND S16

Limiters: Publication Date from 2003 to 2025

Table D1. Summary of studies included in scoping review

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
Burcher et al. (2013), Australia & New Zealand	Quantitative Non-interventional	Survey Researcher-developed	Partial – Developed with expert panel; piloted with 5 professionals; ‘internal reliability’ (Cronbach’s α) reported; no further validation	Oncology health professional: surgeons, oncologists, and breast care nurses Breast care nurses: n=63	Genetic testing (TFGT)	Attitudes: Perceived usefulness and value of TFGT; Perceived impact on treatment decision-making; Attitudes towards future use; Views and preferences for timing and preferred professional to make the initial offer of testing.	Oncology health professionals had ‘positive attitudes’ towards the usefulness and value of TFGT, and the impact of knowledge of <i>BRCA1</i> and <i>BRCA2</i> mutation status on patient decision- making. Majority of the whole sample (n = 139) agreed TFGT would impact treatment decision-making (96%), - Sub-analysis (breast care nurses): Mean perceived impact on treatment decision-making = 10.9 (SD 1.18), - Breast care nurses were more likely to rate TFGT as useful for patient care and treatment/management (mean 27.1, SD 2.86). - Nurses’ preferred initial offer of TFGT: surgeons 43.4%, genetics specialists/counsellors 35.8%, oncologists 13.2%, breast care nurses 7.5%.
Cuthill et al. (2025), UK	Quantitative Cross-sectional	Survey Researcher-developed survey (modelled on Health Education England 2021 genomics in practice survey)	Partial – Based on HEE 2021 survey (itself adapted from AGHA). Trialled with small cancer nursing team. No psychometric statistics reported in this or source surveys.	Cancer nurses n=199	Genomics (practice-based)	Knowledge: Perceived knowledge of Genomics and Genomics in practice Attitudes: Views on relevance to future practice; Preparedness to use genomics in practice; preferences for delivering genomic testing in practice; desire for education Confidence: Genomics, application in practice	Lack/limited knowledge and low confidence. Perceived knowledge/Confidence: - 41–58% reported low confidence across genomics domains; only 9–18% high (highest in consent, lowest in selecting tests/decision-making). - One-third (n=60/180) reported understanding basic concepts (DNA/genes), but advanced topics (penetrance, mosaicism, polygenic risk) were poorly understood. - Only 13% confident using the National Genomic Test Directory. Views: - 95% believed genomics would affect practice within 5 years. - 34% did not feel prepared to use genomics in practice. - 84% said improved knowledge would change their practice. Open-ended questions: Limited knowledge: ‘I have an understanding of genetic mutations but little knowledge and understanding of the full nature of genetics and its impact on treatment.’ Role and advocacy: ‘I think it’s important to remain open to the speed and unpredictability of genetic advancement. It’s vital that we maintain our role as patient advocate by immersing ourselves in this speciality.’

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
							Correlations: Perceived genomic knowledge was highest among nurses in breast, gynaecological, and haematological cancer specialties. Greater confidence in genomic knowledge and test selection was reported among nurses aged 55–64 years.
Dodson (2014), USA	Quantitative Cross-sectional, descriptive	Survey Modified Knowledge & Attitude Questionnaire (Roederer 2012) and Nursing Practice Questionnaire (Brett 1987)	Partial – Both instruments adapted for oncology context. Internal consistency reported (Cronbach's $\alpha = 0.64–0.68$ for knowledge, $\alpha = 0.59$ for practice); no further psychometric testing reported.	Oncology nurses n=368	Pharmacogenomics & Genomics (basic & cancer-specific)	Knowledge: Objective and perceived knowledge of genetics and pharmacogenomics. Attitudes: Attitudes towards pharmacogenomic testing (general & oncology-specific); Fears/concerns (unauthorised access, discrimination, family will be affected); Trust, Perceptions (need of pharmacogenomics, difficult to understand, Nurses should educate patients, decreases adverse events).	Limited knowledge but positive attitudes. Actual knowledge: Genomic M=2.45 (SD=1.40)/5; pharmacogenomic M=2.61 (SD=1.44)/5; total M=5.09 (SD=2.43)/10. Perceived knowledge: Genetics fair/poor 69% (57% fair, 12% poor); pharmacogenomics fair/poor 72% (47% fair, 25% poor). Attitudes: General M=14.1 (SD=3.9)/20; oncology-specific M=9.2 (SD=2.9)/18; overall M=23.3 (SD=6.1)/38. Key items: Perceived need 89%; decreases adverse events 80%; nurses should educate 77%; trust 69% (53% trust, 16% strongly trust). Concerns: Unauthorized access 66% (41% somewhat, 25% concerned/very concerned); discrimination 77% (37% somewhat, 40% concerned/very concerned); family impact 78% (42% somewhat, 36% concerned/very concerned). Correlations: Knowledge correlated with oncology certification, previous genomic education, and prior experience
Dodson (2015), USA	Qualitative Descriptive	Survey Open-ended item from Dodson (2014) survey	N/A	Oncology nurses n=173 responses analysed	Pharmacogenomics	Attitudes: Thoughts and concerns regarding pharmacogenomics	Several positive themes identified as well as some negative concerns. Theme 1: consistency (13%) Theme 2: effectiveness (40%) Theme 3: rise of insurance cost (10%) Theme 4: disparity among the uninsured (12%) Theme 5: genetic counselling needs (5%) Theme 6: need for further education (20%)
Dodson (2017), USA	Qualitative Descriptive	Survey Researcher-developed	No – No pilot, expert input, or psychometric validation reported	Oncology nurses n=28	Pharmacogenomics	Attitudes: Attitudes towards pharmacogenomics	Themes identified: 1) Changing scope of practice, 2) Standardized means of communicating to providers & patients, 3) Access to up-to-date information, 4) Advocacy
Dodson (2018), USA	Quantitative Pre-/Post- test	Survey Modified KAQ-PGx (from Roederer et al., 2012)	Partial – KAQ-PGx adapted with removal of subscales and addition of knowledge questions;	Oncology nurses n=434	Pharmacogenomics & Genomics (basic)	Knowledge: Objective knowledge of genomics and pharmacogenomics	Mean pre-test knowledge score (out of 100): 72.7, - Post-test score: 85.9 ($p < 0.01$) – Poor knowledge of: understanding drug response over a patient's lifetime and the impact of subtle genomic differences on drug response. Correlations:

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
			piloted with oncology nurse panel; internal consistency reported for knowledge scale ($\alpha = 0.81$); no other psychometric testing reported				No difference in knowledge scores was found for any of the correlates assessed.
Dornelles Prolla et al. (2015), Brazil	Quantitative Descriptive, Cross-sectional	Survey Researcher-developed	No – No pilot, expert input, or psychometric validation reported	Nurses involved in the care of oncology patients n=135 (analysed)	Genetics (cancer) & Hereditary breast cancer	Knowledge: Objective knowledge of cancer genetics and hereditary breast cancer (characteristics, risk indicators, knowledge of genetic counselling). Attitudes: Interest in education	Mean correct answers = 67.98% (SD=8.91; range 37.9–91.1). Hereditary cancer knowledge: characteristics 74.9%, risk indicators 66.4%. Low scores: only 26.6% knew most breast cancers are not hereditary; 26.1% recognised male breast cancer as a risk factor. Only 31.1% reported knowing what genetic counselling is. 96.3% interested in learning about hereditary breast cancer and genetic counselling Correlations: Knowledge not associated with age/specialisation, but inversely associated with years since graduation (more experienced nurses performed worse).
Fee-Schroeder and Nelson (2019), USA	Quantitative Pre-/Post-intervention	Survey Established Genomic Nursing Concept Inventory (GNCI, 13 items); Genetic/Genomic Nursing Practice Survey (GGNPS)	Yes – Both GNCI and GGNPS are validated instruments. GNCI used in shortened 13-item form	Oncology nurses (inpatient and ambulatory) n=165	Genetics & Genomics	Knowledge: Objective and perceived knowledge of genetic and genomic concepts (foundations, pharmacogenomics, cancer inheritance patterns, red flags in family history, and the ability to identify relevant educational resources and clinical applications) Attitudes: Attitudes and perceived importance of genetics/genomics Confidence: Genomics knowledge	Baseline (pre-program): Knowledge (GGNPS): 85% (136/160) rated their personal genomic knowledge as fair/poor. Attitudes (GGNPS): 81% (129/160) reported nurses' understanding of genetics/genomics as somewhat to very important
Gonthier et al. (2018), Canada	Quantitative Cross-sectional	Survey Researcher-developed	Partial – Developed by research team using literature, ASCO curriculum, and prior studies; reviewed by cancer genetics experts; pretested with health professionals for understanding; no	Palliative care professionals (Physicians, Nurses, Other) Palliative care nurses: n=19	Familial/hereditary cancer	Knowledge: Objective knowledge of familial cancers (cancer genetics, associated risks, family history, and genetic counselling resources) Attitudes: Interest in education Confidence:	Low confidence. Nurses (sub-analysis): 43% correct answers to knowledge questions. 63% occasionally addressed concerns from patients/relatives about family history of cancer, but reported low confidence in responding. Whole sample (mixed providers): Palliative care providers overall reported low confidence discussing cancer risks associated with family history and did not feel competent to recognise signs of a significant family history. Knowledge gaps were evident in defining

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
			psychometric statistics reported.			Discussing cancer risks associated with family history with terminally ill patients or their families; recognise signs of a significant family history.	features of significant family history. Most (78%) expressed interest in specific training on this topic.
Hébert et al. (2022), Canada	Quantitative Cross-sectional, descriptive	Survey Researcher-developed	Partial – Based on prior studies; pre-tested for face validity; authors note reliability and validity uncertain. No psychometric statistics reported	Nurses working with cancer patients n=40	Genetics (cancer)	Knowledge: Objective and perceived knowledge of cancer genetics, genetic testing, family history Attitudes: Role of nurses in oncogenetics and professional duties (e.g., being someone patients can talk to, referring to resources, empowering families, managing family disagreements); Raising genetic testing w/ patients/families; Discussing Family History and incorporating into practice; interest in education Confidence: Addressing the concerns of cancer patients and their families with respect to their family history of cancer and the associated risks; recognize significant aspects of a family's cancer history	Limited and lack of knowledge undermining confidence. Knowledge: limited; 71% rated understanding as fair–non-existent, none very good/excellent. Misconceptions common (e.g., 56% overestimated proportion hereditary; 45% thought genetic testing applies to cervical cancer; 61% believed mutations can ‘skip’ generations). Awareness highest for breast cancer testing (89%) and lowest for pancreatic (3%). 84% felt unqualified to address patient/family concerns; 79% lacked skills to interpret family history. Attitudes: Majority recognised a role in oncogenetics (e.g., being someone patients can talk to (97%), supporting patients (86%) referring to resources (92%), empowering families (81%), help manage family disagreement (65%)); 77% felt they should raise genetic testing. 58% felt it was essential for Family History to be brought up with patients/families. 63% felt addressing this with patients/families could easily be incorporated into routine follow-up. Strong interest in further education (61%); 77% believed genetics should be part of academic studies.
Hines-Dowell et al. (2024), USA	Mixed-methods Cross-sectional	Survey, Focus groups Researcher-developed survey (with 4 adapted items from Johnson et al., 2019). Qualitative phase used a researcher-developed focus group guide	Partial – Adapted 4 items from survey for parents (Johnson et al., 2019); piloted with 10 genomics-proficient professionals; revisions made for clarity and usability; no psychometric statistics reported.	Pediatric Registered nurses (RNs), nurse practitioners (NPs), nurse anesthetists, or other advanced practice providers or physician assistants (PAs) n= 168: RNs (n=132); NPs (n=29); RN anaesthetists (n=2) PAs (n=2))	Genomics	Knowledge: Objective baseline genetics knowledge (genetic variants, testing utility). Attitudes: Perceived preparedness (answering patient/family questions), perceived role of nurses (educating patients/families, taking family history, requesting referrals, explaining genetics concepts), role clarity; need and desire for education	Quant: Knowledge: 75% (126/168) correctly identified variant types (benign, pathogenic, VUS); 55% (92/168) distinguished germline vs somatic variants; 94% (158/168) recognised utility of genomic testing. Perceived preparedness: 72% reported being ‘not prepared’ to answer patient/family questions about genomics. Perceived role in genomic practice: 66% ranked educating patients/families as the most important role. Taking family history and requesting genetics referrals were also frequently prioritised. 56% did not view explaining genetic test results as part of their role (44% ranked it least important). Qual: Nurses reported lack of structured institutional training/communication, with genomics education directed mainly at physicians. They relied on physicians for information and perceived

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
						Confidence: Genomics understanding; use in practice	genomics as 'for the doctors.' Participants expressed a strong need for more accessible, interactive, and tailored education to build confidence, support patient/family communication, and clarify their role.
Kocatepe et al. (2022), Turkey	Quantitative Descriptive	Survey Researcher-developed	Partial – Developed using National Nursing Core Curriculum; reviewed by 10 experts across nursing, molecular biology, and medical biology; finalized based on expert feedback; no psychometric testing reported.	Oncology and chemotherapy nurses n=101	Genetics	Knowledge: Objective knowledge of genetics (general and conceptual). Attitudes: Caring about advancements in genetics; awareness of their own values/attitudes that may affect care; readiness to provide accurate/suitable genomic information/resources/services; considered social, cultural, legal, or financial issues in genomic care; supported patients' informed decision-making; acknowledged patients' autonomy and informed/enlightened decisions	Knowledge levels were moderate but insufficient. Mean score on Genetic Knowledge Test = 12.43/20 (SD = 3.78). Sub-scores: conceptual genetics 5.01/10 (SD = 2.75); general genetic information 7.43/10 (SD = 1.88). 76% reported caring about advances in genetics. 81% reported awareness of their own values/attitudes that may affect care. 99% supported patients' informed decision-making. 71% acknowledged patients' autonomy and informed/enlightened decisions. 67% reported readiness to provide accurate/suitable genomic information/resources/services. 55% considered social, cultural, legal, or financial issues in genomic care. Correlations: no statistically significant correlations found.
Lester et al. (2014), USA	Quantitative Cross-sectional, descriptive	Survey Researcher-developed	Partial – One genetic risk question included; instrument developed via literature review and expert panel; content validity assessed (CVI = 0.89 then 1.00); no other psychometric testing reported.	Cancer nurses n=223	Genetic risk (patient and family discussion)	Knowledge: Perceived knowledge (discussing genetic risks with patients and families)	Described as a 'knowledge deficit' 17% (n=39) felt knowledgeable about discussing genetic risks with patients and families
Liu et al. (2021), Malaysia	Quantitative Descriptive, cross-sectional	Survey Researcher-developed (knowledge scale adapted from National Health Interview Survey (NHIS))	Partial – Knowledge scale adapted from NHIS; internal consistency reported ($\alpha = 0.78$). Attitude scale developed from literature and reviewed by expert panel; no additional psychometric testing reported.	Nurses from medical and surgical wards, oncology, paediatric, obstetrics, and gynaecology departments Oncology nurses: n=56	Genetic testing (<i>BRCA1/2</i>)	Knowledge: Objective knowledge regarding <i>BRCA1/2</i> testing. Attitudes: Objective attitudes regarding <i>BRCA1/2</i> testing	Attitudes 'positive' and knowledge adequate high-moderate. (oncology nurses): Knowledge: High = 53.6% (n = 30), Moderate = 39.3% (n = 22), Low = 7.1% (n = 4). Attitudes: Strongly positive = 39.3% (n = 22), Positive = 53.6% (n = 30), Negative = 0%, Strongly negative = 7.1% (n = 4). Correlations: Association between specialty area and attitude significant; oncology nurses had the strongest positive attitudes toward <i>BRCA</i> testing compared with other units.

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
Liu et al. (2011), China	Quantitative Cross-sectional	Survey Researcher-developed	No – No pilot testing, expert input, or psychometric validation reported	Oncology physicians or nurses Oncology nurses: n=184	Gene therapy	Knowledge: Perceived understanding of gene therapy. Attitudes: Perceptions of safety of gene therapy; willingness to accept gene therapy	Understanding of gene therapy: 0% 'very much'; 44.6% 'some'; 44% 'little'; 11.4% 'none.' Perceived safety: 78% 'safe' (0% 'very safe'); 20.7% 'not safe'; 2% 'not safe at all.' Willingness to accept gene therapy: If early-stage cancer: 5.4% 'very willing,' 53.8% 'somewhat willing,' 40.2% 'not very willing,' 0.5% 'not willing at all.' If advanced cancer: 7.6% 'very willing,' 75.5% 'willing,' 15.2% 'not willing,' 1.6% 'not willing at all.' Correlations: Effect of cancer stage: Acceptance significantly higher for advanced vs early stage.
Matsumoto et al. (2023), Japan	Quantitative Cross-sectional	Survey Researcher-developed	No – No pilot testing, expert input, or psychometric validation reported	Nurses working in breast cancer care n=317	Hereditary breast and ovarian cancer, genetics (cancer)	Knowledge: Perceived knowledge of hereditary breast and ovarian cancer (characteristics, inheritance patterns, family history taking). Attitudes: Attitudes about learning and education	Nurses had limited knowledge about hereditary breast and ovarian cancer characteristics. Perceived knowledge: -41.6% reported no knowledge of HBOC, 3.5% knew about HBOC disease characteristics, and 6% knew about characteristics that would raise clinical suspicion of HBOC. 63% asked about family history, but only 23% extended to third-degree relatives. A Attitudes about learning about HBOC: 91% were willing to learn about HBOC. 88.6% wished to participate in HBOC study group meetings. The most frequently asked question was 'Can my close relatives (especially my daughter) inherit the cancer from me?' The most common answer to this question was 'I recommended a self-examination and a breast cancer screening test.'
Metcalfe et al. (2010), UK	Mixed-methods Non-interventional	Survey, telephone interview Adapted survey (originally validated by Werrett et al., 2001; Metcalfe et al., 2008)	Partial – Adapted from validated instrument; original $\alpha > 0.80$ with >400 nurses. Modified for hospice setting and piloted locally; no psychometric testing reported for adapted version.	Hospice nurses n=328	Genetics (in hospice/end-of-life)	Knowledge: Perceived knowledge of genetics related activities. Attitudes: Perceived importance of genetics-related activities; perceived relevance to practice; desire for education Confidence: Carrying out genetics-related activities (psychosocial, clinical or biological) within an end-of-life care context.	Confidence was low. Quant: Importance: 60–97% rated genetics-related activities as very important/essential, highest for psychosocial aspects (supporting families, confidentiality, ethics). Confidence: Up to 87% 'not at all confident' in clinical/biological genetics; greater confidence in psychosocial tasks (e.g., 57% very confident on confidentiality). Qual: - Many nurses reported they had not previously considered genetics relevant to hospice care, but through reflection saw it as important/essential. - Expressed a strong need for education, particularly on psychosocial aspects of genetics (communication, supporting families, ethical concerns).

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
							- Nurses highlighted challenges around confidentiality, disclosure, and family communication. - Telephone interviews reinforced that training opportunities were limited, but there was strong desire for practical and educational support. Correlations: Senior managerial staff reported higher confidence than staff nurses; confidence increased with seniority and prior genetics education, but overall levels remained low.
Quinn et al. (2014), USA	Quantitative Non-interventional	Survey Modified consumer survey on PGD (from Kalfoglou et al., 2004)	No - Adapted from non-validated patient/consumer survey. No psychometric validation reported for original or modified versions	Oncology nurses n=201	Pre-implantation Genetic Diagnosis (PGD)	Knowledge: Perceived knowledge and awareness of PGD and genetic counselling programs. Attitudes: Acceptability towards PGD; concerns regarding PGD (affordability, misuse, 'playing god', social/religious concerns). Confidence: Knowledge of PGD	Limited knowledge but PGD was 'generally accepted' with some negative concerns. Knowledge/awareness: 78% had not heard of PGD. Among those aware (n=45), 59% rated knowledge limited, 41% adequate. 29% overall said they would consider using PGD themselves. 64% were aware of genetic counselling programs. Acceptability/concerns: 66% thought PGD acceptable for hereditary cancer families; 81% felt individuals with strong family/personal history should receive information. Main concerns were affordability (40%), misuse (22%), and 'playing God' (16%). Barriers: 89% reported lack of confidence in knowledge; 53% lack of time; 39% social/religious concerns; 35% believed topic should be physician-initiated.
Seven et al. (2017), Turkey	Quantitative Descriptive	Survey Researcher-developed	No – Developed by authors (experts in genetics and oncology nursing) and informed by literature. No pilot testing or psychometric statistics reported	Oncology nurses and nurse academicians with interest areas in oncology n=104	Genetics (hereditary breast and ovarian cancer)	Knowledge: Objective knowledge (inheritance, risk factors, screening, referral criteria); knowledge of referral/use of genetic services. Attitudes: Willingness for further education and priority topics	Knowledge levels were moderate. Knowledge: Mean score $6.74 \pm 3.85/13$. 71.4% recognised family history as a risk factor; 67.3% knew <i>BRCA1/2</i> link; only 25.5% knew <i>BRCA1</i> can be inherited from the father. Referral knowledge/practice: 57.7% recognised referral for breast cancer <50 years; 53.8% for ≥3 HBOC-related cancers. Least recognised: Ashkenazi ancestry (25%), lobular breast/diffuse gastric cancer (21.2%). 29.9% had referred at least one patient for genetic counselling. Educational needs: 59.6% expressed willingness for further education. Priority topics: inheritance, genetic screening/diagnostic tests, treatment based on genetics. Less interest in family history taking (29.8%), prognosis (36.5%), and local genetic centers (38.5%). Correlations: Knowledge levels were significantly associated with nurses' practice area and their interest in genetics continuing education.

Citation & country	Methodology & study design	Data collection method & instrument	Validation	Participants & sample size	Genetics/ Genomics focus	Concept focus	Findings
Wright et al. (2020), Australia	Qualitative Non-interventional	Semi-structured interviews Researcher-developed semi-structured interview guide	No	Cancer nurses n=9	Genomics	Knowledge: Perceived knowledge of genomics for practice. Attitudes: Perceived relevance to practice; perceived application in practice; interest in learning.	Nurses have limited knowledge and applying at reduced capacity. Adequacy of knowledge: Most rated genomic knowledge as poor/average; none very good/excellent. No participant could adequately define 'genomics.' Few recalled genomics in nursing education. Interest in learning expressed, but barriers included time, finances, availability. Relevance of knowledge to practice: Most said genomics was relevant/very relevant, linked to personalised care. A minority felt it was not relevant to daily tasks. Some viewed it as doctors'/specialists' responsibility. Applying knowledge in practice: Application limited, mainly via targeted/precision treatments. Some used genomics in family history taking or psychosocial support. Patients often asked genomics questions (media-triggered); nurses referred to doctors or gave simplistic answers. Several said genomics did not alter daily nursing tasks.
Zhao et al. (2022), China	Quantitative Cross-sectional	Survey GGNPS-CV (Chinese adaptation of GGNPS)	Cross-cultural adaptation of GGNPS using AAOS (2002) guidelines; content validity tested (S-CVI = 0.94); internal consistency reported ($\alpha = 0.867$); pilot tested with 30 nurses.	General hospital nurses and Oncology nurses (defined as working in oncology hospitals) Cancer hospital nurses: n=1166	Genetics & Genomics (general & cancer)	Knowledge: Objective and perceived knowledge of genomics and genetics of common diseases; genetic test results support clinical decisions. Attitudes: Attitudes, receptivity; perceived importance for nurses to be educated; Perceived advantages (treatment decisions); Perceived Disadvantages (need to 're-tool' professionally); intention to learn more Confidence: Discussing genetics with patient; deciding what family history information is relevant to assessing genetic susceptibility; determining the availability, risks, benefits and limitations of genetic testing; facilitating referrals for genetic service	Knowledge levels were moderate. Objective knowledge: Mean genomic knowledge score = 8.38 (SD = 2.08). Perceived knowledge: 63.5% (n=740) rated overall genomic knowledge as poor; 58.4% (n=681) said they understood genetics of common diseases; 85.4% (n=996) recognised that genetic test results are essential to support clinical decisions. Attitudes: 43.6% (n=508) felt it was very important for nurses to become more educated in genetics/genomics of common diseases. 94% considered 'better treatment decisions' to be advantage of integration. 68.9% felt 'need to 're-tool' professional knowledge and skills' as disadvantage. Confidence: 68.7% reported confidence discussing risks, 72.0% benefits, and 64.8% limitations of genetic testing. 60.6% intended to learn more about genetics/genomics.

Table E.1. Correlates examined in studies reporting correlation analyses (n=10)

Study	Correlates examined
Cuthill et al. (2025)	Cancer specialties, age
Dodson (2014)	Age, degree, certification in oncology, current practice, work setting, demographic, previous genetic education, perceived genetic and pharmacogenomic knowledge, previous pharmacogenomic education, available pharmacogenomic tests, prior experience, perceived need
Dodson (2018)	Practice setting (urban, community, outpatient), geographic location, previous pharmacogenomic education, degree, oncology certification.
Dornelles Prolla et al. (2015)	Age, specialisation, years since graduation
Kocatepe et al. (2022)	Duration of professional experience, duration of experience with cancer patients, previous training on genetics and genetics disease, 6 attitudinal questions
Liu et al. (2021)	Socio-demographic variables (age group, gender, ethnicity, highest nursing degree, years of experience, specialised working area, and years of working experience) and knowledge and attitude level.
Liu et al. (2011)	Age, gender, marital status, occupation, education, religiousness, monthly income, time working in oncology, being a cancer patient, relatives with cancer, hypothetical questions related to suffering from cancer
Metcalfe et al. (2010)	Age, job role, time worked at hospice, time since qualified, highest qualification,
Quinn et al. (2014)	Gender, ethnicity, race, education, inpatient/outpatient, clinic type, age, religion, have children, want future children
Seven et al. (2017)	Age, place of residence, highest qualification in nursing, years working in oncology, area of work, marital status, desire for continuing education

3.3 Chapter summary

This chapter has presented a scoping review in the form of a manuscript submitted for publication. The chapter addressed Objective 1 of the thesis by scoping and critically examining published research on oncology nurses' knowledge of and attitudes to genetics and genomics. Through this review, the existing evidence base was mapped and key conceptual and methodological gaps were identified. Collectively, these insights clarified the limited scope of current inquiry and reinforced the need for rigorous, contextually grounded research to advance understanding of how nurses engage with genomics in practice. The next chapter outlines the methodological approach undertaken to address these gaps within the Australian oncology nursing context.

Chapter 4 – Methods

4.1 Introduction

This purpose of this chapter is to outline the methodological approach underpinning this doctoral study. The chapter begins with a reiteration of the research questions, aims and objectives followed by an outline of the philosophical underpinnings and the worldview assumptions that guided this project. Subsequently, a justification for selecting a mixed methods approach for the study is presented. The research design framework is discussed, followed by a description of the methods employed in phase one and two of the study. This discussion includes explanation of the development of the research instrument, recruitment, sampling, data collection, and data analysis. The chapter concludes with a discussion of the ethical considerations for both phases of the study.

4.2 Research question, aims and objectives

4.2.1 Research questions

How do oncology nurses in Australia engage with genomics, and what individual characteristics and perceived barriers or enablers influence its adoption into practice?

4.2.2 Aims

1. To assess oncology nurses' knowledge, engagement, and adoption of genomics in practice across Australia.
2. To identify individual characteristics associated with the uptake of genomics in nursing practice.
3. To explore perceived barriers and enablers to integrating genomics into oncology nursing practice.

4.2.3 Objectives

1. To scope and critically examine existing research on oncology nurses' knowledge and attitudes towards genetics and genomics (scoping review – supports Aim 1).

2. To assess levels of genomic knowledge, engagement, and adoption among Australian oncology nurses, and explore associations with individual, professional, and demographic characteristics (quantitative survey – supports Aims 1 & 2).
3. To explore perceived barriers and enablers to genomic uptake in oncology nursing across diverse clinical roles and healthcare contexts (qualitative interviews – supports Aim 3)

4.3 Philosophical underpinnings

Every research project is shaped by the researcher's underlying philosophical stance, an implicit or explicit framework that guides decisions about what constitutes valid knowledge and how that knowledge can be acquired. These philosophical assumptions, often referred to as a paradigm, encompass views about the nature of reality (ontology), the nature of knowledge (epistemology), and the role of values (axiology) in the research process (Crotty, 1998; Denzin & Lincoln, 2017). This study adopts pragmatism as its guiding philosophical paradigm.

Pragmatism is particularly well-suited to real-world, applied research. Rooted in the work of classical American philosophers including Charles Sanders Peirce, William James, and John Dewey, pragmatism views knowledge as something that arises through interaction with the world, is contextually situated, and is ultimately judged by its usefulness (Dewey, 1916; James, 1907; Peirce, 1903). Rather than being committed to a singular form of truth or reality, pragmatism is fundamentally pluralistic as it allows for multiple, often conflicting, perspectives to coexist, provided they contribute to practical understanding or resolution of the research problem (Biesta, 2010; Feilzer, 2010).

Ontologically, pragmatism rejects binary oppositions such as realism vs relativism. Instead, it embraces a transactional ontology in which reality is not seen as entirely external and objective, nor as wholly constructed and subjective. Rather, it is shaped through experiential and social interactions, evolving as people engage with and interpret their environments (Morgan, 2007). In this way, reality is understood as provisional and negotiated, making pragmatism a valuable stance when investigating complex, situated phenomena such as healthcare innovation adoption.

From an epistemological standpoint, pragmatism holds that knowledge is generated through active inquiry—through 'doing' as much as 'knowing'. Dewey (1938) argued that knowledge arises in response to problems and is refined through cycles of action, reflection, and

adjustment. This epistemology supports the notion that truth is not static, but instead must be continually tested and re-evaluated in light of its consequences. As Morgan (2014) explains, this view positions the researcher not as a detached observer nor as a purely subjective participant but as an *inter-subjective agent*, someone engaged in meaning-making through reciprocal interaction with their context.

Importantly, pragmatism also provides a robust response to the limitations of paradigmatic purism. While some philosophical positions (e.g., positivism or constructivism) can imply that only certain types of data or methods are valid, pragmatism rejects these rigid boundaries. Instead, it centres the research question itself as the primary driver of design decisions and supports methodological flexibility based on what will generate the most useful understanding of the problem at hand (Greene & Hall, 2010; Teddlie & Tashakkori, 2009). This makes it particularly relevant for studying practice-based issues in healthcare, where both quantifiable patterns and contextual nuances may be needed to inform actionable conclusions.

In applied fields such as nursing and genomic medicine, where evidence must often be translated swiftly into practice, pragmatism enables a responsive and context-sensitive approach to inquiry. It aligns with the complexity of clinical environments, where knowledge is often co-produced by patients, practitioners, and systems, and where interventions must be judged not only by theoretical coherence but by practical effectiveness. Pragmatism's emphasis on outcomes and consequences thus resonates with the goals of translational research in oncology nursing.

Furthermore, by recognising that the researcher operates within social, political, and institutional contexts, pragmatism encourages critical reflection on the purposes and implications of inquiry. It does not assume neutrality but instead invites transparency about the researcher's position and priorities. In this study, the goal of contributing to improved genomic care practices within nursing is not viewed as separate from the research process but as an integral part of its philosophical grounding.

Real-world change, such as improving the adoption of genomic innovations, requires an understanding of both broad patterns revealed through quantitative data and the rich, lived experiences captured through qualitative inquiry, in order to design solutions that are contextually grounded and practically effective. The specific methodological implications of this philosophical stance are explored in the following section.

4.4 Methodology and sequencing

Mixed-methods research refers to a methodological approach that integrates both quantitative and qualitative methods within a single study to provide a more comprehensive understanding of complex research problems (Creswell & Plano Clark, 2018). By drawing on the strengths of both paradigms—quantitative approaches for identifying patterns and measuring variables, and qualitative approaches for interpreting experiences and meanings—a mixed-methods design allows researchers to explore phenomena from multiple perspectives (Johnson & Onwuegbuzie, 2004; Teddlie & Tashakkori, 2009).

In health and nursing research, mixed methods designs are particularly valuable given the complexity of human behaviour, clinical systems, and context-dependent decision-making, which are often insufficiently captured through a single methodological lens (Halcomb & Hickman, 2015; Wasti et al., 2022). This is especially relevant to this thesis given that the scoping review in Chapter 3 identified a scarcity of qualitative and mixed-methods studies examining nurses' knowledge and attitudes towards genomics, underscoring the need for approaches that capture both measurable patterns and experiential dimensions of practice. The integration of numeric data with experiential accounts enables a richer, more holistic understanding of professional practices and innovation adoption, which is central to this study's focus on genomics in oncology nursing. The quantitative component helps to delineate *what* patterns, relationships, and trends exist, while the qualitative strand explores *how* and *why* these occur within particular contexts. This complementary relationship allows for insights that not only deepen understanding but also inform the development of policies and practices that are responsive and tailored to the needs of specific populations (Gilson, 2014; Rana et al., 2023).

This doctoral research study comprised two phases of data collection aligned with the research aims outlined earlier. Phase 1 involved an online national survey to examine oncology nurses' genomic knowledge, engagement, and adoption patterns, while Phase 2 comprised semi-structured telephone interviews with oncology nurses from a range of clinical and professional contexts. These two strands were designed to address different aspects of the research questions using distinct but complementary methods.

This study was initially conceptualised as an explanatory sequential mixed-methods design (Creswell & Plano Clark, 2018), in which the quantitative data collected in Phase 1 would inform the development of the qualitative interview schedule for Phase 2. Survey data were collected and subjected to descriptive statistical analysis, with the aim of identifying patterns

to guide the qualitative phase. In practice, however, an early-stage analysis indicated that the survey findings, while informative in their own right, offered limited direction for shaping the interview questions. As such, the qualitative phase proceeded semi-independently, informed primarily by the overarching research aims and conceptual framing, rather than directly by the quantitative results.

This shift in strategy represents a modification of the original explanatory sequential design. While data collection remained temporally sequential, Phase 1 findings did not substantially shape the qualitative instruments. Instead, integration occurred during interpretive synthesis, consistent with pragmatic mixed methods approaches that emphasise flexibility and responsiveness to real-world research constraints (Creswell & Creswell, 2018; Morgan, 2014). The mixed-methods approach adopted in this study established the foundation for a triangulated analysis, in which multiple sources of data were examined for convergence and complementarity. The following section outlines the triangulation strategy used and describes how the integration of qualitative and quantitative findings contributed to the generation of robust, practice-informed insights.

4.5 Data integration and triangulation

Integration of findings is a defining characteristic of mixed methods research and serves as the central mechanism through which quantitative and qualitative strands are brought together (Creswell & Plano Clark, 2018; Fetters, 2019; Fetters et al., 2013; Skamagki et al., 2024). In this doctoral research, integration occurred during the interpretive phase, in which the results from the survey and interview datasets were compared, contrasted, and synthesised to develop a more holistic understanding of the factors influencing genomic adoption in oncology nursing. Rather than treating each dataset as isolated or independently explanatory, the interpretive synthesis allowed for both convergence and complementarity to be explored. Convergence was examined by identifying instances where qualitative insights aligned with quantitative patterns—for example, where expressed attitudes toward genomics were reflected in survey scores related to engagement. Conversely, divergence was also considered valuable, revealing where the interview narratives either challenged or expanded on trends observed in the survey. This process of interpretive integration is consistent with what Teddlie and Tashakkori (2009) refer to as *methodological complementarity*, where findings are not merely verified across methods but instead used to elaborate, illuminate, or contextualise each other.

The integration strategy employed in this study was largely interpretive and comparative, aligned with a recent guide published by Skamagki and colleagues (2024). Separate analysis of the survey and interview data was conducted, after which findings were reviewed in relation to one another. This side-by-side examination enabled exploration of key themes, including barriers and enablers to genomic adoption, contextual variability in practice, and differing attitudes towards this innovation across both data sources. Particular attention was paid to areas of thematic alignment, amplification, or contradiction, with the aim of generating what Creswell and Plano Clark (2018) term *meta-inferences*: insights that arise specifically from the integration of multiple datasets.

Although triangulation is sometimes understood strictly as a form of validation, this study adopts a broader, pragmatist-informed interpretation. Data triangulation here refers not only to the use of multiple methods but also to the layering of different types of insight such as numeric trends and narrative depth, to address the research questions more comprehensively. Denzin (1978) and Patton (1999) identify four forms of triangulation: methodological triangulation (using more than one method), data triangulation (drawing from multiple data sources), investigator triangulation (involving multiple analysts), and theory triangulation (applying multiple theoretical perspectives). While the current doctoral study employed the first two forms, its central emphasis was on methodological triangulation through the sequential integration of quantitative and qualitative strands. Within the qualitative component, triangulation was complemented by a commitment to reflexivity, following Braun and Clarke's (2006, 2013, 2019, 2021) guidance for ensuring rigour in reflexive thematic analysis. Braun and Clarke caution against treating triangulation as an external validation mechanism that assumes a single, fixed reality; instead, they emphasise researcher reflexivity as the cornerstone of quality. In line with this view, reflexive practices, such as maintaining a coding journal, engaging in ongoing self-reflection on positionality and decision-making, and discussing interpretive choices with the supervisory team, were incorporated to enhance rigour, transparency, credibility, and analytic depth. This dual focus on integration across methods and reflexivity within methods strengthened the coherence and trustworthiness of the study's overall design.

Importantly, this approach to data integration and triangulation aligns with the study's pragmatic positioning, in which the aim is not epistemological purity but the generation of actionable, practice-relevant knowledge through the integration of diverse forms of evidence (Morgan, 2014; Feilzer, 2010). Rather than seeking convergence for its own sake, the process

of integration was directed toward answering the study's overarching research questions. Bringing together the breadth of the survey findings and the richness of the interview data provided a more comprehensive understanding of the factors influencing the uptake of genomics in oncology nursing. This integration of findings strengthened the explanatory power of the study and informed the development of its conclusions. The following chapters present the findings from each phase in detail before bringing them into discussion through a process of interpretive synthesis.

4.6 Phase 1 research

This section explains the method used for the quantitative phase of the study (Phase 1) and how this method was developed. It begins by outlining the rationale for selecting a quantitative survey design and describes the process of adapting an existing instrument, followed by the piloting of the survey. The section then details the sampling strategy, participant recruitment, data collection procedures, and the analytic approach used to address the study's quantitative research questions.

4.6.1 Method

The quantitative phase (Phase 1) adopted a cross-sectional descriptive survey design, building on the work of Andrews et al. (2014b). A survey approach was selected to capture a snapshot of current knowledge, engagement, and adoption of genomics among oncology nurses in Australia. In alignment with Rogers' (2003) Diffusion of Innovations (DOI) theory, and the study aims, the survey also sought to identify personal and professional characteristics associated with likely genomic adopters.

Survey research is well-suited to descriptive and exploratory aims, providing a systematic means of quantifying patterns, behaviours, and attitudes across a target population (Creswell & Creswell, 2018; Fowler, 2014). Online surveys offer logistical advantages in large-scale studies, including cost-efficiency, rapid data collection, and accessibility for geographically dispersed participants (Wright, 2005). These benefits were particularly relevant in the present study, which aimed to capture national perspectives across diverse clinical contexts.

Data were collected via a secure, web-based REDCap® (Research Electronic Data Capture) platform, hosted by the University of Technology Sydney. REDCap enables researchers to build and administer structured online surveys without requiring specialised software or infrastructure (Harris et al., 2009). Participants were invited to complete the survey via a unique

link, allowing for anonymous, flexible, and remote participation. This approach also minimised non-response bias by enhancing accessibility and participant convenience, which was particularly important in the aftermath of the COVID-19 pandemic when clinical workloads and physical distancing measures constrained research participation.

This survey study was reported in accordance with the *Consensus-Based Checklist for Reporting of Survey Studies* (CROSS) (Sharma et al., 2021). The CROSS checklist provides structured guidance for transparent and comprehensive reporting of survey methodology and findings. A completed CROSS checklist, with page references indicating where each item is addressed within this thesis, is provided in Appendix A. The following sections describe the development and piloting of the survey instrument, followed by procedures for sampling, recruitment, data collection, and analysis.

4.6.2 Development of the survey instrument

The survey instrument used in this study was adapted from a previous study by Andrews et al. (2014a, 2014b), which aimed to identify the characteristics of nurse adopters of genetics, particularly among oncology and primary care nurses. The original instrument was part of a theoretically grounded study designed to classify adopters based on behavioural, demographic, and attitudinal traits, with the broader goal of informing how genetics could be integrated more effectively into nursing practice. It was underpinned by DOI theory, as extended by Leach et al. (2016), who proposed that recognising adopter categories, such as genetic adopters and opinion leaders, can accelerate the integration of genomics into nursing. Building on this foundation, the current study applied and extended these concepts to the Australian oncology nursing context, comparing likely adopters and non-adopters across demographic, professional, and personality variables.

As outlined in Chapter 3, the scoping review identified a significant gap in validated tools capable of measuring genomic adoption in nursing, particularly within oncology contexts. Given the emergent and niche nature of this field, and the need for theory-aligned yet context-sensitive tools, this survey represented the most appropriate foundation for addressing the research aims of this current study. Its strong grounding in DOI theory, supported by constructs from the Theory of Planned Behaviour (Ajzen, 1991) and other behavioural frameworks, made it an appropriate basis for adaptation in this study.

The Genetics & Genomics Nursing Practice Survey (GGNPS; Plavskin et al., 2019) was also considered during instrument selection. While the GGNPS is a psychometrically robust and widely used tool for assessing nurses' genomic knowledge, attitudes, and practice behaviours, it was developed for general nursing populations within the United States. Its emphasis on common chronic diseases (e.g., diabetes, cardiovascular disease), inclusion of USA-specific policy and competency references, and context-dependent items such as insurance discrimination may limit its applicability to oncology nursing and to the Australian healthcare context. In contrast, the Andrews et al. (2014b) instrument was designed for oncology and primary care nurses within the United Kingdom, whose healthcare system and nursing scope of practice are more comparable to Australia. Although not formally validated, it aligns closely with the aims of the present study and captures a range of variables associated with adoption, including personality traits, familiarity with genomic resources, barriers/enablers, and environmental and social influences, alongside key behavioural indicators defined through expert consensus as Genetic Indicators of Adoption (GIAs; described in Section 4.6.2.1). For these reasons, the Andrews et al. survey was selected and adapted to enhance contextual relevance, theoretical alignment, and methodological rigour. These theoretical and practical foundations made it suitable for adaptation and refinement to the Australian oncology nursing context and were highly relevant to this doctoral study's aims and objectives.

4.6.2.1 Structure and origins of the original Andrews et al. survey

The original instrument was developed as part of a two-phase mixed-methods study conducted in the United Kingdom (Andrews et al., 2014b). In Phase 1 of their study, expert consultation was used to define a set of Genetic Indicators of Adoption (GIAs), which are key behaviours that signify the integration of genetics/genomics into nursing practice. These four GIAs, which formed the conceptual foundation for the Phase 2 questionnaire, are:

- Knowing how to access and use genetic services.
- Providing information on support services to patients and families.
- Asking relevant questions about family history.
- Being open to the role of genomics in all aspects of care.

These four GIAs also align with the genomic nursing competency frameworks described in 1.4.4.

In Phase 2 of their study they developed and deployed a structured questionnaire designed to identify adopters based on the GIAs and aimed to explore associated personal, professional, and contextual factors, which is in alignment with aims 1 and 2 of this doctoral study. Items in this survey were drawn from a combination of validated scales and custom-developed content. These included:

- Measures of personality traits, particularly Openness to Experience (John et al., 1991, 2008).
- Constructs relating to perceived influence and opinion leadership (Grimshaw et al., 2006; Weimann et al., 2007).
- Items addressing stages of adoption and environmental and societal effects on adoption (Brown et al., 2007; Chen et al., 2008; Francis et al., 2004).

The final instrument consisted of a variety of question formats: Likert scales, scenario-based questions, closed-ended items, and ranking tasks, which were organised into nine thematic sections. These formats were chosen as they are designed to capture demographic characteristics as well as both behavioural indicators and broader contextual variables associated with the adoption of genomics in nursing practice.

4.6.2.2 Adaptation for the current study

The survey instrument developed by Andrews et al., (2014b) was adapted for use in the present study to ensure relevance to the Australian oncology nursing context, improve methodological rigour, and align with the study's quantitative design. While the original instrument provided a strong theoretical and empirical foundation, several adaptations were necessary due to differences in healthcare systems, advances in genomic nursing practice over the past decade, and opportunities to strengthen the survey's clarity, inclusivity, and analytical utility.

Adaptations fell into four main categories:

1. **Contextual modifications:** Items referencing UK healthcare systems, organisations, or initiatives were revised to reflect Australian equivalents and, where appropriate, supplemented with relevant international resources.
2. **Content adjustments:** New items were added to address constructs relevant to contemporary oncology nursing and DOI theory (e.g., cosmopolitanism, specific hereditary cancer scenarios), while outdated or non-applicable items were removed.

3. **Design and response scale improvements:** Inconsistent Likert scales and optional open-ended items in the original instrument were replaced with standardised five-point scales and forced-choice formats to enhance comparability, reduce respondent burden, and improve data quality.
4. **Language, inclusivity, and clarity:** Wording and terminology were refined to improve comprehension, align with current professional language, and ensure inclusivity in demographic questions (e.g., gender identity). Additionally, the term *genomics*, which was scarcely mentioned in the original instrument, was incorporated where appropriate to reflect contemporary terminology and the current study objectives.

Examples of the specific adaptations made, along with their justifications, are presented in Table 4.1. The final adapted survey comprised 33 items, including nine demographic questions and 24 core items addressing the study objectives (Appendix B).

Table 4.1. Survey adaptation

Original item (Andrews et al., 2014)	Adapted item	Justification
Q#2: What characteristics would you say are typical of people you know who are open to new ideas and concepts? Please write down some key words to describe them	Removed	This open-ended item was removed to align with the quantitative design of the adapted instrument. The original question produced highly variable responses with limited comparability, and its exclusion supports cleaner statistical analysis, improved response consistency, and reduced participant burden.
Q#3: <i>Are colleagues who you think are open to change and new ideas likely to be the people from whom you would seek professional advice?</i> (Yes, No, Don't know) <i>If no: Where do you seek professional advice?</i> <i>What type of personality does she/he have?</i>	Removed	This open-ended item was removed to align with the quantitative design of the adapted instrument. The original question produced highly variable responses with limited comparability, and its exclusion supports cleaner statistical analysis, improved response consistency, and reduced participant burden.
Q#5: Please rate your familiarity with the following resources: A) The UK genetic competency standard statements for nurses, midwives and health visitors B) NHS National Genetics Education and Development Centre C) Your local specialist genetic services D) Telling Stories Understanding Real Life Genetics website E) Human Genome Project Response options: Never heard of them; Somewhat familiar; Very familiar; Completely familiar	Q#3: Please rate your familiarity with the following resources: A) The Australian College of Nursing (ACN) 2021 position statement: <i>Nurses, Genomics and Clinical Practice</i> B) The Australian Genomics Health Alliance C) Your state's health department strategic plan for genomics (e.g., NSW Health) D) Your local specialist genetics service E) Centre for Genetics Education website: www.genetics.edu.au F) Human Genome Project G) International Society of Nurses in Genetics (ISONG) H) Global Genomics Nursing Alliance (G2NA) Response options: Familiar; Somewhat familiar; Moderately familiar; Extremely familiar.	The content was updated to reflect the Australian genomic healthcare context, replacing UK-specific organisations and frameworks with relevant national equivalents (e.g., ACN, Australian Genomics, state-based strategic plans). Items were added to reflect important global and professional resources that have emerged or gained relevance since the original survey was developed, ensuring currency and comprehensiveness (e.g., ISONG, G2NA). The original Likert-style response scale was restructured for clarity and internal consistency, addressing inconsistencies in wording and scale structure noted in the original instrument. This aligns with best practice in survey design for forced-choice scaling and response discrimination (DeCastellarnau, 2018; Revilla et al., 2014) The rewording also aimed to improve respondent comprehension and reduce cognitive burden, in line with contemporary scale development recommendations.

Original item (Andrews et al., 2014)	Adapted item	Justification
Q#6: Please indicate your response to each statement by ticking one option for each statement: a) Nurses should regularly keep up to date with new areas of practice b) Nurses should be able to decide which areas of knowledge they want to expand, whilst not being at a cost to safe practice if other areas are de-prioritised c) Taking a patient's family history is an important aspect of my role d) Continued professional development in genetics should be encouraged for all nurses e) I have a good awareness of how genetics impacts on my own specialty f) Developments in genetics offer real potential to improve health outcomes for all patient groups Response options: Strongly Agree; Agree; Neither Agree or Disagree; Disagree; Strongly Disagree; Not sure	Q#4: Items a–e: Unchanged Item f (reworded): <i>Developments in genomics offer limited potential to improve health outcomes for all patient groups</i> Response scale revised for all items: Strongly disagree; Disagree; Neither agree nor disagree; Agree; Strongly agree	Item f was rephrased in the negative to reduce response bias introduced by its original strongly affirmative framing. Negative wording is a common strategy used to counter acquiescence bias, encouraging more deliberate engagement with the item (Colman et al., 1997). The Likert response scale was re-ordered to maintain directional consistency (from negative to positive) throughout the survey. Additionally, the 'Not sure' option was removed to create a forced-choice format, which encourages cognitive engagement and prevents satisficing behaviours that can reduce data quality (DeCastellarnau, 2018; Revilla et al., 2014).
Q#7: A 23 year old patient is admitted with dizziness, palpitations and fainting episodes after exercising. The patient mentions to you that this has happened before during strenuous exercise. a) How important would it be in this situation to take a family history? (1 = extremely important, 6 = not at all important) b) If you felt you needed advice would you consider discussing the patient's situation with your colleague? (tick Extremely likely, somewhat likely, not likely, unsure) c) What possible explanations would you provide for the patient's symptoms? (Please give some very brief comments e.g. it might have been a hot day or they may have low blood sugar)(Optional free text) d) How confident would you feel dealing with this scenario? (1 = confident, 10 = not confident)	Q#5: A 43-year-old woman is admitted for symptom management and treatment of endometrial cancer. While caring for her, she mentions in passing that she had several colon polyps removed during a routine colonoscopy last year. Based on this: a) How important would it be in this situation to take a family history? b) How confident would you feel educating the person in this scenario? c) How confident would you feel managing this scenario in practice? Response options for all: Not at all important/confident; Slightly; Somewhat; Moderately; Extremely	The scenario was modified to focus on oncology care, aligning more closely with the study's target population. The new scenario presents a similar 'red flag' suggesting possible hereditary cancer risk, preserving the original intent. All qualitative (open-ended) items were removed to support the quantitative-only design of this study and reduce interpretive ambiguity. This also increased consistency in analysis and reduced participant burden. Items that were previously optional were made mandatory to reduce missing data. Response scales were revised for directionality, clarity, and standardisation across the survey. This included use of symmetrical 5-point Likert scales, consistent ordering, and removal of 'unsure' or ambiguous middle categories (DeCastellarnau, 2018; Revilla et al., 2014).

Original item (Andrews et al., 2014)	Adapted item	Justification
		Item (d) was adapted into two discrete confidence-based items, aligning with best practices for assessing self-efficacy in clinical scenarios. Item (b) response options were mismatched (a yes/no question with a likelihood scale), which introduced methodological ambiguity.
<i>Q#11:</i> Please tick as many as apply: Which of the following questions should be included when taking a genetic history? a) Familial medical conditions b) Whether the patient had received private or NHS treatment c) Births, pregnancy loss and deaths d) Ages of family disease onset e) Exposure to environmental toxins f) Information about the patient's partners family g) History of road accidents h) If partners are related in any way i) In a patient with e.g. bowel cancer, asking about other cancers in the family	<i>Q#09:</i> Which of the following should be included when taking a genetic family history for an adult with cancer? (Tick as many as apply) a) Familial medical conditions b) Whether the patient received treatment as a private or public patient c) Births, pregnancy loss and deaths d) Ages of family disease onset e) Exposure to environmental toxins f) Information about the patient's partner's family g) History of road accidents h) If partners are blood-related in any way (e.g., cousins) i) Asking about other cancers in the family j) Including grandparents when collecting family history	Wording was updated to align with Australian healthcare terminology (e.g., <i>public/private patient</i> rather than <i>NHS</i>). An additional item (j) was included to reflect standard cancer genetic practice in family history taking, such as, the inclusion of grandparents in the pedigree. Item (h) was revised to clarify the concept of consanguinity, with 'cousins' added as an accessible example. Minor changes were made to grammar and item phrasing for clarity and consistency. The question prompt was narrowed to focus specifically on cancer settings, which better aligns with the scope of the present study.
<i>Q#12:</i> Regional Genetic Centres (RGC) are situated throughout the country and are concerned with the cause, course, diagnosis and treatment of genetic disorders and also provide education and resources for the NHS. Which statement best represents you? A) I am unaware of Regional Genetic Centres and services B) I am aware of Regional Genetic Centres but not about its services C) I know about them and have used them	<i>Q#10:</i> Public clinical genetic services are available throughout Australian states and territories, providing diagnosis, screening, testing and counselling for inherited disorders. Genetic counselling is provided by a team of health professionals who work together to provide the most up-to-date information and support to people and their families who have a health condition that may have a genetic basis. Which statement best represents your understanding of genetic services? (Tick all that apply)	Item was adapted to reflect the Australian healthcare system in place of the UK-specific <i>Regional Genetic Centres</i> and NHS references. The description preceding the question was updated to improve clarity and contextual accuracy for Australian respondents. The response format was changed from single-choice to 'tick all that apply', enabling a more nuanced understanding of participants' familiarity with genetic services.

Original item (Andrews et al., 2014)	Adapted item	Justification
D) I know about them and have recommended them to colleagues/patients E) I know the genetic counsellor that serves the local area by name <i>Response type: Select one only</i>	A) I am unaware of available genetic services B) I am aware of genetic services C) I know about available genetic services and have used them D) I know about these genetic services and have recommended them to colleagues/patients E) I know the genetic counsellors who work for genetics services F) I know the genetic counsellor that works for my local genetics service by name	Additional response option (E) was added to capture broader awareness of counselling personnel, while (F) retained the personalised item from the original tool. Minor wording changes were made for clarity, grammatical consistency, and alignment with Australian terminology.
<i>Q#13:</i> <i>What resources can Regional Genetic Centres provide?</i> <i>Response type: Free-text (qualitative)</i>	Removed	This item was removed because it elicited open-ended qualitative responses, which were outside the scope of this study's quantitative survey design. Additionally, the reference to UK-based <i>Regional Genetic Centres</i> was not applicable within the Australian healthcare context.
<i>Q#14:</i> <i>What types of support services are available to patients and their families with or at risk of a genetic condition?</i> Options: A) Genetic counselling B) Specific charities C) Medical insurance D) Patient support groups E) Personal and social care <i>Response: Select all that apply</i>	<i>Q#11:</i> <i>What resources are available through your local genetic services?</i> Options: A) Genetic screening B) Genetic risk assessment C) Genetic counselling D) Pregnancy terminations E) Access to support groups F) Access to research opportunities G) I don't know <i>Response: Select all that apply</i>	The item was adapted to reflect the structure and services of Australian clinical genetics departments, aligning more closely with what nurses in this context may actually encounter. Several options were revised or replaced to ensure cultural and systemic relevance (e.g., 'medical insurance' is less applicable in Australia's public healthcare system). A deliberate misconception item was added (Option D: Pregnancy terminations), reflecting a common misunderstanding that termination is provided <i>directly</i> through genetics services. The inclusion of plausible yet incorrect options is a validated technique for assessing actual familiarity and reducing guesswork (Jones et al., 2015; Miller & Baker-Prewitt, 2009). 'I don't know' was also added as a meaningful response option, which can help distinguish uncertainty from incorrect selections (Revilla et al., 2014).

Original item (Andrews et al., 2014)	Adapted item	Justification
Q#15: a) Approximately how many times have you identified an individual who should/could be referred to genetic specialist services since qualifying? b) If you have never identified an individual to be referred is it because: 1) I have never encountered an individual who should be referred 2) Not relevant to my practice 3) I would not recognise when this was appropriate 4) Other – <i>free text</i> Response type: Qualitative free text for (a); single-choice for (b)	Q#12: <i>In the last month, how many times have you referred a patient to genetic services?</i> 1) 0 times 2) 1–10 times 3) More than 10 times If 0 times: <i>If you have not identified an individual to be referred, is it because: (Select as many as you like)</i> 1) I have never encountered an individual who should be referred 2) Not relevant to my practice 3) I would not recognise when this was appropriate 4) I do not have the resources to do this 5) I do not have the support of my organisation to do this 6) Other	The timeframe was adjusted from ‘since qualifying’ to ‘in the last month’ to enhance recall accuracy and reduce recall bias, which is a known issue in retrospective self-reporting (Bradburn et al., 1987). A one-month recall window strikes a balance between feasibility and relevance for capturing recent clinical behaviours. Free-text responses were removed in favour of quantitative categorical options to allow for standardised analysis and improve data comparability. The ‘if not’ options were expanded to include structural barriers (e.g., lack of resources or organisational support), reflecting known implementation challenges in genomic referral pathways (Morrow et al., 2021). Response format was changed from single- to multiple-response selection to better reflect the complexity of barriers to referral.
Q#17: <i>Think of a situation where you have had an idea in your professional practice.</i> a) If you were unable to implement it, what prevented you from doing so? b) If you were able to implement your idea, what enabled you to do this? <i>Response format: Free-text (qualitative)</i>	Removed	This question was removed due to its open-ended qualitative format, which did not align with the quantitative design of the adapted survey. Additionally, the content focus: perceived barriers and enablers to implementation, was explored in depth through the semi-structured interviews conducted in Phase 2 of the current study.
Q#25: <i>Have you ever sought genetic information for the following people?</i> a) Self b) Family c) Client/patients family d) For a colleague e) I have never sought genetic information	Q#22: <i>Have you ever sought genetic information for the following people?</i> a) Self b) Family c) Client/patient’s family d) For a colleague e) Friend	The response format was simplified from a three-category scale (‘never asked,’ ‘asked,’ ‘asked and acted’) to a binary Yes/No option. This change was made to reduce respondent burden, minimise ambiguity between ‘asked’ and ‘acted,’ and align with the study’s focus on whether the behaviour occurred rather than the circumstances prompting it.

Original item (Andrews et al., 2014)	Adapted item	Justification
f) Friend g) Other Response scale: 1) I have never been asked to seek advice 2) I have been asked to seek advice 3) I have been asked to seek advice and have acted	f) I have never sought genetic information g) Other Response scale: Yes / No	Minor wording edits were made for clarity (e.g., adding apostrophe to 'patient's' and consistent capitalisation). This simplification is consistent with best practices in survey design when the primary goal is prevalence estimation rather than detailed behavioural sequencing (Dillman et al., 2014; Fowler, 2014).
Q#26: <i>Which of the following interventions/people encourage you to incorporate new areas of knowledge into your practice?</i> a) Peers b) Heads of department e.g. line managers c) Contacts with specific professional services d) Other health professionals e) Attending study days f) Having a mentor g) Case studies h) Attending short presentations (e.g. lunchtime seminars) i) Patients Response scale: Please tick as many options as you deem necessary (Optional)	Q#23: <i>Which of the following interventions/people encourage you to incorporate new areas of knowledge into your practice?</i> A) Peers B) Heads of department (e.g., NUM) C) Contact with specific professional services D) Other health professionals E) Attending study days F) Having a mentor G) Case studies H) Attending short presentations (e.g., lunchtime in-service) I) Patients Response scale: Please tick as many options as you like	Adaptations were made to reflect the Australian healthcare context. 'Line managers' was replaced with 'NUM' (Nurse Unit Manager) to reflect local terminology. 'Lunchtime seminars' was changed to 'lunchtime in-service' to align with common Australian hospital and clinical education terminology. Minor wording and punctuation changes were made for clarity and consistency. Retention of a 'select all that apply' format preserves the original item's intention to capture multiple influences on professional learning, while removing the 'optional' note avoids signalling that the item is non-essential, which can reduce response rates (Dillman et al., 2014).
<i>When you need advice for a particular patient or medical issue, who do you usually ask for advice?</i> A) High grade asks low grade B) Low grade asks high grade C) Low grade asks low grade D) High grade asks high grade E) Grade doesn't matter, anyone is asked	<i>If you need advice for a particular patient or medical issue, who would you consult with first?</i> 1) I would consult a junior colleague 2) I would consult a senior colleague 3) I would consult a colleague practising at my level of experience 4) I would consult anyone, level of experience doesn't matter	The question was adapted due to concerns over wording clarity and interpretability. The original wording was ambiguous and relied on hierarchical terminology ('high grade' / 'low grade') that is not commonly used in the Australian nursing context and may be interpreted inconsistently by respondents. This adaptation is supported by best practice guidelines for survey translation/adaptation, which recommend replacing unclear or locally unfamiliar terms with culturally equivalent descriptors (Behr, 2017; Harkness et al., 2010).

Original item (Andrews et al., 2014)	Adapted item	Justification
<i>Q#30:</i> <i>At what grade are you currently practising?</i> Response options: a) 5 b) 6 c) 7 d) 8 e) 9	<i>DemoQ4:</i> <i>At what grade are you currently practising?</i> Response options: 1) Registered Nurse (RN) 2) Clinical Nurse Specialist (CNS) 3) Clinical Nurse Consultant (CNC) 4) Clinical Nurse Educator (CNE) 5) Nursing Unit Manager (NUM) 6) Nurse Practitioner (NP) 7) Other	The original UK <i>Agenda for Change</i> banding system (grades 5–9) was replaced with terminology and role titles used in the Australian nursing workforce to ensure cultural and professional relevance. This adaptation preserves the original intent, capturing the participant’s seniority level, while providing categories that are both recognisable and meaningful to Australian respondents.
<i>Q#31:</i> <i>What is your highest level of academic achievement?</i> Response options: a) Diploma b) Degree c) Masters d) PhD	<i>DemoQ5:</i> <i>What is your highest level of academic achievement?</i> Response options: 1) TAFE/Vocational training 2) Bachelor’s degree 3) Graduate certificate/diploma 4) Master’s degree 5) PhD/post-graduate research degree	The original UK-centric education categories were adapted to reflect the Australian tertiary and vocational education frameworks.
<i>Q#33:</i> <i>Please indicate your gender:</i> Response options: a) Male b) Female	<i>DemoQ7:</i> <i>Please indicate your gender:</i> Response options: 1) Female 2) Male 3) Non-binary 4) I do not have a gender identity 5) Prefer not to say 6) Prefer to self-describe/other	The original binary gender options (‘Male’ / ‘Female’) were expanded to align with current best practice for inclusivity in demographic data collection (Australian Bureau of Statistics, 2020). Additional categories were included to reflect diverse gender identities, allow respondents to opt out (‘Prefer not to say’), and provide a free-text self-description option. This adaptation reflects updated guidance from the Australian Bureau of Statistics (2020), which emphasises using separate and inclusive measures for sex and gender, and is supported by recent scholarly recommendations for gender measurement in health and social science research (Bauer et al., 2017; Cameron & Stinson, 2019; Fraser, 2018). Updating demographic questions in this way enhances respondent comfort, reduces misclassification, and improves data accuracy while meeting contemporary ethical standards.

Original item (Andrews et al., 2014)	Adapted item	Justification
Q#34: <i>Are you or any members of your family affected by a genetic condition?</i> Response options: a) Yes b) No	DemoQ8: <i>Have you or anyone in your family had experience with genetic counselling or genetic testing?</i> Response options: a) Yes b) No	The item was reworded following advice from the ethics committee to avoid directly eliciting personal or familial medical information, which could be considered sensitive and potentially distressing for participants. The revised question retains the core intent: assessing whether personal familiarity with genetics services may influence adoption-related behaviours, while framing the inquiry in a way that focuses on service experience rather than medical diagnosis. This approach aligns with ethical principles for minimising potential harm and respecting participant privacy in health research (National Health and Medical Research Council, 2018).
Q#35: Please indicate your ethnic background by ticking the correct box: a) English b) Welsh c) Scottish d) Northern Irish e) British f) Irish g) White & black Caribbean h) White & black African i) White & Asian j) Indian k) Pakistani l) Bangladeshi m) Chinese n) African o) Caribbean p) South American q) North American r) Canadian s) New Zealander t) Australian u) Other	DemoQ9: What is your ethnic background? (tick any that apply) 1) Australian 2) Indigenous or Torres Strait Islander 3) New Zealander 4) Asian 5) Indian 6) Middle Eastern 7) European 8) Caribbean 9) North American 10) South American 11) African 12) Jewish 13) Decline to answer 14) Other	The list of categories was revised to reflect relevance to the Australian population and contemporary classification practices, including recognition of <i>Aboriginal and Torres Strait Islander peoples</i> as distinct groups. Several categories were consolidated to improve clarity and statistical analysis while maintaining inclusivity. Minor spelling and wording adjustments were made to align with current Australian Bureau of Statistics (ABS) terminology and ensure cultural sensitivity. The option 'Decline to answer' was added to respect participant autonomy and support ethical best practice in demographic data collection (Australian Bureau of Statistics, 2022; National Health and Medical Research Council, 2018).

Original item (Andrews et al., 2014)	Adapted item	Justification
	<i>Q#14:</i> <i>Please select the answer that best reflects your level of agreement/disagreement with each statement:</i> A) I use research articles for information to make practice decisions B) I use information I learn from conferences to guide my practice C) I use information learnt from continuing professional development (CPD) to make practice decisions D) I use scholarly database searches for information to make practice decisions E) I use internet sources (e.g., Google search) for information to make practice decisions Response scale: 1) Never 2) Rarely 3) Sometimes 4) Often 5) Always	This item was newly introduced to assess cosmopolitanism and information-seeking behaviour, consistent with Rogers' (2003) <i>Diffusion of Innovations</i> theory. These dimensions are recognised traits of early adopters but were not fully explored in the original Andrews et al. instrument. The question and items were adapted from Section 4 (Information Sources) of the School Nurse Evidence-Based Practice Questionnaire (Adams & Barron, 2010), which was previously applied in Bourgault's (2012) study (Bourgault, 2012; Bourgault et al., 2014). The original 4-point frequency scale was modified to a 5-point scale to incorporate a neutral midpoint and improve response granularity, in line with best practices in behavioural survey design (Upton & Upton, 2006). This also reflects scaling used in similar nursing studies on research utilisation (Majid et al., 2011). Though no psychometric testing was conducted on the adapted scale, the item wording and intent remained aligned with validated constructs.
Multiple items in the original survey (Questions 8, 10, 16, 19, 21, 22, 23, and 24) used inconsistent Likert-type scales, varying in range from 5-, 6-, 7-, and 10-point formats, with irregular ordering and inconsistent inclusion of neutral or 'unsure' options.	All Likert-type scales were standardised to a consistent 5-point format with a neutral midpoint. The wording of anchors was retained where possible but restructured for clarity and directional consistency (e.g., <i>Strongly disagree</i> → <i>Strongly agree</i>; <i>Very difficult</i> → <i>Very easy</i>). For example: - 1) Strongly disagree; 2) Disagree; 3) Neither agree nor disagree; 4) Agree; 5) Strongly agree	Standardising the response scales improved measurement reliability, respondent comprehension, and comparability across items (Colman et al., 1997; DeCastellarnau, 2018). Using a consistent 5-point scale with a central neutral option is supported in the survey methods literature for reducing cognitive burden, promoting balanced responding, and facilitating interpretation in statistical analyses (Revilla et al., 2014). The reordering of anchors from negative to positive ensured consistency with the rest of the instrument and minimised potential response bias. Additionally, the 'Not sure' option was removed to create a forced-choice format, which encourages cognitive engagement and prevents satisficing behaviours that can reduce data quality (Revilla et al., 2014; DeCastellarnau, 2018).

4.6.2.3 Survey construct grouping

The survey instrument developed by Andrews et al. (2014b) was originally organised into nine thematic sections. For the purpose of this doctoral study, these thematic groupings were reconceptualised into 11 constructs that more clearly captured the intent of each question and aligned with the study's specific aims and objectives.

The final adapted survey included 33 items, consisting of nine demographic questions and 24 core items addressing the study objectives. Some of the constructs (demographic characteristics, perceived knowledge/awareness, objective knowledge, confidence, attitudes, engagement/adoption, barriers/enablers, cosmopolitanism and information-seeking behaviours) were reported using descriptive statistics to provide a profile of the sample, consistent with Aim 1.

The remaining constructs (demographic characteristics, barriers/enablers, personality traits, opinion leadership, cosmopolitanism and information-seeking, and professional role expectations and influences) were examined using inferential statistics to explore characteristics associated with likely adopters and non-adopters, in line with Aim 2. Table 4.2 provides an overview of the survey constructs and the questions included under each construct.

Table 4.2. Survey constructs

Survey Construct	Survey Questions
Perceived knowledge/awareness	Q3, Q4(e), Q10
Objective knowledge	Q7, Q9, Q11
Confidence	Q5(b–c), Q8
Attitudinal variables	Q4 (a–d, f), Q5(a), Q6, Q20, Q21
Engagement/Adoption	Q12(a), Q22, Q19
Barriers/Enabler	Q12(b), Q15, Q16, Q23
Personality traits	Q1
Opinion Leadership	Q2, Q13
Cosmopolitanism/ information-seeking	Q14
Professional role expectations and influences	Q17, Q18
Demographics	DQ1–9

4.6.3 Pilot

To ensure the clarity, usability, and functional integrity of the survey instrument, a pre-test pilot was conducted prior to formal data collection. Ten individuals, comprising oncology nurses and academic colleagues with relevant clinical or methodological expertise, were invited to complete the survey and provide structured feedback. The purpose of the pilot was to evaluate aspects such as question clarity, layout and formatting, technical functionality (e.g., dropdown menus, navigation), and the overall respondent experience.

Feedback from pilot participants highlighted minor areas where wording could be improved for clarity and interpretability. In particular, adjustments were made to ensure consistent terminology across sections and to refine the flow of certain items for logical sequencing. No major structural or conceptual changes were required as the core content was considered appropriate and well-aligned with the study's objectives. This process aligns with recommendations by Thomas (2004), who emphasises the importance of pilot testing questionnaires to determine their usability, participant burden, and interpretive clarity. The final version of the survey, as revised following the pilot phase, is included in Appendix B.

4.6.4 Sampling

The sample for this study consisted of registered nurses working in oncology settings across Australia. A combination of purposive and snowball sampling strategies was employed to recruit participants with diverse roles, experiences, and geographic contexts within cancer care, irrespective of their familiarity with genomics.

Purposive sampling was used as the primary strategy to ensure that participants met the core inclusion criteria: being registered with the Australian Health Practitioner Regulation Agency (Ahpra) and currently employed in oncology or cancer care settings. This approach is commonly used in descriptive and exploratory components of research, such as the first phase of this study, as it enables the deliberate selection of individuals positioned to provide insight into the topic under investigation—in this case, the current landscape of genomic knowledge, engagement, and practice among oncology nurses (Maxwell, 2013; Neuman, 2013). Purposive sampling involves the deliberate selection of participants based on their capacity to contribute information-rich perspectives aligned with the research objectives (Patton, 2014). Importantly, the sample was not limited to nurses already engaged with genomics and aimed to capture non-

genomics nurses experts and ideally reflect the experiences of the broader oncology nursing workforce in Australia.

To broaden the sample and facilitate recruitment across geographically and professionally dispersed groups, snowball sampling (also known as chain-referral sampling) was also employed. Snowball sampling is another non-randomised strategy in which research participants are asked to recommend other potential participants who meet the eligibility criteria (Neuman, 2013). As existing participants recruit future participants from among their colleagues, the sample grows and a ‘snowball effect’ is established. This approach is particularly useful when recruiting from professional communities where formal registries are insufficient to identify all potential participants, and where trust within professional networks can support engagement (Faugier & Sargeant, 1997; Given, 2008; Parker et al., 2020; Sheu et al., 2009). While non-probability methods such as these do not support statistical generalisation, they are well suited for studies prioritising depth, diversity, and contextual relevance (Faugier & Sargeant, 1997; Noy, 2008). Findings derived from such approaches may support analytical generalisation, whereby insights are extended to comparable settings or theoretical propositions (Yin, 2017). This sampling approach aligned with the pragmatic underpinnings of the study and the mixed-methods design, and supported the collection of targeted data from a cross-section of the oncology nursing workforce. Based on an estimated Cancer Nurses Society of Australia (CNSA) membership of approximately 1,500 nurses at the time of data collection, a target sample size of 306 was calculated using a 95% confidence interval and a 5% margin of error.

4.6.5 Recruitment

Following ethics approval from the University of Technology Sydney Human Research Ethics Committee (HREC) (see Appendix C), permission to recruit members was sought from the Research Standing Committee (RSC) of the CNSA. This process involved the submission of a formal research proposal detailing the study’s aims, methodology, and participant information materials.

Upon approval, an email invitation (see Appendix D) was distributed to CNSA members on 1 October 2022. The invitation contained a secure link to the online survey and a plain language participant information statement. Consistent with ethical guidelines for minimal-risk research, implied consent was assumed upon completion of the survey. To maximise reach, the survey invitation was also promoted through professional social media platforms, including LinkedIn,

Twitter, and Facebook (see Appendix E). These posts were shared in relevant oncology nursing groups and networks, encouraging both direct participation and snowball referral.

Two weeks following the initial email, a reminder invitation was sent to CNSA members, and additional posts were disseminated via social media to sustain engagement. This strategy helped to support broad, profession-wide reach across geographic and institutional contexts.

4.6.6 Data collection procedure

As noted in Section 4.6.1, data collection for the quantitative phase was conducted using a secure, web-based REDCap® platform hosted by the University of Technology Sydney. The survey was accessible online between October 2022 and June 2023 and was designed for self-completion via desktop or mobile devices. Participants were not required to register or provide identifying details, supporting anonymity and ease of access.

At the conclusion of the survey, participants were presented with a separate REDCap form via which they could express interest in participating in a follow-up telephone interview for Phase 2 of the study. This mechanism enabled linkage between the two study phases while maintaining separation between survey responses and interview recruitment, thus protecting participant confidentiality.

4.6.7 Data analysis

Quantitative data analysis was conducted with guidance from a specialist biostatistician. Survey data were exported from REDCap and analysed using R (Version 4.5.1; R Core Team, 2025). Descriptive statistics of the survey variables were estimated as appropriate for the type of variable. For categorical (binary and multi-category) variables, the number of participants responding to each level of the variable was reported, as well as the percentage of the appropriate denominator (total, or subset of total) who selected each level. Continuous variables were reported using the mean and standard deviation.

When comparing between two groups in categorical variables, the absolute percentage difference with a 95% confidence interval was reported. For continuous variables, the mean difference with 95% confidence interval was estimated. To test against a null hypothesis of no difference between groups in continuous variables, a Welch's *t*-test was used, which makes fewer assumptions (equal variance between groups) than a standard *t*-test. For categorical variables, a chi-square test was used as the first preference, with Fisher's exact test applied

where the expected number in a cell was less than 5. Given that the study was exploratory and not confirmatory in nature, the analysis was not concerned with controlling the family-wise error rate. There was no single universal null hypothesis for the study, and accordingly, no adjustments for multiplicity were made (Rothman, 1990).

Where the survey included items designed to measure a latent construct, internal consistency was assessed before using the measure. Two indices were used for this purpose. The first was Cronbach's alpha, which provides a measure from 0 to 1 based on the correlation of individual items with the overall score, relative to the variance for each item (Cronbach, 1951). The second was McDonald's omega, an index between 0 and 1 indicating the general saturation or consistency of a test (McDonald, 1999). Values greater than 0.70 on both indices were considered acceptable, indicating that the items could be reliably combined into an overall construct and treated as a continuous variable in subsequent analyses.

To address Aim 2 of the study, which was to identify individual characteristics associated with the uptake of genomics in nursing practice, participants were classified into two groups: likely adopters and likely non-adopters. This classification was based on a median split of a composite adoption score derived from relevant survey items. The following section describes this classification process and outlines the inferential analyses conducted to compare these two groups.

4.6.7.1 Distinguishing likely adopters and non-adopters

To address Aim 2 of the study, identifying individual characteristics associated with the uptake of genomics in nursing practice, a composite adopter score was developed to classify participants according to their likelihood of adopting genomics into oncology nursing. This score was based on 14 items adapted from the original survey tool by Andrews et al. (2014b), which was designed to capture four key GIAs (see Section 4.6.2.1). In the original Andrews et al. study, each of the 14 questions was individually scored according to competency expectations and, in some cases, the relative position of the response option (e.g., 'top 20% of response options'). However, in the current study some items in the original scoring framework were revised. These revisions were informed by advances in the field, changes in practice contexts, and extensive consultation with the supervisory team about what constitutes meaningful genomic engagement in modern Australian oncology nursing. Some of the original cut-offs were no longer considered fit for purpose, and a revised set of scoring thresholds was

applied to better reflect contemporary practice realities. The likely adopter score was revised to a range of 0–14 (see Table 4.3 for scoring criteria).

A total adoption score was calculated for each participant based on their responses to the 14 questions. As the distribution of scores did not reveal a clear natural break or theoretically derived cut-point for classification, a median split was applied to divide participants into two groups: those scoring above the median were classified as *likely adopters*, and those scoring below as *likely non-adopters*. This pragmatic approach generated balanced group sizes and enabled meaningful inferential comparisons across the sample.

Importantly, this updated scoring and classification framework represents a novel contribution of the current study. It adapts and extends a previously developed instrument in a way that accounts for both recent advances and the specific context of genomic nursing in Australia. The resulting classification enabled subsequent inferential analyses examining associations between adoption likelihood and a range of factors, including demographic characteristics, perceived barriers and enablers, personality traits, opinion leadership, cosmopolitanness and information-seeking behaviours, and role expectations and influences. These findings provided critical context for interpreting the results and integrating them with the Phase 2 interview data.

Table 4.3. Adoption scoring

Question	Likely adopter
Q1: Please tick the relevant answer for the following statements (Strongly Disagree; Disagree; Neither Agree nor Disagree; Agree; Strongly Agree) I am someone who: a) Is original, comes up with new ideas b) Is curious about many different things c) Is ingenious, a deep thinker d) Has an active imagination e) Is inventive f) Values artistic, aesthetic experiences g) Prefers work that is routine h) Likes to reflect, play with ideas i) Has few artistic interests j) Is sophisticated in art, music or literature	‘Agree’ or ‘Strongly Agree’ = 1 ‘Neither agree or disagree’, ‘disagree’, ‘strongly disagree’ = 0

Question	Likely adopter
Q3: Please rate your familiarity with the following resources (Not at all familiar; Slightly familiar; Somewhat familiar; Moderately familiar; Extremely familiar). Please tick one option for each resource: a) The Australian College of Nursing (ACN) 2021 position statement: Nurses, Genomics and Clinical Practice b) The Australian Genomics Health Alliance c) Your state's health department strategic plan for genomics (e.g., NSW health) d) Your local specialist genetics service e) Centre for Genetics Education website: www.genetics.edu.au f) Human Genome Project g) International Society of Nurses in Genetics (ISONG) h) Global Genomics Nurses Alliance (G2NA)	'Extremely familiar' or 'Moderately familiar' to all of: a), b) and f) = 1 'Somewhat familiar', 'Slightly familiar', 'Not at all familiar' = 0
Q4: Please indicate your response to each statement (Strongly Disagree; Disagree; Neither Agree nor Disagree; Agree; Strongly Agree): a) Nurses should regularly keep up to date with new areas of practice b) Nurses should be able to decide which areas of knowledge they want to expand c) Taking a patient's family history is an important aspect of my role d) Continual professional development in genetics and genomics should be encouraged for all nurses e) I have a good awareness of how genetics and genomics impacts my own specialty f) Developments in genomics offer limited potential to improve health outcomes for all patient groups	'Agree' or 'Strongly Agree' for all questions (except for c) = 1 Question f) is reverse scored 'Neither Agree nor Disagree', 'Disagree', 'Strongly Disagree' = 0
Q5: Scenario Question a) How important would it be in this situation to take a family history? (Not at all important; Slightly important; Somewhat important; Moderately important; Extremely important) b) How confident would you feel educating the person in this scenario? (Not at all confident; Slightly confident; Somewhat confident; Moderately confident; Extremely confident) c) How confident would you feel managing this scenario in practice? (Not at all confident; Slightly confident; Somewhat confident; Moderately confident; Extremely confident)	'Extremely' or 'Moderately' for all three questions = 1 'Not at all confident', 'Slightly confident', 'Somewhat confident' = 0
Q6: Do you think the application of genomics is relevant to your patient group? (Not at all relevant; Slightly relevant; Somewhat relevant; Moderately relevant; Extremely relevant)	'Extremely' or 'Moderately' = 1 'Not at all relevant', 'Slightly relevant',

Question	Likely adopter
	‘Somewhat relevant’ = 0
Q7: Which of the following areas of care are linked to genetics? a) Peoples response to particular medication b) Appendicitis c) Weight d) Blood pressure e) Blood volume f) Ethnic origin g) Cholesterol levels h) Cancer	Answer all correctly. b) and e) are incorrect red herrings = 1
Q8: Would you feel confident asking patients about their genetic family history? (Not at all confident; Slightly confident; Somewhat confident; Moderately confident; Extremely confident)	‘Extremely confident’ or ‘moderately confident’ = 1 ‘Not at all confident’, ‘Slightly confident’ ‘Somewhat confident’ = 0
Q9: Which of the following should be included when taking a genetic family history for an Adult with cancer? (tick as many as you like) a) Familial medical conditions b) Whether the patient received treatment as a private or public patient c) Births, pregnancy loss and deaths d) Ages of family disease onset e) Exposure to environmental toxins f) Information about the patient’s partner’s family g) History of road accidents h) If partners are blood-related in any way (e.g., cousins) i) Asking about other cancers in the family j) Including grandparents when collecting family history	Answer at least 6 correctly =1 (However, if they answered one of the red herrings = 0 f) and g) are red herrings)
Q10: Which statement best represents your understanding of genetic services? a) I am unaware of available genetic services b) I am aware of genetic services c) I know about available genetic services and have used them d) I know about these genetic services and have recommended them to colleagues/patients	Tick at least one of c), d), e) or f) = 1

Question	Likely adopter
e) I know the genetic counsellors work for genetics services f) I know the genetic counsellor that works for my local genetics service by name	
Q11: What resources are available through your local genetic services? (Tick as many as you like): a) Genetic screening b) Genetic risk assessment c) Genetic counselling d) Pregnancy terminations e) Access to support groups f) Access to research opportunities g) I don't know	Tick a), b) and c) = 1 If they ticked d) or g) = 0
Q19: How often do you speak to your colleagues about genetics/genomics? (Never; Rarely; Sometimes; Often; Always)	'Sometimes', 'Often' and 'Always' = 1 'Never', 'Rarely' = 0
Q20: Would you like to incorporate more genetics/genomics as part of your everyday practice? (Definitely not; Probably not; Possibly; Probably; Definitely)	'Definitely' and 'Probably' = 1 'Definitely not', 'Probably not', 'Possibly' = 0
Q21: Are you interested in new areas of genetic and genomic knowledge within your practice? (Not at all interested; Slightly interested; Somewhat interested; Moderately interested; Extremely interested)	'Extremely' or 'Moderately' = 1 'Not at all interested', 'Slightly interested', 'Somewhat interested' = 0
Q22: Have you ever sought genetic information for the following people? a) Self b) Family c) Client/ patient's family d) For a colleague e) Friend f) I have never sought genetic information g) Other	Tick at least 1 answer between a)-e) = 1

4.7 Phase 2 qualitative research

This section outlines the method used for the qualitative phase of the study (Phase 2) and the strategies employed to ensure its rigour and relevance. It begins by presenting the rationale for adopting semi-structured telephone interviews as the primary mode of qualitative inquiry, in alignment with the study's pragmatic foundations and aims. The development of the interview guide is then described, including the processes undertaken to support its validity, such as mock interviews, observational review, and researcher reflexivity. This is followed by a description of the sample and recruitment strategy for Phase 2, and a detailed account of the interview procedures, including scheduling, verbal consent, audio recording, and transcription. The final part of the section explains the analytic approach used to interpret the qualitative data in alignment with the study's aims and theoretical framework.

4.7.1 Method

Phase 2 of this study employed semi-structured telephone interviews to explore the conditions, barriers, and enablers shaping the uptake of genomics in oncology nursing. This method was selected for its capacity to elicit rich, contextualised accounts of nurses' experiences and perspectives, in alignment with the study's pragmatic orientation and its emphasis on generating practice-relevant knowledge. While the interviews were designed to explore factors influencing engagement with genomic innovation, adoption status was not a criterion for inclusion, nor was it explicitly assessed. Rather, participants were encouraged to reflect on their roles, settings, and attitudes, with references to adoption often emerging organically in the data.

Semi-structured interviewing offers a balance between consistency and flexibility. The interview guide provided a structured framework to ensure that key topics relevant to the research aims were addressed, while still allowing the conversation to unfold responsively to each participant's narrative. This adaptability is particularly suited to pragmatic inquiry, which values methods that are both systematic and context-sensitive (Galletta & Cross, 2013; Greene & Hall, 2010; Teddlie & Tashakkori, 2009). While the schedule served as a guide, it was not always followed sequentially. Instead, participants were encouraged to shape the flow of the discussion, enabling the researcher to pursue emergent themes in real time.

Telephone interviews were selected for both practical and epistemological reasons, with the study design developed during a period of ongoing COVID-19-related uncertainty. Logistically, this mode allowed access to participants from across Australia, overcoming

geographic constraints and supporting the inclusion of diverse professional and institutional contexts (McCoyd & Kerson, 2006; Sturges & Hanrahan, 2004). This approach was also cost-effective and reduced potential barriers to participation such as time constraints and scheduling burden (Novick, 2008). The use of telephone rather than face-to-face interviewing also provided participants with the flexibility to engage from a setting of their choice, while also offering a degree of anonymity that may have enhanced comfort, particularly when sharing professional uncertainties or sensitive reflections related to clinical practice.

While the absence of visual cues is often cited as a limitation of telephone interviewing (Novick, 2008), this study considered the trade-off in light of both methodological and pragmatic priorities. The researcher's background in counselling and experience conducting health-related interviews supported the development of rapport and sensitivity to verbal nuances. Techniques such as attentive listening, verbal affirmations, and adaptive pacing were used to sustain conversational flow and participant engagement (Carr & Worth, 2001; Fontana & Frey, 2005). Although nonverbal communication can add richness to in-person interviews, it is also susceptible to interpretive bias and may not always be essential for meaning-making (Burnard, 1994). In this context, the advantages of extended reach, scheduling flexibility, and the relative anonymity of telephone interviews were considered to outweigh limitations associated with reduced visual input, particularly given the exploratory aims and pragmatic positioning of the study.

4.7.2 Development of interview guide

The interview guide used in Phase 2 was developed to explore the factors influencing the uptake of genomics in oncology nursing, with a focus on identifying the perceived barriers and enablers to integration into practice. This qualitative phase was designed to complement and expand upon the quantitative findings of Phase 1, and the guide was therefore developed to allow deeper exploration of themes that may have emerged in the survey, as well as to uncover new perspectives not captured through closed-ended items.

The initial development process involved the drafting of an extensive pool of potential interview questions, informed by the third research objective and designed to probe professional attitudes, clinical experiences, and systemic factors related to the use of genomics in nursing. These questions were then iteratively refined in collaboration with the supervisory team to ensure focus, relevance, and alignment with the study's aims.

To support conceptual rigour, the development of the guide was informed by key constructs from DOI theory, which also guided the overall design of the study. Concepts such as *relative advantage*, *compatibility*, *complexity*, *observability*, and *trialability* were used to frame potential areas of inquiry. However, while these constructs influenced the content and structure of the interview questions, the analysis was not deductively coded against the DOI framework. This decision was made to preserve the openness of the data and allow unanticipated themes to emerge, in keeping with the exploratory and inductive nature of qualitative research (Patton, 2014). Over-reliance on a pre-existing theoretical lens during analysis was seen as potentially limiting, with the risk of prematurely categorising participant accounts into pre-defined constructs rather than allowing meanings to surface from the data itself. As such, DOI theory was used as a conceptual scaffold in the guide's development, but not as a coding frame during analysis.

The resulting interview guide consisted of a structured set of open-ended questions accompanied by prompts and probes designed to elicit rich, contextualised narratives. The guide began with an introduction and consent script, which was read aloud at the start of each interview. This included a plain language explanation of the study's purpose, reassurances about confidentiality, information about voluntary participation and withdrawal, and a request for verbal consent to proceed with both the interview and audio recording.

An opening, rapport-building question invited participants to describe their understanding of and experience with genomics. This was followed by a series of content questions aligned with the research focus, framed in accessible and conversational language. Probing questions were used flexibly to invite elaboration or clarification, especially when participants touched on topics related to clinical practice, decision-making, professional development, or organisational context. These probes were not standardised but used responsively, in line with the semi-structured nature of the interviews (Galletta & Cross, 2013; Kallio et al., 2016). The sequencing of the guide was intentionally flexible, allowing the interviewer to follow the natural flow of each conversation while ensuring coverage of key topics.

The interview concluded with a summary prompt inviting participants to ask questions, share any final reflections or offer perspectives they felt had not yet been addressed. This final prompt helped to ensure participants had adequate opportunity to express views that may not have been anticipated by the guide. The full interview guide is included in Appendix F.

4.7.3 Validity

7.4.3.1 Mock interviews

To support the validity and functionality of the interview guide, mock interviews were conducted with members of the supervisory team prior to commencing data collection. These mock sessions served several purposes: they allowed the researcher to practise her interviewing technique, refine question phrasing, and rehearse transitions and pacing within a semi-structured format. Attention was also given to the practicalities of data collection, including the use of recording equipment, testing of devices, and ensuring audio quality for transcription purposes.

Feedback from the mock interviews was used to enhance the clarity and accessibility of the interview schedule, and to ensure the questions were not only logically sequenced but also capable of eliciting meaningful, context-rich responses. These sessions also allowed the supervisory team to observe and provide guidance on the researcher's approach, including how follow-up prompts were used, how consent procedures were explained, and how rapport was established.

This process supported both the technical reliability and conceptual validity of the interview instrument, helping to ensure that the tool was sufficiently robust to address the research aims while remaining flexible and ethically responsive to participants' needs (Kallio et al., 2016; Galletta & Cross, 2013).

4.7.3.2 Reflexivity

Reflexivity was a central component of the qualitative research process, recognised as a critical strategy for ensuring the integrity and rigour of data collection and interpretation (see Section 1.12). In this study, reflexivity was particularly important given the researcher's dual professional background in nursing and genetic counselling, both of which carried the potential to shape expectations, interpersonal dynamics, and interpretive frames.

In alignment with Braun and Clarke's (2021) emphasis on the active and situated nature of qualitative research, the researcher approached the interviews as a co-constructed encounter, remaining attentive to how her professional identity and assumptions could influence the research process. A structured reflexive process was adopted throughout data collection. Immediately after each interview, the researcher recorded a short audio reflection noting her

initial impressions, affective responses, and any contextual factors that might have influenced the interaction. These were complemented by a written reflection guided by prompts such as: *How did the interview go? What stood out? What do I feel and think in this moment? What do I wish I had asked but didn't? What could have gone better?*

These reflections supported an ongoing appraisal of the researcher's positioning and facilitated greater transparency in the interpretive process. On several occasions, the researcher also engaged in post-interview debriefings with her supervisors, summarising the content and emotional tone of the interview and receiving feedback on her performance as interviewer.

While reflexivity is an accepted standard in qualitative inquiry (Braun & Clarke, 2013, 2019), it was especially vital in this study due to the niche nature of the genomic nursing workforce and the proximity of the researcher to the professional community under investigation. By maintaining a practice of critical self-awareness, the researcher sought to mitigate the risk of interpretive bias and uphold the ethical and epistemological rigour of the study.

4.7.4 Sample

The sample for Phase 2 comprised nine oncology nurses who had participated in the earlier quantitative phase of the study and expressed interest in a follow-up interview. These participants represented a diverse cross-section of oncology nursing practice in Australia, with variation in geographic location, clinical role, and level of engagement with genomics.

The use of purposive sampling is well established in qualitative research, particularly when the goal is to generate rich, contextualised insights from individuals who hold relevant experiences or perspectives (Patton, 2014). In this study, while purposive selection ensured that all participants were registered nurses working in oncology, no prior knowledge or engagement with genomics was required, allowing for diverse perspectives on the phenomenon of interest.

The sample size of nine was deemed sufficient based on both conceptual and practical considerations. Consistent with qualitative research principles, interviews continued until no substantially new insights emerged, and the narratives began to display repetition in themes and patterns, indicating that data saturation had been reached (Guest et al., 2006; Mason, 2010). This point of saturation coincided with the number of participants who were both eligible and available to take part in interviews during the data collection period. Although debates persist regarding the applicability of saturation in reflexive thematic analysis (Braun & Clarke, 2019), the decision to conclude interviews was informed by the richness, relevance, and consistency

of the data, as well as the pragmatic constraints of the study's recruitment process. The sample thus reflected both analytical sufficiency and the practical boundaries of the participant pool.

4.7.5 Recruitment

Participants for the qualitative phase of this study (Phase 2) were recruited from the pool of respondents who had completed the Phase 1 survey. At the conclusion of the survey, participants were directed to a separate, secure REDCap form via which they could voluntarily express interest in taking part in a follow-up telephone interview. This separation of forms preserved the anonymity of the survey responses while enabling ethical and efficient recruitment for the second phase.

Those who indicated interest in Phase 2 were subsequently contacted via email. Each email contained a formal invitation to participate, as well as a copy of the Participant Information Statement (PIS) outlining the aims, procedures, voluntary nature, and ethical considerations of the interview process (see Appendix G). Interested participants were invited to review this material and contact the researcher to arrange a suitable interview time.

Of the 32 oncology nurses who initially expressed interest in being interviewed, nine ultimately participated. Despite follow-up contact attempts, the remaining 23 individuals did not respond to the email invitation. No participants actively withdrew or declined; rather, non-response was interpreted as passive withdrawal. Interviews continued until all available and responsive participants had been interviewed, at which point no new themes emerged from the data, suggesting that data saturation had been reached. This outcome aligns with established guidance that qualitative sample sizes should be sufficient to generate depth and nuance without redundancy (Braun & Clarke, 2016).

4.7.6 Procedure

4.7.6.1 Interview scheduling

Following receipt of expressions of interest via the separate REDCap form at the conclusion of the Phase 1 survey, participants who responded to the Phase 2 invitation email were contacted directly by the researcher to arrange a suitable time and date for a telephone interview. Scheduling was participant-driven, with efforts made to remain flexible to accommodate the nurses' clinical workloads and personal preferences. Interview times ranged across standard business hours and after-hours, depending on participant availability.

4.7.6.2 Consent and rapport building

At the beginning of each interview, the researcher verbally reiterated the purpose of the study, explained the voluntary nature of participation, reviewed confidentiality assurances, and obtained verbal consent to proceed with both the interview and its audio recording. This process followed a standardised introductory script included in the interview guide, developed to support consistency and transparency in the consent process.

4.7.6.3 Interview conduct and audio-recording

All interviews were conducted via telephone and ranged from 40 to 60 minutes in duration. With participant consent, interviews were audio-recorded using a secure digital recording device to ensure accuracy in capturing participants' narratives and to support subsequent transcription. Interviews followed a semi-structured format as outlined in the interview guide.

4.7.6.4 Immediate post-interview observations and reflexivity

Immediately after each interview, the researcher undertook a structured reflexive process to document impressions, contextual observations, and methodological notes. These included audio-recorded voice memos followed by written reflections addressing what stood out, what could have gone better, and any questions or thoughts that emerged. These reflections were shared with the supervisory team, allowing space for discussion and ongoing methodological refinement. This practice supported transparency and enhanced the researcher's reflexive engagement with the data generation process (Braun & Clarke, 2021).

A follow-up thank-you email was then sent to the participant, which included a movie voucher and a reminder that they could request a copy of their transcript for review prior to analysis. No participants made such requests.

4.7.6.5 Transcription and data preparation

Audio recordings were transcribed verbatim by a professional transcription service, following a signed confidentiality agreement with the transcriber. Each transcript was then reviewed and edited by the researcher for accuracy, with all identifying information removed to ensure participant anonymity. Once transcription was complete, audio files and any identifiable material were permanently deleted in accordance with the data management plan (see Section 4.9). De-identified transcripts were stored in both hard copy and digital formats and uploaded to NVivo (QSR International) to facilitate subsequent coding and thematic analysis. This step

marked the beginning of data familiarisation and immersion (Braun & Clarke, 2019, 2021; Davidson, 2009).

4.7.7 Data analysis

4.7.7.1 Analytical approach

Thematic analysis (TA) was selected as the method of qualitative data analysis for this study, guided by the six-phase reflexive approach developed by Braun and Clarke (2006). Reflexive thematic analysis (RTA) offers a theoretically flexible yet methodologically rigorous framework for identifying, analysing, and interpreting patterns of meaning across qualitative data. It is grounded in participants' lived experiences while attending to the active, interpretive role of the researcher in meaning-making. This made RTA particularly well-suited to the aims of the present study, which sought to explore the perceived barriers and enablers to the integration of genomics into oncology nursing practice. A primarily inductive and experiential orientation was adopted, allowing themes to be developed from the 'bottom-up' (where the process is to code the data without attempting to fit it into a pre-existing coding frame) and closely aligned with participants' accounts, while still guided by the overarching research aims.

Reflexive TA was chosen over other forms of thematic analysis (e.g., codebook or coding reliability approaches) due to its compatibility with the study's interpretivist-leaning epistemology and exploratory qualitative design. In RTA, themes are not assumed to pre-exist within the data but are constructed through an iterative and reflexive engagement between the researcher and the dataset. Knowledge is seen as partial, situated, and co-constructed through interpretive practices, rather than passively discovered (Braun & Clarke, 2021).

While the development of the interview guide was informed by DOI theory, the analytic process itself remained primarily inductive. Codes and themes were generated from the content of the data rather than imposed through a pre-existing theoretical framework. DOI theory served as a sensitising lens during data generation but was not used as a deductive scaffold during analysis, in keeping with RTA's emphasis on openness to unexpected meanings and the importance of remaining grounded in participants' accounts.

To support both depth and analytic rigour, an integrative approach was used in the process of coding and theme development. Specifically, both manual techniques (such as physical hard-copy annotation, printed transcripts, using coloured pens, paper, and sticky notes) and digital tools (primarily NVivo 12 software) were employed at different stages of the analysis. While

NVivo was used to streamline data management, retrieval, and visualisation of patterns across the dataset, manual methods were invaluable during early data immersion, initial coding, and theme conceptualisation. This hybrid approach allowed for a recursive and flexible engagement with the data, consistent with Braun and Clarke's (2021) emphasis on active and iterative theme development rather than mechanistic code aggregation.

Throughout the process, analysis was conducted by the primary researcher in ongoing consultation with the supervisory team. Team discussions served as opportunities for reflexive dialogue, critical questioning, and refinement of analytic interpretations. Braun and Clarke's six-step model of analysis was used as a structural guide, encompassing: (1) familiarisation with the data, (2) generating initial codes, (3) searching for themes, (4) reviewing themes, (5) defining and naming themes, and (6) producing the final report. These steps are elaborated below.

Step 1: Familiarisation with the data. The process of familiarisation marked the beginning of the analytic journey and was essential to developing a deep and intimate understanding of the dataset. Following Braun and Clarke's (2021) RTA framework, this phase was not merely preparatory but analytic in nature, laying the foundation for subsequent theme development.

Once interview transcripts were returned from the professional transcription service, each was reviewed against the original audio recordings to ensure accuracy and completeness. This process not only served to verify the fidelity of the transcription but also allowed the researcher to begin reconnecting with the nuances of participants' speech, tone, and expression. During this phase, any identifiable information was systematically removed from the transcripts to ensure anonymity and adhere to ethical data management and storage protocols.

Each transcript was then read several times to support full immersion in the data. The initial reading was done for general comprehension and flow; a second reading focused on making editorial corrections and removing identifiers; a third, more analytic reading was used to begin noting early observations, points of interest, and preliminary patterns in the data. These impressions were recorded in a coding journal and supplemented by notes made on printed transcripts using coloured pens, highlighters, and sticky notes, techniques that enhanced visual and conceptual engagement with the material. This process reflected Braun and Clarke's (2013, 2021) emphasis on active, thoughtful engagement rather than passive reading.

Familiarisation also involved reviewing reflexive materials recorded throughout the data collection process, including post-interview voice memos, written reflections, and field notes. These reflections helped the researcher consider how prior assumptions, professional background, and interactions with participants might shape data interpretation. Such reflexive engagement was particularly important given the researcher's dual clinical background as both a nurse and genetic counsellor.

Finally, familiarisation continued during the transition to NVivo software, where transcripts were imported, organised, and initially explored. While NVivo would later serve as a key tool for data management and coding, its early use in this phase supported the identification of potential patterns and links between data items, further deepening the researcher's analytic orientation to the dataset.

Step 2: Generating initial codes. The second stage of reflexive thematic analysis involved systematically generating initial codes across the full dataset. According to Braun and Clarke (2021), coding refers to the process of identifying and labelling features of the data that appear potentially meaningful or relevant to the research questions. In this study, coding was approached from a primarily inductive, semantic orientation, focused on capturing participants' explicit meanings rather than interpreting underlying assumptions or ideologies at this stage.

A strategy of 'complete coding' was employed. This involved coding all segments of the data that appeared pertinent to answering the research questions (rather than selecting only the most striking or frequent content), ensuring a comprehensive analytic foundation. Braun and Clarke (2013, 2021) advocate complete coding as a way of preserving analytic openness in the early stages of theme development, enabling the identification of both dominant patterns and subtler, yet important, meanings.

Initial coding began in a manual, paper-based format to facilitate close data engagement. Transcripts were printed and annotated by hand using coloured pens, sticky notes, and margin comments to identify phrases or sentences that were interesting, emotionally resonant, or theoretically relevant. Codes at this stage often consisted of short phrases or words that reflected participants' meanings as closely as possible, preserving the semantic integrity of their narratives.

These initial codes were later revisited, refined, and formalised within NVivo 12 (QSR International), which supported systematic data management, retrieval, and comparison. Each

code was documented with a label and brief description in a coding journal, which also included reflexive notes about the researcher's evolving analytic ideas, uncertainties, and questions. This iterative coding process involved repeatedly returning to the data to refine code boundaries and clarify meanings.

Although codes were primarily inductive, the interview guide's structure and the study's overarching aims provided a loose framework that guided attention towards relevant content (e.g., organisational context, professional roles, perceived barriers). This analytic orientation reflects Braun and Clarke's (2006, 2021) notion of a continuum between inductive and theoretically driven thematic analysis, where coding remains grounded in participants' accounts while being informed by the study's conceptual focus.

The reflexive nature of coding was maintained throughout, with analytic decisions discussed and refined in supervisory meetings. Coding was conducted by the primary researcher, but the collaborative review process contributed to reflexivity and transparency. Consistent with Braun and Clarke's (2021) stance, coding was not viewed as a mechanical task but as a flexible and creative analytic activity that set the foundation for theme development.

Step 3: Searching for themes. Following the completion of initial coding, the third step of reflexive thematic analysis involved moving from codes to candidate themes. This stage required the clustering of similar or conceptually related codes and the generation of broader patterns of meaning across the dataset. As described by Braun and Clarke (2021), themes are not simply categories that emerge from the data but are interpretive stories about what the data means in relation to the research questions.

The process began with a review and refinement of the coding framework developed in Phase 2. Redundant, overlapping, or ambiguous codes were collapsed, renamed, or removed, and related codes were clustered together based on shared content and meaning. Codes were re-read within context to ensure analytic coherence, and decisions about merging or modifying codes were carefully documented in a coding journal to maintain an audit trail and support transparency.

At this point, the researcher shifted from working in NVivo to a more tactile, visual approach to deepen interpretive engagement. Using printed versions of codes and segments of data, codes were physically arranged on large sheets of paper and across the floor using sticky notes, allowing for an expansive and flexible mapping of potential thematic connections (see Figure 4.1.). This hands-on, paper-based clustering method helped to visualise the conceptual

relationships between codes, enabling the identification of central organising concepts that could serve as the basis for initial themes.

This mapping process was iterative and recursive. Codes were moved, grouped, regrouped, and occasionally re-coded as emerging patterns were considered and challenged. Candidate themes were developed through this process of analytic clustering, guided by the research questions and the principles of experiential reflexive thematic analysis. Each theme reflected a pattern of shared meaning, underpinned by a central organising concept, rather than merely a collection of frequent or similar codes (Braun & Clarke, 2021).

At the conclusion of this step, several candidate themes and sub-themes had been identified, which provided a working structure for further refinement. These were later revisited and critically reviewed in collaboration with the supervisory team.

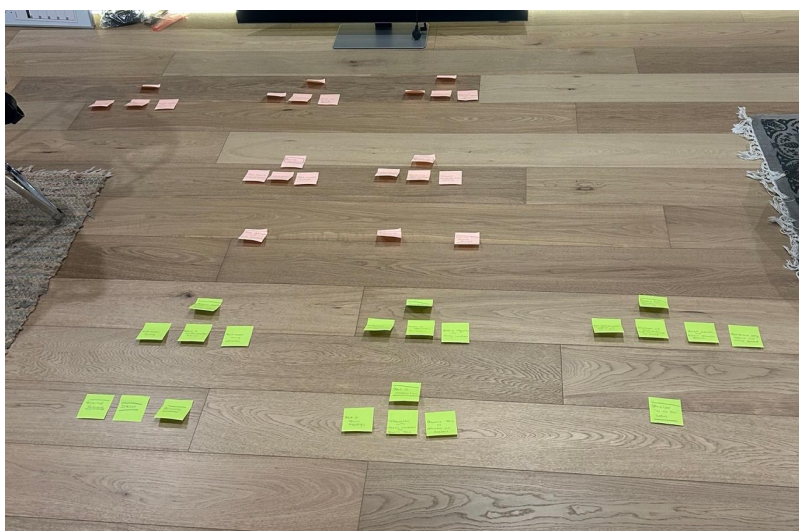
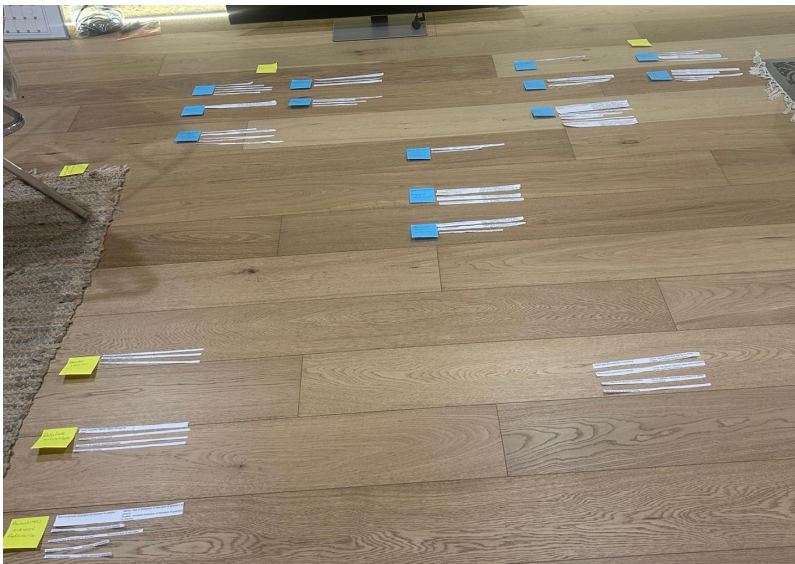


Figure 4.1. Searching for themes.

Step 4: Reviewing the themes. In Step 4, the candidate themes developed during the previous phase were reviewed, refined, and evaluated for coherence, clarity, and alignment with the dataset and the research aims. Braun and Clarke (2021) describe this as a recursive and iterative process, involving continual movement between the data, the coded extracts, and the emerging analysis to ensure that the themes meaningfully captured patterned responses across the dataset.

The first stage of this review involved reading all coded data extracts within each theme to assess internal coherence and analytic clarity. Overlapping, redundant, or insufficiently supported candidate themes were refined, merged, or discarded as needed. Next, the entire dataset was re-examined to ensure that the thematic structure adequately represented the participants' accounts and that no significant patterns had been overlooked. Particular attention was paid to the central organising concept of each theme, following Braun and Clarke's (2021) recommendation that each theme should be conceptually distinct and offer a coherent analytic story.

Throughout this process, both manual and digital methods were used to interrogate the developing themes. NVivo was used to collate coded data under each theme and subtheme, while early thematic maps were developed through physical rearrangement of printed codes and handwritten annotations. Discussions with the supervisory team served as an additional level of analytic reflexivity and helped ensure that the resulting thematic structure was both compelling and methodologically robust.

Step 5: Defining and naming themes. In this stage, the provisional themes developed during earlier steps were refined, defined, and named in order to clearly articulate their central organising concepts. This involved a return to the full dataset to ensure that each theme captured a coherent and analytically rich story grounded in the participants' accounts and aligned with the research aims. According to Braun and Clarke (2021), this step is critical for clarifying the scope and content of each theme, refining boundaries between themes, and ensuring that each theme is internally coherent and externally distinctive.

This process began by critically reviewing each theme's coded data extracts to determine whether the theme was conceptually robust, well-evidenced, and capable of supporting a compelling analytic narrative. Theme names, definitions, and supporting quotes were refined by the researcher and validated in consultation with the supervisory team. To aid in this process, NVivo was used to visually map theme hierarchies and to collate supporting data extracts. Manual techniques also played a role, particularly in supporting the development of theme

names and definitions that reflected the language and meanings embedded in participants' own words.

The final theme definitions were refined to clearly articulate each theme's focus and boundaries. These are presented in Appendix H in a comprehensive thematic table that outlines each theme, its definition, and illustrative quotes

In the final stages of defining and naming themes, a broader conceptual structure began to emerge. Through reflective engagement with the data and critical analysis of the interrelationships between themes, it became clear that the themes clustered meaningfully into five overarching domains: (1) Attributes of the Innovation, (2) Education-Related Factors, (3) Professional Factors, (4) Organisational Factors, and (5) Individual Factors. These domains were not pre-determined or imposed but, rather, evolved organically through the iterative and reflexive analytic process, consistent with Braun and Clarke's (2021) emphasis on flexibility and theoretical openness in RTA. They serve as a high-level organising framework for the analytic narrative and enhance the interpretive coherence of the findings, without reducing the richness or complexity of individual themes. This domain structure is used to guide the presentation of results in the following phase.

Step 6: Producing the final report. The sixth and final stage of RTA involved the formal write-up of the findings, presenting a coherent and compelling analytic narrative grounded in the data. This entailed selecting vivid, illustrative data extracts that supported each theme and communicating how these themes addressed the research aims and questions. As Braun and Clarke (2021) emphasise, writing is not a separate activity from analysis but an integral part of the interpretive process, enabling the researcher to refine and deepen their understanding of the data while crafting the analytic story.

The final report of the findings is structured around the five overarching domains developed in Phase 5 (Attributes of the Innovation, Education-Related Factors, Professional Factors, Organisational Factors, and Individual Factors), each of which contains several themes supported by key quotes from the interviews. Each theme is introduced with a clear definition and situated within its broader domain, accompanied by participant quotes that exemplify key analytic points. This structure allows the findings to be presented in a way that preserves the richness and complexity of participants' perspectives while highlighting conceptual patterns across the dataset. The narrative presentation of the findings is presented in Chapter 6

(Qualitative Results), where the themes are examined in depth, linked back to the research questions, and later situated within the existing literature in the discussion chapter.

4.7.7.2 Qualitative rigour and validity

Rigour in qualitative research was embedded throughout the analytic process, informed by Lincoln and Guba's (1985) model of trustworthiness and aligned with established frameworks and best practices (Ahmed, 2024; Anney, 2014; Koch, 1994; Patton, 1999). The approach to ensuring trustworthiness was reflexive and transparent, consistent with the principles of reflexive thematic analysis (Braun & Clarke, 2021), and attended to the criteria of credibility, dependability, transferability, and confirmability.

Credibility. This refers to the confidence that can be placed in the truth and plausibility of qualitative findings and the extent to which they accurately reflect participants' experiences (Lincoln & Guba, 1985). In this study, credibility was enhanced through a rigorous and iterative analytic process guided by Braun and Clarke's six-step framework for reflexive thematic analysis, which required prolonged engagement with the data. This included repeated listening to interview recordings, multiple readings of transcripts, and sustained immersion during coding and theme development. Reflexive engagement was maintained throughout through ongoing documentation in field notes and a coding journal, which captured analytic decisions and shifts in interpretive stance. Credibility was further strengthened through regular supervisory consultations that served as a form of peer debriefing, as well as triangulation with quantitative findings from the earlier phase of the study and interpretive discussions within the supervisory team. Participants were also offered the opportunity to review and comment on their transcripts and preliminary interpretations (member checking), providing an additional layer of transparency and rigour, although none elected to do so. Finally, the use of verbatim data extracts in the findings chapter provides direct evidence supporting each theme, ensuring that interpretations remain grounded in participants' voices.

Dependability. Dependability refers to the stability and consistency of research findings over time and across conditions, reflecting the extent to which the study's processes are logical, traceable, and well documented (Lincoln & Guba, 1985). To enhance dependability, the analytic process was systematically documented at all stages, including the rationale for methodological decisions, the evolution of codes and themes, and reflections recorded in field notes and the coding journal. NVivo software was used to manage and visualise the developing code structure, while manual approaches such as clustering and mapping with sticky notes

facilitated theme development and conceptual coherence. Regular supervisory input and discussion supported consistency and transparency in analytic decisions, ensuring that interpretations were grounded in the data rather than shaped by isolated researcher assumptions. An excerpt from the coding journal is provided in Appendix I to illustrate an audit trail of how codes were refined and themes conceptualised throughout the analytic process.

Transferability. This refers to the degree to which the findings of qualitative research can be applied or transferred to other contexts or groups, representing the interpretive equivalent of quantitative generalisability (Lincoln & Guba, 1985). In this study, transferability was supported through transparency in methodological reporting, sampling strategy and detailed presentation of the analytic outcomes, enabling readers to assess the applicability of the findings to other settings. Purposive sampling facilitated the inclusion of oncology nurses working across varied roles and practice contexts, thereby generating insights that may resonate with similar professional settings. A comprehensive thematic table outlining each theme, its definition, and illustrative quotes is provided in Appendix H to allow readers to evaluate the coherence and scope of the findings. Rich contextual detail about participants was intentionally limited to protect anonymity, given the small and specialised nature of the participant pool (see Section 4.8.3). While this constrains the use of ‘thick description’ in the traditional sense, the interpretive clarity of the findings and inclusion of verbatim excerpts enable readers to determine the extent to which these findings may resonate with comparable professional contexts.

Confirmability. Confirmability refers to the extent to which the findings of a study are shaped by the participants and the data rather than researcher bias or preconceptions (Lincoln & Guba, 1985). In RTA, confirmability is achieved not through claims of neutrality but, rather, through transparency in the analytic process and reflexive awareness of the researcher’s influence. In this study, confirmability was supported through ongoing reflexive practice and detailed journaling that captured analytic decisions, evolving interpretations, and reflections on positionality. Regular peer debriefing and consultation with the supervisory team provided additional opportunities to interrogate assumptions and enhance the coherence and credibility of interpretations. Reflexive engagement throughout the analytic process helped to mitigate potential bias and ensure that interpretations remained grounded in participants’ accounts.

4.8 Ethical considerations

This study adhered to the ethical principles and standards outlined in the *National Statement on Ethical Conduct in Human Research* (NHMRC, 2018), with particular attention to respect, beneficence, and non-maleficence. Ethical approval for this project was granted by the University of Technology Sydney Human Research Ethics Committee (HREC) [Approval number: ETH22-6852] (see Appendix C), following submission of a detailed application outlining the study's aims, methodology, and ethical safeguards.

4.8.1 Informed consent and participant autonomy

Informed consent was obtained in both phases of the study in accordance with national guidelines (NHMRC, 2018). For Phase 1, consent was implied by completion of the anonymous REDCap survey, which included an embedded Participant Information Statement (PIS) on the opening page (Appendix B). Participants were required to review the PIS before proceeding to the survey questions. For Phase 2, written information was emailed to participants prior to scheduling their telephone interview, and verbal consent was obtained at the beginning of each interview. Participants were also asked to provide verbal consent for audio recording. In both phases, participation was entirely voluntary, and individuals were informed of their right to withdraw at any time without consequence.

Every effort was made to communicate research information using accessible, lay-friendly language appropriate to the target population. This was supported by the researcher's professional experience in health communication and clinical research.

4.8.2 Minimising risk and managing potential distress

The primary inconvenience anticipated for participants was time commitment: approximately 10–15 minutes for the online survey and up to 60 minutes for the optional follow-up interview. To mitigate this, the REDCap platform allowed participants to complete the survey at a time and pace that suited them. Telephone interviews similarly offered convenience and flexibility, with no financial or logistical burden to participants. In addition, this mode of data collection minimised potential risks associated with face-to-face interaction during the COVID-19 pandemic.

Although the research topics were not inherently sensitive, the possibility of distress or fatigue during the interviews was acknowledged. The researcher, a trained counsellor, was prepared to

respond appropriately, and a distress protocol was developed and included in the project's appendix (Appendix J). Participants were advised they could pause or terminate the interview at any time and were provided with contact details for support services such as Lifeline and their workplace Employee Assistance Programs (EAPs). Additional strategies were included to address risks to the researcher as well.

A separate protocol (Appendix K) was established to guide the researcher in the event of incidental disclosure of illegal activity, professional misconduct, or experience of victimisation. Participants were informed in advance about the potential consequences of such disclosures, and this information was communicated in plain language prior to obtaining consent.

4.8.3 Confidentiality and risk of deductive disclosure

Confidentiality was a central ethical consideration in this study, particularly in Phase 2, which involved interviews with nurses working in the highly specialised field of cancer genomics. While all participants were registered nurses working in oncology settings, a small proportion had roles or interests specifically related to genomics. Given the emerging and niche nature of this workforce in Australia, where only a limited number of nurses have formal or informal involvement in genomic practice, the risk of deductive disclosure was deemed significant.

As outlined in Section 2.2 of the *National Statement on Ethical Conduct in Human Research* (NHMRC, 2018), researchers must 'respect the privacy, confidentiality and cultural sensitivities of the participants and communities involved in the research' and take steps to avoid harm that may arise from inadvertent identification. The NHMRC further states in Section 3.1.50 that in qualitative research, researchers must consider whether the use of pseudonyms alone is adequate to protect participant identities in small or specialised populations where indirect identifiers may be easily inferred.

In this context, assigning pseudonyms and including role titles, demographic descriptors, or contextual information in the reporting of interview data was considered ethically inappropriate. Even minimal identifiers such as participant role, organisation type, or location could have allowed others within professional networks to deduce the identity of specific individuals, especially those known to be working in the limited field of genomic nursing. The potential consequences of such identification included reputational harm, professional discomfort, and in some cases, breaches of confidentiality within closely connected clinical settings.

To mitigate these risks, following consultation with the supervisory team and UTS HREC, the decision was made not to attribute interview quotations to individual pseudonyms or to include any potentially identifying descriptors in the reporting of results. While this departs from common practice in qualitative research, the decision reflects a deliberate and ethically defensible strategy grounded in the principle of non-maleficence—that is, the obligation to minimise risk of harm to participants.

Participants were informed of these confidentiality measures in advance, including the rationale for de-identifying data at both the collection and reporting stages. They were also offered the opportunity to review their de-identified transcripts prior to analysis, providing an additional layer of transparency and reinforcing their control over the use of their narrative contributions. Interview transcripts were carefully reviewed and edited to remove indirect identifiers, and no link was retained between participants' contact details and their qualitative data. These strategies were designed not only to ensure anonymity, but also to foster participant trust and protect the professional standing of nurses who may be among a very small number practising in this field.

In line with the NHMRC's emphasis on reflexivity and proportionality in qualitative ethics (NHMRC, 2018, Sections 3.1.16–3.1.19), this decision was not made lightly but was the result of sustained reflection, supervisory consultation, and formal ethical review. While this approach may reduce some contextual richness in the data presentation, it was considered necessary to uphold the ethical responsibilities of privacy, trust, and non-maleficence.

4.9 Data management and storage

All data were managed in accordance with the NHMRC *Australian Code for the Responsible Conduct of Research* and the UTS *Guidelines for the Management of Research Data*. A comprehensive data management plan was created and maintained in 'Stash', the UTS research data management system, which supports compliance with Australian Research Council (ARC) and NHMRC requirements and records essential documentation, including ethical approvals and data licences.

Consistent with this plan, survey data were collected anonymously and stored on the secure, password-protected UTS REDCap server. Interview audio recordings were captured using a password-protected device and securely transferred to a professional transcription service operating under a signed confidentiality agreement. Following transcription, all audio files were

permanently deleted. Transcripts were de-identified during the transcription process, and any residual identifying information was removed during analysis. No linkage files connecting participant contact details to qualitative data were retained.

All electronic research files (survey datasets, de-identified transcripts, codebooks, and analytic documents) were stored on UTS's encrypted cloud storage system with access restricted to members of the research team. In accordance with institutional and national policy, all research data will be securely stored for a minimum of five years following publication, after which they will be permanently destroyed.

4.10 Participant compensation

Participants who completed the optional telephone interview in Phase 2 were offered a movie voucher valued at AU\$25 as a token of appreciation for their time. While participation was entirely voluntary and uncompensated in Phase 1, this small gesture for interviewees in Phase 2 was intended to acknowledge the time and effort involved in contributing to the qualitative component of the study. The value of the voucher was considered reasonably proportionate to the anticipated time commitment (up to 60 minutes) and was benchmarked against the average hourly wage of Registered Nurses in Australia (approximately AU\$33.90 per hour). Importantly, the reimbursement was framed as a gesture of appreciation rather than an inducement, and participants were informed that accepting or declining the voucher would not affect their involvement in the study or the use of their data.

4.11 Conclusion

This chapter detailed the philosophical foundations of the study and its mixed-methods design, outlining the rationale, methodology, sampling strategy, data collection instruments, and analytic procedures for both the quantitative and qualitative phases. Considerations of rigour, ethics, and researcher reflexivity were also addressed. The following chapter presents the quantitative results from Phase 1, examining oncology nurses' knowledge, engagement, and adoption of genomics in clinical practice

Chapter 5 – Quantitative Results

5.1 Introduction

This chapter presents the findings from the quantitative phase (Phase 1) of the study, which examined the current landscape of genomic knowledge, engagement, and adoption among oncology nurses in Australia, as well as the individual characteristics associated with adoption. The results are presented in four sections. First, the sample is characterised in terms of personal and demographic attributes. Second, participants' knowledge, engagement, and adoption of genomics in practice are described. Finally, participants are classified into two groups, *likely adopters* and *likely non-adopters*, based on a median split of a composite adoption score, and inferential analyses are conducted to compare these groups. Finally, a summary of the key quantitative findings is provided to support integration with the qualitative phase in the subsequent chapter.

5.1.1 Reiteration of research questions, aim and objective

The quantitative phase addresses the research question:

How do oncology nurses in Australia engage with genomics, and what individual characteristics and perceived barriers or enablers influence its adoption into practice?

These analyses primarily support Aim 1 and Aim 2 of the study:

1. To assess oncology nurses' knowledge, engagement, and adoption of genomics in practice across Australia.
2. To identify individual characteristics associated with the uptake of genomics in nursing practice.

They also address Objective 2: To assess levels of genomic knowledge, engagement, and adoption among Australian oncology nurses, and explore associations with individual, professional, and demographic characteristics.

Although the main exploration of barriers and enablers (Aim 3) is presented in the qualitative results chapter (Chapter 6), several survey items relating to perceived barriers and enablers are included here to complement those findings and provide quantitative context.

5.1.2 Overview of analyses

A total of 127 surveys were returned between October 2022 and June 2023, distributed via the Cancer Nurses Society of Australia (CNSA), relevant social media channels, and snowball recruitment. Of these, 106 were complete and included in the analyses.

Descriptive statistics were first calculated for the whole sample. For categorical variables, frequencies and percentages were reported. For continuous variables, means and standard deviations were presented. When comparing between adopters and non-adopters, absolute percentage differences with 95% confidence intervals were reported for categorical data, and mean differences with 95% confidence intervals for continuous data. Welch's *t*-tests were used for continuous variables, as it makes less assumptions (equal variance between groups) than a standard *t*-test. For categorical variables, Pearson's chi-square tests were used, with Fisher's exact tests applied when expected cell counts were less than 5.

Where individual items were used to measure latent constructs (e.g., personality traits, opinion leadership), internal consistency was assessed prior to scale construction. Both Cronbach's alpha and McDonald's omega were estimated (with 95% CI), with thresholds of >0.70 interpreted as evidence that the items could be combined into a composite measure.

The statistical approach was exploratory rather than confirmatory. Analyses were not designed to test a single universal null hypothesis but, rather, to identify group differences and associations relevant to adoption of genomics in oncology nursing. Accordingly, no adjustments were made for multiple comparisons. These exploratory results provided essential context for interpreting patterns of adoption and for integrating findings with the qualitative phase.

5.2 Participant characteristics

Based on an estimated CNSA membership of approximately 1,500 nurses at the time of data collection, a target sample size of 306 was calculated using a 95% confidence interval and a 5% margin of error (see Chapter 4.6.4). We received responses from 127 oncology nurses who participated in the survey who met our study inclusion criteria. While the achieved sample was below this target, it nonetheless provided sufficient data for descriptive analyses and for exploratory inferential comparisons between groups. Participant characteristics are summarised in Table 5.1. As one of the study's aims was to compare likely adopters to likely non-adopters, responses that were incomplete for the items used to generate the likely-adopter score were

excluded (see Section 4.6.7.1 for more details on scoring). Twenty-one responses were incomplete, leaving 106 complete cases for analysis. This approach assumes that there were no systematic differences between those missing data and those without missing data (missing completely at random).

Table 5.1 shows most respondents identified as female (93%), and were aged 25–64 years, with similar representation across the 25–34 (27%), 35–44 (22%), 45–54 (20%), and 55–64 (21%) brackets. Smaller proportions were aged 18–24 years (6.6%) or 65 years and older (3.8%). The most frequently reported highest level of academic achievement was a bachelor's degree (37%), followed by a graduate certificate or diploma (31%) and a master's degree (29%). On average, participants reported 18.8 years of nursing experience (SD = 13.5, range 0.17–48.00 years) and 10.2 years in their current role (SD = 9.76, range 0–41 years). The most common grade at which nurses were practising was Registered Nurse (36%), followed by Clinical Nurse Specialist (19%) and Clinical Nurse Consultant (18%). Over half of participants identified as Australian (57%), with 25% identifying as European and smaller proportions across other ethnic groups. In addition, 22% reported having personal or family experience with genetic counselling or genetic testing.

5.3 Descriptive statistics: Aim 1

5.3.1 Perceived knowledge and awareness of genomics

Table 5.2 presents descriptive statistics for items related to perceived knowledge and awareness of genomics. Perceived knowledge and awareness and familiarity with genomic resources and initiatives was generally low across the sample. The majority of nurses reported being not at all familiar with national policy or educational resources, including the Australian College of Nursing (ACN) position statement (62%), the Australian Genomics Health Alliance (73%), state health department strategic plans for genomics (75%), and the Centre for Genetics Education (63%). Notably, 39% of participants reported being not at all familiar with their local specialist genetics service. International nursing organisations were even less well recognised, with 78% reporting no familiarity with the International Society of Nurses in Genetics (ISONG) and 81% with the Global Genomics Nurses Alliance (G2NA). The Human Genome Project was the most widely recognised resource overall, yet 43% of respondents still reported being not at all familiar with it, while 40% indicated at least some familiarity.

Table 5.1. Descriptive information of participants (N=106)

Characteristic	n (%)
Gender	
Female	99 (93%)
Male	7 (6.6%)
Age	
18–24	7 (6.6%)
25–34	29 (27%)
35–44	23 (22%)
45–54	21 (20%)
55–64	22 (21%)
65+	4 (3.8%)
Highest level of academic achievement	
TAFE/vocational training	3 (2.8%)
Bachelors degree	39 (37%)
Graduate certificate/diploma	33 (31%)
Masters degree	31 (29%)
PhD/post-graduate research degree	0 (0%)
Grade currently practicing in	
Registered Nurse (RN)	38 (36%)
Clinical Nurse Specialist (CNS)	20 (19%)
Clinical Nurse Consultant (CNC)	19 (18%)
Clinical Nurse Educator (CNE)	12 (11%)
Nursing Unit Manager (NUM)	5 (4.7%)
Nurse Practitioner (NP)	5 (4.7%)
Other	7 (6.6%)
Time in nursing (years)	Mean: 18.8 SD: 13.5 Range: 0.17–48
Time in role (years)	Mean: 10.20 SD: 9.76 Range: 0.00–41
Ethnic background	Australian: 60 (57%) New Zealander: 4 (3.8%) Asian: 13 (12%) Indian: 2 (1.9%) Middle Eastern: 1 (0.9%) European: 26 (25%) North American: 2 (1.9%) South American: 3 (2.8%) African: 1 (0.9%) Jewish: 1 (0.9%) Other: 4 (3.8%)
Have you or anyone in your family had experience with genetic counselling or genetic testing?	Yes: 23 (22%) No: 83 (78%)

Participants reported varying levels of awareness and engagement with genetic services. Over one-third (36%) were unaware of available services, while almost half (49%) indicated general awareness. Around one-quarter reported having used genetic services themselves (24%) or recommended them to colleagues or patients (26%). Just over one-third (34%) were aware that genetic counsellors work within these services, and 19% reported personally knowing the counsellor at their local service by name.

When asked about their awareness of the impact of genetics and genomics on their own specialty, just over half of participants (55%) agreed or strongly agreed that they had good awareness. Almost one-quarter (23%) neither agreed nor disagreed, while 22.5% reported that they did not feel they had good awareness.

Table 5.2. Perceived knowledge and awareness

Characteristic	N = 106 ¹
Familiarity with these resources:	
The Australian College of Nursing (ACN) 2021 position statement: Nurses, Genomics and Clinical Practice	
Not at all familiar	66/106 (62%)
Slightly familiar	17/106 (16%)
Somewhat familiar	16/106 (15%)
Moderately familiar	6/106 (5.7%)
Extremely familiar	1/106 (0.9%)
The Australian Genomics Health Alliance	
Not at all familiar	77/106 (73%)
Slightly familiar	14/106 (13%)
Somewhat familiar	10/106 (9.4%)
Moderately familiar	5/106 (4.7%)
Extremely familiar	0/106 (0%)
Your states health department strategic plan for genomics (e.g., NSW health)	
Not at all familiar	79/106 (75%)
Slightly familiar	10/106 (9.4%)
Somewhat familiar	10/106 (9.4%)
Moderately familiar	6/106 (5.7%)
Extremely familiar	1/106 (0.9%)
Your local specialist genetics service	
Not at all familiar	41/106 (39%)
Slightly familiar	19/106 (18%)
Somewhat familiar	13/106 (12%)
Moderately familiar	17/106 (16%)
Extremely familiar	16/106 (15%)
Centre for Genetics Education website: www.genetics.edu.au	
Not at all familiar	67/106 (63%)
Slightly familiar	14/106 (13%)
Somewhat familiar	12/106 (11%)
Moderately familiar	8/106 (7.5%)
Extremely familiar	5/106 (4.7%)
Human Genome Project	
Not at all familiar	46/106 (43%)
Slightly familiar	17/106 (16%)
Somewhat familiar	25/106 (24%)
Moderately familiar	17/106 (16%)
Extremely familiar	1/106 (0.9%)
International Society of Nurses in Genetics (ISONG)	
Not at all familiar	83/106 (78%)
Slightly familiar	9/106 (8.5%)
Somewhat familiar	11/106 (10%)
Moderately familiar	3/106 (2.8%)
Extremely familiar	0/106 (0%)
Global Genomics Nurses Alliance (G2NA)	
Not at all familiar	86/106 (81%)
Slightly familiar	9/106 (8.5%)
Somewhat familiar	9/106 (8.5%)
Moderately familiar	2/106 (1.9%)
Extremely familiar	0/106 (0%)
What represents your understanding of genetic services?	
I am unaware of available genetic services	38/106 (36%)
I am aware of genetic services	52/106 (49%)
I know about available genetic services and have used them	25/106 (24%)
I know about these genetic services and have recommended them to colleagues/ patients	28/106 (26%)
I know that genetic counsellors work for genetics services	36/106 (34%)
I have a good awareness of how genetics and genomics impacts my own specialty	
Strongly Disagree	8/106 (7.5%)
Disagree	16/106 (15%)
Neither Agree or Disagree	24/106 (23%)
Agree	39/106 (37%)
Strongly Agree	19/106 (18%)

¹ n/N (%)

5.3.2 Objective knowledge

Objective knowledge of genomics was assessed through items requiring participants to correctly identify genomic applications, essential elements of family history taking, and resources available through local genetic services. These items were designed to measure factual understanding rather than self-reported familiarity or confidence. These findings are shown in Table 5.3.

As illustrated in Figure 5.1, participants were asked to identify which areas of care are linked to genomics. The majority correctly recognised cancer (94%) and ethnic origin (81%) as genomically linked. Around two-thirds identified weight (73%) and blood pressure (68%), while 58% identified cholesterol level. Notably, just over half (57%) identified response to medication, an area of care where genomic influence is well established. In contrast, only small numbers incorrectly selected unrelated options such as appendicitis (8.5%) or blood volume (14%).

When asked which information should be included in a genetic family history for an adult with cancer, most participants identified other cancers in the family (97%), familial medical conditions (94%), inclusion of grandparents (87%), and ages of disease onset (86%) as relevant. Around three-quarters selected exposure to environmental toxins (73%), while just over half included consanguinity, such as partners being blood-related (59%). Fewer participants selected births, pregnancy loss, and deaths (45%). Some respondents also selected items not generally relevant to a genetic family history, including information about the patient's partner's family (22%), whether the patient was treated as a private or public patient (7.5%), and history of road accidents (2.8%).

Participants were asked to identify which resources were available through their local genetic services. Almost three-quarters correctly selected genetic screening (72%), while 63% identified genetic counselling and 60% identified genetic risk assessment. Smaller proportions identified access to research opportunities (24%) and support groups (19%). A minority (7.5%) incorrectly identified pregnancy terminations as being offered by genetic services. Notably, 28% of participants indicated that they did not know what resources were available through their local service.

Table 5.3. Objective knowledge

Characteristic	N = 106 ¹
Which of the following areas of care are linked to genomics:	
People's response to medication	60/106 (57%)
Appendicitis	9/106 (8.5%)
Weight	77/106 (73%)
Blood pressure	72/106 (68%)
Blood volume	15/106 (14%)
Ethnic origin	86/106 (81%)
Cholesterol level	62/106 (58%)
Cancer	100/106 (94%)
What should be included when taking a genetic family history for an Adult with cancer?	
Familial medical conditions	100/106 (94%)
Whether the patient received treatment as a private or public patient	8/106 (7.5%)
Births, pregnancy loss and deaths	48/106 (45%)
Ages of family disease onset	91/106 (86%)
Exposure to environmental toxins	77/106 (73%)
Information about the patient's partners' family	23/106 (22%)
History of road accidents	3/106 (2.8%)
If partners are blood-related in any way (e.g., cousins)	63/106 (59%)
Asking about other cancers in the family	103/106 (97%)
Including grandparents when collecting a family history	92/106 (87%)
What resources are available to you through your local genetic services?	
Genetic screening	76/106 (72%)
Genetic risk assessment	64/106 (60%)
Genetic counselling	67/106 (63%)
Pregnancy terminations	8/106 (7.5%)
Access to support groups	20/106 (19%)
Access to research opportunities	25/106 (24%)
I don't know	30/106 (28%)

¹n/N (%)

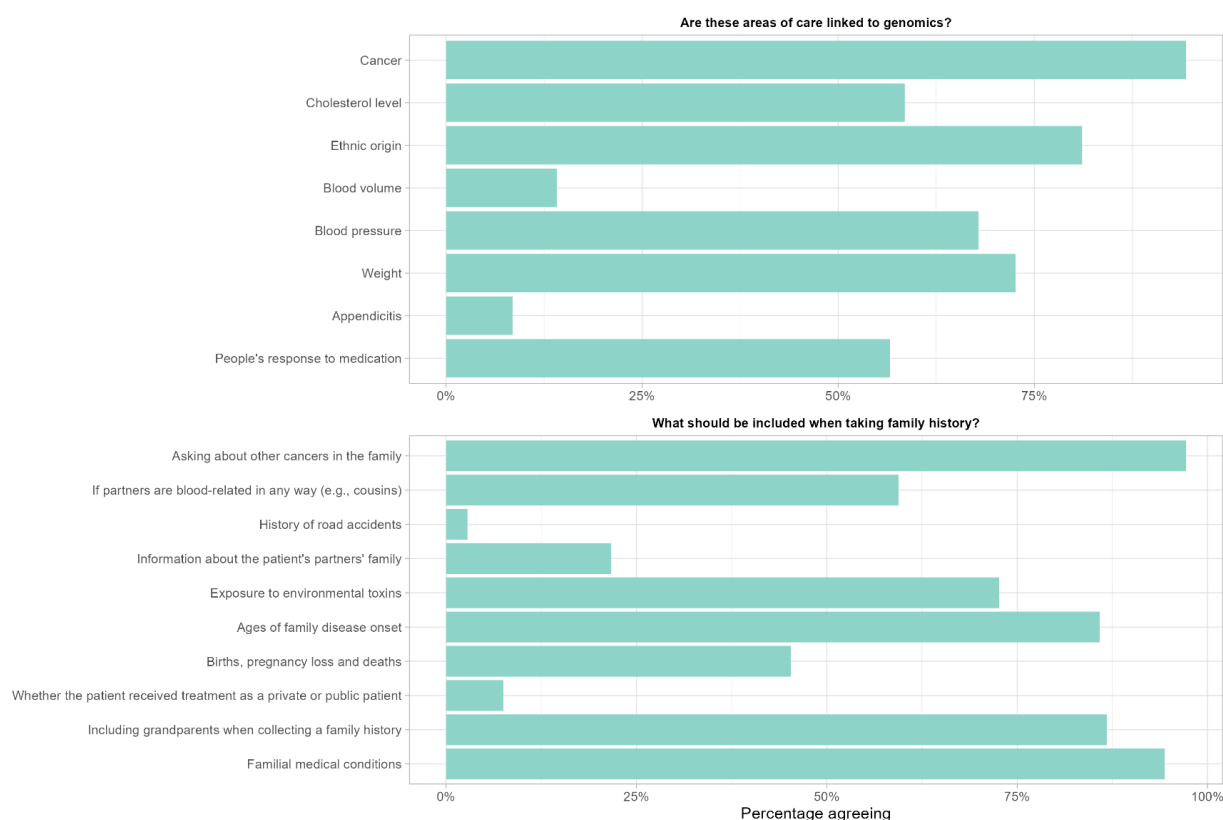


Figure 5.1. Participants' responses to objective knowledge items on genomics-linked care and components of family history taking.

5.3.3 Confidence

This section reports participants' confidence in engaging with genomics in practice, including asking about family history, educating patients, and managing genomically relevant scenarios (see Table 5.4). Overall, levels of confidence were widely distributed across the sample, with relatively few participants reporting high confidence and larger proportions positioned in the lower and middle categories (see Figure 5.2).

Confidence in asking patients about their genetic family history was variable across the sample. One-quarter of participants (25%) reported being not at all confident, while a further 16% felt only slightly confident and 17% somewhat confident. In contrast, 28% indicated they were moderately confident and 14% reported being extremely confident.

In a clinical scenario involving a woman with endometrial cancer and a history of colon polyps, when asked about educating the patient, 26% reported being not at all confident, 17% slightly confident, 25% somewhat confident, 23% moderately confident, and 9.4% extremely confident. Similarly, confidence in managing the scenario was distributed across the lower categories, with 21% not at all confident, 23% slightly confident, 22% somewhat confident, 27% moderately confident, and 7.5% extremely confident.

Table 5.4. Confidence

Characteristic	N = 106 ¹
Feel confident asking patients about their genetic family history	
No at all confident	26/106 (25%)
Slightly confident	17/106 (16%)
Somewhat confident	18/106 (17%)
Moderately confident	30/106 (28%)
Extremely confident	15/106 (14%)
How confident would you feel educating the person in this scenario?	
No at all confident	28/106 (26%)
Slightly confident	18/106 (17%)
Somewhat confident	26/106 (25%)
Moderately confident	24/106 (23%)
Extremely confident	10/106 (9.4%)
How confident would you feel managing this scenario in practice?	
No at all confident	22/106 (21%)
Slightly confident	24/106 (23%)
Somewhat confident	23/106 (22%)
Moderately confident	29/106 (27%)
Extremely confident	8/106 (7.5%)

¹n/N (%)

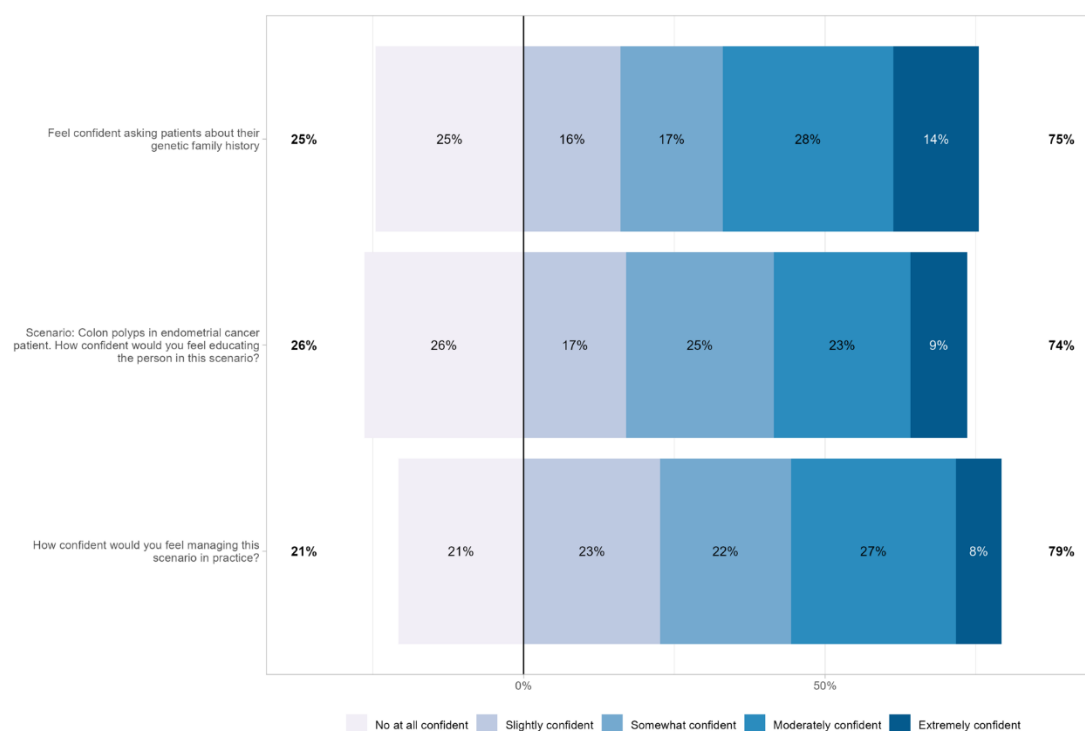


Figure 5.2. Participants' Likert-scale confidence ratings for family history taking and genomics-related clinical scenarios.

5.3.4 Attitudes

Attitudinal variables were assessed through items examining participants' views on the role of genomics in nursing practice, the importance of professional development, and the perceived relevance of genomics to patient care. Responses also explored interest in expanding genomics within everyday practice and openness to new areas of genomic knowledge. Overall, participants generally expressed supportive attitudes toward the inclusion of genomics in oncology nursing, although levels of certainty and confidence varied across specific domains (see Table 5.5).

In response to a number of genomic nursing statements, most participants recognised family history as an important aspect of their nursing role, with 63% agreeing or strongly agreeing with this statement. Around one-quarter (24.9%) disagreed, and a further 12% were neutral.

The majority of participants supported the need for continual professional development (CPD) in genetics and genomics for nurses, with 69% agreeing or strongly agreeing that such training should be encouraged. Around one-quarter (26%) were neutral, while only 4.7% disagreed.

Most participants rejected the notion that genomics offers only limited potential to improve health outcomes across patient groups, with 60% disagreeing or strongly disagreeing with this statement. One-quarter (25%) were neutral, while a minority (15.1%) agreed or strongly agreed.

In a clinical scenario involving a woman with endometrial cancer and a history of colon polyps, most participants rated taking a family history as extremely important (60%), with a further 19% rating it as moderately important (Table 5.4). Confidence in responding to this scenario was lower.

Most participants considered the application of genomics to be highly relevant to their patient group. Nearly two-thirds (64%) rated genomics as extremely relevant, with a further 20% rating it as moderately relevant. Smaller proportions reported it as somewhat relevant (11%) or slightly relevant (4.7%), and no participants indicated that genomics was not at all relevant.

When asked whether they would like to incorporate more genetics or genomics into their everyday practice, almost half of participants (48%) responded ‘possibly’. A further 41% expressed a clear intention to do so, with 18% indicating ‘probably’ and 23% ‘definitely’. By contrast, 11% reported ‘probably not,’ and no participants selected ‘definitely not’.

Most participants expressed an interest in new areas of genetic and genomic knowledge within their practice. Over half (52%) reported being moderately or extremely interested, while 32% indicated they were somewhat interested. A minority expressed limited interest, with 14% slightly interested and 1.9% not at all interested.

Table 5.5. Attitudes

Characteristic	N = 106 ¹
Taking a patient’s FAMILY HISTORY is an important aspect of my role	
Strongly Disagree	1/106 (0.9%)
Disagree	25/106 (24%)
Neither Agree or Disagree	13/106 (12%)
Agree	34/106 (32%)
Strongly Agree	33/106 (31%)
Continual professional development in genetics and genomics should be encouraged for all nurses	
Strongly Disagree	0/106 (0%)
Disagree	5/106 (4.7%)
Neither Agree or Disagree	28/106 (26%)
Agree	50/106 (47%)
Strongly Agree	23/106 (22%)
Developments in genomics offer limited potential to improve health outcomes for all patient groups	
Strongly Disagree	23/106 (22%)
Disagree	40/106 (38%)
Neither Agree or Disagree	27/106 (25%)
Agree	6/106 (5.7%)
Strongly Agree	10/106 (9.4%)
Scenario: endometrial cancer	
How important would it be in this situation to take a family history ?	
Not at all important	3/106 (2.8%)
Slightly important	5/106 (4.7%)
Somewhat important	14/106 (13%)

Characteristic	N = 106 ¹
Moderately important	20/106 (19%)
Extremely important	64/106 (60%)
Do you think that the application of genomics is relevant to your patient group?	
Not at all relevant	0/106 (0%)
Slightly relevant	5/106 (4.7%)
Somewhat relevant	12/106 (11%)
Moderately relevant	21/106 (20%)
Extremely relevant	68/106 (64%)
Would you like to incorporate more genetics/genomics as part of your everyday practice?	
Definitely not	0/106 (0%)
Probably not	12/106 (11%)
Possibly	51/106 (48%)
Probably	19/106 (18%)
Definitely	24/106 (23%)
Are you interested in new areas of genetic and genomic knowledge within your practice?	
Not at all interested	2/106 (1.9%)
Slightly interested	15/106 (14%)
Somewhat interested	34/106 (32%)
Moderately interested	24/106 (23%)
Extremely interested	31/106 (29%)

¹n/N (%)

5.3.5 Engagement and adoption

Engagement and adoption behaviours were assessed through survey items capturing participants' practical involvement with genomics, including referral activity, professional discussions with colleagues, and seeking genetic information for themselves, patients, or others. These findings are presented in Table 5.6. Overall, reported engagement in these activities was relatively limited, with most participants indicating few or no recent referrals, infrequent discussion with colleagues, and mixed patterns of information-seeking.

When asked how many times they had referred a patient to genetic services in the past month, most participants (76%) reported no referrals. One-fifth (20%) reported making between one and ten referrals, while 3.8% indicated more than ten referrals.

Most participants reported that they did not regularly discuss genetics or genomics with colleagues. One-third (33%) indicated they never did so and a further 25% said rarely. Around one-quarter (24%) reported sometimes discussing genetics or genomics with colleagues, while 16% said they often did and only 1.9% reported always doing so.

Participants were asked whether they had ever sought genetic information for different purposes. The most common response was on behalf of a client or patient's family (42%), followed by seeking information for their own family (30%) or themselves (23%). Smaller

proportions reported doing so for a colleague (12%) or a friend (9.4%). Notably, 41% indicated that they had never sought genetic information.

Table 5.6. Engagement and adoption

Characteristic	N = 106 ¹
In the last month, how many times have you referred a patient to genetic services?	
0 times	81/106 (76%)
1–10 times	21/106 (20%)
>10 times	4/106 (3.8%)
How often do you speak to your colleagues about genetics/genomics?	
Never	35/106 (33%)
Rarely	27/106 (25%)
Sometimes	25/106 (24%)
Often	17/106 (16%)
Always	2/106 (1.9%)
Have you ever sought genetic information for:	
Self	24/106 (23%)
Family	32/106 (30%)
Client / patients family	44/106 (42%)
For a colleague	13/106 (12%)
Friend	10/106 (9.4%)
I have never sought genetic information	43/106 (41%)
Other	2/106 (1.9%)

¹n/N (%)

5.3.6 Barriers and enablers

Barriers and enablers to the uptake of genomics in nursing practice were explored through several survey items and are presented in Table 5.7. Barriers were assessed in relation to referral activity, perceived obstacles to using genomics more broadly, and the perceived difficulty of undertaking genomics-related actions in practice. Enablers were assessed by asking participants to identify interventions or sources of support that encouraged them to incorporate new areas of knowledge into their work. Overall, participants reported a range of barriers, including lack of confidence, resources, and time, while study days, peers, and professional support were most frequently cited as enablers.

Among participants who had not referred a patient to genetic services in the past month, several barriers were identified. The most frequently reported reasons were not recognising when referral would be appropriate (32%) and perceiving it as not relevant to their practice (30%). One-fifth indicated that they had never encountered an individual requiring referral (20%). Other barriers included a lack of resources to make referrals (22%) and lack of organisational support (15%).

Participants were asked which issues or problems prevented them from using genomics more in their nursing role, with multiple responses permitted. The most frequently reported barriers were time constraints (41%), the perception that using genomics was not their decision to make (32%), and the view that it was the doctors' job (31%). Almost one-third also reported a lack of understanding of genomics (30%). Additional barriers included patients not raising the topic (25%), lack of relevant resources (26%), and absence of local study sessions (21%). Less frequently reported barriers included perceptions that genomics was not relevant (3.8%), lack of support from a manager (2.8%), dislike of science (2.8%), and lack of support from colleagues (1.9%).

Participants were asked to rate how difficult it would be to achieve several actions relating to genomics in practice. Attending study days or courses on genomics was most commonly reported as difficult or very difficult (54%), with only 17.8% describing this as easy. In contrast, applying new knowledge into practice was largely seen as achievable, with 62% rating it as easy or very easy, while 7.5% described it as difficult. Requesting access to new resources from senior management was reported as easy or very easy by 46.6% of participants, while 18.8% described it as difficult. Talking to colleagues about genomics was rated as easy or very easy by 36.5% of participants, though one-quarter (25%) found this difficult. Seeking support from senior nurses and management was the most challenging, with 40% reporting difficulty and only 21.7% reporting ease.

Participants were asked to identify enablers that encouraged them to incorporate new areas of knowledge into their practice, with multiple responses permitted. The most frequently reported enabler was attending study days (71%), followed by peers (60%) and short presentations such as lunchtime in-services (60%). Other health professionals (54%) and heads of department (51%) were also commonly selected. Less frequently reported enablers included contacts with specific professional services (44%), patients (44%), case studies (35%), and having a mentor (30%).

Table 5.7. Barriers and enablers

Characteristic	N = 106 ¹
Reason haven't referred a patient	
I have never encountered an individual who should be referred	16/81 (20%)
Not relevant to my practice	24/81 (30%)
I would not recognise when this was appropriate	26/81 (32%)
I do not have the resources to do this	18/81 (22%)
I do not have the support of my organisation to do this	12/81 (15%)
Other	16/81 (20%)
Which issues/problems prevent you from using genomics more in your nursing role	

Characteristic	N = 106 ¹
Genomics is not relevant	4/106 (3.8%)
I don't understand genomics	32/106 (30%)
My colleagues don't support my interests	2/106 (1.9%)
There are no relevant resources to help me learn	28/106 (26%)
There are too many time constraints	43/106 (41%)
My boss doesn't think it's important	3/106 (2.8%)
I don't like science	3/106 (2.8%)
There are no local study sessions	22/106 (21%)
It's the doctor's job	33/106 (31%)
Patients never talk to me about genomics	26/106 (25%)
It isn't my decision	34/106 (32%)
Other	28/106 (26%)
How difficult is it for you to achieve the following actions:	
Attend study days/courses that include genomics in practice	
Very difficult	29/106 (27%)
Difficult	29/106 (27%)
Neutral	29/106 (27%)
Easy	15/106 (14%)
Very easy	4/106 (3.8%)
Apply new knowledge into your nursing practice	
Very difficult	1/106 (0.9%)
Difficult	7/106 (6.6%)
Neutral	33/106 (31%)
Easy	55/106 (52%)
Very easy	10/106 (9.4%)
Request access from senior management to new resources	
Very difficult	4/106 (3.8%)
Difficult	16/106 (15%)
Neutral	37/106 (35%)
Easy	42/106 (40%)
Very easy	7/106 (6.6%)
Talk to colleagues about genomics	
Very difficult	14/106 (13%)
Difficult	13/106 (12%)
Neutral	40/106 (38%)
Easy	31/106 (29%)
Very easy	8/106 (7.5%)
Seek support from senior nurses and management to include genomics in your role	
Very difficult	16/106 (15%)
Difficult	27/106 (25%)
Neutral	40/106 (38%)
Easy	17/106 (16%)
Very easy	6/106 (5.7%)
Do these interventions/people encourage you to incorporate new areas of knowledge into your practice?	
Peers	64/106 (60%)
Heads of department	54/106 (51%)
Contacts with specific professional services	47/106 (44%)
Other health professionals	57/106 (54%)
Attending study days	75/106 (71%)
Having a mentor	32/106 (30%)
Case studies	37/106 (35%)
Attending short presentations (e.g. lunchtime in-service)	64/106 (60%)
Patients	47/106 (44%)

¹n/N (%)

5.3.7 Cosmopolitanism and information-seeking behaviours

Participants were also asked about the sources of information they use to inform their practice, including research articles, conferences, CPD, scholarly databases, and internet searches (Table 5.8). These items provide an indication of the types of knowledge resources nurses draw on in their everyday work.

As illustrated in Figure 5.3, participants reported drawing on a range of sources to inform their practice. Over half indicated that they often or always used research articles (53.5%) and conference information (54.4%), while the majority (72%) reported using CPD to guide practice decisions. Use of scholarly database searches was more variable, with 41% reporting frequent use and 26% reporting rare or no use. Internet sources such as Google were used less consistently than other resources. Around two-thirds of participants reported using them rarely or sometimes (67%), while one-quarter reported frequent use (often or always, 24.8%), and 8.5% reported never using them.

Table 5.8. Cosmopolitanism and information seeking behaviours

Characteristic	N = 106 ¹
I use research articles for information to make practice decisions	
Never	7/106 (6.6%)
Rarely	11/106 (10%)
Sometimes	31/106 (29%)
Often	48/106 (45%)
Always	9/106 (8.5%)
I use information I learn from conferences to guide my practice	
Never	14/106 (13%)
Rarely	5/106 (4.7%)
Sometimes	29/106 (27%)
Often	48/106 (45%)
Always	10/106 (9.4%)
I use information learnt from continuing professional development (CPD) to make practice decisions	
Never	1/106 (0.9%)
Rarely	5/106 (4.7%)
Sometimes	24/106 (23%)
Often	60/106 (57%)
Always	16/106 (15%)
I use scholarly database searches for information to make practice decisions	
Never	13/106 (12%)
Rarely	15/106 (14%)
Sometimes	34/106 (32%)
Often	33/106 (31%)
Always	11/106 (10%)
I use internet sources (e.g., google search) for information to make practice decisions	
Never	9/106 (8.5%)
Rarely	36/106 (34%)
Sometimes	35/106 (33%)
Often	22/106 (21%)
Always	4/106 (3.8%)

¹n/N (%)

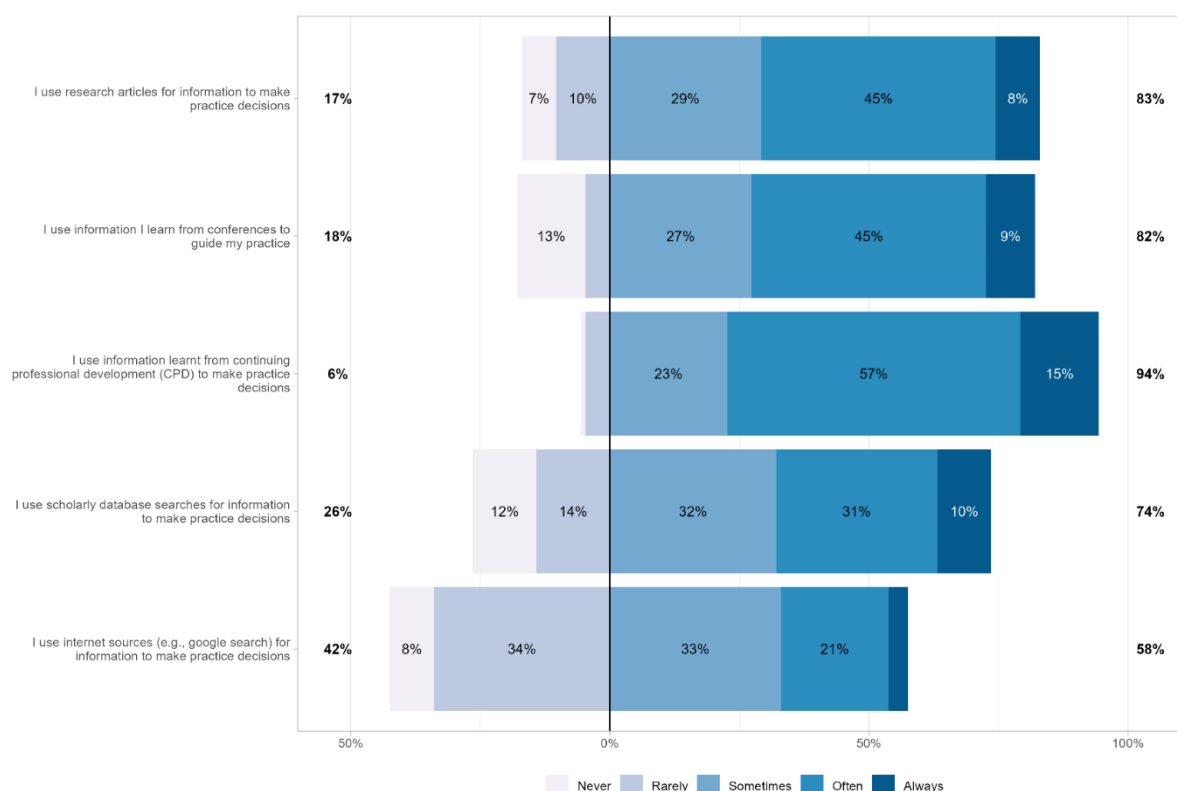


Figure 5.3. Participants' Likert-scale responses on cosmopolitanism and information-seeking behaviours.

5.4 Aim 2: Distinguishing likely adopters from likely non-adopters

A composite adopter score was developed to differentiate between oncology nurses more or less likely to integrate genomics into their practice. The score was based on 14 survey components (see Section 4.6.7.1) as summarised in Table 5.9. Each item was coded according to predefined criteria (e.g., correct responses, agreement thresholds, or demonstration of relevant behaviours). The scoring framework drew on the original cut-off approach described by Andrews et al. (2014b) but was revised following discussion with the supervisory team to reflect the Australian oncology nursing context and contemporary indicators of genomic adoption (see Table 4.3). This represents a novel contribution of the study, extending prior instruments to create a context-sensitive measure of adoption.

Table 5.9. Summary of components of the adopter score

Characteristic	N = 106 ¹
Q1 component - Openness to experience	15 (14%)
Q3 component - Familiarity w/ initiatives/resources	2 (1.9%)
Q4 component - Attitudes to genomic nursing statements	8 (7.5%)
Q5 component - Scenario	30 (28%)
Q6 component - Relevance of application	89 (84%)
Q7 component - Areas of care linked to genetics	19 (18%)
Q8 component - Confidence taking Family History	45 (42%)

Q9 component - Knowledge needed for Family History	57 (54%)
Q10 component - Awareness of genetic services	101 (95%)
Q11 component - Resources available through services	55 (52%)
Q19 component - Talking to colleagues about genetics/genomics	44 (42%)
Q20 component - Intent to incorporate into practice	43 (41%)
Q21 component - Interest in new areas of genetics/genomic knowledge	55 (52%)
Q22 component - Sought genetic/genomic information	33 (31%)

¹n (%)

Adopter scores ranged from 0 to 14, with a mean of 5.6, standard deviation 2.7, and a median of 6. The distribution appeared bimodal, but there was no obvious cut-off point between adopter types (Figure 5.4). Participants were divided into two groups using a median split: those above the median were classified as ‘likely adopters,’ and those below the median as ‘likely non-adopters.’ This approach provided balanced group sizes ([n = 54] adopters, [n = 52] non-adopters) and allowed for inferential comparisons in subsequent analyses.

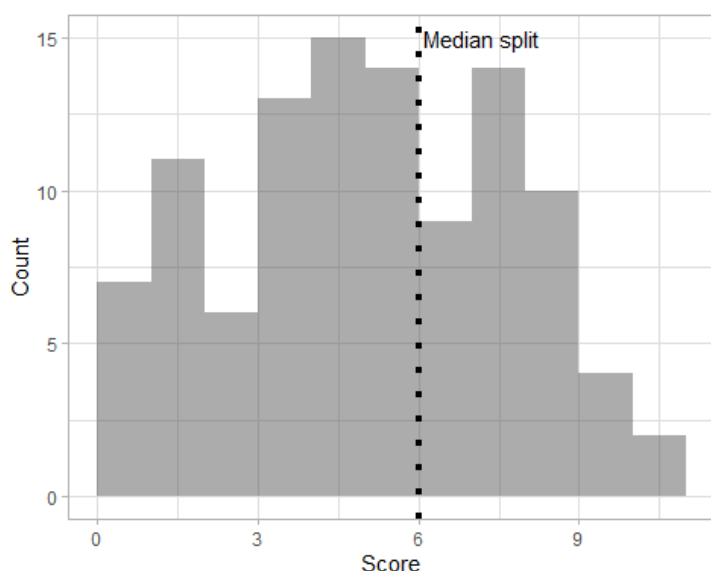


Figure 5.4. Distribution of adopter score.

5.4.1 Inferential statistics

5.4.1.1 Demographic and professional variables

Group comparisons revealed statistically significant demographic and professional differences between likely adopters and likely non-adopters (Table 5.10). Likely adopters had significantly more years of nursing experience ($M = 24.1$) than likely non-adopters ($M = 13.4$ years; mean difference = -11 , 95% CI [-11 , -5.9]) with good evidence of a difference (Welch’s t -test, $p < .001$). There was good evidence that age group distributions differed significantly between adopters and non-adopters ($p = .002$), with non-adopters more concentrated in younger

brackets, particularly 25–34 years (37% vs 19%), while adopters were more frequently represented in older groups, including 55–64 years (31% vs 9.6%).

Grade of practice distributions differed significantly between groups ($p < .001$). Likely non-adopters were more frequently practising as Registered Nurses (52% vs 20%), while likely adopters were more often working in advanced practice roles, including Clinical Nurse Consultants (30% vs 5.8%) and Clinical Nurse Specialists (24% vs 13%). Highest level of academic achievement also differed significantly between groups ($p = .033$). Non-adopters were more likely to report a bachelor's degree as their highest qualification (50% vs 24%), whereas adopters were more likely to hold a master's degree (37% vs 21%). Graduate certificate or diploma attainment was also more common among adopters (35% vs 27%).

No significant differences were observed between groups by gender ($p > .99$). The sample overall was predominantly female (94%), with similar proportions across both groups. While a higher proportion of adopters reported personal or family experience of genetic counselling or testing compared to non-adopters (30% vs 13%), there was no evidence for this difference ($p = .075$).

Table 5.10. Demographics and work experience of participants

Characteristic	Overall	Non-adopter	Adopter	Difference ³	95% CI ³	p-value ³
	N = 106 ¹	N = 52 ²	N = 54 ²			
Time in nursing (years)	18.8 (13.5)	13.4	24.1	−11	−11, −5.9	<0.001
Time in role (years)	10.2 (9.5)	7.6	12.7	−5.0	−5.0, −1.5	0.006
Personal or family experience of genetic counselling	23 (22%)	7/52 (13%)	16/54 (30%)	−16%	−16%, 1.0%	0.075
Grade of practice						<0.001
Registered Nurse (RN)	38 (36%)	27/52 (52%)	11/54 (20%)			
Clinical Nurse Specialist (CNS)	20 (19%)	7/52 (13%)	13/54 (24%)			
Clinical Nurse Consultant (CNC)	19 (18%)	3/52 (5.8%)	16/54 (30%)			
Clinical Nurse Educator (CNE)	12 (11%)	9/52 (17%)	3/54 (5.6%)			
Nursing Unit Manager (NUM)	5 (4.7%)	3/52 (5.8%)	2/54 (3.7%)			
Nurse Practitioner (NP)	5 (4.7%)	1/52 (1.9%)	4/54 (7.4%)			
Other	7 (6.6%)	2/52 (3.8%)	5/54 (9.3%)			
Highest level of academic achievement						0.033
TAFE/vocational training	3 (2.8%)	1/52 (1.9%)	2/54 (3.7%)			
Bachelors degree	39 (37%)	26/52 (50%)	13/54 (24%)			
Graduate certificate/diploma	33 (31%)	14/52 (27%)	19/54 (35%)			
Masters degree	31 (29%)	11/52 (21%)	20/54 (37%)			
PhD/post-graduate research degree	0 (0%)	0/52 (0%)	0/54 (0%)			
Age (years)						0.002
18 - 24	7 (6.6%)	7/52 (13%)	0/54 (0%)			
25 - 34	29 (27%)	19/52 (37%)	10/54 (19%)			
35 - 44	23 (22%)	10/52 (19%)	13/54 (24%)			
45 - 54	21 (20%)	10/52 (19%)	11/54 (20%)			
55 - 64	22 (21%)	5/52 (9.6%)	17/54 (31%)			
65+	4 (3.8%)	1/52 (1.9%)	3/54 (5.6%)			
Gender						>0.99
Female	99 (93%)	49/52 (94%)	50/54 (93%)			
Male	7 (6.6%)	3/52 (5.8%)	4/54 (7.4%)			
Ethnic background						
Australian	60 (57%)	24/52 (46%)	36/54 (67%)			
Indigenous Australian or Torres Strait Islander	0 (0%)	0/52 (0%)	0/54 (0%)			
New Zealander	4 (3.8%)	3/52 (5.8%)	1/54 (1.9%)			

Characteristic	Overall	Non-adopter	Adopter	Difference ³	95% CI ³	p-value ³
	N = 106 ¹	N = 52 ²	N = 54 ²			
Asian	13 (12%)	8/52 (15%)	5/54 (9.3%)			
Indian	2 (1.9%)	2/52 (3.8%)	0/54 (0%)			
Middle Eastern	1 (0.9%)	0/52 (0%)	1/54 (1.9%)			
European	26 (25%)	13/52 (25%)	13/54 (24%)			
Caribbean	0 (0%)	0/52 (0%)	0/54 (0%)			
North American	2 (1.9%)	0/52 (0%)	2/54 (3.7%)			
South American	3 (2.8%)	1/52 (1.9%)	2/54 (3.7%)			
African	1 (0.9%)	1/52 (1.9%)	0/54 (0%)			
Jewish	1 (0.9%)	1/52 (1.9%)	0/54 (0%)			
Decline to answer	0 (0%)	0/52 (0%)	0/54 (0%)			
Other	4 (3.8%)	3/52 (5.8%)	1/54 (1.9%)			

¹Mean (SD); n (%)

²Mean; n/N (%)

³Welch Two Sample *t*-test; 2-sample test for equality of proportions with continuity correction

Abbreviation: CI = Confidence Interval

5.4.1.2 Personality traits

As illustrated in Figure 5.5, openness to experience and opinion leadership showed more density at higher score levels in adopters, while the density of perceived influence over others was very similar between likely adopters and non-adopters.

Openness to Experience scale.

As per Table 5.11, openness to experience was assessed using the 10-item subscale of the Big Five Inventory (John et al., 1991, 2008). Items were rated on a five-point Likert scale (1 = strongly disagree to 5 = strongly agree), with two items reverse-scored. Higher scores reflected greater openness to experience. Internal consistency for the scale was acceptable, with McDonald's omega of 0.78 (95% CI [0.70–0.85]) and Cronbach's alpha of 0.75 (95% CI [0.67–0.81]).

Mean openness scores differed significantly between groups ($p = .003$). Likely adopters had a higher mean score ($M = 37.7$, $SD = 5.5$) compared with non-adopters ($M = 34.2$, $SD = 5.7$). This difference of 3.5 points (95% CI [1.2–5.7]) suggests that adopters tended to report greater openness to experience than non-adopters.

5.4.1.3 Opinion Leadership

Opinion leadership was assessed using two complementary measures:

Perceived influence (Personality Strength scale). Perceived influence over others was measured with the 10-item Personality Strength scale (Noelle-Neumann, 1983, 1985; Weimann, 2007). Each Yes/No response was scored with item-specific weights (Yes = 12–18; No = 6–9), summed to yield a total PS score ranging from 75 to 149, with higher scores

indicating greater perceived influence. Internal consistency was acceptable (McDonald's $\omega = 0.77$, 95% CI [0.71–0.84]); Cronbach's $\alpha = 0.76$, 95% CI [0.69–0.82]). Mean scores did not differ significantly between groups, with adopters ($M = 119$) and non-adopters ($M = 118$) reporting very similar levels of perceived influence ($p = .85$) (see Table 5.11).

Opinion Leadership scale.

Opinion leadership was also assessed using four items adapted from Grimshaw et al. (2006), rated on a 5-point Likert scale (Never–Always) and summed to give a total score (range 4–20). Reliability for this scale was excellent (McDonald's $\omega = 0.90$, 95% CI [0.87–0.93]; Cronbach's $\alpha = 0.89$, 95% CI [0.86–0.92]). Adopters reported significantly higher mean scores than non-adopters ($M = 14.8$ vs. 11.8 , $p < .001$) (see Table 5.11).

Following Andrews' (2014a) approach, overall opinion leadership scores were combined and a fixed cut-off of 16–20 was used to classify participants as opinion leaders. Using this criterion, 34% of the total sample were identified as opinion leaders. Adopters were significantly more likely than non-adopters to be classified in this way ($p < .001$). Within the adopter group, participants were evenly divided, with half scoring above the cut-off and half below, compared with only 17% of non-adopters exceeding the cut-off.

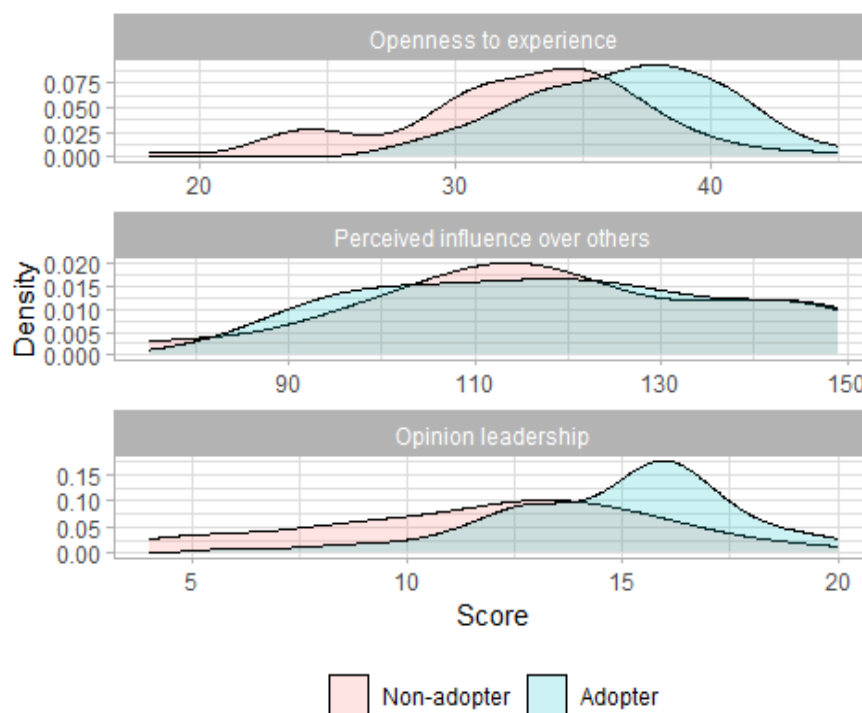


Figure 5.5. Distribution of personality scores in likely non-adopters and likely adopters.

Table 5.11. Personality traits

Characteristic	Overall	Non-adopter	Adopter	Difference ³	95% CI ³	p-value ³
	N = 106 ¹	N = 52 ²	N = 54 ²			
Openness to experience	34.6 (4.9)	32.5	36.7	-4.2	-5.9, -2.4	<0.001
Perceived influence over others	118.7 (19.4)	118	119	-0.71	-8.2, 6.8	0.85
Opinion leadership	13.3 (3.7)	11.8	14.8	-3.0	-4.3, -1.7	<0.001
Opinion leader (≥ 16)						<0.001
Not opinion leader	70/106 (66%)	43/52 (83%)	27/54 (50%)			
Opinion leader	36/106 (34%)	9/52 (17%)	27/54 (50%)			
I use research articles for information to make practice decisions						<0.001
Never	7/106 (6.6%)	7/52 (13%)	0/54 (0%)			
Rarely	11/106 (10%)	8/52 (15%)	3/54 (5.6%)			
Sometimes	31/106 (29%)	20/52 (38%)	11/54 (20%)			
Often	48/106 (45%)	15/52 (29%)	33/54 (61%)			
Always	9/106 (8.5%)	2/52 (3.8%)	7/54 (13%)			
I use information I learn from conferences to guide my practice						0.003
Never	14/106 (13%)	12/52 (23%)	2/54 (3.7%)			
Rarely	5/106 (4.7%)	4/52 (7.7%)	1/54 (1.9%)			
Sometimes	29/106 (27%)	16/52 (31%)	13/54 (24%)			
Often	48/106 (45%)	16/52 (31%)	32/54 (59%)			
Always	10/106 (9.4%)	4/52 (7.7%)	6/54 (11%)			
I use information learnt from continuing professional development (CPD) to make practice decisions						0.024
Never	1/106 (0.9%)	1/52 (1.9%)	0/54 (0%)			
Rarely	5/106 (4.7%)	5/52 (9.6%)	0/54 (0%)			
Sometimes	24/106 (23%)	15/52 (29%)	9/54 (17%)			
Often	60/106 (57%)	24/52 (46%)	36/54 (67%)			
Always	16/106 (15%)	7/52 (13%)	9/54 (17%)			
I use scholarly database searches for information to make practice decisions						0.009
Never	13/106 (12%)	10/52 (19%)	3/54 (5.6%)			
Rarely	15/106 (14%)	12/52 (23%)	3/54 (5.6%)			
Sometimes	34/106 (32%)	14/52 (27%)	20/54 (37%)			
Often	33/106 (31%)	12/52 (23%)	21/54 (39%)			
Always	11/106 (10%)	4/52 (7.7%)	7/54 (13%)			
I use internet sources (e.g., google search) for information to make practice decisions						0.87
Never	9/106 (8.5%)	5/52 (9.6%)	4/54 (7.4%)			
Rarely	36/106 (34%)	19/52 (37%)	17/54 (31%)			
Sometimes	35/106 (33%)	16/52 (31%)	19/54 (35%)			
Often	22/106 (21%)	11/52 (21%)	11/54 (20%)			
Always	4/106 (3.8%)	1/52 (1.9%)	3/54 (5.6%)			

¹Mean (SD)²Mean³Welch Two Sample *t*-test

Abbreviation: CI = Confidence Interval

5.4.1.4 Cosmopolitanness and information-seeking behaviour

Group comparisons revealed significant differences on four of the five information-seeking items (Table 5.11). There was good evidence that compared with non-adopters, a greater proportion of likely adopters reported frequent use ('often' or 'always') of research articles (74% vs 32.8%, $p < .001$), conferences (70% vs 38.7%, $p = .003$), and reasonable evidence of a difference in reporting continuing professional development (CPD) activities (84% vs 59%, $p = .024$), and scholarly database searches (52% vs 30.7%, $p = .009$). In contrast, there was no significant group difference in the use of internet sources such as Google ($p = .87$), with both adopters and non-adopters most often reporting 'sometimes' or 'rarely'.

5.4.1.5 Barriers and enablers

Referral activity differed significantly between groups (Fisher's exact test, $p < .001$). The majority of non-adopters (96%) reported no referrals in the past month, compared with 57% of adopters. In contrast, 37% of adopters reported 1–10 referrals, compared with only 1.9% of non-adopters. A further 5.6% of adopters reported more than ten referrals, compared with 1.9% of non-adopters (see Table 5.12). Among participants who had not referred a patient to genetic services in the past month, reported barriers varied between groups. There was some evidence that non-adopters were more likely than adopters to report that they would not recognise when referral was appropriate (42% vs 16%; Fisher's exact test, $p = .029$; difference = 26%, 95% CI [4.4%, 47%]). A greater proportion of adopters reported never having encountered an individual requiring referral (32% vs 12%), although this difference was only marginally non-significant ($p = .053$; difference = -20%, 95% CI [-42%, 1.1%]). Other reported reasons, including lack of resources, lack of organisational support, and perceptions that referral was not relevant to practice, did not differ significantly between groups (see Table 5.12). Non-adopters were more likely than adopters to report not understanding genomics (52% vs 9.3%; Fisher's exact test, $p < .001$; difference = 43%, 95% CI [25%, 60%]). They were also more likely to report the barrier that genomics was primarily the doctor's responsibility (44% vs 19%; $p = .008$; difference = 26%, 95% CI [6.8%, 45%]).

Other reported barriers, including time constraints (42% vs 39%), perceptions that decisions about genomics were not theirs to make (35% vs 30%), lack of relevant resources (33% vs 20%), absence of local study sessions (17% vs 24%), and patients not raising the topic (29% vs 20%), were not statistically significant (all $p > .05$). Less frequently endorsed barriers such as lack of support from colleagues or managers, perceptions of irrelevance, or dislike of science also did not differ between groups.

Perceived difficulty in genomics-related activities differed between adopters and non-adopters. There was good evidence that adopters were more likely to describe applying new knowledge in practice as easy or very easy compared with non-adopters (74% vs 47.9%; $p < .001$). Talking to colleagues about genomics also showed group differences, with nearly 59% of adopters rating this as easy or very easy compared with only 13.4% of non-adopters ($p < .001$). Adopters additionally reported greater ease in seeking support from senior nurses and management (52% vs 30%; $p = .031$). In contrast, there were no significant group differences in the perceived

difficulty of attending study days or requesting access to new resources, with both adopters and non-adopters reporting a mix of neutral and moderately difficult responses.

Enabling factors for incorporating new knowledge into practice differed across groups. Adopters were significantly more likely than non-adopters to identify contacts with specific professional services (57% vs 31%; $p = .010$; difference = -27% , 95% CI $[-47\%, -6.5\%]$) and other health professionals (69% vs 38%; $p = .004$; difference = -30% , 95% CI $[-50\%, -10\%]$) as enablers. They were also more likely to select case studies (46% vs 23%; $p = .021$; difference = -23% , 95% CI $[-43\%, -3.8\%]$) and patients (61% vs 27%; $p < .001$; difference = -34% , 95% CI $[-54\%, -15\%]$) as encouraging them to incorporate new knowledge. Other potential enablers, such as peers, heads of department, attending study days, having a mentor, and short presentations, did not differ significantly between groups.

Table 5.12. Stages of adoption, barriers and enablers

Characteristic	Overall N = 106 ¹	Non-adopter N = 52 ¹	Adopter N = 54 ¹	p- value ²	Difference ³	95% CI ³
In the last month, how many times have you referred a patient to genetic services?				<0.001		
0 times	81/106 (76%)	50/52 (96%)	31/54 (57%)			
1-10 times	21/106 (20%)	1/52 (1.9%)	20/54 (37%)			
>10 times	4/106 (3.8%)	1/52 (1.9%)	3/54 (5.6%)			
Reason haven't referred a patient						
I have never encountered an individual who should be referred	16/81 (20%)	6/50 (12%)	10/31 (32%)	0.053	-20%	-42%, 1.1%
Not relevant to my practice	24/81 (30%)	17/50 (34%)	7/31 (23%)	0.40	11%	-11%, 34%
I would not recognise when this was appropriate	26/81 (32%)	21/50 (42%)	5/31 (16%)	0.029	26%	4.4%, 47%
I do not have the resources to do this	18/81 (22%)	9/50 (18%)	9/31 (29%)	0.38	-11%	-33%, 11%
I do not have the support of my organisation to do this	12/81 (15%)	8/50 (16%)	4/31 (13%)	0.95	3.1%	-15%, 21%
Other	16/81 (20%)	8/50 (16%)	8/31 (26%)	0.43	-9.8%	-31%, 11%
Which issues/problems prevent you from using genomics more in your nursing role						
Genomics is not relevant	4/106 (3.8%)	4/52 (7.7%)	0/54 (0%)	0.12	7.7%	-1.4%, 17%
I don't understand genomics	32/106 (30%)	27/52 (52%)	5/54 (9.3%)	<0.001	43%	25%, 60%
My colleagues don't support my interests	2/106 (1.9%)	0/52 (0%)	2/54 (3.7%)	0.49	-3.7%	-11%, 3.2%
There are no relevant resources to help me learn	28/106 (26%)	17/52 (33%)	11/54 (20%)	0.22	12%	-6.2%, 31%
There are too many time constraints	43/106 (41%)	22/52 (42%)	21/54 (39%)	0.87	3.4%	-17%, 24%
My boss doesn't think it's important	3/106 (2.8%)	1/52 (1.9%)	2/54 (3.7%)	>0.99	-1.8%	-9.8%, 6.3%
I don't like science	3/106 (2.8%)	3/52 (5.8%)	0/54 (0%)	0.23	5.8%	-2.5%, 14%
There are no local study sessions	22/106 (21%)	9/52 (17%)	13/54 (24%)	0.54	-6.8%	-24%, 10%
It's the doctor's job	33/106 (31%)	23/52 (44%)	10/54 (19%)	0.008	26%	6.8%, 45%
Patients never talk to me about genomics	26/106 (25%)	15/52 (29%)	11/54 (20%)	0.43	8.5%	-9.8%, 27%
It isn't my decision	34/106 (32%)	18/52 (35%)	16/54 (30%)	0.73	5.0%	-15%, 25%
Other	28/106 (26%)	5/52 (9.6%)	23/54 (43%)	<0.001	-33%	-50%, -16%
Do these interventions/people encourage you to incorporate new areas of knowledge into your practice?						
Peers	64/106 (60%)	29/52 (56%)	35/54 (65%)	0.45	-9.0%	-29%, 11%
Heads of department	54/106 (51%)	28/52 (54%)	26/54 (48%)	0.69	5.7%	-15%, 27%
Contacts with specific professional services	47/106 (44%)	16/52 (31%)	31/54 (57%)	0.010	-27%	-47%, -6.5%
Other health professionals	57/106 (54%)	20/52 (38%)	37/54 (69%)	0.004	-30%	-50%, -10%
Attending study days	75/106 (71%)	35/52 (67%)	40/54 (74%)	0.58	-6.8%	-26%, 12%

Characteristic	Overall	Non-adopter	Adopter	p-value ²	Difference ³	95% CI ³
	N = 106 ¹	N = 52 ¹	N = 54 ¹			
Having a mentor	32/106 (30%)	13/52 (25%)	19/54 (35%)	0.35	-10%	-29%, 9.0%
Case studies	37/106 (35%)	12/52 (23%)	25/54 (46%)	0.021	-23%	-43%, -3.8%
Attending short presentations (e.g. lunchtime in-service)	64/106 (60%)	27/52 (52%)	37/54 (69%)	0.12	-17%	-37%, 3.7%
Patients	47/106 (44%)	14/52 (27%)	33/54 (61%)	<0.001	-34%	-54%, -15%
How difficult is it for you to achieve the following actions:						
Attend study days/courses that include genomics in practice				0.062		
Very difficult	29/106 (27%)	17/52 (33%)	12/54 (22%)			
Difficult	29/106 (27%)	14/52 (27%)	15/54 (28%)			
Neutral	29/106 (27%)	17/52 (33%)	12/54 (22%)			
Easy	15/106 (14%)	4/52 (7.7%)	11/54 (20%)			
Very easy	4/106 (3.8%)	0/52 (0%)	4/54 (7.4%)			
Apply new knowledge into your nursing practice				<0.001		
Very difficult	1/106 (0.9%)	1/52 (1.9%)	0/54 (0%)			
Difficult	7/106 (6.6%)	7/52 (13%)	0/54 (0%)			
Neutral	33/106 (31%)	19/52 (37%)	14/54 (26%)			
Easy	55/106 (52%)	24/52 (46%)	31/54 (57%)			
Very easy	10/106 (9.4%)	1/52 (1.9%)	9/54 (17%)			
Request access from senior management to new resources				0.53		
Very difficult	4/106 (3.8%)	3/52 (5.8%)	1/54 (1.9%)			
Difficult	16/106 (15%)	6/52 (12%)	10/54 (19%)			
Neutral	37/106 (35%)	19/52 (37%)	18/54 (33%)			
Easy	42/106 (40%)	22/52 (42%)	20/54 (37%)			
Very easy	7/106 (6.6%)	2/52 (3.8%)	5/54 (9.3%)			
Talk to colleagues about genomics				<0.001		
Very difficult	14/106 (13%)	12/52 (23%)	2/54 (3.7%)			
Difficult	13/106 (12%)	9/52 (17%)	4/54 (7.4%)			
Neutral	40/106 (38%)	24/52 (46%)	16/54 (30%)			
Easy	31/106 (29%)	5/52 (9.6%)	26/54 (48%)			
Very easy	8/106 (7.5%)	2/52 (3.8%)	6/54 (11%)			
Seek support from senior nurses and management to include genomics in your role				0.031		
Very difficult	16/106 (15%)	10/52 (19%)	6/54 (11%)			
Difficult	27/106 (25%)	17/52 (33%)	10/54 (19%)			
Neutral	40/106 (38%)	19/52 (37%)	21/54 (39%)			
Easy	17/106 (16%)	6/52 (12%)	11/54 (20%)			
Very easy	6/106 (5.7%)	0/52 (0%)	6/54 (11%)			

¹n/N (%)

²Fisher's exact test

³2-sample test for equality of proportions with continuity correction

5.4.1.6 Professional role expectations and influences

Differences between likely adopters and non-adopters were also apparent in participants' perceptions of their professional responsibilities, expectations, and influences across two clinical scenarios (Figure 5.6). Inferential statistics for these items are provided in Table 5.13. Responses to the clinical scenario involving a 42-year-old patient with breast cancer and a strong family history of early-onset disease showed significant group differences across all three items (Fisher's exact test; Pearson's chi-squared test, all $p < .001$).

There was good evidence that adopters were more likely to agree it was their responsibility to highlight the need for in-depth patient investigation, with 89% agreeing or strongly agreeing

compared with 63% of non-adopters. Conversely, 19% of non-adopters disagreed, compared with none of the adopters.

Non-adopters were also more than twice as likely to disagree that their colleagues expected them to ensure the patient's family was followed up by genetic services (66% vs 32%). In contrast, 47% of adopters agreed or strongly agreed compared with only 12% of non-adopters. Notably, 19% of adopters strongly agreed, whereas none of the non-adopters did so.

Finally, adopters were more likely than non-adopters to view follow-up of genetic consultations as part of their role, with 50% agreeing or strongly agreeing compared to 13% of non-adopters. Nearly two-thirds of non-adopters (62%) disagreed or strongly disagreed, compared with 34% of adopters.

Responses to the clinical scenario involving a 20-year-old man presenting with abdominal symptoms and a family history of bowel cancer showed significant group differences for two of the five items (Fisher's exact test; Pearson's chi-squared test).

There was reasonable evidence that adopters were more likely than non-adopters to believe their manager would approve of them highlighting the need for further investigation (82% agreeing or strongly agreeing vs 50%; $p = .008$), and good evidence that adopters were more likely to view it as their responsibility to raise the possibility of a genetic link with the patient's doctors, with 72% agreeing or strongly agreeing compared with 37% of non-adopters ($p < .001$). Notably, 28% of adopters strongly agreed compared with only 5.8% of non-adopters.

Although adopters were more likely than non-adopters to perceive that patients and relatives expected them to refer to a genetics service (25% vs 12% agreeing or strongly agreeing), this difference was not statistically significant ($p = .12$). Similarly, adopters and non-adopters did not differ significantly in their reported willingness to act without being influenced by colleagues' views ($p = .059$). Comparable proportions agreed overall (38% vs 39%), although adopters were more likely to strongly agree (20% vs 3.8%). Finally, there were no significant differences between groups in making decisions without seeking others' opinions ($p = .79$).

Table 5.13. Scenario questions

Characteristic	Overall N = 106 ¹	Non-adopter N = 52 ¹	Adopter N = 54 ¹	p-value ²
Scenario: 42-year-old patient with breast cancer mentions to you her concerns about her daughter's and granddaughter's chances of developing breast cancer				
It is my responsibility to highlight the possible need for more in-depth patient investigation				<0.001
Strongly Disagree	3/106 (2.8%)	1/52 (1.9%)	2/54 (3.7%)	
Disagree	10/106 (9.4%)	10/52 (19%)	0/54 (0%)	
Neither Agree or Disagree	12/106 (11%)	8/52 (15%)	4/54 (7.4%)	
Agree	37/106 (35%)	21/52 (40%)	16/54 (30%)	
Strongly Agree	44/106 (42%)	12/52 (23%)	32/54 (59%)	
My colleagues expect me to make sure the patients family is followed up by genetic services				<0.001
Strongly Disagree	23/106 (22%)	15/52 (29%)	8/54 (15%)	
Disagree	28/106 (26%)	19/52 (37%)	9/54 (17%)	
Neither Agree or Disagree	24/106 (23%)	12/52 (23%)	12/54 (22%)	
Agree	21/106 (20%)	6/52 (12%)	15/54 (28%)	
Strongly Agree	10/106 (9.4%)	0/52 (0%)	10/54 (19%)	
It is part of my role to follow up genetic consultations for the family either directly or via my manager				<0.001
Strongly Disagree	27/106 (25%)	17/52 (33%)	10/54 (19%)	
Disagree	23/106 (22%)	15/52 (29%)	8/54 (15%)	
Neither Agree or Disagree	22/106 (21%)	13/52 (25%)	9/54 (17%)	
Agree	21/106 (20%)	7/52 (13%)	14/54 (26%)	
Strongly Agree	13/106 (12%)	0/52 (0%)	13/54 (24%)	
A 20-year-old man presents with abdominal pain, unexplained weight loss and regular diarrhoea. Upon completing his family history, you discover that his mother's brother (uncle) aged 45 is recovering from bowel cancer				
Patients and relatives expect me to refer to a specialist genetics service				0.12
Strongly Disagree	17/106 (16%)	11/52 (21%)	6/54 (11%)	
Disagree	38/106 (36%)	22/52 (42%)	16/54 (30%)	
Neither Agree or Disagree	32/106 (30%)	13/52 (25%)	19/54 (35%)	
Agree	16/106 (15%)	6/52 (12%)	10/54 (19%)	
Strongly Agree	3/106 (2.8%)	0/52 (0%)	3/54 (5.6%)	
My manager would approve of me highlighting the need for further patient investigation				0.008
Strongly Disagree	1/106 (0.9%)	1/52 (1.9%)	0/54 (0%)	
Disagree	10/106 (9.4%)	7/52 (13%)	3/54 (5.6%)	
Neither Agree or Disagree	25/106 (24%)	18/52 (35%)	7/54 (13%)	
Agree	49/106 (46%)	20/52 (38%)	29/54 (54%)	
Strongly Agree	21/106 (20%)	6/52 (12%)	15/54 (28%)	
It is my responsibility to raise the possibility of a genetic link with this patients doctors				<0.001
Strongly Disagree	2/106 (1.9%)	1/52 (1.9%)	1/54 (1.9%)	
Disagree	20/106 (19%)	16/52 (31%)	4/54 (7.4%)	
Neither Agree or Disagree	26/106 (25%)	16/52 (31%)	10/54 (19%)	
Agree	40/106 (38%)	16/52 (31%)	24/54 (44%)	
Strongly Agree	18/106 (17%)	3/52 (5.8%)	15/54 (28%)	
If I thought my actions with this patient were appropriate, I would not be influenced by my colleagues views				0.059
Strongly Disagree	3/106 (2.8%)	1/52 (1.9%)	2/54 (3.7%)	
Disagree	20/106 (19%)	11/52 (21%)	9/54 (17%)	
Neither Agree or Disagree	29/106 (27%)	18/52 (35%)	11/54 (20%)	
Agree	41/106 (39%)	20/52 (38%)	21/54 (39%)	
Strongly Agree	13/106 (12%)	2/52 (3.8%)	11/54 (20%)	
I would make decisions regarding this patient without seeking the opinions of others				0.79
Strongly Disagree	32/106 (30%)	15/52 (29%)	17/54 (31%)	
Disagree	46/106 (43%)	23/52 (44%)	23/54 (43%)	
Neither Agree or Disagree	20/106 (19%)	11/52 (21%)	9/54 (17%)	
Agree	6/106 (5.7%)	3/52 (5.8%)	3/54 (5.6%)	
Strongly Agree	2/106 (1.9%)	0/52 (0%)	2/54 (3.7%)	

¹n/N (%)

²Fisher's exact test; Pearson's Chi-squared test

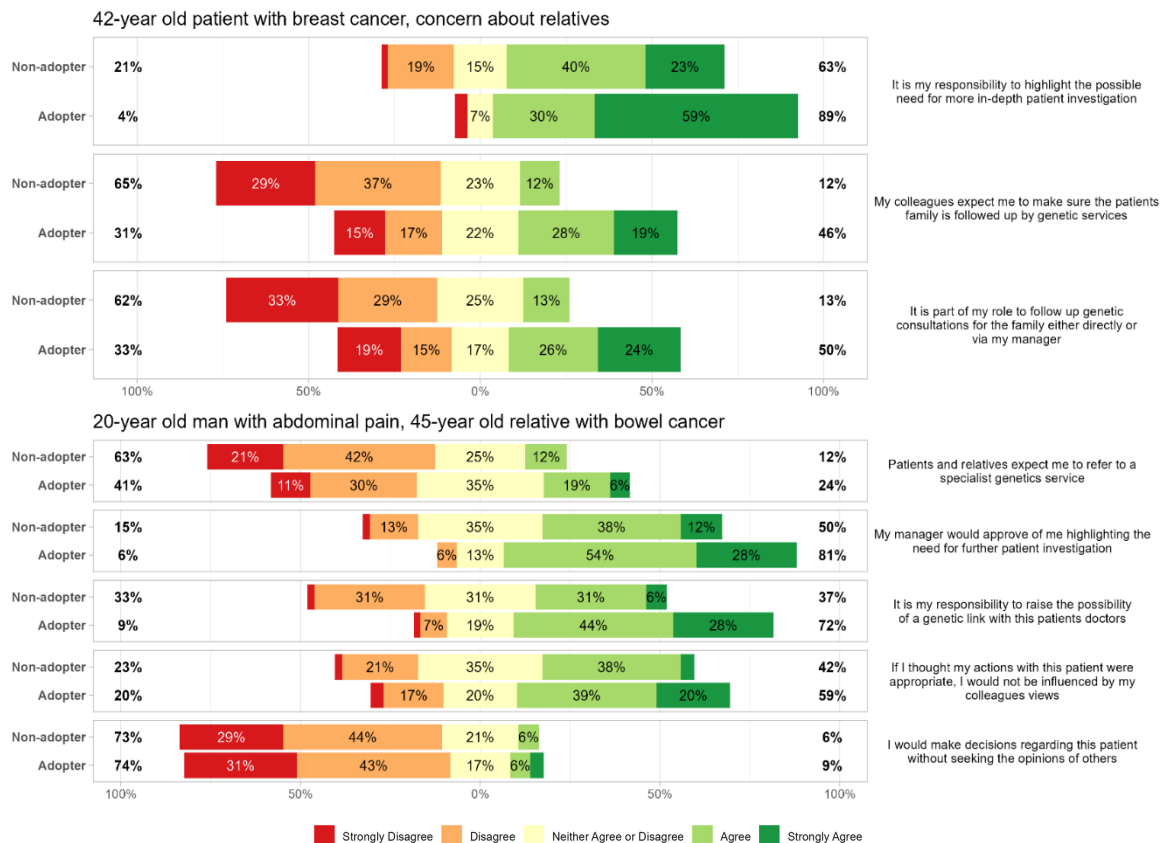


Figure 5.6. Adopters' and non-adopters' responses to professional role expectations and influences across two clinical scenarios.

5.5 Summary of results

5.5.1 Oncology nurses' knowledge, engagement, and adoption of genomics in practice

Overall, oncology nurses in this study demonstrated limited familiarity with national and international genomic resources and initiatives, with many reporting little or no awareness of specialist genetics services and their available resources. Objective knowledge of genomics was mixed: while most participants recognised core genomic applications such as cancer and family history, fewer identified pharmacogenomic influences such as response to medication.

Confidence in engaging with genomics was generally low, particularly in patient education and managing genomically relevant clinical scenarios. Attitudinal responses, however, were largely supportive: most participants endorsed the importance of family history, the relevance of genomics to oncology practice, and the need for continuing professional development. Levels of interest in incorporating genomics into practice were also high, though accompanied with uncertainty.

In terms of engagement, most participants reported few or no referrals to genetic services, infrequent discussions with colleagues about genomics, and variable patterns of information-seeking. Common barriers included time constraints, limited knowledge, and perceptions that genomics was either the responsibility of doctors or beyond nurses' decision-making authority. Enablers most often cited were study days, peer support, and opportunities for short educational sessions.

Together, these findings indicate that while oncology nurses recognise the importance and potential relevance of genomics in their practice, current levels of knowledge, confidence, and practical engagement remain limited and are shaped by both structural barriers and available supports.

5.5.2 Identifying individual characteristics associated with the uptake of genomics in nursing practice

Comparisons between likely adopters and likely non-adopters revealed significant differences across several domains. Adopters tended to have more years of nursing experience and were more frequently represented in older age brackets and advanced practice roles, whereas non-adopters were more commonly younger nurses and those practising at the Registered Nurse grade. Adopters were also more likely to hold postgraduate qualifications such as master's degrees, while non-adopters more often reported a bachelor's degree as their highest qualification.

Personality and individual characteristics also distinguished the groups. Adopters reported significantly higher levels of openness to experience and scored higher on the opinion leadership scale, with a greater proportion meeting the cut-off for self-designated opinion leaders. In contrast, no group difference was observed in perceived influence as measured by the personality strength scale.

In relation to cosmopolitanism and information-seeking, adopters reported more frequent use of research articles, conferences, CPD activities, and scholarly databases to inform their practice, although both groups reported similar levels of reliance on internet sources.

Referral activity clearly differentiated the groups, with adopters more likely to have engaged in recent referrals to genetics services compared with non-adopters, reinforcing referral behaviour as a central marker of adoption. Adopters were also distinguished by their lower endorsement of barriers to referral and uptake. Non-adopters were significantly more likely to report not

understanding genomics and to identify genomics as primarily the doctor's responsibility, whereas adopters were more likely to perceive greater ease in applying new knowledge, discussing genomics with colleagues, and seeking support from senior nurses and management. Enabling factors such as support from other health professionals, patients, professional services, and case studies were more frequently cited by adopters. Finally, scenario-based responses demonstrated that adopters were more likely to endorse responsibility for identifying potential genetic concerns, expect managerial approval, and view follow-up of genetic consultations as part of their role. Non-adopters, in contrast, were more likely to disagree with these responsibilities or remain neutral.

5.6 Conclusion

This chapter has presented the findings from the quantitative phase (Phase 1) of the study, which examined the current landscape of genomic knowledge, engagement, and adoption among oncology nurses in Australia, as well as the individual characteristics associated with adoption. The next chapter presents the qualitative findings (Phase 2), which explore nurses' perceived barriers and enablers to uptake of genomics into oncology nursing practice.

Chapter 6 – Qualitative Results

6.1 Introduction

The results of the qualitative phase of this doctoral research are reported in this chapter, with the aim of exploring perceived barriers and enablers to genomic uptake in oncology nursing. This chapter begins with a brief description of the characteristics of the interview participants. This is followed by a comprehensive analysis of the data collected in the Phase 2 qualitative semi-structured interviews where several key themes related to the barriers and enablers to genomic adoption into nursing practice are reported. These themes are subsequently mapped into five broad domains: 1) *attributes of the innovation*, 2) *education-related factors*, 3) *professional factors*, 4) *organisational factors*, and 5) *individual factors*. Within each of these domains, specific themes were outlined and contextualised with key quotes from the participants to provide further insight into the experiences and perspectives shared during the interviews. While the following themes are grouped under five analytical domains, several barriers and enablers are shared by more than one domain and as a result, cross these boundaries. In such cases, themes are positioned within the domain most reflective of participants' framing and context. Where relevant, links to overlapping domains are noted to reflect the multidimensional and dynamic nature of the experiences reflected by the data.

6.2 Participant characteristics

Nine registered nurses from four different Australian states and territories were interviewed. Given the highly specialised and niche nature of genomic nursing, alongside the limited number of practitioners working in this space, the risk of deductive disclosure was considerable (see Section 4.8.3). To protect participant confidentiality, direct identifiers (including location, specific role titles, and individual demographic details) have been withheld, and quotations are not attributed to specific participants. While demographic variables such as gender were collected, they were deemed analytically irrelevant and are not reported. Most participants occupied senior clinical positions, including Clinical Nurse Consultants (CNCs), Clinical Nurse Educators (CNEs), and Clinical Nurse Specialists (CNSs), with most having over 20 years of nursing experience. Notably, two CNEs were within five years of registration, reflecting early-career perspectives within educator roles. Of the nine participants, three were employed in formal genomic nursing positions; four described varying levels of genomic adoption integrated into their existing roles—ranging from referrals to genetics services to facilitating patient

education and consenting for mainstream genetic testing; and two reported no involvement with genomic practice, citing minimal exposure or perceived relevance in their current settings. The participants worked across a variety of oncology healthcare settings, including metropolitan and regional areas, within public hospitals, specialty cancer hospitals, and private healthcare facilities.

6.3 Findings

6.3.1 Domain 1: Attributes of the innovation

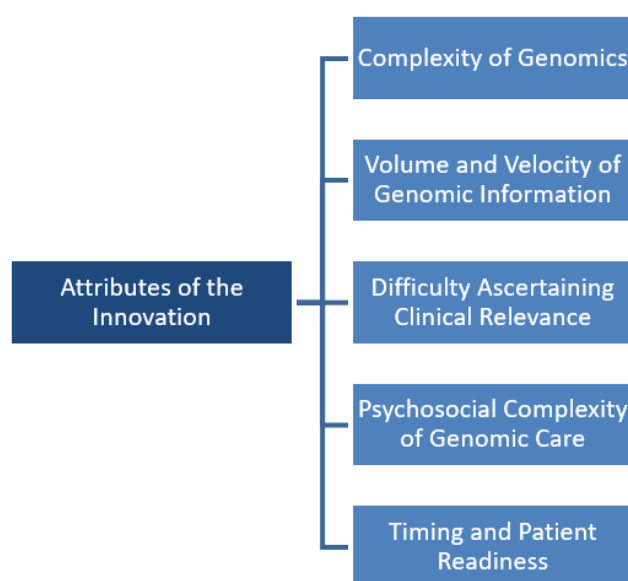


Figure 6.1. Domain 1: Attributes of the innovation.

This domain explores how specific attributes of genomics as a clinical innovation (e.g., genomic concepts, testing, risk assessment, family history-taking, referral, genomic education) were experienced by participants and how these attributes shaped their ability to adopt and deliver genomically informed care. Participants consistently described genomics as distinct from other medical or nursing knowledge, characterised by scientific and psychosocial complexity, rapid information growth, and ambiguous clinical relevance. These perceived genomic attributes often posed challenges for the participants to comprehend, integrate, and confidently apply genomics in their practice.

6.3.1.1 Theme 1: Complexity of genomics

This theme reflects nurses' perceptions of genomic innovations as complex, abstract, and technically demanding. The scientific language, unfamiliar terminology, and conceptual depth were viewed as barriers to comprehension and integration into existing knowledge frameworks.

Many participants likened genomics to learning a new language and cited this as a significant barrier to adoption. As one participant explained, ‘I actually just feel like... it’s like a foreign language to me, almost’. Another echoed this sentiment: ‘It’s like me reading Chinese. I have no idea. I don’t know what I’m looking at.’ A third participant similarly noted, ‘It was just like I was speaking a different language’.

These accounts underscore how the perceived technical and linguistic complexity of genomics acts as a foundational barrier to its integration into everyday nursing practice. Participants described genomic concepts, terminology, and data as difficult to interpret and apply without specialised training. This complexity reduced their confidence in discussing genomic information with patients and colleagues, creating uncertainty about when and how genomics was relevant to their role.

6.3.1.2 Theme 2: Volume and velocity of emerging genomic information

This theme highlights nurses’ feelings of being overwhelmed by the sheer volume of emerging genomic information and the rapid pace of change. One nurse described this barrier:

It does get bigger and bigger every time I look at another paper on what the next genetic marker is... You think, ‘Oh my goodness,’ every time I get a new referral when I was working and I’d look at it and say, ‘Well, what’s this new gene in this?’ It’s becoming more and more a minefield... Yeah, the information is quite vast.

The exponential growth in genomic discoveries and evolving practices was consistently cited as a challenge, with several nurses expressing difficulty keeping up, leading to a sense of ‘information overload’. A participant explicitly stated this struggle: ‘I’m finding it’s actually a struggle to—it’s starting to be a struggle to keep up with all of the rapid pace of knowledge and changes that are coming out’.

These accounts illustrate how the volume and rapid evolution of genomic information were experienced as barriers to engagement. Some noted that while guidelines were intended to provide direction, they were often complex, inconsistent, or difficult to access, further compounding the challenge of staying current. Participants described feeling swamped by the volume of new information and uncertain about how to identify which updates were most relevant to their clinical practice, a challenge that also intersects with the difficulty of ascertaining clinical relevance, explored further in the following theme.

6.3.1.3 Theme 3: Difficulty ascertaining clinical relevance

This theme refers to uncertainty about which aspects of genomic information were relevant to clinical practice. The vastness of the topic, coupled with the lack of clear guidance on what knowledge was necessary for their role, created confusion and was reported as a barrier to engagement. This issue was expressed by participants irrespective of their level of experience with genomics. One participant in a dedicated genomics role shared their struggle as they prepared for their position as a genomic nurse: ‘I didn’t know what I did need to know and what I didn’t need to know... I kind of got lost in that for a bit’. Similarly, a participant who works in an environment where genomics is not embedded faced the same difficulty in determining the clinical relevance of genomic information as they independently sought to expand their knowledge: ‘Some information may be relevant, it may not be relevant, I don’t know.’ Participants described varied responses to this uncertainty. Some reported feeling discouraged or disengaging from further learning when the information seemed overwhelming, while others attempted to ‘wade through it’ by independently seeking resources or peer support to clarify what was most relevant. These self-directed strategies are explored further in the education factors domain.

6.3.1.4 Theme 4: Psychosocial complexity of genomic care

Participants highlighted the psychosocial attributes of genomic innovations as a significant barrier to their engagement with and adoption of genomics in clinical practice. Unlike many other forms of medical information, genetic data were described as familial in nature and carrying a prophetic quality, which nurses perceived as heightening patient anxiety. Conversations about genetic risk and family history were therefore characterised as emotionally taxing and psychosocially complex, making it challenging for nurses to navigate these discussions and incorporate genomics into routine care.

There was broad agreement among participants that genomic information frequently elicited strong emotional responses from patients, including anxiety, fear, and uncertainty, particularly when hereditary implications or difficult treatment decisions were involved. Nurses described this psychosocial burden as complicating the provision of genomic care, especially in contexts where patients lacked adequate emotional support or where access to genetic counselling services was limited.

One participant conveyed this emotional burden: ‘There’s just a general kind of anxiety, “Will my family get it?” and all those things.’ Another participant discussed the reluctance to engage with genomic topics due to the potential for re-traumatisation or the unintended consequences of delving into sensitive family histories: ‘If you talk about families and talk about family history, I think we’ve got to be mindful we could open up a can of worms. So it could be a bit traumatic.’

Notably, this psychosocial weight, which is intrinsic to the nature of genomic innovations, often prompted patient information-seeking and emotionally charged questions. These inquiries were frequently directed at nurses, given their close proximity to patients and the trust embedded in the nurse–patient relationship. This dynamic is further explored in Domain 3, Theme 3, which examines the role of nurses as opportunistic facilitators. Importantly, such interactions also revealed gaps in preparedness and knowledge among nurses. While this lack of confidence posed a barrier for many, it also paradoxically served as an enabler for others, who described feeling motivated to upskill in order to better support their patients. These intersecting dynamics are further examined in Domain 2, Theme 1, which explores deficits in training and preparedness, as well as in Domain 5, Theme 1, which discusses individual knowledge and confidence in this context.

6.3.1.5 Theme 5: Timing and patient readiness

This theme underscores the importance of patient readiness and timing in genomic care. Given the complex psychosocial attributes of this innovation, nurses emphasised that genomic conversations require an appropriate emotional context, adequate time within the clinical schedule, and careful pacing. The emotional weight of genomic information demands precise timing and patient readiness, which can be difficult to manage within everyday clinical workflows. Time constraints and emotionally overwhelmed patients were identified as significant barriers to the adoption of genomics.

These barriers were particularly explicit amongst nurses who work in formal genomic roles. One participant articulated these barriers, highlighting the critical role of timing due to the emotional weight of genomic information:

It’s quite time sensitive. You can’t rush telling somebody about all of this. They need to take it in. In the ward, if they’re just post-op, they’re often overwhelmed by

information, so we've just got to kind of titrate it to how they're feeling and maybe pick a time with them, with a relative there.

Similarly, another nurse in a formal genomic role discussed the challenge of identifying the right time to speak with patients about genetic studies:

Finding when they're on the ward, are there any psychosocial barriers, getting approval from the oncologists, and making sure that they don't have anything else challenging that day—having the conversation about the study means that a whole lot of things need to align, and then me actually having time to go and do it.

This theme is reported within the *attributes of the innovation* domain to highlight participants' views that these timing challenges were unique to genomics itself. They described genomic care as fundamentally different from other medical and nursing interactions due to its emotional intensity and layered implications, which necessitated greater sensitivity to timing and patient readiness. Including this theme within this domain underscores how nurses perceived the distinctive features of genomics as shaping their ability to engage with it in practice. However, this theme also dynamically intersects with other domains. For instance, it overlaps with the theme of *time poverty* (Domain 3, Theme 1), organisational conditions reported in Domain 4, and *opportunistic facilitators* (Domain 3, Theme 3), where nurses' proximity and rapport with patients often positioned them as the primary recipients of emotionally charged genomic questions. Additionally, it aligns with themes related to *knowledge and confidence* (Domain 5, Theme 1), since nurses' confidence in managing these nuanced conversations was influenced by these individual attributes.

6.3.2 Domain 2: Education-related factors

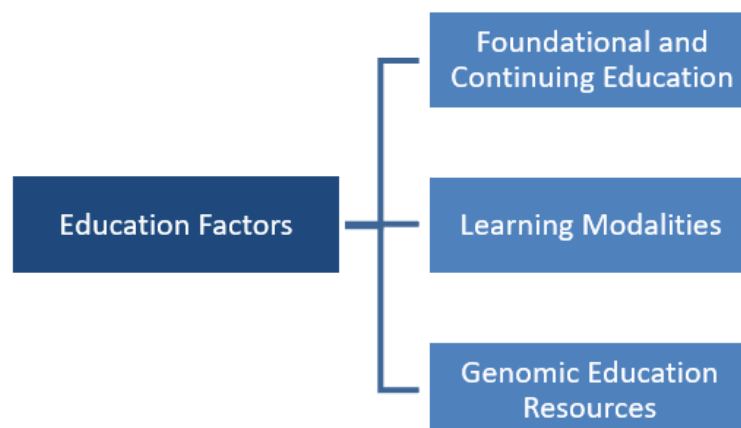


Figure 6.2. Domain 2: Education-related factors.

This domain explores how nurses' exposure to genomics through formal education, ongoing training, and access to resources shaped their engagement with genomic care. Participants identified limited pre-registration exposure and minimal workplace-based education as foundational barriers, often resulting in uncertainty and reduced confidence. Access to structured, clinically relevant content was frequently described as inconsistent and poorly aligned with nursing roles.

Conversely, participants identified several educational enablers that supported engagement, including experiential learning opportunities, trusted platforms such as eviQ and the Cancer Nurses Society of Australia (CNSA), and diverse learning modalities such as webinars, university courses, and self-directed study. Across interviews, participants consistently emphasised the need for simplified, centralised, and nursing-specific genomic education resources to bridge the gap between theoretical knowledge and practical application.

6.3.2.1 Theme 1: Foundational and continuing genomic education

This theme refers to participants' reports of limited exposure to genomics during their pre-registration training and minimal opportunities for continuing education post-registration. These educational gaps were identified as key barriers that contributed to ongoing uncertainty and limited confidence in genomic practice. While the absence of genomics in formal nursing education was viewed as a foundational deficit, participants also highlighted the lack of workplace-based education and training as a barrier to further engagement. Conversely, participants identified continuing education, such as in-services, as a valuable enabler that supported their interest and confidence in genomic practice.

Several nurses recalled little to no exposure to genomics in their pre-registration nursing programs. One participant noted, 'Looking back... at my degree... I don't recall ever having a thorough or comprehensive—even a single lecture slide dedicated to it. I don't recall that.' Another discussed how this absence was common among colleagues: 'Across the board genetic and genomics knowledge was not something that they came across while they were training.'

One participant reflected on the clinical implications of these foundational knowledge gaps, describing a situation in which she was confronted with a genomic care need she felt unprepared to manage. She described how the lack of genomic content in her formal education left her without the clinical competency required to respond effectively to the patient's needs:

I mean, you learn about disease progression. Genetics component, okay, *BRCA* genes. We just—that's the only thing we learn. We don't learn anything else. How to approach this situation with the patient, how to—if something like this happens, how are you dealing with it? What services are available? How are you managing all these situations? You never learn all those things, and then you land in a situation like this and most of the nurses are clueless. What do we do? We don't know.

This account underscores the significance of educational preparation in shaping genomic competency and highlights how these training deficits form a foundational barrier to confident clinical engagement. While situated within the theme of education, the example also demonstrates the close relationship between training gaps and individual knowledge and confidence—an issue explored further in Domain 5, Theme 1.

In addition to foundational gaps, participants also reported limited access to ongoing genomic education in their workplaces. There was a general sense that genomics was rarely addressed through in-services or professional development programs. As one nurse noted, 'Yeah, not too many in-services like directly related to that information and how it affects patient care for nurses'. Conversely, some participants viewed continued education as a potential enabler and expressed a desire for more opportunities in this area. One participant voiced this aspiration: 'I really wish that, yeah, work would do a bit more in-depth in-services regarding that aspect of oncology.' Another described a positive experience in delivering an in-service including genomic concepts, noting its impact on junior nurses: 'I have had a new grad, that after my [in-service] talk come to me and be like, 'wow this is really interesting. I want to know more about this in cancer.'

Importantly, this theme intersects closely with Domain 5, Theme 1, which explores individual-level knowledge and confidence. While knowledge and confidence are reported as individual factors, participants consistently linked these deficits to gaps in their education and training, underscoring how individual competence is shaped by structural conditions within the workforce. This dynamic was particularly evident in the context of patient information-seeking, a common occurrence driven by the psychosocial attributes of genomics (as discussed in Domain 1, Theme 4) and nurses' proximity to patients (explored further in Domain 3, Theme 3). One participant captured this intersection, stating:

I think when you are working in the unit with the patients, they'll often ask questions... some of them worry about their children's future and those sorts of things; what should they do?... [W]e need counselling training.

This account exemplifies how patient expectations can expose knowledge gaps and amplify the consequences of educational deficits, reinforcing the urgent need for accessible and ongoing genomic education.

While this theme is centred within the domain of *education-related factors*, it also intersects with Domain 4 (*organisational factors*), particularly in relation to workplace-based learning. Participants' experiences with in-services, professional development, and access to structured continuing education were often shaped by institutional priorities and support. As such, the availability and integration of ongoing genomic education cannot be fully disentangled from the broader organisational context in which nursing practice occurs.

6.3.2.2 Theme 2: Learning modalities

This theme captures the diverse educational approaches participants engaged with in order to build their genomic knowledge, as well as the particular value they placed on hands-on, experiential learning. Participants described using a variety of modalities—including university courses, webinars, newsletters, and online self-directed study—which they found beneficial in developing their understanding of genomics. In addition to these flexible learning formats, several nurses highlighted the impact of immersive experiences such as secondments, mentorships, and observational learning. These experiential opportunities were viewed as especially effective in building confidence and translating theoretical knowledge into clinical practice.

Many participants shared examples of multimodal learning strategies they had accessed, often informally or through personal initiative. One nurse explained, 'I started learning about this through university doing a Master's level Introduction to Genetics'. Another described attending online education: 'I think it was four online webinars... the last one, you sat in and listened to a Molecular Tumour Board discussion.' Informal learning through professional networks and self-study was also commonly reported. Participants noted, 'I subscribe to a few oncology-related newsletters... that's one way of keeping abreast of what's happening', and 'When I'm reading through a patient's history... I just do a bit of a Google search to learn a little bit more about it'. Others reported drawing on seminars and webinars from trusted sources:

‘I would ask my educator, or I’d look at seminars, or webinars that CNSA would put on.’ One participant highlighted the benefit of conferences, noting, ‘I’ve managed to go to some of the conferences, doing them virtually over the last few years’.

Among these approaches, experiential learning stood out as a particularly valued enabler. Several participants described how secondments, mentorships, or observing genomic consultations helped solidify their understanding and improve their comfort with genomic concepts in clinical settings. As one participant explained, ‘Going up to see what happens to the samples and where they go and speak to genetic counsellors is really good’. Another genomic nurse described encouraging colleagues to take on consent roles after guided exposure: ‘We arranged for her to go up to [redacted genetics service] and have a mentor up there. She sat in on about three or four interviews... now she does them herself.’ One nurse summarised the value of experiential learning simply: ‘I was seconded to [Redacted: specialist cancer centre]... It was really, really useful. It was fantastic.’

These accounts suggest that while flexible, multimodal education formats provide accessible ways for nurses to engage with genomics, experiential learning plays a distinct and powerful role in building confidence, supporting translation to practice, and facilitating adoption. Although this theme is situated within the *education-related factors* domain, the accessibility of experiential learning is closely tied to institutional support, highlighting an important overlap with the domain of *organisational factors*.

6.3.2.3 Theme 3: Genomic education resources

This theme explores how the accessibility, clarity, and relevance of genomic education resources shaped participants’ engagement with genomics. Nurses described existing resources as often too complex, poorly aligned with nursing practice, and difficult to translate into clinical application. These issues were reported as barriers that discouraged self-directed learning. Conversely, trusted platforms such as eviQ and CNSA were identified as important sources of genomic information, offering reliable resources that supported knowledge acquisition and informed clinical decision-making. Participants also strongly articulated a need for a simplified, centralised, and nursing-specific resource to better support genomic education in practice.

Several nurses commented on the limitations of currently available resources, particularly regarding their usability and relevance. One participant shared:

I think they are not resources that are easy to understand... it's more like—they don't relate back to practice, like how do you use that day to day. I think that would discourage nurses from accessing them.

This sentiment was echoed across levels of genomic engagement, with participants from both high- and low-exposure settings expressing difficulty in finding materials that were accessible and practically applicable.

Across the interviews, participants consistently voiced the need for genomic education materials that were tailored specifically to nurses. This included simplifying complex content, ensuring clinical relevance, and centralising access. One nurse expressed the importance of striking the right balance in content: 'it needs to be relevant and clinically appropriate and it needs to help facilitate discussion, but not necessarily get into too much of the nitty gritty as working on the floor'. Another participant similarly described what would be most helpful for nurses is a resource that is: 'for nurses that isn't quite as high-powered but gives enough information to be useful onsite in the hospitals'.

In addition to these content-related needs, participants emphasised accessibility. They advocated for genomic resources to be housed in a central, regularly updated location to support ease of use and practical application. One nurse highlighted this need explicitly, stating, 'Like if there was a central spot that you could go and look at all the updates for ovarian cancer, that'd be great'. This emphasis on centralisation was framed as critical for enabling timely access to information at the point of care.

Despite these limitations in existing resources, participants identified some trusted platforms that they actively used to support their genomic learning. eviQ, in particular, was frequently referenced as a hospital-supported, reliable educational source. Of the nine nurses interviewed, seven cited eviQ as their preferred platform for accessing genomic information. One nurse described its credibility simply: 'eviQ is the Gold Standard for cancer care.'

Similarly, CNSA was identified as a dependable source of webinars, seminars, and specialised content through its online portal and cancer-specific subgroups. One nurse highlighted its practical relevance: 'CNSA, that would be a really good body to link in with, because they already help to run the ovarian cancer nurses' support.'

Participants also discussed how these trusted platforms could serve as valuable sources for future genomic education. One nurse reflected on the potential of expanding structured content through established systems:

[O]nline training like HETI [Health Education and Training Institute] modules and things like that could be really valuable, or eviQ modules specific to genetic syndromes I think would be really valuable, just so that there's that consistency of knowledge.

These findings highlight how the complexity and misalignment of many existing resources pose barriers to engagement, while trusted tools like eviQ and CNSA can support genomic learning. Importantly, participants' call for a simplified, centralised, and nursing-specific educational resource signals a key area for future intervention to enable broader genomic integration into nursing care.

6.3.3 Domain 3: Professional factors



Figure 6.3. Domain 3: Professional factors.

This domain presents how characteristics of the nursing profession, including workforce issues such as time pressures, staffing instability, professional scope boundaries, and the nature of nurse–patient relationships, were experienced by participants as shaping their ability to engage with and adopt genomics in clinical practice. While several barriers were identified, such as

workforce constraints, scope uncertainty, and variable role delineation, participants also described clear workforce-level enablers. These included the compatibility of genomics with advanced practice nursing roles, access to ‘on the floor’ genomic nurse specialists and the unique positioning of nurses as opportunistic facilitators of genomic care. Although some of these factors may intersect with broader organisational structures, participants primarily discussed them in relation to workforce norms and conditions.

6.3.3.1 Theme 1: Workforce constraints

This theme captures how time scarcity and broader workforce instability shaped nurses’ capacity to engage with genomic education and incorporate genomics into clinical practice. Participants consistently described competing clinical demands, limited protected learning time, and understaffing as key barriers to genomic integration. These constraints were seen as systemic issues across the nursing workforce, affecting both educational access and clinical application.

Several participants highlighted how intense workloads and staffing shortages limited opportunities to engage with genomics during routine care. One nurse noted:

I think time constraint is one of them. Time and staff. Staff availability. Looking at the number of patients and the amount of work we have and the lack of resource which we have, it definitely is a time-consuming process. Staff, availability of staff.

Another reflected on how this affected their ability to pursue further training:

With nurses these days, we are always constantly trying to upgrade and study, but it’s something that gets harder and harder and harder with the hours that we work.

Others described the specific challenge of accessing uninterrupted time for learning: ‘It’s so hard to just cover staff for at least 20 minutes without some sort of interruption where they can just have a consolidated protected learning time.’ These time constraints also limited the ability to engage meaningfully with patients around genomic issues: ‘You don’t have time—nurses don’t have time to sit down with that and engage with the person.’

In addition to time poverty, participants described a broader sense of workforce strain affecting the nursing profession. Staff shortages, high turnover, and a junior nursing workforce were identified as contributing factors. One participant explained, ‘It’s something the younger ones struggle with because they are so busy. I think it’s a time-poor thing... it’s a minefield at the

moment to actually get enough cancer care nurses.’ Another pointed to the difficulty of even coordinating in-services in this context: ‘It’s tricky to run in-services... getting more than two people is a win when you’ve only got eight, nine staff on the ward.’

The impact of workforce turnover and lack of senior staff was also raised:

I know there’s a high turnover in nursing, so our workforce is so junior at the moment, I think we’ve got a two or three year out of uni is the majority... they’re such junior nurses leading the ward. So I think part of it is just a massive education drain.

A small number of participants also reflected on how these workforce pressures may shape professional norms, suggesting that the demand for efficiency can discourage reflective learning. One nurse observed:

[Y]ou are more pushed to focus on your work and just do your work, that’s it... Even if you have questions, this is not relevant, you can do research in your own time. Let’s now focus on this work at hand. We need to do chemotherapy, we are not encouraging the curiosity I don’t think. We aren’t developing a very curious workforce.

These accounts reflect how time constraints and workforce instability are experienced as structural and widespread barriers to genomic engagement, limiting both individual learning and systemic capacity to build genomic competency in nursing practice. While this theme is reported within the *workforce-related factors* domain due to the way participants framed time poverty and staffing pressures as profession-wide challenges, it also intersects with Domain 4, *organisational factors*. Access to protected learning time and staffing levels may vary across institutions, suggesting that organisational culture and resourcing may also shape how these workforce constraints are experienced.

6.3.3.2 Theme 2: Scope boundaries and role delineation

This theme reflects participants’ varying understandings of where genomic responsibilities sit within nursing scope, with evidence of both uncertainty and professional gatekeeping. Among nurses not in formal genomic roles, there was no clear consensus. Some viewed genomics as falling outside their scope, others described a default deference to medical staff, and a few actively questioned these assumptions. In contrast, nurses in dedicated genomic roles described genomic care as routine and firmly within their clinical remit.

One nurse described detailed genomic education as explicitly beyond their scope, stating, ‘I can give them an overview but it’s outside of my scope to go into lots of details’. This perspective was echoed in other accounts, which described deferring to medical staff as standard practice. One participant explained, ‘Patients that haven’t been through genetic testing but that I have suspected them needing to be referred to genetic testing, is kind of something like, you refer to the doctor. You just don’t do it yourself.’ This response points not only to scope uncertainty but also to a culture of professional gatekeeping, where nurses adopt a passive role despite recognising genomic need.

Another participant reflected on the blurred boundaries between professions, acknowledging both a lack of clarity and the consequences when responsibilities are left unclaimed:

I think some of it is what is the doctor’s role versus what’s the nurse’s role. Generally, we would expect that it’s the doctors that talk about—to patients about genomics. However, I’ve found that, often, it doesn’t happen.

While scope uncertainty was common, some participants challenged the idea that genomics lies outside nursing. One nurse articulated a strong view that understanding disease processes, including genomics, is integral to nursing care:

That’s a bit of a thing that people say, ‘That’s the doctors job’, but that’s not what it is. We need to understand the disease and how it affects, because that’s where we come in... How it affects them in every aspect of their life because that’s where us nurses could help. That’s what we need to know, and I think that [we’re lacking]. Where do we come in.

In contrast to these varied and sometimes conflicted accounts, participants working in formal genomic roles described no ambiguity. They routinely engaged in tasks such as taking family histories, providing genomic education, and obtaining consent for genetic testing, and viewed these as fully consistent with their scope of practice. Together, these findings highlight an important gap between perceived and actual scope in nursing genomic care. While specialised nurses demonstrated clear integration of genomics into their role, many others remained uncertain or hesitant, reinforcing a barrier to broader adoption.

6.3.3.3 Theme 3: Nurses as opportunistic facilitators

This theme captures how nurses' sustained presence, relational proximity, and communication skills position them as opportunistic facilitators of genomic care. Nurses are often the first to elicit family histories, identify potential genomic red flags, and provide patient education. This intrinsic feature of nursing practice, where clinical tasks are interwoven with interpersonal connection, was described as a key workforce-level enabler of genomic engagement. This view was shared consistently across participants, regardless of their role, level of genomic adoption, or clinical setting.

Several participants highlighted nurses' proximity to patients as a central factor enabling genomic facilitation. One noted, 'I think with training, nurses can be very useful because we're in the ward – at the coalface, if you like – and able to facilitate the testing quickly for patients'. Another described nurses as ideally placed to support not only patients but their families, particularly when genetic risk was a concern:

Nurses are such a perfect position to be providing education and a little bit more support in those areas. Just making sure that they are aware of the risk, not only to themselves but to families. Also making sure that they do have on hand, services that they can be referred to if they do want to have further testing. Or just making sure you bridge that for them to pass that information to their relatives as well.

Participants consistently emphasised that nurses' role in genomic facilitation is not just about physical access but also about relational depth. The trust and rapport developed through day-to-day interactions created safe spaces for patient disclosure and education. One participant explained:

The amount of time we spend with patients. Most of the time we build a lot more rapport with them. As you're doing things with them, like giving medications, or changing their beds, you're always chatting to them. Getting to know when patients also start seeing you as a person that they have a good rapport with, that they trust and disclose a lot of information. They are very open to education coming from nurses. I think because nurses are a little bit more connected with the patients, they kind of know how to break down information in a way that they understand much easier than let's say, the doctors. It's not uncommon for a patient to be like, 'oh the

doctor said this and that but I don't understand what does that mean, what does this mean?' Kind of like, they feel safe having those conversations with you'.

This perception of nurses as health communicators was echoed by another participant who described the complementary role of nurses in clarifying and contextualising medical information:

I think nurses recognise in general that a doctor says something to a patient and then that's facilitated to understand with the nurse backing it up, to say 'well this is what it means in normal language'.

This interpretive and supportive function was framed as a natural extension of nursing practice, and one that made genomics a particularly fitting area for nursing engagement.

The potential impact of this enabler was clearly illustrated in participants' accounts of real-world practice. One nurse recalled a critical intervention that arose from a routine nurse–patient conversation, demonstrating how nurses can identify unmet genomic need in real time during everyday clinical encounters and help prevent patients from falling through systemic gaps with potential adverse health consequences:

I've picked up on someone who've slipped through the cracks. I've been doing my assessment of the patient and they've started telling me about their family history of different cancers and such. I thought, 'Gee, that's an awful lot of cancers in one family'. I've asked the patient if anybody has spoken to them about genetics or genetic testing or anything like that and they've said no. Then I've gone to contact the genetics team at [REDACTED] and discussed the patient and their family history with them. They've then said that they feel that, yes, this person warrants having a full assessment.

Together, these accounts reinforce the view that nurses' routine engagement with patients, rooted in trust, proximity, and skilled communication, creates opportunities for facilitating genomic care. As such, this relational and communicative dimension of nursing is a key workforce-level enabler for future genomic integration.

6.3.3.4 Theme 4: Compatibility with advanced practice nursing

This theme identifies the perceived compatibility between genomics and advanced practice nursing roles, particularly CNSs and CNCs, as an enabler for genomic integration within the

nursing workforce. Participants described these roles as already encompassing leadership, coordination, complex clinical knowledge, and patient education, making them a logical and appropriate fit for genomic responsibilities.

Importantly, this view was expressed by both nurses working in formal genomic roles and those who had not adopted genomics into their practice. One nurse currently in a genomic role explained:

I think there's a lot of value in having advanced practice nurses that can be champions and leaders in this area and I think there are certain positions that you need to have the navigator, coordinator, advanced practice role in. But I think everybody should have an understanding of it and every oncology nurse in particular should understand how genomics, at least at a broad level, impacts the care that we're delivering, impacts the role that cancer plays, treatment and the prognosis and the tumour genesis even. So for example, we've got oncology nurses and we also have advanced practice oncology nurses. I think the same should be done for genetics.

Similarly, a nurse who did not report engaging with genomic care or working alongside genetics services nonetheless recognised the potential relevance of genomics within CNS and CNC positions. They reflected:

I think about the types of NUM [Nursing Unit Manager], CNSs and CNCs. We have breast CNCs and CNSs, we have supportive care CNSs that work in our outpatient clinic for, like, massage therapy and acupuncture and things like that. So I wouldn't see why it wouldn't be relevant—it would be quite relevant, I think, to have someone to have that discussion with patients and to specialise in that area and be able to give them a better understanding as to how to communicate their illness diagnoses and their trajectory—potential trajectory with family'.

Together, these accounts suggest that embedding genomics within advanced nursing roles is not only feasible but already seen by participants as aligned with the broader scope and expectations of specialist nursing practice. This alignment was viewed as a practical and credible workforce-level enabler for future integration of genomics into cancer nursing.

6.3.3.5 Theme 5: Support ‘on the floor’ – Genomic nurse specialists

This theme explores participants’ experiences and reflections on the value of having a genetics nurse specialist embedded within the clinical environment. Where such roles existed, they were described as highly beneficial for adoption. Participants highlighted that access to a knowledgeable, approachable resource person could improve their ability to navigate patient queries, integrate genomics into practice, and build their own genomic literacy. Even where no such specialist was available, participants suggested that introducing these roles would strengthen the adoption of genomics in nursing practice.

One participant described working with a genomic nurse in the past:

It’s such an involved field I think that you need a specialised nurse that can be a support person for other nurses. In the past I’ve worked in an area where we actually had a particular nurse in that role and it was in that way we were able to ask them for support and help or even ask them to come and help us with a patient that might have asked about the genetics in regards to their family and risk and so on. That was good.

Another nurse highlighted the potential benefits of having a genomic nurse specialist:

At least we could have someone in our team who knows what it is. It’s like me reading Chinese. I have no idea. I don’t know what I’m looking at. So, at least if someone has knowledge about that—and that will really help us because that person can act as an educator. They can teach us what’s happening. So, in the future if we encounter something like this, we know what we’re dealing with. So, it can help us to—how to manage a patient. The patient management and patient care will be far better. The quality of care which we’re going to provide is far better than what we’re providing now’.

A further participant touched on the motivational aspect of having such a resource:

If I have someone in the department who knows about it, a resource person or a resource where I could go and get all of the information, it would be a very good thing to have in our department. Then that’ll motivate not me, everyone, even the grads, to go and get that information.

While this theme fits within the domain of workforce-related factors, it also intersects with *organisational factors* (Domain 4). The establishment and support of genomic nurse specialist

roles require organisational commitment, including resource allocation and structural integration.

6.3.4 Domain 4: Organisational factors

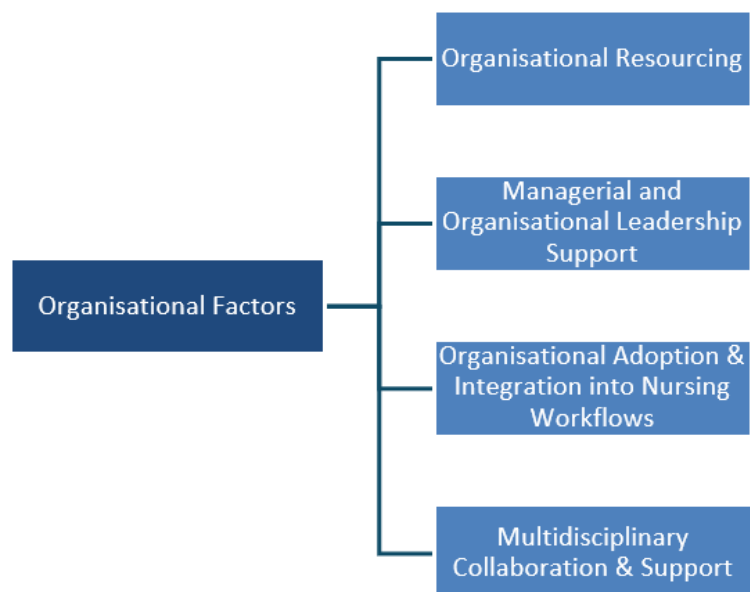


Figure 6.4. Domain 4: Organisational factors.

This domain presents how organisational factors, including funding, leadership engagement, service integration, and multidisciplinary collaboration, were experienced by participants as shaping their ability to adopt and deliver genomically informed care in clinical practice. Participants described both enablers and barriers at the organisational level, including limited financial investment, absent or disengaged leadership, and lack of embedded genetics services. Conversely, organisational support, the integration of genomics into nursing workflows, and access to multidisciplinary collaboration were reported to facilitate engagement and adoption. While these findings often intersected with individual or workforce-level experiences, participants primarily framed them as dependent on broader organisational priorities and structures.

6.3.4.1 Theme 1: Organisational resourcing

This theme captures how organisational investment shaped nurses' capacity to engage with and adopt genomics in clinical practice. Participants identified resourcing as a critical determinant of genomic integration, encompassing financial support for education and training, the creation of specialist roles, and structural provisions such as protected learning time.

A lack of organisational funding was frequently cited as a barrier, particularly where nurses were expected to self-fund their genomic education. One participant was unequivocal: ‘There’s that financial cost if your workplace is not willing to supplement or assist.’

Another participant reflected on how access to genomic training was shaped by organisational support, identifying both an enabler and a barrier within the same account. They described how their hospital’s provision of scholarships made further education possible, while also acknowledging that the lack of such support posed a broader challenge for nurses:

All these things cost, and nurses can’t afford to pay for them. We’re lucky at this hospital that we have a lot of scholarships offered which can pay for things like that, but it’s difficult if you haven’t got that to afford to pay for university things.

This account illustrates how organisational investment could enable their own genomic learning, but also underscored the systemic barrier faced by nurses without such institutional backing.

The lack of organisational funding for specialist roles was also described as a key barrier. One nurse, reflecting on the challenges of introducing a genomic nursing position, explained:

To have the hospitals recognise the need for specialists in these fields and specialists is hard with the financial side of it. I think that’s probably the biggest barrier at the moment that I see... I think that they don’t see the relevance as to the priority that we do. So creating a role that would be funded is hard.

While this comment highlights financial barriers to organisational resourcing, it also reveals a deeper issue of perceived relevance, specifically, the disconnect between nurses’ recognition of genomic care as a priority and the limited acknowledgment of its importance at the organisational level. This issue of perceived relevance is further explored in Theme 2 of this domain and also discussed from an individual perspective in Domain 5, Theme 5.

Participants also described the provision (or lack) of protected time for learning as a resourcing issue. While this was discussed in the context of broader workforce barriers in Domain 3, several participants also framed this as an organisational failure to allocate structural support for continuing education.

Despite these barriers, participants also pointed to organisational resourcing as an enabler. Three participants held formal genomic nursing roles, funded by their hospitals, which provided

dedicated time and recognition for their involvement in genomic care. These roles were seen as clear indicators of organisational commitment and facilitated wider genomic adoption by embedding genomic advanced nursing practice within the clinical team.

6.3.4.2 Theme 2: Managerial and organisational leadership support

This theme captures participants' perceptions of limited engagement and support from managerial and senior nursing leadership in the integration of genomics into nursing practice. Participants described a lack of awareness, understanding, and prioritisation of genomic innovation among leadership. This disengagement ranged from passive disinterest to active resistance, creating organisational inertia that, in some cases, undermined nurse-led initiatives or requests for genomics training.

One participant highlighted the knowledge gap among educators: 'The educators aren't necessarily... upskilled or knowledgeable in genomics.' This reflected a broader concern raised by some nurses about the challenge of upskilling when those in positions of guidance (such as clinical nurse educators and managers) lacked foundational genomic knowledge themselves.

Another genomic nurse noted a lack of understanding from their manager: 'I don't think my manager quite knows what I do.' This example illustrated the potential disconnect between individual genomic roles and broader managerial comprehension of their purpose or potential impact.

When asked about barriers to adopting more genomics into daily practice, one nurse pointed to the role of leadership perceptions:

On paper it sounds really easy but I think because a lot of like middle and senior management doesn't see the point... it doesn't really give us room at the moment to do that... Given that middle management and senior management don't even see the applicability of this yet on our day to day. They're not really keen to help us bridge that gap.

This account highlights how managerial disengagement was closely linked to a lack of perceived relevance at the organisational level. While individual perceptions of relevance are explored in Domain 5 (Theme 5), this example illustrates how similar dynamics operate at a structural level, with leadership's failure to recognise applicability stalling broader implementation efforts.

Another participant recounted their experience proposing a genomics in-service to management: ‘It’s always “Yes, but...” or “Yeah, we can—absolutely I’m supportive of an in service”, but again only one person turns up, because there was a clinical priority.’ This reflects a superficial endorsement from management without the corresponding structural support, such as protected learning time. As noted in Theme 1 of this domain, and previously discussed at the workforce level in Domain 3, Theme 1, these constraints on education access are framed as significant barriers to engagement with and adoption of genomics.

In one instance, a participant faced direct opposition when attempting to incorporate genomics into their practice. This nurse recalled:

Every attempt I have made and been like, ‘Oh maybe I could do a case study on the haematology patient and link it back to the genetics’. Talking a little bit about the basics so the nurses can understand this a bit better, I was shut down by my manager and education department.

6.3.4.3 Theme 3: Organisational adoption and integration into nursing workflows

This theme captures how the integration of genomics into routine nursing workflows and the organisational adoption of genomic testing into clinical pathways functioned as key enablers of genomic practice. As genomics became embedded in some institutional protocols, particularly through initiatives such as mainstream genetic testing, nurses working in these settings reported increased engagement, comfort, and role clarity in genomic care delivery. These changes positioned genomics as a standard component of oncology care, fostering familiarity through necessity and routine exposure.

The organisational adoption of genomics into standardised care models emerged as a significant driver of nursing engagement. Nurses described how mainstream testing programs were embedded within clinical routines, shifting genomics from a peripheral interest to a central feature of nursing work. One participant, reflecting on this transition, noted: ‘Most recent change in the last few years has probably been introduction of mainstream testing, particularly for breast cancer.’

‘Mainstream [genetic] testing’ in Australia refers to a government-funded program enabling oncology teams to offer genetic testing directly to eligible patients as part of routine care (see 1.2.7). This initiative aims to improve the early identification of inherited cancer predispositions by streamlining referral pathways, diagnosis, and proactive management. In settings where this

program is offered, nurses commonly facilitated key steps in the testing process, such as consent and patient education. As one participant described:

If there's an oncologist who's got patients coming into day oncology that wants a test here, I just go over and explain it and consent them... I provide the explanation and introduction to it and explain what it's all about to get consent for the test.

This integration of genomics into existing workflows, such as consent, sample collection, and multidisciplinary coordination, enabled nurses to engage with genomic care without requiring formal titles or specialised roles. Several nurses reported that these responsibilities aligned naturally with their scope of practice, providing opportunities for skill development through hands-on engagement. One nurse noted that their organisation adopting mainstream testing was their entry-point to the topic, reporting that their initial exposure to genomics occurred through '[l]earning about the mainstreaming genetics program'.

This exposure contributed to growing awareness of genomics, reinforcing patterns observed in Domain 5, Theme 3 in the context of individual-level-factors. As one nurse put it, 'There's also a little bit more awareness of mainstreaming testing, which has changed quite a bit'. The routinisation of genomic processes enhanced visibility and helped normalise genomics in everyday practice. As clinical workflows evolved and genomics became embedded into standard practice, nurses increasingly viewed it not as a niche or specialised domain, but as an expected element of comprehensive cancer care.

6.3.4.4 Theme 4: Multidisciplinary collaboration and support

This theme captures how organisational structures that fostered collaboration across disciplines supported nurses' engagement with genomics. Participants highlighted the value of working alongside genetic counsellors, clinical geneticists, consultants, pathology services, and research staff. They described how embedded roles within multidisciplinary teams, regular multidisciplinary meetings, and proximity to specialised expertise contributed to skill development, increased awareness, and confidence. These collaborative environments were seen to make genomics more accessible, visible, and embedded in routine nursing care.

Multidisciplinary team (MDT) meetings were frequently described as valuable opportunities for informal learning. Participants highlighted how structured discussions, including weekly molecular tumour boards and departmental MDT meetings, exposed nurses to real-time clinical reasoning and case-based knowledge related to genomics. Through observation, discussion, and

case review, nurses reported developing a contextual understanding of genomic concepts within the complexities of cancer care. One participant explained, ‘We have weekly multidisciplinary team meetings... so you sort of just listen and learn’. Another nurse similarly reflected, ‘Our team meetings are very much talking about patients... to build up that knowledge and kind of baseline understanding of it’, while a third noted, ‘We run a Molecular Tumour Board once a week... that has been huge learning’.

Collaboration with consultants and oncology specialists further supported nurses’ engagement with genomics, particularly when those clinicians were supportive or willing to share updates. One nurse explained, ‘All the oncologists will update the staff there about the new therapies and things like that’. Genomic nurses especially described strong working relationships with clinicians as enabling: ‘The clinicians that I worked with were really supportive... the oncologist in particular’, and ‘I feel that the oncologists here are very aware of the service and very supportive’.

However, some participants described a more hierarchical dynamic in which genomic decision-making was predominantly led by medical consultants. These accounts suggest that organisational structures and cultural norms within certain services shaped the extent of nursing involvement. One nurse observed:

When we’ve had our triple negative breast cancer patients and we look at testing, genetic testing. We have terminology thrown around, but it’s been mainly like say, consultants, medical oncologist consultants that discuss this while we do the notes.

While this quote aligns with the workforce-level dynamics discussed in Domain 3, Theme 2 (*scope boundaries and role delineation*), it also reflects broader organisational patterns that influence how nursing roles are operationalised within genomic care. Another nurse emphasised the variability between settings:

It may depend on the location, so where they are... a lot of the mainstreaming happens at our cancer centre with the oncologists who do it. Some of them, they just control that process and do the process of the mainstreaming.

These examples illustrate that while collaboration with consultants was often reported as an enabler, it was not universal and appeared contingent on the organisational context.

In addition to medical consultants, collaboration with surgical and pathology teams was also reported as an enabler. One nurse, when asked to reflect on what supported her ability to adopt genomics into practice, described how efficient interdepartmental coordination and timely communication facilitated the referral process:

The biggest one is the pathology service... [they] have a turnaround of about four days... After the multidisciplinary team meeting, the surgeons will come around and tell the patients their results and then I'm usually with them then... The enabler is the speed that we get the histopathology back and the cooperation between the surgeons, and the pathologists, and the theatre staff to get the samples over there, so it's streamlined.

Strong working relationships with clinical genetics services, particularly genetic counsellors, were another reported enabler of genomic adoption. These relationships provided support, clarification, and education, often through informal interactions or shared clinical roles. One nurse explained that when issues arose in practice related to genomics, she would often seek guidance from genetics colleagues: 'I will often... go back to one of the genetic counsellors that I work closely with, or with the geneticist, and talk to them about it.' Another described a more structured arrangement, noting, 'I meet with the geneticist every week, so if there are any questions, or anything coming up, we can talk about any changes. I meet with the genetic counsellor once a fortnight.' Several participants highlighted the value of proximity to genetics staff in building confidence and knowledge. One nurse commented:

The genetic counsellors did the training, which was a half hour session particularly around ethics and that kind of aspect of it and then just build on it. Because I work in the team with the genetic counsellors, they're very easy to just have that conversation with and if there was something I didn't know.

Another reflected:

When you get to know the genetic counsellors and that they're passionate about their field as well, so they're more than happy to share their knowledge to help, I guess, spread the word. I guess I could see them as enablers in helping.

Conversely, limited access to genetic services was reported as a barrier to adoption. Three participants who described minimal or no engagement with genomics also reported working in organisations without onsite genetic counsellors or clinical geneticists. One nurse, working in

a regional hospital without integrated genetics support, reflected on how this organisational isolation impeded coordinated care and limited shared knowledge:

That blindness... are we aware? are we liaising with the other hospital?—which we are not—but then if we have service here with us, we know what’s happening. Then we have a bit more cohesion of the care rather than people working in isolation. At the moment our department, we are working in isolation.

In this account, ‘blindness’ refers to the absence of communication and visibility between services, which results in fragmented and disconnected care. The quote underscores both the barrier, organisational isolation, and the potential enabler: that co-locating genetics services within the organisation could enhance cohesion and collaboration.

Finally, collaboration with research nurses and clinical trials teams was also described as an organisational enabler of genomic engagement. These collaborations exposed nurses to emerging therapies and genomic principles in an applied context, often fostering informal learning and increasing awareness. In some settings, research staff provided informal education and invited clinical staff into trial-related activities, creating opportunities for skill development without requiring formal training. Nurses described learning ‘by osmosis’ through trial-related tasks, blood sample collection, and study involvement. One participant, reflecting on how this integration supported learning, explained:

Often we would have two or three patients where we would be required by our research team to take bloods and help with them gathering as much data as possible. So the staff on the floor as such became over the months, particularly last year with some of the newer discoveries coming out, began to see the importance of why we did this particular part of the work... So I must admit our research team do a little bit of education in that area as well and involve the staff as much as they can too. So it does bring the awareness there.

This account illustrates how research activity intersected with routine nursing work, reinforcing themes of *workflow integration* (Theme 3), *growing awareness* (Domain 5, Theme 3), and the *increasing perceived relevance of genomics in contemporary cancer care* (Domain 5, Theme 5).

Another nurse echoed this view, describing how exposure to novel therapies within research-focused settings fostered organic, contextualised learning:

Because we are seeing all these new novel agents and we're trialling a whole lot of stuff... this sort of high quality care environment, where you're participating in research... And possibly a little bit of knowledge through osmosis I think.

These reflections suggest that involvement in research and clinical trials not only facilitated practical genomic literacy but also helped reposition genomics as a routine and relevant component of high-quality cancer care.

These accounts highlight how collaboration with specialist colleagues and inclusion within multidisciplinary structures enabled genomic engagement across diverse nursing roles. Organisational models that fostered these collaborations were seen as integral to supporting knowledge-building, practice integration, and confidence in delivering genomics-informed care.

6.3.5 Domain 5: Individual factors

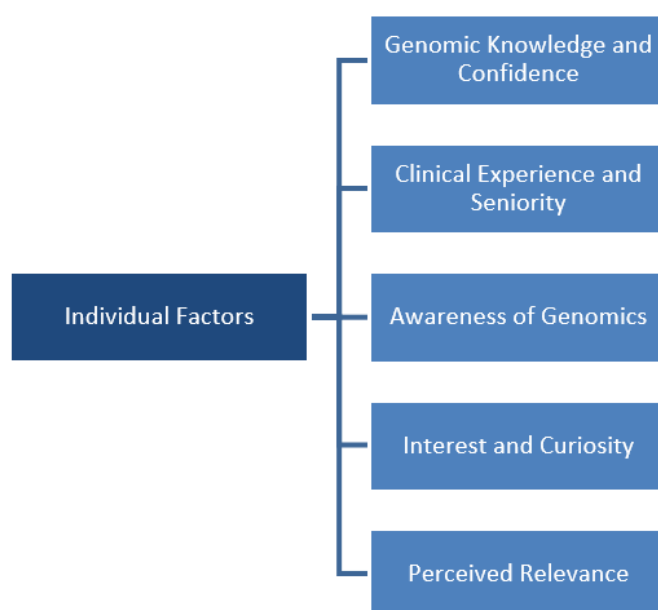


Figure 6.5. Domain 5: Individual factors.

This domain explores how nurses' individual characteristics, such as personal knowledge, clinical experience, baseline awareness, personal interest, and perceived relevance, shaped their engagement with genomics in cancer care. While experienced nurses often described greater comfort with and integration of genomics, early-career nurses were perceived to encounter more barriers, including limited exposure and competing clinical priorities. Although these factors intersected with broader educational and organisational conditions, they were

consistently framed as key enablers or barriers arising from within the individual. The following themes examine how these internal dispositions supported or constrained genomic adoption.

6.3.5.1 Theme 1: Genomic knowledge and confidence

This theme reflects participants' reports of limited genomic knowledge and minimal clinical experience, which contributed to a lack of confidence in engaging with genomic care. Nurses who were not in formal genomic roles consistently described knowledge and confidence as foundational barriers to adoption. Participants reported uncertainty about genomic concepts, discomfort in applying them in practice, and hesitancy in initiating patient conversations due to fear of providing incorrect or insufficient information.

One nurse clearly articulated this barrier, stating, 'I guess one of the barriers is having enough knowledge to feel confident in talking about this'. Even among nurses who reported some genomic engagement, such as facilitating consent, limitations in knowledge were evident. As one participant explained, 'Like, I only have really the basic understanding of genetics and it's very specific to ovarian cancer'.

Participants in formal genomic roles echoed these observations, describing significant knowledge gaps among their colleagues. One such nurse noted a fundamental misunderstanding of genetics relates to cancer: 'I think there's still a lack of, you know, even a lack of that somatic understanding of that even a cancer cell has got some genetic change in it.'

This lack of knowledge was closely linked to a perceived lack of preparedness for genomic and psychosocial conversations. The emotional weight of genomic innovations was discussed in Domain 1, Theme 4, and this intersects with how nurses described feeling under-equipped to support patients navigating genomic uncertainty, with several citing difficulty answering patient questions and concern about inadvertently causing distress. As one nurse explained, 'I find that there's a lot of areas where the nurses are unsure of how to ask the questions, how to broach the more difficult topics and how to manage the patients' response'. Another participant reflected on this issue, describing herself and her colleagues as ill-equipped and lacking in the necessary knowledge to manage patient questions:

Many female—specifically female patients—they come ask, 'Is my daughter going to get this disease?' Then it's a very difficult thing to answer. We don't know... we don't know how to deliver this talk.

This challenge was particularly evident in settings where genomics had not been integrated into practice, or where nurses did not perceive themselves as genomic adopters. Patient expectations and information-seeking behaviours, often prompted by familial risk concerns, frequently exposed nurses' knowledge gaps. One nurse reflected:

We do have patients that come in and say, you know, 'I don't have a history of, say, breast or pancreatic or colorectal cancer in my family. You know, this doesn't run in my family, why is this happening?' I just genuinely don't have an explanation for them... wish I did... I just feel like I'd have a bit more in my toolkit to be able to know what to say. I just feel like I don't know what I don't know when it comes to the topic. So, when those sorts of things are raised, when, you know, you're by the bedside and someone says, 'I don't know why this is happening to me. I've been healthy all my life. Is it because of my genes, or is it because of my—like, my aunt had something like this?', I actually don't know what to say.

These emotionally charged interactions, often directed to nurses due to their close proximity and trusted relationships with patients (as discussed in Domain 3, Theme 3), underscored not only the emotional complexity of genomic care but also the practical challenges nurses faced in the absence of adequate training. While these deficits were consistently described as barriers, they also paradoxically acted as enablers by prompting self-reflection and motivating nurses to pursue further education.

This dynamic was particularly evident when a participant described a clinical encounter in which a lack of genomic knowledge and limited access to genetic counselling contributed to adverse patient outcomes. The patient in question had a significant family history of cancer, with all affected relatives having died from the condition. Upon learning of a genetic cause underlying the cancer in their family, the patient appeared to interpret this information fatalistically, believing she was destined to suffer the same fate as her deceased relatives. This case occurred in a small regional hospital where genetic counselling was not embedded in her primary treatment pathway. The participant, a nurse who was caring for the patient during her chemotherapy admission, recounted the emotional impact of the genetic information, which led the patient to abruptly discontinue treatment: 'She just dropped out of the treatment completely. She said "I don't want to do it, anyway I'm going to die".' The experience had a profound impact on this nurse and prompted them to pursue further education on the topic: 'I think I wish

I would have had a bit more knowledge about it. I went ahead and researched about it, but I think it was too late. She didn't turn up, she didn't come back.'

Together, these accounts underscore how deficits in genomic knowledge and confidence constrained participants' ability to engage with genomic care and respond meaningfully to patient needs, while also highlighting the potential for such deficits to catalyse professional growth.

6.3.5.2 Theme 2: Clinical experience and seniority

This theme captures the way some nurses described years of experience and clinical seniority as shaping their confidence and ability to engage with genomics in practice. Participants who held formal genomic roles or regularly facilitated mainstream testing and genomic consenting consistently framed their own longevity of experience as a key enabler of genomic adoption. These individuals emphasised how cumulative exposure over time, through observation, case familiarity, and ongoing practice, built their comfort with genomic conversations and processes.

One participant reflected on their capacity to learn more about genomics: 'I've probably absorbed a lot of knowledge over many, many years. So for me it's not a big issue.' Another participant commented on their ability to manage complex questions: 'I've been nursing for a long time, so it's hard to stump me and throw me off.' These nurses described being confident in broaching genomics with patients and integrating it into care, particularly when discussing complex issues such as familial risk.

However, it is important to note that these views were shared almost exclusively by senior nurses who are either in genomic roles or who actively adopt genomics in practice (e.g., by facilitating mainstream testing). In contrast, these more experienced participants described early-career nurses as facing greater barriers to genomic engagement. They suggested that less experienced nurses lacked the clinical maturity and exposure necessary to confidently engage with genomics. One senior nurse commented, 'I feel quite comfortable in having those sorts of conversations. I think there probably needs to be more education available for younger nurses.'

Another spoke of how a junior nurse might experience a Molecular Tumour Board meeting, remarked: 'You throw a junior nurse into that, they're going to walk off either half asleep or crying.' Similarly, early-career nurses were perceived to struggle due to high workloads and limited genomic exposure: 'It's something the younger ones struggle with because they are so busy. I think it's a time-poor thing.'

Importantly, these perspectives were offered by senior nurses and were not echoed by the two participants who were <5 years post-registration. Nonetheless, these accounts collectively illustrate how clinical experience was framed as an internal enabler of confidence and capability, while early-career status was often constructed as a barrier.

6.3.5.3 Theme 3: Awareness of genomics

This theme captures how participants framed awareness as a foundational individual-level factor shaping genomic engagement. Several nurses described general awareness of genomics as limited among their peers, noting that without visibility or promotion, genomics remained peripheral to many nurses' practice. Lack of awareness was seen not only as a barrier to knowledge acquisition but also as limiting curiosity and perceived relevance.

One participant reflected on the role of awareness in driving genomic engagement:

More awareness. Knowledge is powerful... So I think more education I think is the key. Being aware of the relevance of genetics as well. What the relevance and why it is important.

Another participant emphasised the need for broader visibility of genomics in oncology settings:

I think overall promotion of– genomics needs to be promoted. I mean, when we think of oncology, cancer and everything, genomics I believe is not very promoted kind of thing. So, it needs to be more– people need to be more aware of it. It's something to be more aware of. When you're more aware of it, then you try to learn more about it, try to know more about it. You have the curiosity to learn.

These accounts position awareness not as a passive state but as a precondition for motivation, learning, and, ultimately, adoption. As such, low awareness was framed as a barrier, while increased visibility and promotion of genomics were seen as essential enablers for engagement.

6.3.5.4 Theme 4: Interest and curiosity

This theme captures how personal interest and intrinsic curiosity were described as individual-level enablers of genomic engagement. Participants noted that interest in genomics was not uniformly distributed across the nursing workforce and was often the determining factor in whether nurses pursued further knowledge or engaged with genomic innovations.

When asked directly about enablers to genomic adoption, one participant responded succinctly: ‘Interest. Personal interest in the area.’ Another echoed this sentiment, reflecting on the broader applicability of genomic responsibilities and how uptake depends on individual motivation: ‘Well, across Australia the gynaecology clinical nurse consultants could all learn this, and all do it on the spot in their own hospitals, but it’s just a matter of whether they’re interested.’ The importance of interest as a precursor to adoption was also evident in another participant’s comment: ‘You’d really have to have nurses who are interested in genetics and women’s health in the first place.’

While this theme focuses on interest, curiosity also emerged as a linked concept that supported interest and engagement. In the domain of *workforce-related factors* (Domain 3, Theme 1), some participants described an absence of curiosity as a cultural barrier to interest in and adoption of genomics. In contrast, others described how curiosity and interest interplay with exposure to genomic education. One participant recalled: ‘I have had a new grad, that after my [in-service] talk come to me and be like, “Wow this is really interesting. I want to know more about this in cancer”’.

The connection between curiosity, interest, and awareness was also captured in a quote previously used in the analysis of awareness. In that example, the participant reflected on how awareness could foster curiosity: ‘When you’re more aware of it, then you try to learn more about it, try to know more about it. You have the curiosity to learn.’

Together, these accounts highlight how individual curiosity and interest functioned as enablers for learning and engagement.

6.3.5.5 Theme 5: Perceived relevance

Perceived relevance to clinical practice emerged as a critical factor influencing nurses’ engagement with genomics. Participants who had adopted genomics into their roles, either through formal positions or by facilitating mainstream testing, consistently described the integration of genomics as both clinically necessary and professionally motivating. These nurses emphasised its importance in contemporary cancer care and often advocated for increased awareness and uptake among their colleagues.

One participant discussed the increasing relevance of genomics to practice and how this ‘future of cancer nursing’ has motivated their desire to adopt:

I think these things [genomic innovations] will actually motivate everyone including me to take the time out to invest in the future, because this is going to go in the long run. So, if you're going to be an oncology nurse for the next 30, 40 years this is the future of cancer nursing.

Another participant reflected on this shift:

Like the knowledge has exploded in recent years. Especially since the human genome was done. Instead of it just being a niche area, it's now becoming an area where it really needs to be considered in almost every patient's diagnosis.

Participants who perceived genomics as relevant often pushed for wider awareness and education among peers. However, in contexts where genomics was not yet embedded or routinely discussed, nurses described challenges in conveying its significance and how this acted as a barrier to wider adoption. One participant reflected:

If I spoke to any of the colleagues that they still would have no idea about genomics and I'm trying to push that education, but it's not high on the agenda. You know, with febrile neutropenia and sepsis and what is leukaemia and what is daunorubicin, you know, impact their right now daily care, it's hard to push that relevance of what genomics and genetics is and how that impacts their care, particularly when they've come up in a system that doesn't mention it in their training at all.

Another nurse described how relevance was often overshadowed by more immediate concerns in early clinical practice:

I think in the early stages, the important stuff is generally around the main cancer diagnoses and the treatments and side effects of all of those and what they need to do to support patients. Looking at the deeper things, like genomics and stuff is probably, 'Oh yeah, I'll do that later'.

In these cases, the failure to perceive genomics as directly relevant was described as a significant barrier. Similarly, a lack of perceived relevance was framed as a reason for resistance to genomics more broadly:

It is hard because like, I guess if we can make it more apparent how genomics can be applicable, cost and time efficient, we'd probably have a good case. But there will

always going to be resistance on things that they don't see the applicability, like right there.

While this theme focuses on individual perceptions of relevance, it is important to note the interplay with organisational context. As explored in Domain 4 (*organisational factors*), some participants described how their managers or broader institutions did not recognise the clinical value of genomics, which limited systemic support for its integration. These organisational-level barriers further shaped how relevance was understood and acted upon at the individual level.

6.4 Conclusion

This chapter has presented the findings from the qualitative phase (Phase 2) of the study, detailing the themes generated through the analysis of interview data. Five key domains were identified: attributes of the innovation, education-related factors, professional factors, organisational factors, and individual factors, with each domain comprising themes illustrated through participant accounts.

The next chapter brings together the findings from both phases to provide an integrated discussion of the study. It offers theoretical interpretation, situates the results within the wider literature, and explains how the findings contribute to the existing body of knowledge. The chapter also outlines the study's limitations, presents recommendations for research, practice, and policy, and concludes the thesis.

Chapter 7 – Discussion

7.1 Introduction

This chapter discusses the findings of the study in relation to its overarching research question: *How do oncology nurses in Australia engage with genomics, and what individual characteristics and perceived barriers or enablers influence its adoption into practice?* The study was designed to address three aims: (1) to assess oncology nurses' knowledge, engagement, and adoption of genomics in practice across Australia; (2) to identify individual characteristics associated with the uptake of genomics in nursing practice; and (3) to explore perceived barriers and enablers to integrating genomics into oncology nursing practice.

These aims were addressed through a mixed-methods study design underpinned by a pragmatic worldview. A scoping review of the international literature was first conducted to map existing evidence on oncology nurses' knowledge and attitudes towards genetics and genomics (Chapter 3). Subsequently, Phase 1 involved a quantitative survey to assess levels of genomic knowledge, engagement, and adoption among Australian oncology nurses, and Phase 2 comprised semi-structured interviews with a purposive subsample of survey respondents. Together, these strands provided complementary insights into both the scope of current knowledge and adoption, alongside the contextual barriers and enablers shaping genomic integration into oncology nursing practice.

The purpose of this chapter is to integrate and interpret the findings from both quantitative and qualitative phases, situating them within the wider literature and theoretical framework. In line with the mixed-methods design, it begins with an integration of the Phase 1 and Phase 2 results, highlighting points of convergence, divergence, and amplification. The discussion then addresses each research aim in turn, with particular emphasis on the barriers and enablers of genomic adoption as the central focus of the study, interpreted through Rogers' (2003) DOI theory. This is followed by a dedicated section providing theoretical interpretations of the findings. The chapter then outlines the study's limitations, contributions to knowledge, recommendations, and future research directions, before concluding with a summary of the thesis.

7.2 Integration of quantitative and qualitative findings

A defining feature of this study’s mixed-methods design was the integration of findings during the interpretive phase. In line with guidance from Creswell and Plano Clark (2018), Fetter et al. (2013), Fetter (2019), and the more recent guide proposed by Skamagki et al. (2024), integration was approached as a process of systematically comparing, contrasting, and synthesising the quantitative and qualitative strands. This enabled the identification of areas of convergence (alignment between datasets), divergence (where findings pointed in different directions), amplification (where one dataset elaborated or deepened the other), and alignment (where one strand contextualised the other). Through this process, the study was able to generate meta-inferences that extend beyond the scope of either dataset alone (see 4.5). This approach was particularly valuable in the present study, as the survey provided a broad overview of knowledge, adoption, and individual characteristics, while the interviews offered in-depth insight into the contextual barriers and enablers shaping practice. Integrating these strands allowed for a more comprehensive account of genomic adoption than either could achieve alone.

An illustrative excerpt of integrated findings examples is presented in Table 7.1, which maps key areas of convergence, divergence, amplification, and alignment across the survey and interview data. The table shows how integration was undertaken through three selected findings and demonstrates the approach used to compare and synthesise the datasets, forming the basis for the subsequent interpretive synthesis. To extend this, three narrative examples are also presented to illustrate how integration added depth and nuance to the findings.

Table 7.1. Illustrative example of data integration

Theme / Focus Area	Quantitative Finding	Qualitative Finding	Integration Insight (Type)
Adopter characteristic	Adopter traits: older age, higher grade, more experienced	Younger nurses were less confident and struggled more with genomic concepts	Convergence
Barriers	(3%) identified lack of managerial support as a barrier to using genomics	Support from managers was critical; describing the absence of support as a major barrier and its presence as a key enabler.	Divergence
Barriers	26% reported that ‘no relevant resources’ were available to support their learning	Discussed limitations of current resources and opportunities for improvement. Existing resources are overly complex, poorly aligned with nursing practice, and difficult to apply clinically. Trusted sources identified (e.g., CNSA)	Amplification

As outlined in the table, a clear instance of convergence concerned the role of age and experience. Survey results indicated that likely adopters were significantly older and more experienced than non-adopters, and interview participants likewise observed that younger nurses were less confident and struggled more with genomic concepts.

In contrast, managerial support highlighted a point of divergence. Only a small proportion of survey respondents (3%) identified lack of managerial support as a barrier to using genomics, yet interviewees consistently emphasised it as a critical factor, describing the absence of support as a major barrier and its presence as a key enabler.

A further example of integration was provided by genomic education resources, which illustrated amplification. In the survey, 26% of participants reported that ‘no relevant resources’ were available to support their learning. The interviews elaborated on this, revealing that existing resources were often overly complex, poorly aligned with nursing practice, and difficult to apply clinically. At the same time, participants pointed to trusted sources such as eviQ and CNSA as valuable, while calling for simplified, centralised, and nursing-specific resources. This qualitative elaboration deepened the survey insight, highlighting both the limitations of current resources and opportunities for improvement.

These select examples demonstrate how integration strengthened the explanatory power of the study. Convergence reinforced key findings, divergence revealed discrepancies warranting further consideration, and amplification added richness to survey responses. These integration insights provide a bridge into the following sections, where findings are discussed in relation to the study’s three aims, with particular emphasis on the barriers and enablers of genomic adoption.

7.2.1 Oncology nurses’ knowledge, engagement, and adoption of genomics in practice across Australia

Levels of genomic knowledge among participants were variable. While most recognised core applications such as cancer genetics and family history, just over half (57%) correctly identified that genomic variation can influence medication response. This is a significant finding, as understanding of pharmacogenomics and the ability to take a comprehensive family history are increasingly essential concepts for oncology nursing practice (Cheek et al., 2015; Germany & Kueber, 2023; Swadas et al., 2022). The relevance of pharmacogenomics to oncology care is particularly salient in the era of precision healthcare, making this knowledge gap concerning.

These findings parallel other studies that also report low levels of pharmacogenomic knowledge among nurses (Dodson, 2014; Swadas et al., 2022).

In relation to family history, participants demonstrated sound understanding of key elements needing to be included, such as documenting other cancers and medical conditions in the family, including three generations and ages of disease onset; however, only 59% identified consanguinity as information that should be included. Consanguinity is an important consideration in genetic risk assessment, as it increases the likelihood of autosomal recessive conditions and shared genetic variants within families (Bishop et al., 2008; Oniya et al., 2019). This suggests limited knowledge of more complex aspects of genomic concepts and an incomplete understanding of the genetic mechanisms contributing to hereditary cancer risk. This aligns with recent research from the UK which found that nurses possess a basic foundational understanding but lack awareness of more advanced genomic concepts (Cuthill et al., 2025).

Confidence in collecting family history information was also limited, with more than half of participants reporting low to moderate confidence (ranging from not at all to somewhat confident). Similarly, confidence in educating patients about genetics was low. Both actions are established indicators of genomic engagement and are essential components of nurses' competence in this domain (Calzone et al., 2024; Calzone, Jenkins, et al., 2018). Lower confidence in determining which aspects of family history are indicative of genetic susceptibility has been shown to be associated with reduced use of family history in practice (Calzone, Jenkins, et al., 2018). Taken together, these findings underscore the close relationship between knowledge, confidence, and genomic engagement, and highlight an important area for further development within Australian oncology nursing.

Within the Diffusion of Innovations framework, knowledge and awareness represent the earliest stages of adoption, shaping how individuals perceive an innovation's relevance and potential advantage (Rogers, 2003). In this study, familiarity with genomic resources and initiatives was generally limited, particularly in relation to local specialist genetics services. Such limited awareness constrains opportunities for knowledge development and engagement, which are necessary precursors to adoption. From a diffusion perspective, this suggests that many oncology nurses remain positioned in the early knowledge stage of the adoption process, which may impede progression toward active implementation of genomics in practice.

This interpretation is consistent with earlier work by Dearing and Taverner (2018), who identified lack of familiarity with genetic services as a barrier to integrating genetics into practice among palliative healthcare professionals, including nurses. Andrews et al. (2014b) likewise recognised familiarity with genetic services as a key indicator of genetic adoption. Taken together, these findings suggest that while awareness of genomics is emerging, the practical skills and self-efficacy required for implementation may not yet be established among many oncology nurses. This highlights a critical competency gap within the Australian oncology nursing workforce and represents an important empirical contribution to understanding genomic readiness in this context.

Despite gaps in knowledge and awareness, participants' attitudes toward genomics were generally positive. Most agreed that genomics is relevant to oncology nursing and endorsed the importance of incorporating it into continuing professional development. This attitudinal openness is consistent with other studies reporting that oncology nurses value the potential relevance of genomics even when they feel underprepared to apply it in practice (Carpenter-Clawson et al., 2023; Dodson, 2014; Metcalfe et al., 2010; Wright et al., 2020). Within the DOI framework, perceived relevance corresponds to Rogers' attribute of compatibility—the extent to which an innovation aligns with existing professional values and the perceived remit of oncology care. The recognition of genomics as pertinent to cancer care suggests that oncology nurses conceptually accept its utility and congruence with their clinical role. However, positive attitudes alone rarely translate into behavioural adoption; DOI theory emphasises that favourable perceptions must be supported by adequate knowledge and confidence to progress beyond the persuasion stage (Rogers, 2003). The convergence of positive attitudes with limited practical readiness observed here therefore represents an early, receptive phase of diffusion rather than established implementation.

The limited implementation evident in these findings is further reflected in the low levels of engagement reported by participants. Most nurses had made few or no referrals to genetic services, seldom discussed genomics with colleagues, and described variable patterns of information-seeking. Referral to specialist genetic services is recognised as a core competency for oncology nurses, yet limited awareness of these services and their available resources likely contributes to the low referral rate observed. Without adequate knowledge of when and how to refer, nurses are unable to integrate genomics effectively into patient care. This aligns with recent findings by Cuthill et al. (2025), who reported that cancer nurses often lack knowledge about how to order genomic testing, how to communicate with specialist genetic teams, and

how their role fits within these processes. Related findings were noted by Dearing and Taverner (2018), who reported that unfamiliarity with referral pathways, uncertainty about how to access referral guidelines, and limited connection with genetics services were key barriers to integrating genetics into practice.

Within the DOI framework, these engagement behaviours represent early operational expressions of adoption, signalling whether awareness and interest have begun to translate into observable practice change. The infrequency of referrals and professional dialogue observed here further confirms that diffusion remains at an early stage, with genomics yet to achieve normalisation within oncology nursing practice. This limited engagement reinforces the disconnect between conceptual acceptance and practical uptake evident across the dataset, underscoring that positive attitudes alone are insufficient to sustain implementation without the accompanying development of practical competencies and system-level supports. In particular, the need to strengthen nurses' awareness aligns with the findings of Limoges et al. (2022), who emphasise that strengthening nurses' awareness of how genomics intersects with everyday practice is a critical step toward enhancing integration.

Collectively, these findings depict a workforce receptive to genomic practice but still developing the foundational competencies necessary for its broader adoption in oncology nursing. Building on this understanding of nurses' genomic knowledge, confidence, awareness, and engagement, the study also sought to distinguish nurses who are likely to adopt genomics in their practice and to elucidate the individual characteristics associated with adoption. To do so, demographic, professional, and behavioural variables were compared between those identified as likely adopters and those less engaged with genomic practices.

7.2.2 Identifying individual characteristics associated with the uptake of genomics in nursing practice

Building on this understanding, the analysis examined how individual characteristics shape the uptake of genomics in practice. Drawing on Rogers' DOI framework, Leach et al. (2016) proposed that identifying and supporting early nurse adopters is a critical strategy for accelerating genomic integration, emphasising adoption as a social and behavioural process rather than a purely educational one. Similarly, Andrews et al. (2014b) highlighted the importance of distinguishing adopters within nursing contexts to understand how new practices diffuse through professional networks. Extending this work, the present study provides the first empirical examination of adopter characteristics among Australian oncology nurses, exploring

how demographic, professional, and personality attributes, such as openness to experience, opinion leadership, and cosmopolitanism, relate to genomic uptake. A composite adoption score, adapted from Andrews et al. (2014b) for the Australian context, enabled the classification of participants as likely adopters or non-adopters, offering a novel approach for examining diffusion processes within this workforce.

Analyses comparing likely adopters and non-adopters revealed several demographic and professional distinctions. Adopters tended to be older, had more years of oncology experience, and were more frequently represented in advanced practice roles, whereas non-adopters were typically younger and more often employed at the Registered Nurse level. Adopters were also more likely to hold postgraduate qualifications. These findings align with Rogers' proposition (see Section 2.4.2) that earlier adopters tend to have higher formal education and occupy positions of greater social status or occupational prestige, factors that enhance exposure to new ideas and perceived authority within professional networks (Rogers, 2003).

Although age was associated with adoption in this study, this does not contradict Rogers' later position, as he noted that empirical findings on age and innovativeness are inconsistent and therefore concluded that earlier and later adopters do not differ systematically in age (see Table 2.1) (Rogers, 2003). Within this context, the relationship between age and adoption may be non-linear, and the association observed here may reflect a context-specific or role-related pattern rather than a direct effect of age itself. It is possible that among mid-career nurses, age exerts little influence, whereas in more senior age groups greater experience, autonomy, and role breadth may enhance opportunity for trialability.

Comparable work by Andrews et al. (2014b) did not identify significant demographic differences between adopters and non-adopters, a discrepancy that may partly reflect the limited generalisability of their sample. Findings from several studies identified in the present scoping review (Chapter 3) offer a broader context. Cuthill et al.'s (2025) findings strongly align with this study's results; they reported that confidence in genomic knowledge and test selection was higher among respondents aged over 55, attributing this to experiential learning 'on the job'. Liu et al. (2021) likewise found that years of experience significantly influenced genetic knowledge, while Metcalfe et al. (2010) observed that senior nurses expressed greater confidence in managing the psychosocial dimensions of genetic care. Other investigations have not detected such associations (Kocatepe et al., 2022; Liu et al., 2011; Quinn et al., 2014; Seven et al., 2017), and Dornelles-Prolla et al. (2015) even reported lower knowledge among more

experienced clinicians, which they attributed to a lack of training. These mixed findings suggest that the relationship between experience and adoption is context-dependent, potentially shaped by differences in educational access and clinical opportunity.

In terms of personality variables, adopters reported significantly higher levels of openness to experience than non-adopters. Within the DOI framework, this trait reflects a greater willingness to engage with uncertainty and explore new ideas, which are qualities consistently linked to innovativeness, curiosity, and receptivity to change (Ali, 2019; Batey & Furnham, 2006; George & Zhou, 2001; Hammond et al., 2011; McCrae, 1993, 1994; McCrae & Costa, 1985; Patterson & Zibarras, 2017). Individuals high in openness are more likely to experiment, tolerate ambiguity, and integrate novel concepts into practice, aligning with Rogers' description of early adopters as venturesome and information-seeking. Extensive research supports this association between openness and innovative behaviour across diverse contexts, including health-related adoption such as preventive healthcare and vaccination (Iwasa et al., 2009; Mo et al., 2021; Nolan et al., 2019; Pandhi et al., 2016). Of particular relevance, Andrews et al. (2014b) also found significantly higher openness scores among genetic adopters, reinforcing its relevance as a predictor of early adoption in nursing. Openness has additionally been associated with opinion leadership, as open individuals tend to seek diverse information sources and influence peers through role-modelling behaviours (Andrews et al., 2014a; McCrae, 1996). The higher openness observed among adopters in this study therefore suggests a group more cognitively and behaviourally inclined toward exploration and change. From an implementation perspective, these findings indicate that fostering curiosity, critical thinking, and tolerance for uncertainty (features captured by openness) may enhance nurses' readiness to engage with genomics and to model its integration within oncology practice. Given that early adopters play a central role in diffusing innovations within social systems, recognising the association between openness and early adoption may also offer a useful starting point for targeting implementation strategies towards individuals who are more likely to model genomics uptake within oncology nursing.

Adopters also scored higher on the opinion leadership scale. Within the DOI framework, opinion leaders are viewed as pivotal actors in the spread of innovation (Rogers, 2003), and this is particularly true in nursing where peer influence has been reported as the key mechanism by which nurses adopt evidence-based practice (Estabrooks et al., 2005; Fossum et al., 2022). The higher levels of opinion leadership observed among adopters in this study therefore align closely with diffusion theory and previous genomic nursing research. Andrews et al. (2014a,

2014b) similarly reported higher opinion-leadership scores among adopters of genomics, while Leach et al. (2016) emphasised that identifying and supporting early nurse adopters and opinion leaders is a critical strategy for accelerating genomic integration. These findings underscore the social dimension of adoption, suggesting that adopters may not only be early implementers of genomics but also conduits of influence within oncology nursing networks. Strategically engaging these credible peers could enhance diffusion by leveraging their informal authority and professional reach to normalise genomic practice.

In relation to measures of perceived influence over others, no significant difference was observed between adopters and non-adopters in this domain. This measure, reflecting individuals' self-perceived capacity to affect peers' decisions, was included as a related but distinct dimension of opinion leadership. The absence of group difference suggests that perceiving oneself as influential does not necessarily translate into adoption behaviour. A comparable pattern was reported by Andrews et al. (2014a, 2014b), who found that perceived influence was associated with opinion leadership but did not differentiate adopters from non-adopters. This may indicate that the influence of peers in diffusion processes is shaped less by self-perception and more by externally recognised credibility and communication within professional networks.

Finally, communication behaviours were assessed and revealed that adopters demonstrated significantly higher engagement in cosmopolite information-seeking behaviours, reporting more frequent use of research articles, conferences, continuing professional development activities, and scholarly databases to inform their practice. Rogers (2003) identified cosmopoliteness as a defining attribute of early adopters, describing them as individuals who orient beyond their immediate social system to seek knowledge and experiences from external networks. These outward-looking behaviours expand professional horizons, expose individuals to emerging ideas, and reduce uncertainty in the adoption process. The present findings align with this theoretical expectation and extend prior nursing scholarship by empirically demonstrating these patterns in a genomic nursing context (Bourgault et al., 2014; Guilbert et al., 2014).

While some genomic nursing studies have examined oncology nurses' preferences for information sources (Hines-Dowell et al., 2024; Matsumoto et al., 2023), no previous research has explicitly measured cosmopoliteness in relation to genomic adoption. The present study therefore offers a novel contribution, adapting items from Adams and Barron's (2010) *School*

Nurse Evidence-Based Practice Questionnaire, which has been used in prior research by Bourgault and colleagues (2014) who similarly reported a statistically significant correlation between cosmopolite communication behaviours and innovation adoption, supporting the link between external information-seeking and innovation adoption. Broader nursing literature has long noted that engaging with conferences, journals, and professional networks is associated with higher levels of evidence-based practice and integration of new knowledge (Amicucci et al., 2022; Rodgers, 2000). That both adopters and non-adopters in this study reported similar use of general internet sources suggests that it is not mere access to information, but active, deliberate engagement with professional and scholarly channels that distinguishes adopters. These results reinforce cosmopolitanism as an important behavioural characteristic of early adopters and underline the value of fostering professional connectedness and information exchange to support genomic diffusion within oncology nursing. Promotion of genomics through scholarly and professional platforms, such as conferences, specialist journals, and continuing education forums, may therefore be particularly effective for engaging likely adopters, raising awareness, and leveraging their influence to diffuse genomic knowledge to less cosmopolite colleagues.

In summary, this study identified several individual characteristics associated with the uptake of genomics in nursing practice. Likely adopters were typically older, more experienced, and more often held advanced practice roles and postgraduate qualifications. They also exhibited higher openness to experience, stronger opinion-leadership tendencies, and greater engagement with professional and scholarly information sources. Collectively, these traits delineate a distinct adopter profile within the Australian oncology nursing workforce.

7.2.3 Exploring perceived barriers and enablers to integrating genomics into oncology nursing practice

The results for this aim are discussed through a *meso-to-micro* interpretive model that conceptualises the barriers and enablers to genomic uptake as layered and interdependent. Akin to an ‘onion’ structure (Figure 7.1), each layer represents a contextual level influencing adoption: the attributes of the innovation itself, educational factors, workforce and professional factors, organisational factors, and individual factors. This model reflects the complex, multi-level ecosystem in which nurses encounter and engage with genomics, from system conditions that shape access and leadership to individual attributes that influence openness and confidence.

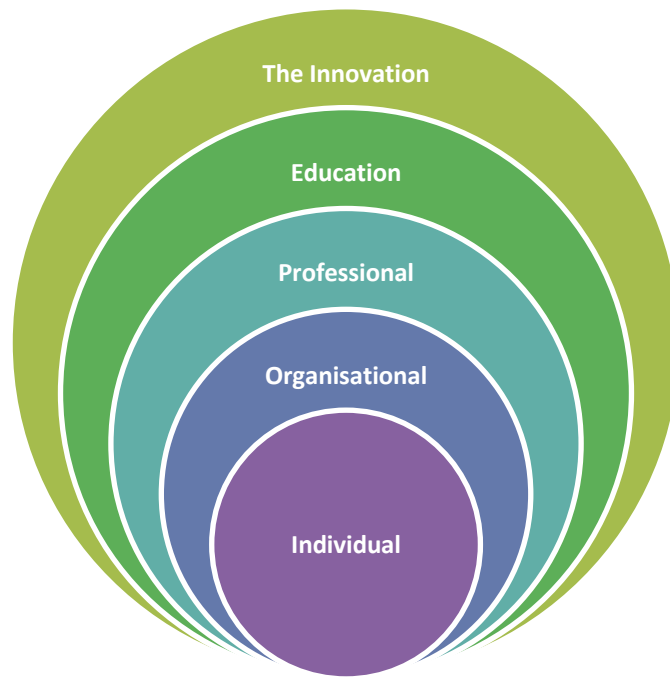


Figure 7.1. Barriers and enablers domains.

7.2.3.1 Domain 1: Attributes of the innovation

Attributes of the innovation emerged as a significant barrier to genomic adoption, with participants repeatedly describing genomics as a ‘foreign language’ and uniquely distinct from other health concepts. Nurses portrayed genomic information as dense, technical, and fast-moving, making it difficult to translate into practice. Indeed, this sense of complexity mirrors Dewell et al.’s (2021) findings in which both nursing students and faculty perceived genomics as aligned with the ‘hard sciences’ and therefore too complex for nurses to readily engage with. The rapid pace of advances further exacerbated this perception, with participants in the present study voicing concerns that the volume and velocity of emerging genomic evidence outstripped their ability to remain up to date.

Within Rogers’ DOI framework, complexity is recognised as a key inhibitor of adoption, with innovations perceived as overly difficult or obscure less likely to be integrated into practice. Perceived complexity is also crucial in shaping attitudes during the persuasion stage of adoption; however, as Rogers observed, a favourable attitude alone does not necessarily guarantee uptake. This appears highly pertinent in the genomic context, where the perceived technical and linguistic barriers may delay the progression from awareness to confident application.

The Australian Genomics Workforce and Education Working Group (Janinski et al., 2018) similarly reported that non-genomic health professionals were often reluctant to engage in genomics education when it was viewed as excessively complex or challenging. Although some education providers acknowledged that genomics can indeed be more conceptually demanding than other areas of practice, others suggested that the issue lay less in its actual difficulty and more in its perceived complexity. This perspective was echoed by participants in the present study.

Beyond technical complexity, participants in this study also emphasised the psychosocial distinctiveness of genomic care, framing it as fundamentally different from other medical and nursing innovations. Unlike conventional clinical information, genetic data is familial in nature and often carries a prophetic quality, which can amplify patient anxiety. Conversations about genetic risk or family history were described as emotionally taxing, and some nurses expressed reluctance to raise genomics for fear of retraumatising patients or triggering unintended consequences within families. These accounts echo findings from White et al.'s (2020) systematic review, which identified that health providers often avoided initiating genomic discussions due to apprehension about ethical, legal, and psychological impacts. In the present study, patient-initiated questions were common and often directed toward nurses, given their proximity to patients and the trust embedded in the nurse–patient relationship. While these encounters frequently exposed gaps in nurses' preparedness, they also highlight that patient demand sometimes functioned as a motivator, prompting nurses to seek further learning to meet patient needs. These findings align with those of Chiu et al. (2024), who similarly reported that nurses were hesitant to engage in genomics due to concerns about causing harm, but that patient questions and expectations often motivated them to address their knowledge gaps. This relational dimension sits at the intersection of professional role and patient expectations and is explored further in Domain 3, where the role of nurses as opportunistic facilitators is considered in depth.

Recognising both the technical and psychosocial attributes of genomics reframes how education and training needs should be conceptualised. Existing initiatives often target technical competence such as knowledge of genomic concepts, pathways, and referral processes, yet the present findings demonstrate that this focus is necessary but insufficient. Nurses also require preparation for the emotional and relational dimensions of genomic care, including strategies for managing patient anxiety, responding to sensitive family histories, and assessing readiness to engage in genomic discussions. These competencies are particularly critical in oncology,

where patients frequently navigate heightened fear and uncertainty. This extends Rogers' concept of 'complexity', indicating that in the genomic context adoption is hindered not only by scientific or technical difficulty but also by the psychosocial weight carried by the innovation. By foregrounding this psychosocial complexity, the present study contributes new insight to genomic-competency frameworks and underscores the need for integrated training models that address both knowledge and psychosocial skills.

Overall, the findings suggest that the intrinsic attributes of genomics as an innovation are multidimensional, encompassing not only technical difficulty but also emotional, relational, and structural barriers. If complexity acts as a barrier to adoption, education represents one of the most direct levers to reduce it, yet current approaches often remain inaccessible, fragmented, and poorly aligned with the realities of oncology nursing practice. Addressing this complexity requires educational approaches that demystify genomic concepts while also equipping nurses to manage the psychosocial implications inherent in genomic care.

7.2.3.2 Domain 2: Education-related factors

Curriculum deficit. A central structural barrier to genomic adoption identified in this study is the curriculum deficit—notably, the limited and inconsistent inclusion of genomics within pre-registration nursing education. Participants uniformly reported that genetics or genomics was either absent from their undergraduate programs or presented only as basic biological content with little connection to clinical practice. This omission reflects a systemic gap in curriculum design rather than an individual failing, with significant implications for workforce preparedness.

The limited integration of genomics in nursing curricula has been documented internationally and within Australia. McLaughlin et al. (2024) note that globally, inconsistent incorporation of genomic content constrains students' knowledge and understanding of the field, while Dewell et al. (2021) similarly identified significant curriculum gaps in Canadian nursing programs. In Australia, the extent of genomic education within nursing programs remains largely unknown, as no national audits or peer-reviewed analyses have yet documented its presence. This lack of visibility represents a critical evidence gap for workforce planning and competency development.

Available Australian evidence, though scarce, demonstrates minimal genomic integration in nursing education. Saleh et al. (2019) reported that most allied health professionals, including

nurses, recalled little or no genetics in their training programs, while McClaren et al. (2018) found no substantive genomics education initiatives beyond isolated examples. The current study both corroborates and extends these observations. Consistent with Wright et al.'s (2020) Australian study, in which Queensland oncology nurses recalled only basic biological concepts, participants here described genomic content as superficial or entirely absent, with several unable to recall any exposure at all. This absence underscores the magnitude of the curriculum deficit and suggests that some nurses may enter the workforce wholly unprepared to engage with genomics in clinical care.

The downstream effects of this educational gap were evident in participants' accounts, as many felt ill-equipped to answer patient questions or to access genomic resources and supports. In one instance, this lack of genomic competence appeared to contribute to an adverse patient outcome (see Section 6.3.5.1), a finding that represents a significant contribution of this study and underscores the urgent need for national reform. Indeed, participants emphasised the need for skills in communication, psychosocial support, and counselling when responding to genomic concerns, indicating that educational needs extend beyond foundational genomic knowledge. This aligns with findings from a Korean study of genetic nursing competencies, in which Shin et al. (2020) describe the importance of 'experiential genetic nursing knowledge' as encompassing the ability to communicate with, educate, and counsel patients effectively.

The call to integrate genomic competencies into nursing curricula is central to the Update to the Essential Genomic Nursing Competencies and Outcome Indicators (Calzone et al., 2024), which advocates embedding genomic content across all levels of nursing education to ensure baseline competence. Similarly, the Assessment of Strategic Integration of Genomics across Nursing (ASIGN) tool developed by the Global Genomics Nursing Alliance (Tonkin et al., 2020a) (see Section 1.6) identifies enhanced education and workforce development as critical success factors for genomic integration. Aligning Australian nursing curricula with these frameworks is therefore essential to developing a genomically capable workforce equipped to meet the clinical and ethical demands of personalised medicine.

Post-registration and continuing education. The lack of genomic preparation in pre-registration programs was compounded by limited opportunities for post-registration and continuing education. Within nursing, continuing professional development (CPD) is a professional and regulatory requirement designed to sustain competence and introduce new skills, thereby protecting the public through ethical, effective, and safe practice (NMBA, 2016).

Ensuring that CPD opportunities include accessible, role-relevant genomic education is therefore not optional but essential to professional accountability and patient safety.

Participants in this study framed CPD and workplace in-services as powerful enablers for building genomic capability. Many expressed strong interest in ongoing education and agreed that CPD in genetics and genomics should be encouraged. This positive orientation aligns with broader Australian evidence emphasising the value of workplace-based learning. The Australian Genomics Workforce and Education Working Group (Janinski et al., 2018) found that health professionals favour short, face-to-face learning opportunities embedded within existing professional activities—a preference echoed by nurses in this study. Similarly, Kim et al. (2022) highlighted that workplace learning beyond formal education is essential to sustaining genomic knowledge and confidence among Australian medical practitioners.

However, despite this enthusiasm, participants consistently described a lack of structured genomic training in their workplaces. Genomics was rarely addressed through in-services or professional development programs, and over half of survey respondents reported difficulty attending genomic learning opportunities. These difficulties were often tied to broader professional and organisational constraints (see Section 6.3.4), illustrating the layered, interdependent nature of the barriers identified in this study. From an ‘onion’ perspective, educational access sits at the interface of multiple layers, shaped not only by individual motivation but also by workforce conditions and institutional resourcing.

Despite in-services offering an accessible and contextually relevant mode of genomic learning, their effectiveness depends on enabling conditions such as organisational endorsement, protected learning time, and managerial advocacy. Many nurses described struggling to balance professional curiosity with operational demands, emphasising that enthusiasm alone is insufficient without institutional facilitation. Consistent with Wright et al.’s (2020) findings, participants preferred informal, practice-based formats such as workshops or in-services over formal postgraduate study, citing accessibility and relevance as key advantages. Yet the feasibility of such learning was frequently undermined by time pressures, financial constraints, and limited managerial support. Saleh et al. (2019) similarly found that integrating continuing education into routine workloads was difficult without explicit endorsement or resourcing from employers.

This challenge is further compounded by the limited availability of genomically competent educators, limited access to expert guidance, and the absence of clear training standards. Prior

research has shown that many nurse educators are tasked with developing and delivering genomic content despite having had little formal education or clinical exposure in the field (Dewell et al., 2024; Tonkin et al., 2011, 2020b; Williams et al., 2011). This situation exposes a critical paradox: while workplace-based education is among the most desired and potentially effective learning formats, it remains one of the most difficult to implement sustainably. Addressing this paradox requires coordinated investment in educator capability, protected learning time, and organisational endorsement to ensure genomic CPD can function as both an educational and structural enabler of adoption.

Learning modalities. Participants described drawing on a range of learning modalities to build their genomic knowledge, often compensating for the absence of structured education through personal initiative. Many reported engaging with postgraduate courses, webinars, newsletters, or self-directed online study, while others relied on seminars and webinars offered by trusted platforms such as the Cancer Nurses Society of Australia (CNSA) and eviQ. These accounts illustrate how nurses actively sought learning opportunities in a fragmented educational landscape.

Among the modalities discussed, experiential learning stood out as a particularly powerful enabler of engagement. Estabrooks et al. (2005) define experiential knowledge as learning gained through observation, identifying it as nurses' most important source of practice knowledge. Participants who had opportunities for secondments, mentorships, or observation of genomic consultations consistently described these experiences as transformative, allowing them to consolidate theoretical knowledge, build confidence, and bridge the gap between abstract understanding and clinical application. Similar benefits of practical exposure are noted by Janinski et al. (2018), who found that Australian education providers viewed hands-on experience and peer discussion as particularly effective for consolidating learning, while McClaren et al. (2020) emphasise the value of embedding genomic learning within authentic clinical settings. Within the present study, such experiences enabled nurses to trial genomic concepts in real-world contexts and to see their relevance to patient care.

From a diffusion perspective, such experiential learning exemplifies Rogers' notion of *trialability*, the extent to which an innovation can be experimented with before full-scale adoption (Rogers, 2003). Allowing nurses to 'try out' genomic practice in a safe and supported environment may reduce perceived complexity and uncertainty, increasing the likelihood of integration into routine care. This interpretation is consistent with diffusion research

demonstrating that perceived complexity can be reduced through practical experience and demonstration (Greenhalgh et al., 2004). Importantly, they also make the *observability* and *relative advantage* of genomics more tangible; when nurses observe or participate in activities such as genomic consultations or consent discussions, they can directly see how genomic information informs patient care, enhances precision in treatment decisions, and improves communication with patients and families. These moments may transform genomics from an abstract scientific concept into a visible, clinically meaningful practice. Evidence suggests that initiatives which make the benefits of an innovation more visible—for example, through demonstrations—increase the likelihood of successful assimilation into practice (Greenhalgh et al., 2004).

Moreover, experiential learning allows nurses to perceive the *compatibility* of genomics with their existing roles and values. For example, witnessing a genetic testing consent process may enable nurses to recognise parallels with familiar aspects of nursing practice, such as patient advocacy, ethical decision-making, and informed consent facilitation. Through this process, genomics becomes not only more comprehensible but also more aligned with the professional identity and moral framework of nursing.

However, the potential of experiential learning must be considered alongside its constraints. Informal and practice-based learning can be difficult to evaluate systematically and may vary in quality compared with structured, didactic education (McClaren et al., 2020). Access also depends on proximity to genetics services, the presence of capable mentors, and organisational willingness to facilitate opportunities. In many clinical contexts, these enabling conditions are limited, rendering experiential learning more aspirational than achievable. Thus, while it represents a powerful pathway for genomic capability building, its impact ultimately hinges on broader system-level supports that determine whether these opportunities can be sustained and equitably distributed.

Peer learning and mentorship also emerged as influential mechanisms for developing genomic competence. Both the survey and interviews highlighted colleagues and professional networks as critical sources of knowledge and motivation. Janinski et al. (2018) reported that peer learning, both informal and as part of structured discussions, is highly valuable, particularly when it involves multidisciplinary participation (explored further in Section 6.3.2). Observational learning from genetic counsellors and geneticists, as described by Saleh et al. (2019), similarly offered authentic insight into genomic communication and clinical reasoning.

More broadly, mentorship has been shown to enhance professional growth, confidence, and attitudinal development (Nowell et al., 2017). In the context of DOI theory, peers and mentors act as *social influencers* and *opinion leaders*, helping to normalise and diffuse genomic practice within professional communities (Rogers, 2003). However, in this study access to these networks was uneven, and for some nurses—particularly those in smaller or regional settings—opportunities for mentorship or peer dialogue may be limited, reinforcing disparities in exposure and support.

Beyond experiential and relational learning, participants described engaging with a mix of multimodal and self-directed approaches, including online modules, webinars, newsletters, and informal Google searches to meet immediate clinical needs. This flexibility reflects the long-standing pedagogical value of varied formats in nursing education; as Kennedy et al. (1998) emphasise, combining written and audiovisual materials supports knowledge integration. Recent evidence from Alexander et al. (2024), who evaluated genomics workshops for nurses and midwives in Queensland, similarly highlights nurses' preference for blended and interactive modalities. Participants in that study favoured formats combining self-study with face-to-face workshops, modular sessions, and online presentations, while static, self-directed resources (such as printed materials or web-based readings) were least preferred. These findings reinforce earlier work by Kirk et al. (2007), who also found that although e-based media were moderately acceptable when combined with traditional resources, they were least popular when used alone. Their analysis suggested that this preference may reflect limited confidence in the subject matter, and a corresponding need for guided rather than self-directed learning. The present study supports aspects of these earlier findings but also diverges in meaningful ways. Several participants described learning effectively through static online materials, a pattern that may reflect contextual differences in accessibility. Unlike the Queensland-based cohort in Alexander et al.'s (2024) study, the present sample included nurses from diverse Australian regions and practice settings. For some, particularly those in rural or remote areas or working variable shifts, asynchronous or text-based resources may represent one of the few practical avenues for continuing professional development (Zureigat et al., 2022). What may appear as a preference for static materials may therefore represent a pragmatic adaptation to structural and geographic constraints. It is also important to consider how technological shifts since 2007 have reshaped both the delivery and perception of online learning. Kirk et al.'s conclusions were drawn in a markedly different digital context, prior to the widespread availability of smart-mobile devices, high-speed internet, and intuitive e-learning platforms. In contrast, contemporary forms of self-

directed digital learning may offer greater flexibility, usability, and engagement, even in the absence of facilitator support (Zureigat et al., 2022). This evolving digital fluency suggests that static resources should not be dismissed outright, but instead understood in relation to learners' needs, digital access, and professional circumstances.

Collectively, these learning strategies reveal both adaptability and inequity. From a DOI perspective, such self-directed efforts can be viewed through Rogers' constructs of information-seeking behaviour and cosmopolitanism. Early adopters typically exhibit greater cosmopolitanism, engaging with professional societies, conferences, and external learning networks to obtain new information. Several participants reflected this outward-looking tendency, describing how they sourced genomic updates through the CNSA or other specialist forums. While experiential, relational, and self-directed learning enable nurses to compensate for systemic educational deficits, they also transfer the burden of professional development to individuals. Schluter (2023) similarly observed that self-directed study remains the primary means by which Australian nurses and midwives build genomic capability, describing it as 'time-consuming, inefficient, and inadequate' (p. 311) for sustaining a competent workforce. The present findings extend this concern, demonstrating that the responsibility for sourcing, interpreting, and applying genomic information often falls to individual nurses. This dependency highlights the need for coherent, accessible, and well-resourced educational infrastructure that supports learning across all levels of practice.

Genomic education resources. Participants described significant challenges in locating genomic education resources that were both comprehensible and relevant to their clinical practice. Across the interviews, nurses expressed frustration at the volume, variability, and technical complexity of available materials, with many finding existing content overly scientific, poorly contextualised for nursing roles, or simply difficult to apply in real-world care. These findings suggest that while genomic resources exist, they are not perceived as accessible or usable within the practical realities of nursing work. This aligns with a global survey of nursing leaders and organisations, which identified limited availability and accessibility of educational resources as major barriers to integrating genomics into nursing practice (Tonkin et al., 2020b).

The challenge of information fragmentation and overload described by participants in this study has been widely reiterated in the literature. Tonkin et al. (2011) observed that the rapidly changing nature of genomics makes it 'time-consuming and daunting' (p. 331) for health

professionals to stay current, while Flynn et al. (2019) noted that the sheer volume of online resources available to oncology nurses can be overwhelming. Similarly, Janinski et al. (2018) identified that genomic education in Australia suffers from ‘unsystematic resources’ (p. 26), making program development both time-intensive and costly. These findings mirror the present study, in which participants described feeling inundated by information yet uncertain which sources were trustworthy or relevant. The lack of a coherent, streamlined approach to genomic education impeded their ability to engage confidently or efficiently. From a DOI perspective, these barriers reflect Rogers’ concept of *complexity*, one of the core attributes influencing adoption. When an innovation—or, in this case, its educational infrastructure—is perceived as difficult to understand or navigate, the likelihood of adoption decreases.

Participants also voiced concern about the pace of emerging genomic evidence and the difficulty of keeping educational content current, which was similarly reported by Janinski et al. (2018), who noted that the rapid evolution of genomics makes regular revision and updating of materials both essential and challenging. In response, nurses strongly advocated a central, regularly updated repository to simplify navigation, ensure currency, and facilitate timely learning. This desire for a ‘one-stop hub’ reflects an intuitive response to the perceived complexity of the current resource environment. Comparable calls for integration have been made internationally; in the United States, Dickman et al. (2024) noted the absence of national repositories consolidating foundational genomic resources for oncology nurses, prompting the creation of the Oncology Nursing Society’s Genomics and Precision Oncology Learning Library. While this initiative illustrates the potential value of a comprehensive, multimodal resource bank, it also highlights the challenge of accessibility, as such platforms often require institutional membership and remain tailored to US-specific contexts.

In Australia, participants frequently cited eviQ as a model for effective genomic education infrastructure. Developed through the Cancer Institute NSW, eviQ provides open-access, evidence-based oncology resources and is widely regarded as the ‘gold standard’ for cancer information (Shingleton et al., 2024). Its credibility, government endorsement, and integration into everyday oncology practice exemplify both compatibility and trustworthiness, which are key enablers within the DOI framework. Because eviQ is already embedded in nurses’ professional routines, it represents a credible and familiar vehicle through which genomics-focused education could be expanded and disseminated. Participants voiced a similar opportunity may exist through the Health Education and Training Institute (HETI), which delivers mandatory training and continuing professional development modules for nurses

across New South Wales (HETI, 2025). Embedding genomic content into such established systems could streamline access, ensure consistency, and leverage existing platforms for sustainable education delivery (Chiu, Limoges, Puddester, et al., 2024).

Despite the abundance of genomic resources, participants repeatedly emphasised that many materials were not designed with nurses in mind. Even when technically accurate, they were often described as overly scientific, conceptually dense, or framed in language disconnected from nursing practice. This disconnect left nurses struggling to translate abstract genomic concepts into clinically relevant actions. These perceptions align with the findings of Calzone et al. (2018a), whose global survey revealed that while numerous educational materials exist, few are specifically targeted to nurses. Janinski et al. (2018) likewise reported that Australian educators regard tailoring genomic education to the learner's discipline and knowledge level as critical, highlighting the need for flexibility and adaptation to professional context.

This study's findings suggest that tailoring genomic education for nurses requires more than simplifying scientific content; it should be framed in the language and clinical context of nursing practice, with examples that reflect real-world patient care—findings and recommendations echoed in Cuthill et al.'s (2025) study. This need for discipline-specific translation is not unique to nursing; Johansen Taber and Dickinson (2014) observed that even among medical physicians, existing pharmacogenomic resources often failed to provide the kind of 'clinician-friendly' information required for confident application. In this context, the call for discipline-relevant genomic education is not merely pedagogical but structural, reflecting the need to reframe genomics through the language, priorities, and scope of nursing practice.

From a DOI perspective, these findings point to the central role of *complexity* and *compatibility* in shaping adoption. When genomic resources are overly technical or misaligned with clinical realities, they heighten perceived complexity and weaken compatibility with nurses' professional roles and values. Conversely, when education is contextualised, written in accessible language, grounded in patient-centred examples, and directly connected to everyday nursing decisions, it not only enhances compatibility and reduces complexity but also clarifies the *relative advantage* of genomics, a key driver of adoption in Rogers' model. Such alignment not only reduces cognitive barriers but also strengthens perceived relevance, a critical precondition for adoption.

7.2.3.3 Domain 3: Profession-related factors

Participants described a range of profession-wide factors and conditions that shaped their capacity to engage with genomics. While many of these intersected with organisational factors such as staffing and access to professional development, they were most often framed as systemic challenges across the nursing profession rather than problems specific to individual workplaces. Accordingly, these findings are discussed within the domain of professional factors, reflecting broader workforce norms, role boundaries, and the structural realities of Australian nursing practice that influence genomic engagement.

Workforce constraints. Time scarcity and workforce instability were consistently described as major barriers to engaging with genomic education and integrating genomics into nursing practice. Nurses portrayed genomic learning as something that must compete with relentless clinical and operational demands. Staffing shortages, high patient acuity, and escalating administrative workload left little room for study or the incorporation of new knowledge. Several participants described the near impossibility of learning amid routine care pressures, with ‘time poverty’ emerging as a defining feature of contemporary nursing. Others reflected more broadly on cumulative workforce pressures such as high turnover, an increasingly junior staff mix, and burnout, which they felt undermined the profession’s overall capacity for upskilling and adoption of new practices such as genomics.

Mounting national evidence supports this interpretation. Inadequate staffing has been identified as a key contributor to missed nursing care in Australia (Mills & Duddle, 2022). In a large cross-sectional study, Bradford et al. (2023) found that 89% of Australian oncology nurses cited workload as their most substantial professional challenge; this was nearly triple the proportion reported two decades earlier (33%). Their follow-up qualitative study similarly identified unsafe staffing ratios, workforce turnover, and limited experience among new graduates as persistent issues contributing to burnout and job dissatisfaction (Bradford et al., 2024). These Australian findings align with international evidence, as Challinor et al. (2020) report substantial global shortages of oncology nurses, exacerbated by the emotional, physical, and cognitive demands of the role. Weller-Newton et al. (2021) likewise highlight that the ageing Australian nursing workforce and the absence of up-to-date national workforce planning data have weakened skill mix and long-term sustainability. Intensifying patient acuity and complexity further intensify demands on nurses, with inadequate resourcing frequently forcing

nurses to reprioritise care tasks (Gustafsson et al., 2020), leaving little capacity to engage with emerging competencies such as genomics.

Although participants framed these barriers as profession-wide, they also intersect with organisational structures, including staffing models, access to protected learning time, and institutional priorities. These interdependencies are explored further in Domain 4 (*organisational factors*).

From a DOI perspective, adoption is shaped by the interaction between the innovation itself, the intended adopters, and the context in which implementation occurs (Greenhalgh et al., 2004). In this study, these cumulative pressures created a working environment in which the demands of genomics were often perceived as incompatible with existing professional realities, a critical determinant of uptake. The findings suggest that under conditions of time poverty, role strain, and workforce instability, genomics may be viewed as incongruent with established nursing workflows. Even where nurses expressed interest in genomics or recognised its clinical relevance, the structural constraints of their roles left little opportunity to meaningfully pursue genomic knowledge or apply it in practice.

Scope and role delineation. Participants expressed varying and sometimes conflicting views about the place of genomics within the nursing scope of practice. Among those not working in formal genomic roles, there was little consensus. Some viewed genomics as outside their remit; others described deferring to medical staff; a few actively challenged these assumptions. This ambiguity manifested not only as individual uncertainty but also as a form of professional gatekeeping, in which nurses recognised genomic needs yet refrained from acting. As one participant reflected:

Patients that haven't been through genetic testing but that I have suspected them needing to be referred to genetic testing, is kind of something like, you refer to the doctor. You just don't do it yourself.

Another noted the consequences of such ambiguity:

I think some of it is what is the doctor's role versus what's the nurse's role. Generally, we would expect that it's the doctors that talk to patients about genomics. However, I've found that, often, it doesn't happen.

In contrast, several nurses contested the notion that genomics belongs solely to the medical domain. Participants in dedicated genomic roles, in particular, expressed no such uncertainty. They described tasks such as taking family histories, educating patients, and facilitating genetic testing as routine, within scope, and entirely congruent with nursing practice.

Quantitative findings mirrored this divergence. Non-adopters were more than twice as likely as adopters to report that genomics was primarily a doctor's responsibility (44% vs 19%). Scenario-based survey items reinforced this distinction, as adopters were significantly more likely to assume responsibility for identifying genomic needs and following up with the medical team. Collectively, these results suggest that nurses who actively engage with genomics tend to hold an expansive view of scope, one in which identifying and acting on genomic risk is consistent with their professional role. Engagement with genomics therefore appears to be influenced not only by knowledge or resource access but by how nurses perceive the fit between genomics and their professional identity.

These findings reflect long-standing challenges surrounding nursing scope and role identity in Australia. Wiggins et al. (2022) identified that confusion surrounding professional identity and poorly defined roles remain persistent challenges in Australian health care, often leading to frustration, conflict, and inhibited collaboration, while Birks et al. (2016, 2019) found that inconsistent terminology and variable role delineation contribute to scope ambiguity across the profession. Context also plays a key role: in rural or resource-limited settings, nurses frequently extend their scope to meet patient needs—an adaptation that may hold particular relevance in genomics, where access to specialist services is uneven. The NMBA (2019) further defines scope of practice as that in which nurses are educated, competent, and permitted by law, while recognising that actual scope is influenced by setting, competence, and service policy. This definition positions genomics as potentially within the nursing remit, provided appropriate education and support are in place. The barrier, therefore, arguably lies less in regulation than in perception and confidence.

Findings from genomic nursing research reinforce this interpretation. Wright et al. (2020) reported that some Australian oncology nurses felt they had little input into patient-care decisions and therefore viewed genomics as the doctor's domain. Internationally, Hines-Dowell et al. (2024) found that over half of paediatric oncology nurses were uncertain whether genomics fell within their scope, with one participant remarking, 'When we see the word *genomic*, it's for the doctors'. An integrative review by Barr et al. (2018) likewise identified

role ambiguity between nurses and genetic counsellors as a persistent challenge to genomic integration. Across Canada, multiple studies have highlighted role clarity and scope of practice as persistent barriers to integrating genomics into nursing. Oncology nurses, students, and faculty alike reported uncertainty about whether genomics falls within their scope and role, with authors emphasising the need for clearer definitions of roles, responsibilities, and scope to guide clinical practice, nursing policy infrastructure, and curriculum development (Chiu, Limoges, Puddester, et al., 2024; Dewell et al., 2021; Limoges et al., 2022). Thus, clarifying scope and strengthening confidence in nurses' genomic contribution will be essential to bridging the gap between potential and perceived practice, thereby enabling more equitable diffusion of genomics across the nursing workforce.

From a diffusion perspective, these dynamics illustrate how perceptions of *compatibility* shape adoption. Diffusion research demonstrates that innovations perceived as compatible with adopters' values, norms, and ways of working are more readily adopted and more successfully assimilated into practice (Greenhalgh et al., 2004). In this study, genomic uptake appeared intrinsically linked to how nurses perceived genomics in relation to their scope of practice. For non-adopters, genomics was often viewed as lying outside established professional boundaries, suggesting a misalignment between the innovation and nurses' perceived roles. Addressing this perceptual misalignment requires more than increasing genomic knowledge alone; it also demands clearer articulation of how genomics complements and extends established nursing roles and values. Within the Australian context, clarifying scope and building confidence in nurses' genomic contribution will be essential to bridging the gap between potential and perceived practice, thereby enabling more equitable diffusion of genomics across the nursing workforce.

Nurses as opportunistic facilitators. Participants framed nurses' sustained presence, interpersonal connection, and communication skills as positioning them to act as *opportunistic facilitators* of genomic care. Across the interviews, nurses described how routine practices such as holistic assessment, rapport building, and patient education, created natural openings for genomic engagement. These opportunities often arose spontaneously through family history discussions, recognition of hereditary 'red flags', or patient queries about genetic risk. Notably, this perception was shared across diverse participants, including those with limited genomic training or non-specialist roles, suggesting that nurses' facilitation of genomics is not contingent on formal expertise but embedded within core nursing functions.

Several participants identified nurses' proximity to and consistent contact with patients as key enablers of genomic engagement. However, they emphasised that this facilitation role extended beyond physical access to encompass relational depth. As one participant explained, 'I've picked up on someone who'd slipped through the cracks', describing a moment during a routine assessment when family history concerns emerged and prompted a timely genetics referral (see Section 6.3.3.3). This patient had met criteria for referral but had not previously been identified within the system, illustrating how nurses can detect unmet genomic need during routine encounters. Such accounts highlight nurses' potential to act as safety nets, identifying genomic need in real time and preventing patients from falling through systemic gaps and preventing adverse health outcomes. Importantly, this finding directly addresses a gap repeatedly identified in the nursing genomics literature: despite widespread discussion of genomic competencies, there remains limited empirical evidence demonstrating nurses' application of genomic knowledge in ways that *tangibly* benefit patient care (Dewell, Benzies, & Ginn, 2020; Keels et al., 2024). This observation therefore adds new empirical insight to the literature, which has acknowledged nurses' role in family history collection and patient education, but has rarely captured such direct examples of genomic intervention prompted by nursing vigilance and relational practice.

This capacity is underpinned by well-documented nursing strengths in therapeutic communication and patient advocacy, particularly in contexts requiring explanation of complex, emotionally charged information (see 1.4.1). In genomic care, where uncertainty and familial implications are common, these established relational competencies align closely with the demands of supporting informed decision-making and coordinating care (Allande-Cussó et al., 2022; Crivelli et al., 2024; Moore et al., 2018; Grant et al., 2025).

Emerging evidence further indicates that patients often direct genetic questions to the nurses caring for them (Chiu, Limoges, Puddester, et al., 2024; Hébert et al., 2022; Limoges, Puddester, Pike, et al., 2024), reflecting the trust and accessibility that characterise the nurse–patient relationship. These patient-initiated enquiries may serve as a catalyst for nurses to pursue further genomic learning (Chiu, Limoges, Puddester, et al., 2024; Matsumoto et al., 2023). The present findings extend this evidence, illustrating how nurses' everyday interactions can become gateways for genomic engagement, positioning them as critical intermediaries between patients, medical teams, and specialist genetics services.

From a DOI perspective, this alignment between core nursing functions and the demands of genomic practice illustrates high compatibility. Genomic care is not necessarily an add-on for nurses; it arguably complements and amplifies their existing responsibilities in patient assessment, education, and advocacy. Recognising this natural fit may be essential for strengthening implementation efforts, as it reframes genomics not as a specialist domain, but as a compatible extension of everyday nursing work.

Compatibility with advanced nursing practice. Genomics was widely perceived to align with the existing roles and responsibilities of advanced practice nurses, particularly Clinical Nurse Specialists (CNSs) and Clinical Nurse Consultants (CNCs). Across the interviews, participants identified these roles as natural conduits for genomic integration, citing their existing responsibilities in clinical leadership, complex decision-making, care coordination, and patient education. Importantly, this compatibility was recognised not only by nurses currently engaged in genomics but also by those without formal genomic roles, suggesting a shared professional belief that genomics fits within the broader scope of advanced nursing practice in Australia.

This alignment is consistent with the NMBA definition of advanced nursing practice, which emphasises complex decision-making, autonomous practice, and responsibilities across leadership, education, and systems-level support (NMBA, 2016). These attributes position advanced practice nurses (e.g., breast CNCs or sarcoma CNSs) at the intersection of clinical expertise and workforce development, making them ideally placed to facilitate genomic integration both through direct patient care and as change agents within multidisciplinary teams.

A recurring enabler identified in the data was the presence—or desired presence—of a genomic nurse specialist ‘on the floor’. Participants consistently described the value of having an accessible, knowledgeable peer who could act as a resource person for clinical queries, support decision-making, and build team capacity through informal education. This emphasis on an accessible genomic resource role aligns with broader evidence that clinical nurse specialists and research-active nurses help enable evidence-based practice in clinical settings, suggesting that similar mechanisms may support genomic implementation (Smith & Johnson, 2023). While several countries have recognised specialist genetics nursing roles (nurses with specialised training in genetics) (Calzone, Kirk, et al., 2018b), the Australian context remains far less developed. As Bradford et al. (2023) observe, even within oncology nursing advanced practice titles and scopes remain inconsistent and often ambiguous. The present findings suggest that some nurses are already performing genomic support functions informally, without official

recognition or structural backing. This underscores the need for national workforce mapping and the development of clearer frameworks for genomic nursing.

Crucially, the data also point to two complementary pathways for advancing genomic nursing in Australia. First, embedding genomic capability within existing advanced practice roles offers an immediate, pragmatic avenue for integration. Second, there is clear potential to establish dedicated advanced genomic nursing roles, designed to provide expert clinical leadership, education, and systems-level coordination across cancer care and beyond. Participants' repeated calls for an accessible 'genomic nurse on the floor' highlight both the workforce appetite and the clinical justification for such positions.

Moreover, the clear enthusiasm for embedded genomic support points to a broader systems-level opportunity. Participants recognised the relative advantage of having such roles available, this aligns closely with DOI theory, which emphasises that innovations are more readily adopted when they are perceived as both *compatible* with existing values and practices, and offering *clear relative advantages* over the status quo (Rogers, 2003). By positioning genomic nurse specialists within clinical teams, health services may not only enhance immediate care but also catalyse broader adoption through peer influence and experiential learning.

Together, these findings indicate that advanced practice nurses are well positioned to lead the integration of genomics into cancer care. Whether through enhanced capability within existing roles or the creation of specialised genomic positions, embedding genomic expertise within nursing teams represents a powerful workforce enabler. However, realising this potential will require more than educational initiatives—it will depend on structural investment, defined career pathways, and coordinated national workforce planning to sustain genomic leadership within the profession.

7.2.3.4 Domain 4: Organisational factors

Organisational resourcing. Participants identified organisational investment as a critical determinant of nurses' capacity to engage with and adopt genomics in clinical practice. Resourcing was discussed in concrete terms such as financial support for education and training, the creation of specialist roles, and the provision of protected learning time. Across the interviews, nurses emphasised that meaningful engagement with genomics requires not only personal motivation but also sustained organisational support. A notable concern voiced was

the expectation that nurses self-fund genomic education, this was deemed a significant barrier to upskilling and pursuing further education.

Despite these constraints, participants also provided examples where organisational commitment directly enabled engagement. Three nurses in the sample held genomic roles funded by their hospitals, providing dedicated time and institutional recognition for their genomic responsibilities. These positions were viewed as clear indicators of organisational endorsement and were described as catalysts for broader diffusion, as embedded expertise within clinical teams made genomics more visible, accessible, and normalised in everyday care.

Although empirical work examining organisational influences on genomics adoption in nursing is scarce, there is evidence for the centrality of organisational, resource and leadership support and the availability of adequate infrastructure for successful integration (Calzone, Jenkins, et al., 2018; Flynn et al., 2019). Findings from adjacent fields lend support. Yan et al. (2022) identified limited organisational resources and economic support as among the most significant barriers to innovation adoption in nursing, recommending investment in infrastructure and professional development to foster a culture of growth. Similarly, Furtado et al. (2024), in their scoping review of organisational context factors influencing nurses' adoption of evidence-based practice, reported that resourcing and infrastructure were key determinants of successful implementation. The present findings suggest that the challenges described by participants are not unique to genomics but reflect a broader pattern in which under-resourced environments inhibit innovation in clinical nursing.

These observations align closely with the G2NA Roadmap and ASIGN tool (see Section 1.6), which recognise the role of organisational capital in supporting genomic integration and identify infrastructure and resources as critical success factors. Together, they emphasise that sustainable implementation requires organisational investment in education, workforce, and systems capacity (Tonkin et al., 2020b, 2020a). Viewed through this lens, the current study provides local evidence that without such resourcing, nurses' enthusiasm and readiness alone are insufficient to embed genomics into practice.

From a DOI perspective, this theme speaks to the concept of *organisational slack*—the availability of surplus resources, such as time, training capacity, or financial investment, that can be allocated toward experimentation and implementation (Rogers, 2003) (see Section 2.4.4). Organisations with greater slack are more likely to support the adoption of new practices (Damanpour, 1991), such as genomics, by reducing the opportunity cost for nurses. In this

sense, the gap between theoretical readiness and practical implementation lies not only in organisational readiness but in structural capacity.

Managerial and organisational leadership support. Participants consistently identified limited engagement from managerial and senior organisational leadership as a major constraint on genomic integration. The quantitative findings presented a nuanced picture. On the one hand, only 2.8% of respondents selected ‘lack of support from a manager’ as a direct barrier to incorporating genomics into their role. On the other hand, seeking support from senior nurses and management was rated as the most difficult genomics-related action. Moreover, more than half of respondents identified heads of department as enablers of new knowledge uptake, and adopters of genomics reported significantly greater ease in seeking managerial support compared with non-adopters (52% vs 30%). Adopters were also more likely to believe their manager would approve efforts to highlight the need for further genomic investigation (82% vs 50%). Taken together, these results suggest that managerial support is inconsistently experienced and perhaps under-recognised when framed as a discrete ‘barrier’ item, despite its strong influence on adoption behaviour.

The qualitative interviews provided crucial context for these patterns. Many participants described a lack of visible engagement from managerial or senior nursing leadership, often attributed to limited awareness of genomics or its perceived irrelevance to nursing practice. In some cases, attempts to initiate genomics-related projects were discouraged or actively opposed (see Section 6.3.4.2). As one participant reflected, ‘I was shut down by my manager and education department’. Such accounts illustrate how managerial disengagement, whether through passive disinterest or active resistance, creates organisational inertia that suppresses nurse-led innovation and constrains capacity for genomic integration.

From a DOI perspective, these findings underscore the importance of the ‘social system’ and its gatekeeping effect on adoption. In highly professionalised and hierarchical systems such as nursing, the influence of immediate supervisors and senior leaders is pivotal. Their endorsement signals whether genomics is viewed as legitimate, relevant, and worth prioritising. This interpretation aligns with a substantial body of literature on nursing innovation. Van der Weide and Smits (2004) demonstrated that the immediate supervisor’s attitude is one of the strongest predictors of nurses’ willingness to adopt innovations, with supportive leadership accelerating uptake. Similarly, Furtado et al. (2024) found that nurse managers’ authority legitimises evidence-based practice implementation, while a lack of leadership orientation amplifies

obstacles. Leadership support operates not only through policy but also through modelling, as leaders who use evidence, empower staff, and recognise initiative create the psychological safety and operational space for innovation to flourish. Smith and Johnson (2023) further emphasised that managerial leadership functions as an ‘agent of change’, embedding new knowledge into departmental norms and reducing staff resistance to new practices.

Evidence from genomic nursing research mirrors these conclusions, as a systematic review by Cao et al. (2025) identified leadership support as the ‘driving force’ behind genomics integration, influencing both access to training and the cultivation of a genomic culture within institutions. However, they also reported wide variability in leadership engagement across studies, leading to inconsistent perceptions among nurses regarding the adequacy of managerial support. Earlier research by Kirk et al. (2007) similarly highlighted the role of senior nursing staff in promoting genetics competence, yet found that fewer than 20% of nurses agreed their manager viewed genetics as part of their role. Calzone et al. (2018) demonstrated that leadership-led initiatives were more effective in motivating nurses to apply genomics in practice.

As efforts to embed genomics into nursing practice continue, organisational leadership will be pivotal not only in addressing structural challenges but also in shaping professional culture. Managers and senior nurses serve as the interpretive bridge between policy and practice: their engagement may determine whether genomics is seen as peripheral or integral to nursing identity. Cultivating leadership capacity and accountability in this area is therefore essential to creating environments where genomic nursing is recognised, valued, and sustained.

Organisational adoption and integration into nursing workflows. The organisational integration of genomics into established care pathways emerged as a powerful enabler of nursing engagement and competency development. Participants described how genomics became increasingly routine through the embedding of mainstream testing programs (see Section 6.3.4), which positioned genetic assessment and patient education as standard components of oncology nursing practice. Mainstream genetic testing, a government-funded initiative in Australia, allows oncology teams to offer genetic testing directly to eligible patients as part of standard care. Nurses in these settings frequently played key roles in this process, including obtaining consent, educating patients, and facilitating coordination with multidisciplinary teams. These responsibilities aligned with core nursing tasks and did not require formal specialist roles or genomic titles, which in turn facilitated hands-on learning and

reduced the distance between generalist practice and genomic care. This process reflects Rogers' DOI constructs of *compatibility* and *observability*, whereby alignment with existing roles and the visible demonstration of genomic practices and outcomes both facilitated engagement and reinforced legitimacy.

Organisations that had implemented mainstream testing functioned as *organisational adopters* of genomics, creating local conditions that normalised genomic practice and directly shaped how nurses engaged with it. Within these settings, institutional endorsement, embedded workflows, and visible infrastructure fostered both confidence and capability among nurses, who described genomics as an expected and routine part of care. In contrast, those working in sites without mainstream programs experienced genomics as peripheral, something dependent on individual initiative rather than collective support.

These findings parallel observations by Kim et al. (2022), who found that access to genomic resources was largely determined by workplace context. In their study of non-genetic medical physicians, clinicians employed at well-resourced, research-active hospitals reported far greater exposure to genomics and acknowledged feeling 'lucky' compared with colleagues in settings where such infrastructure was absent. Likewise, nurses in the present study who worked in mainstreaming environments benefited from the same diffusion effect. These findings emphasise that organisational adoption actively shapes individual engagement. When genomics is institutionally embedded, nurses encounter it as part of routine care rather than as an optional or unfamiliar domain, accelerating diffusion and strengthening the workforce's collective capability.

Multidisciplinary collaboration and support. Nurses in this study consistently described multidisciplinary collaboration as a key organisational enabler of genomics adoption. Working alongside clinical geneticists, genetic counsellors, pathology teams, consultants, and researcher teams offered opportunities for experiential learning, skill development, and role clarity. These collaborative environments enhanced awareness and confidence by making genomics more visible and accessible in everyday practice. Regular MDT meetings, co-located services, and embedded roles within clinical teams fostered a setting where genomics could be learned through interaction, not just formal training. Importantly, nurses framed these interactions—often informal conversations, shared case discussions, or observational learning opportunities—as a resource facilitated by their organisation particularly with accessible proximity to genetics services. Within Rogers' DOI framework, these multidisciplinary settings

exemplify *interconnectedness*, operating as vital interpersonal communication channels and enhance observability, enabling nurses to witness genomic practice firsthand and exchange tacit knowledge through everyday collaboration.

In contrast, organisational isolation was perceived as a major barrier. Three participants who reported minimal or no engagement with genomics also described working in facilities without onsite genetics support. One nurse, working in a regional hospital without integrated genetics support, reflected on how this organisational isolation impeded coordinated care and limited shared knowledge:

That blindness... are we aware? are we liaising with the other hospital?—which we are not—but then if we have service here with us, we know what’s happening. Then we have a bit more cohesion of the care rather than people working in isolation. At the moment our department, we are working in isolation.

In this account, ‘blindness’ captured the impact of siloed practice on visibility, cohesion, and care coordination. This is consistent with findings from Janinski et al., (2018) that a lack of proximity to genomic practice provides less opportunity to consolidate and apply learning. Interview accounts agreed that without proximity to genetics teams or clear inter-service communication, non-genomic health professionals experience a disconnect from both genomic knowledge and the systems needed to implement it effectively.

These findings reflect longstanding challenges in health systems regarding siloed disciplines and fragmented care. Smith and Johnson (2023) identified discipline-based silos as a persistent barrier to embedding research and evidence into clinical practice. Their review highlights how transdisciplinary teams—where different professions work together to develop shared frameworks—improve understanding, communication, and the capacity for guideline implementation. Multidisciplinary and transdisciplinary approaches are also linked to greater empowerment, team decision-making, and the dismantling of hierarchical structures that undermine collaborative care (Smith & Johnson, 2023; Urquhart et al., 2013). Bradford et al. (2024), reporting on Australian cancer nurses, echoed these concerns, noting that siloed professional identities hinder teamwork and limit innovation. They argued that shared governance, mutual respect, and inclusion of nurses in clinical decisions can significantly improve workplace culture and the adoption of new practices.

Genomic healthcare research aligns strongly with this position, with broad consensus that healthcare professionals must collaborate across disciplines and promote interdisciplinary education to meet the genomic needs of patients (Campion et al., 2019; Chiu, Limoges, Pike, et al., 2024; Evanoff & Bierut, 2017; Limoges et al., 2022). Importantly for nursing, Chiu et al. (2024) found that Canadian oncology nurses emphasised the importance of coordinated interprofessional teams and a shared understanding of each discipline's scope and role, particularly as patients encounter genomics-informed care for the first time. Collaboration among team members was viewed as essential to ensuring that patients receive consistent and accurate information, reinforcing how multidisciplinary environments enhance both care quality and workforce capability in genomic practice. Consistent with these findings, the present study identified that organisations fostering such collaboration served as critical enablers of nurses' engagement, confidence, and integration of genomics into everyday practice.

7.2.3.5 Domain 5: Individual factors

Knowledge and confidence. Participants consistently identified limited genomic knowledge and low confidence as key barriers to integrating genomics into their nursing practice. Nurses who were not in formal genomic roles expressed uncertainty about core concepts, discomfort in clinical application, and hesitancy in engaging patients in genomics-related conversations, primarily due to fears of providing incorrect or insufficient information. These individual-level limitations were not described in isolation but often intertwined with broader organisational gaps in training and exposure.

Quantitative findings supported these perceptions. As noted above, while most nurses correctly identified core applications of genomics, such as the role of family history in cancer risk, fewer recognised the relevance of pharmacogenomics and its impact on medication responses. This knowledge gap was further reflected in referral behaviour, with survey data indicating that among participants who had not referred a patient to genetics services in the previous month, the most frequently reported barrier was not recognising when referral would be appropriate. Confidence was also generally low, particularly in domains requiring patient-facing engagement, such as providing education or managing genomically relevant clinical situations. These patterns suggest that while awareness of genomics may be increasing, deeper knowledge and applied competence remain underdeveloped.

These findings are consistent with international evidence positioning knowledge and confidence as critical determinants of nurses' ability to engage with genomics. A recent systematic review by Cao et al. (2025) identified genomic knowledge and self-confidence as key determinants of nurses' ability to perform tasks effectively, emphasising that confidence mediates the translation of knowledge into practice. Similarly, Dante et al. (2025) found in their scoping review that nurses, students, and educators reported alarmingly low levels of genomic literacy, which in turn constrained competence, practical application, and confidence. This pattern is also reflected in recent empirical work, where practising nurses report high perceived relevance of genomics but consistently low knowledge and confidence (Carpenter-Clawson et al., 2023; Dagan et al., 2021).

These findings align with DOI theory, in which knowledge initiates the adoption process and functions as a prerequisite for later stages of persuasion and implementation. Inadequate knowledge and low confidence therefore represent not only individual barriers but structural interruptions in the diffusion process itself. Evidence from the Australian context reflects this same pattern. The only national survey of nurses and midwives' genomic literacy found that overall knowledge levels were low (Wright et al., 2019), a finding that mirrors participants' reports in the present study. White et al. (2020) likewise identified inadequate genetic knowledge among nurses as a major barrier to mainstreaming genomics within healthcare systems. Janinski et al.'s (2018) Australian genomics workforce and education report explicitly stated that lack of confidence surrounding genomics is a critical barrier to education and training among non-genomic health professionals. Collectively, this evidence reinforces that limited knowledge and confidence are intertwined and act as foundational barriers to genomic engagement.

Awareness. Participants identified awareness as a foundational individual-level factor shaping engagement with genomics. Several nurses described general awareness among their peers as limited, noting that without visibility or promotion, genomics remained peripheral to everyday nursing practice. Participants viewed increased visibility and active promotion of genomics as essential enablers for fostering engagement and awareness across the workforce. Low awareness was not only viewed as a barrier to knowledge acquisition but also as limiting curiosity and perceived relevance. Participants emphasised that awareness functions as a precursor to motivation, learning, and eventual adoption; without it, genomics fails to enter the professional consciousness needed to prompt further inquiry or engagement.

Quantitative findings supported these perceptions. Oncology nurses in this study demonstrated limited familiarity with national and international genomic initiatives, with many reporting little or no awareness of specialist genetics services or available educational resources. Together, these findings suggest that awareness operates as an early but critical stage in the diffusion process: increasing the visibility of genomics within nursing is essential to stimulating interest, building confidence, and normalising genomic engagement in practice.

These findings are consistent with broader evidence positioning *awareness* as the first and most influential stage in the adoption of innovation. In the context of genetic nursing, Cao et al. (2025) identified genetic awareness as a critical motivator underpinning nurses' development of genomic competence. Similarly, Newcomb et al. (2019) found that nurses' awareness of genetic and genomic information significantly influenced their ability to provide effective care, with higher awareness levels associated with improved family history assessment, risk appraisal, and patient education, core competencies for early detection and prevention. In the Australian context, Janinski et al. (2018) likewise reported that lack of awareness or interest in genomics may lead individuals to ignore or even avoid using it in favour of more familiar practices. This evidence reinforces the present study's interpretation of awareness as an *active precursor* rather than a passive condition. Awareness stimulates curiosity, fosters perceived relevance, and initiates the cognitive and motivational processes that precede knowledge acquisition and confidence building. Within the DOI framework, awareness thus represents the essential entry point of the adoption process—without visibility and exposure, the opportunity for learning and engagement cannot occur.

Perceived relevance. Perceived relevance to clinical practice emerged as a critical factor shaping nurses' engagement with genomics. Participants who had incorporated genomics into their roles, whether through formal genomic positions or by facilitating mainstream testing, consistently described it as both clinically necessary and professionally motivating. These nurses framed genomics as integral to contemporary cancer care and often acted as advocates for wider awareness and education among their peers. Perceived relevance aligns with the constructs of relative advantage and compatibility; when genomics is experienced as beneficial and congruent with existing nursing roles and workflows, favourable attitudes form and advocacy is more likely. Indeed, there is significant evidence that if the innovation is perceived as relevant to the performance of the intended adopter's work it will be adopted more easily (Greenhalgh et al., 2004).

In contrast, participants working in settings where genomics was not routinely discussed or embedded described difficulty conveying its importance to colleagues. In such environments, limited visibility and institutional support diminished perceptions of relevance, reinforcing genomics as peripheral to nursing work. While this theme centres on individual perceptions, the findings highlight the interplay between personal belief and organisational context: when leaders or institutions did not recognise the relative advantage of genomics as clinically valuable, nurses found it harder to prioritise or legitimise engagement. From a diffusion perspective, low organisational visibility may weaken observability within the local social system, reducing perceived relative advantage and blunting the persuasion mechanisms that convert awareness into active engagement.

Survey results supported the strong sense of relevance reported by participants. Only 3.8% of respondents indicated that genomics was ‘not relevant’ as a barrier to adoption. Most participants endorsed the importance of family history, recognised the relevance of genomics to oncology practice, and expressed interest in continuing professional development in this area. However, this interest was frequently moderated by low confidence and uncertainty, indicating that while many nurses believe genomics is important, gaps in knowledge and support limit their ability to act on this belief. These findings suggest a complex but actionable relationship: perceived relevance is present, but it must be reinforced by confidence-building, workplace support, and visible opportunities for application. In DOI terms, relevance appears established at the persuasion stage; without confidence, supportive context, and visible use cases, progression to decision and implementation is likely to stall.

These findings mirror those from Wright et al.’s (2019) survey of Australian nurses and midwives, and Wright et al.’s (2020) seminal Australian study of oncology nursing practice which also identified perceived relevance to practice as a central theme. Similarly to the present study, Wright and colleagues found that nurses mostly recognised genomics as important and relevant; however, systemic and educational limitations constrained their ability to apply this knowledge in practice. Internationally, studies also suggest that nurses may perceive genomics as relevant or important despite having limited genetic knowledge (Calzone et al., 2012; Calzone, Jenkins, et al., 2018; Dagan et al., 2021), with further evidence highlighting that establishing relevance is a key enabler for wider uptake and integration of genomics into nursing practice (Calzone, Kirk, et al., 2018a, 2018b). Indeed, there also appears to be a dynamic relationship between knowledge gain and perceived relevance. Wong et al. (2020) found that increased exposure to a topic enhances motivation to learn more about it, suggesting

that the process of learning itself can reinforce perceptions of relevance. Hines-Dowell et al., (2024) similarly argue that low interest in genomics may reflect a suboptimal understanding of its significance. Their study found that participants valued genomics knowledge and were interested in education, but those who reported a lack of interest may simply have lacked the conceptual foundation to fully appreciate its clinical value. In this way, education and awareness are not just strategies to increase knowledge, they are also critical for building the sense of relevance that motivates adoption. Accordingly, education and exposure operate as levers that heighten perceived relative advantage and increase observability, strengthening the pathway from awareness to adoption within the innovation-decision process.

Interest and curiosity. Individual interest and curiosity in genomics emerged as foundational enablers of engagement. Across interviews, participants described interest as a catalyst for learning, uptake, and confidence-building in genomic practice. While interest alone was rarely sufficient for adoption, it often determined whether nurses pursued further education or engaged with new opportunities. Curiosity was frequently framed as a desire to understand genomic concepts more deeply and was closely intertwined with interest, reinforcing a cycle of self-directed learning, growing confidence, and more active participation in genomic care.

While interest and curiosity were acknowledged by participants as powerful drivers, they also recognised that these traits were not uniformly distributed across the nursing workforce. Some participants described an absence of curiosity as a cultural barrier within their teams or organisations. Others observed that curiosity was often reinforced through exposure and education: those who encountered genomics in clinical practice (e.g., mainstreaming) were more likely to become curious, ask questions, and pursue further learning. This points to the dynamic relationship between individual motivation and structural enablers; curiosity fosters engagement, but curiosity itself may be shaped by the environment in which a nurse works.

This interplay was echoed in the broader dataset, with most participants expressing interest in gaining more knowledge about genetics and genomics. However, despite this widespread interest, actual engagement remained uneven, highlighting a key theme across this study: interest may be necessary, but it is not sufficient for adoption. Nurses may want to learn about genomics, but without clear pathways for learning, role clarity, and institutional support, that interest can stagnate. As other domains in this chapter demonstrate, individual motivation is deeply shaped, and sometimes constrained, by organisational culture, access to resources, and professional structures.

Theoretical models of curiosity provide a useful lens for understanding these dynamics. Loewenstein's (1994) 'information-gap theory' defines curiosity as a sense of deprivation that occurs when one becomes aware of a gap in knowledge. This feeling motivates individuals to seek out information that resolves the gap. Arnone et al. (2011) similarly argue that curiosity leads to increasingly deeper engagement when it is nurtured and supported. These ideas are highly relevant in the context of genomic nursing, where many nurses have just enough exposure to recognise a knowledge gap, but lack the scaffolding to pursue further inquiry. This framework is particularly useful in explaining participants' accounts of becoming interested in genomics after being asked questions by patients they could not confidently answer. For some, these moments of uncertainty created a strong sense of responsibility and motivation to learn more in order to meet patients' informational needs. In this way, the 'information gap' becomes not just a personal experience of not knowing, but a professionally meaningful trigger for learning, driven by the desire to provide competent and informed care.

Research in nursing and education supports this interpretation. Curiosity has been linked to improved critical thinking, evidence-based practice, and lifelong learning (Cheung, 2024; Hendekci, 2025). Hendecki (2025) also argues that fostering curiosity in nursing students is a vital strategy for developing innovation-ready professionals. Soleas (2020), in a systematic review, found that curiosity and interest were among the most powerful intrinsic motivators for innovation adoption, often more influential than extrinsic rewards. When individuals were genuinely interested in a topic, they were more likely to explore, experiment, and sustain engagement over time.

These traits align closely with DOI theory. The earliest adopters are typically characterised by high levels of curiosity, openness to experience, and willingness to try new ideas. However, DOI theory also makes clear that interest alone does not guarantee adoption. Without organisational visibility, support, and structural integration, even highly interested individuals may struggle to implement new innovations.

This point is particularly salient in the context of genomics. While interest was widely expressed in this study, which aligns with the wider genomic oncology nursing literature (Gonthier et al., 2018; Hébert et al., 2022; Wright et al., 2020), participants also made clear that contextual factors matter. Organisational culture, leadership engagement, access to resources, and role clarity all influence whether interest can translate into action. Even when nurses move through the *persuasion* stage of adoption, enablers are still required for implementation to

occur. As such, fostering curiosity and interest is vital, but must be accompanied by structural strategies to support application.

Clinical experience and seniority. While the earlier analysis in this chapter (see Section 7.4) explored how age and nursing experience correlate with adoption, a related theme identified in this study focused more specifically on how clinical experience and seniority function as enablers of genomic engagement in practice. Nurses who held formal genomic roles or who regularly facilitated mainstream testing described their confidence and comfort with genomics as something that had developed cumulatively over time, through repeated exposure, case familiarity, and hands-on engagement. For these participants, years of clinical practice were seen as having created a foundation for confidently managing genomic conversations, navigating consent processes, and integrating genomic considerations into patient care.

These perspectives were largely shared by senior nurses who had already adopted genomics in some form. Importantly, they also reflected on early-career nurses as facing greater barriers to engagement, attributing this not only to a lack of clinical maturity, experience, and exposure, but also to professional and organisational constraints that shape the early years of nursing practice. Genomics was often described as something that could be deprioritised or sidelined in junior roles, where immediate demands, lack of autonomy, and minimal exposure to specialist practice environments may limit opportunities for genomic engagement. However, these views were not echoed by the two early-career participants in this study (see Section 6.3.5.2). This suggests a need for some reflexivity: the characterisation of clinical experience as a prerequisite for genomic engagement may reflect assumptions from within the adopter group itself. Further research would be useful to explore whether early-career nurses experience the same barriers, or whether targeted education and support could offset the perceived need for long-term clinical exposure.

This theme aligns with patterns in the quantitative data, with adopters tending to be older, more experienced in oncology, and more likely to occupy advanced practice roles. As discussed earlier, these demographic and professional characteristics were statistically associated with adoption. What the current theme adds, however, is an understanding of how nurses themselves interpret experience as a resource—not simply as demographic background, but as something that actively supports genomic engagement. In this way, individual experience was framed by nurses as a practical enabler of confidence, comfort, and competence in genomic practice.

These findings are consistent with the broader innovation literature. Tsarfati and Cojocaru (2023) found that years of professional experience positively predicted receptiveness to technological change among nurses. In a related study, they report that seniority was associated with greater perceived ease of use, higher perceived relevance, and greater benefit recognition for technological innovations in nursing (Tsarfati & Cojocaru, 2022). Similarly, Sariköse and Türkmen (2020) found that nurses in senior positions (e.g., nurse managers and educators) exhibited higher levels of innovativeness and were more likely to adopt new practices earlier. While these findings stem from different technological contexts, they support the idea that experience and seniority can cultivate not only confidence, but also a mindset more open to innovation, particularly when change is complex or knowledge-intensive, as is the case with genomics.

This interpretation aligns with DOI theory, which posits that early adopters are typically individuals with higher social status, greater professional credibility, and strong interpersonal networks. These characteristics enable them to exert informal influence across their systems, effectively endorsing the innovation and facilitating its spread. In nursing contexts, senior and experienced practitioners often have greater autonomy, visibility, and authority, allowing them not only to adopt new practices such as genomics but also to signal their legitimacy and embed them more broadly within clinical workflows.

In summary, clinical experience and seniority were perceived by many participants as important enablers of genomic engagement, offering opportunities for exposure, practice, and the development of confidence. However, this view was most strongly articulated by those already working in advanced or genomics-specific roles. Future work may benefit from exploring how best to support early-career nurses, and whether structured exposure and targeted training can replicate the confidence currently attributed to time and experience.

7.3 Theoretical interpretations

This section synthesises the study's findings through DOI theory as the primary interpretive lens. While DOI principles have been applied throughout the discussion, this section consolidates the core constructs to illustrate the broader conceptual patterns influencing the adoption of genomics among oncology nurses. The accompanying table (Table 7.2) summarises these theoretical interpretations, linking each construct to empirical findings and implementation implications discussed in the subsequent narrative.

Table 7.2. Theoretical interpretations

DOI Construct	Definition	Study Interpretation	Theoretical interpretation	Implementation implications
Relative Advantage	The degree to which an innovation is perceived as being better than the idea it supersedes	Enablers: Engagement increases when genomics was seen to enhance care quality (e.g., mainstream testing, risk stratification, targeted therapies, multidisciplinary collaboration). Barriers: When benefits and relevance to practice were unclear, unsupported, or not visible, engagement and confidence declines.	The study suggests that perceived <i>relevance</i> is underpinned by perceptions of <i>relative advantage</i> ; adoption is driven by the visible, contextualised value of genomics rather than awareness alone. This extends DOI by showing that in nursing contexts, individual, professional and organisational validation of value is central to diffusion.	Implementation efforts should explicitly demonstrate the clinical and professional benefits of genomics through targeted education, experiential learning, and role-modelling. Framing genomics as an essential and relevant component of evidence-based oncology care can strengthen perceived advantage and support diffusion.
Observability	The degree to which the results of an innovation are visible to others	Enablers: Integration of genomics into clinical workflows (e.g., mainstream testing), visible clinical utility, experiential learning opportunities, and organisational adoption/ on-site genetics services increase observability and enable adoption. Barriers: Indirect or delayed genomic outcomes, limited visibility of patient benefit, and organisational isolation or siloed practice from genetics reduce observability and hinder engagement.	Findings reinforce DOI interpretations of observability as a factor that accelerates diffusion by making an innovation's value visible within a social system. While genomic outcomes are not always directly observable, opportunities to witness genomics embedded in everyday practice enhance its perceived relevance and legitimacy. Such visibility normalises genomics and promotes diffusion through peer modelling and social reinforcement.	Strengthen observability by embedding genomics into everyday workflows, providing experiential learning opportunities, and supporting visible genomic roles within teams. Making outcomes and processes more tangible can enhance awareness, normalise genomics, and foster workforce diffusion.
Compatibility	The degree to which an innovation is perceived as compatible with existing values, experiences, practices, and needs	Enablers: Viewing genomics as a natural extension of nursing roles (education, consent, coordination), alignment with nursing scope and advanced practice roles, and reinforcement through experiential learning and visible modelling enhanced perceptions of fit and enabled adoption. Barriers: When genomics was perceived as external to nursing, marked by unclear scope or role delineation, lack of organisational embedding, or constrained by workforce pressures, it appeared incompatible and impeded adoption.	Compatibility extended beyond individual perception to encompass professional identity, practice norms, and organisational context. It functioned as a process of professional and social alignment, where resonance with nursing identity conferred legitimacy and lowered barriers to engagement. Leadership endorsement and peer modelling reinforced this fit, illustrating that in healthcare, compatibility is collectively constructed through organisational and professional norms rather than determined by individual fit alone.	To foster adoption, genomics should be positioned in ways that visibly and meaningfully align with nurses' clinical contributions and professional identity. Promote integration by embedding genomics within routine workflows and existing scopes of practice, and by providing opportunities for experiential learning. Leadership and interdisciplinary teams should actively model genomic care and articulate its alignment with nursing values to strengthen perceived fit and support diffusion.

DOI Construct	Definition	Study Interpretation	Theoretical interpretation	Implementation implications
Complexity	The degree to which an innovation is perceived as difficult to understand or use	Barriers: Nurses perceived genomics as complex both technically and psychosocially, struggling with the volume and pace of emerging information, the emotional and psychosocial dimensions of care, and the lack of accessible, nursing-focused educational resources. This perceived complexity contributed to disengagement, uncertainty, and low confidence in practice. Enablers: Several ‘potential enablers’ identified and outlined in implementation implications.	Complexity in this study extended beyond cognitive difficulty to encompass psychosocial and contextual dimensions that inhibited adoption. This broadens the DOI construct by showing that in healthcare, perceived complexity includes relational confidence, emotional readiness, and organisational support, not just technical skill or knowledge.	Reduce perceived complexity by developing nursing-specific, applied genomic education (including genomics and counselling training) and consolidating regularly updated resources delivered through trusted platforms. Provide structured opportunities for experiential learning, mentorship, and team-based support to build confidence and applied knowledge. Embedding genomics within curricula and continuing education can further accelerate adoption.
Trialability	The degree to which an innovation may be experimented with on a limited basis	Enablers: Opportunities to observe or assist with genomic tasks (e.g., consent discussions, referrals, shadowing) increased understanding, confidence, and engagement. Organisational integration of genomics facilitated such exposure, enhancing observability, perceived advantage, and reducing complexity in practice. Barriers: Limited exposure, restricted access, and lack of organisational embedding reduced opportunities to safely ‘try out’ genomics within nursing workflows.	Trialability functioned as a form of experiential learning that allowed nurses to safely test genomic practices and build confidence. Consistent with DOI, opportunities to ‘try out’ genomics reduced perceived complexity and uncertainty while enhancing observability and perceived advantage. These findings extend DOI by showing that in healthcare, trialability is shaped by organisational embedding and access to supportive practice environments.	Promote trialability by providing structured, low-pressure opportunities for nurses to engage with genomics through simulation, observation, and interdisciplinary collaboration. Embedding such experiences within clinical workflows can build applied competence, normalise practice, and accelerate diffusion.
Opinion Leadership	The degree to which an individual is able to influence others’ attitudes or behaviours informally in a desired way and with relative frequency	Enablers: Nurses engaged with genomics often held informal influence within teams, providing peer support, visible role modelling, and accessible guidance that fostered confidence and normalised genomic practice. Barriers: Absence of recognised opinion leaders, limited access to experienced peers, and lack of structured mentorship reduced opportunities for peer diffusion and slowed adoption.	Likely adopters demonstrated higher levels of opinion leadership, supporting Rogers’ proposition that influential individuals play a central role in legitimising and accelerating innovation uptake within peer networks. Nurses’ framing of genomic nurse specialists as enablers reflected the relational nature of diffusion, where peer credibility and visible role modelling legitimised genomic practice. Consistent with DOI, social influence accelerated adoption, while absence of recognised leaders constrained diffusion.	Identify and support genomic opinion leaders to act as mentors and champions. Leveraging peer credibility, visible role modelling, and structured mentorship can legitimise genomics in practice, foster professional confidence, and accelerate diffusion across nursing teams.

7.3.1 Relative advantage

Rogers (2003) identifies relative advantage—the perceived superiority of an innovation over current practice—as one of the strongest predictors of adoption. Thus, understanding whether genomics is seen as adding value, whether clinically, professionally, or organisationally, offers critical insight into its uptake among nurses.

While earlier sections of this chapter explored how nurses described genomics as relevant and meaningful, DOI theory clarifies why these perceptions matter: when genomics is perceived to enhance care, whether through improved risk stratification, targeted therapies, or contribution to multidisciplinary practice, it becomes easier for individuals to justify its integration, even amid competing demands. Conversely, where this relative advantage was less visible or institutionally reinforced, nurses described lower engagement and uncertainty. This mirrors Rogers' view that innovations must demonstrate their benefits clearly to facilitate diffusion.

Importantly, the findings suggest that perceived relevance, which is an enabler explored throughout this study, may be underpinned by nurses' perceptions of genomics' relative advantage. Conversely, where that advantage is unclear, uptake is more difficult to justify. Rogers (2003) stresses that relative advantage is a central element of message content about an innovation and that clearly communicating this benefit is essential to accelerate its adoption. From a practical perspective, this highlights the value of educational strategies and implementation efforts that explicitly showcase the clinical and professional value of genomics, whether through experiential learning, targeted education resources, or embedded advanced practice roles. Emphasising relative advantage may therefore serve not only to build awareness, but also to shift perceptions of genomics from optional to essential within evidence-based oncology nursing practice.

7.3.2 Observability

Observability—the degree to which the outcomes of an innovation are visible to others—is positively associated with its rate of adoption; the more visible the results of an innovation, the more likely it is to be adopted and diffused through peer influence within a social system (Rogers, 2003). However, observability is a complex construct in the context of genomics. Many genomic interventions are indirect, delayed, or managed outside of nursing roles, making it difficult for nurses to see the immediate impact on patient care. Additionally, the benefits of

genomics often manifest over time or across family members, further reducing their visibility within routine practice.

Nonetheless, this study found that in settings where genomics was embedded into clinical workflows (e.g., mainstream testing) its outcomes became more observable and its value more widely recognised. Nurses who routinely engaged in consent processes, patient education, or care planning described increased comfort and understanding, reinforced through repeated exposure. Observability was also enhanced when genomics directly informed treatment decisions, such as guiding targeted therapies, making its clinical utility tangible. These visible outcomes played an important role in raising awareness, normalising genomics in practice, and prompting curiosity among peers.

Opportunities for experiential learning—such as observing or participating in genomic care—further amplified observability and were repeatedly described as enablers of adoption. In particular, the presence of on-site genetic services or embedded genomic nursing roles increased the visibility of genomics in daily practice, offering nurses tangible examples of how genomics could be integrated into care. Conversely, siloed work environments, where genetics expertise was absent or fragmented across services, reduced observability and contributed to uncertainty, isolation, and low engagement. These findings suggest that increasing opportunities for observability of genomic outcomes in practice may therefore be a critical strategy in promoting its diffusion across oncology nursing.

7.3.3 Compatibility

Compatibility refers to the degree to which an innovation aligns with individuals' values, experiences, and work practices (Rogers, 2003). In this study, compatibility emerged as a key enabler of genomic integration when genomics was embedded into routine nursing workflows such as patient education, consent processes, and care coordination.

Participants who adopted genomics commonly described it as a natural extension of their role rather than a distinct or specialised task. This perceived fit reduced disruption, enhanced role clarity, and supported confidence in delivering genomic care. Mainstream testing, in particular, positioned genomic responsibilities within familiar scopes of practice, making engagement more accessible. In contrast, where genomics was not institutionally embedded or was framed as external to nursing, it was perceived as less compatible and more readily deprioritised.

Perceptions of compatibility were especially evident among nurses in advanced practice roles (e.g. CNCs, CNSs), who described genomics as aligning with their responsibilities in clinical leadership, complex decision-making, and multidisciplinary care. Experiential learning further strengthened compatibility, as observing or participating in activities such as consent or care planning enabled nurses to recognise parallels with familiar nursing practices, reinforcing alignment with professional values and identity.

Conversely, under conditions of workforce strain, rigid role definitions, or limited organisational support, genomics was often perceived as incompatible with existing workloads or institutional expectations. Even where interest or clinical relevance was acknowledged, structural constraints limited the perceived feasibility of adoption. Importantly, compatibility was shaped not only by individual judgement but also by organisational structures, leadership signalling, and team practices. Where genomic care was visibly modelled and supported, nurses' perceptions of fit were reinforced, highlighting the importance of positioning genomics in ways that clearly align with nursing roles, values, and contributions.

7.3.4 Complexity

Complexity—the degree to which an innovation is perceived as difficult to understand or use—is inversely associated with its rate of adoption (Rogers, 2003). In this study, perceived complexity emerged as a significant barrier to genomic engagement, particularly among nurses without formal training, structured exposure, or embedded genomic responsibilities.

Participants often described genomics as abstract or complicated, with many expressing discomfort in discussing genomic issues with patients due to fear of providing incorrect information or causing emotional upset. This aligns with survey findings indicating low confidence in applying genomics in practice, despite high levels of interest and perceived relevance. Importantly, complexity was not only linked to scientific or technical content, but also to the psychosocial dimensions of genomic care. Nurses highlighted challenges in managing patients' emotions, fear of psychosocial harm, and addressing family implications, areas where they felt underprepared particularly in terms of counselling skills.

Educational complexity was frequently cited, with participants noting that existing resources were too advanced or poorly tailored to nursing needs. Simplifying content and designing nursing-specific genomic education were seen as essential enablers. In addition, experiential learning, multidisciplinary collaboration, and proximity to genomic professionals were

described as important supports that reduced complexity in practice. These interactions helped nurses clarify concepts, ask questions in real time, and develop applied confidence.

From a diffusion perspective, these findings reinforce Rogers' assertion that reducing perceived complexity is critical to accelerating adoption. Practical strategies may include embedding genomics into nursing curricula, increasing access to continuing education, designing education interventions targeted at nurses including genomic and counselling skills, providing structured opportunities for experiential learning, and ensuring team-based support in clinical settings. In this way, complexity is not merely a cognitive barrier but also a contextual and relational one, shaped by organisational culture, available resources, and the degree of support nurses receive when engaging with genomic care.

7.3.5 Trialability

In DOI theory, trialability refers to the extent to which an innovation can be experimented with before full-scale adoption (Rogers, 2003). In the context of this study, trialability was visible through accounts of experiential learning, secondments, and observation of genomic consultations.

Participants who had opportunities to observe or assist with genomic tasks such as participating in genetic consent discussions, reviewing referrals, or shadowing genomic nurse specialists, often described these experiences as formative. Such exposure allowed nurses to 'try on' aspects of genomic practice within the safety of existing workflows, without requiring a formal title or immediate expertise. These opportunities were most often reported in contexts where genomics had been integrated into routine care (e.g., through mainstream testing pathways), suggesting that organisational adoption facilitates individual trialability.

The ability to trial genomic care also contributed to increased observability, relative advantage and reduction in perceived complexity. This aligns with Rogers' argument that trialability lowers the barrier to entry, especially for innovations that are perceived as complex or disruptive. From a practical standpoint, these findings underscore the importance of creating structured, low-pressure opportunities for nurses to engage with genomics, through simulation, shadowing, interdisciplinary collaboration, or supported nursing initiatives.

7.3.6 Opinion leaders

Rogers (2003) identifies opinion leaders as key agents in the diffusion process, defined as individuals who are respected, well-connected, and able to influence others' attitudes or behaviours within a social system. Unlike innovators, who may adopt ahead of the curve but have limited influence, opinion leaders are embedded in their peer networks and serve as trusted sources of information and validation. When they adopt an innovation, they effectively 'legitimise' it for others, accelerating broader uptake.

In this study, survey findings indicated that adopters were significantly more likely to score higher on the opinion leadership scale. This suggests that nurses already engaged with genomics may also hold positions of informal influence within their teams. Such individuals could serve as powerful change agents, helping to raise awareness, model innovative practice, and normalise genomics as a routine part of oncology nursing care.

Although the qualitative data did not explicitly frame participants as opinion leaders, several accounts highlighted the value of working alongside genomic nurse specialists or more experienced colleagues. These individuals provided accessible sources of guidance and learning, particularly through informal, peer-based support. In this way, even where formal leadership structures were lacking, proximal expertise played an enabling role by fostering comfort, confidence, and curiosity among less experienced staff. This aligns with the findings of Leach et al. (2016) and Andrews et al. (2014a, 2014b), who propose that recognising adopter categories, such as genetic adopters and opinion leaders, can be a useful strategy to accelerate the integration of genomics into nursing. As such, identifying and supporting these informal leaders, particularly those already adopting genomic practices, may represent a powerful strategy for accelerating diffusion. By leveraging peer influence and creating structures that support mentorship and visible role modelling, health services can foster broader workforce engagement and cultural readiness for genomic integration.

7.3.7 Conceptual alignment with implementation frameworks

In addition to DOI theory, several findings from this study also aligned conceptually with constructs from the Consolidated Framework for Implementation Research (CFIR) (Damschroder et al., 2009) (see Section 2.4.9). While CFIR was not used as a guiding or analytical framework in this research, it is briefly included here because of its influence on international strategies for genomic nursing implementation, particularly the G2NA roadmap

and ASIGN tool, which are explicitly structured around CFIR's domains (see Section 1.6) (Tonkin et al., 2020b, 2020a).

Although the analysis in this study was grounded in DOI theory, several of the themes identified (attributes of the innovation, education factors, professional factors, organisational factors, and individual factors) show conceptual resonance with CFIR's five core domains (intervention, individuals, inner context, outer context, and process). While this does not constitute a formal mapping to CFIR, the conceptual convergence strengthens confidence in the interpretations presented here, suggesting that the diffusion processes experienced by nurses are closely interwoven with the organisational and contextual determinants emphasised in implementation science. In this way, CFIR complements DOI theory by illustrating how individual adoption occurs within broader systems shaped by leadership, culture, resources, and workforce capability—conditions that are central to large-scale genomic integration.

This conceptual alignment also resonates with international efforts to structure implementation strategies for genomic nursing. For example, the G2NA roadmap draws on CFIR to guide the identification of barriers and enablers, while the accompanying Maturity Matrix (Tonkin et al., 2020a) provides a mechanism for benchmarking progress (see Section 1.6). Tonkin et al. (2020b) describe the early phases of the roadmap as centring on the identification of contextual factors that may influence change, alongside readiness activities such as assessing organisational and workforce needs. Although the present study focused on nurses' perceived barriers and enablers at the individual and practice levels, these findings offer locally derived insights that may inform these foundational stages of the roadmap process. In this way, the study contributes conceptually to the broader implementation agenda by providing early evidence that can support planning processes and foster collaboration with the nursing workforce and key stakeholders as Australia progresses toward integrating genomics into oncology nursing practice and education.

7.4 Limitations

While this study provides important insights into how oncology nurses in Australia engage with genomics, it is necessary to acknowledge several limitations that influence the interpretation, scope, and generalisability of the findings. These limitations arise across multiple dimensions, including the theoretical framework, sampling strategies, survey design and validation, contextual conditions of data collection, and the qualitative phase of the study.

7.4.1 Theoretical framework limitations

The study was guided by Rogers' (2003) DOI theory, which offers a valuable lens for exploring the uptake of new practices in healthcare. However, DOI theory has notable limitations (see Section 2.4.5). It has been critiqued for its pro-innovation bias (Rogers, 2003), which assumes that adoption is inherently positive and should be maximised, potentially overlooking legitimate contextual or ethical reasons for resisting innovation. Additionally, the theory carries an individual-blame bias, whereby barriers to adoption are often attributed to the individual rather than the system (Rogers, 2003). In the context of genomics in oncology nursing, this may obscure the influence of structural factors such as institutional support, access to training, or policy environments. While DOI theory remains widely used in health research and was appropriate for the study's aims, its limitations warrant consideration when interpreting the findings. Notably, some of these broader organisational and system-level influences emerged organically in the qualitative data and were considered during thematic interpretation.

7.4.2 Sampling and generalisability

Sampling and recruitment strategies in this study introduce several important limitations that affect the generalisability of the findings. In Phase 1, participants were recruited primarily through the Cancer Nurses Society of Australia (CNSA), supported by purposive and snowball sampling approaches. While this strategy enabled the inclusion of nurses from diverse oncology roles and practice settings, it also likely introduced self-selection bias. Nurses who are members of professional societies and who volunteer to participate in research may differ systematically from those who do not, particularly in terms of professional engagement, openness to innovation, or cosmopolitanism, traits that are themselves relevant within DOI theory. As a result, the sample may overrepresent individuals with a pre-existing interest in genomics or professional development, potentially skewing the findings toward more favourable views of adoption. This potential for self-selection bias may have been further amplified in the qualitative phase, as interview participants were drawn from survey respondents who had already expressed interest in genomics and willingness to discuss it.

Furthermore, it was not possible to determine the exact number of nurses who received the survey invitation. Because a third-party mailing list was used and snowball recruitment occurred through peer networks, the denominator required to calculate a response rate was unknown. This limits the ability to assess non-response bias or the representativeness of the final sample. However, purposive and snowball sampling were necessary given the absence of

a publicly accessible database of Australian oncology nurses or a means to directly contact CNSA members. Alternative recruitment strategies, such as site-based or employer-mediated contact, were not feasible as they would have required individual institutional approvals across multiple healthcare settings. While 127 nurses completed the survey and 106 complete responses were analysed, providing a rich dataset for descriptive and exploratory analyses, this number fell below the original target sample size of 306, which had been calculated based on an estimated CNSA membership of 1,500.

A further sampling limitation relates to the lack of geographic practice data, particularly concerning rurality. Geographic location plays a critical role in shaping access to innovation, professional networks, and continuing education. The absence of information on whether participants practised in metropolitan, regional, or remote areas therefore represents a missed opportunity for deeper contextual analysis. In the Australian healthcare landscape, rural and remote nurses often face distinct structural challenges, and their underrepresentation or invisibility within the data constrains the study's ability to comment meaningfully on these dimensions of genomic adoption.

7.4.3 Context of data collection

The timing of data collection represents an important contextual factor that may have influenced both the response rate and the content of participants' responses. The survey was administered in early 2022, during Australia's recovery from the COVID-19 pandemic and a period marked by strict nation-wide lockdowns, systemic disruption, and healthcare fatigue. Oncology nurses, like much of the broader health workforce, were operating under significant and prolonged pressure due to staffing shortages, shifting clinical priorities, and emotional exhaustion (Butow et al., 2022). These circumstances likely had implications for how participants engaged with the study, as well as how they perceived and responded to questions about genomics in clinical practice.

Specifically, it is possible that participation rates were suppressed due to the extraordinary demands placed on nurses during this period. Time constraints, psychological fatigue, and the reprioritisation of professional responsibilities may have limited nurses' capacity to engage with voluntary research activities (Fernandez et al., 2020; Halcomb et al., 2020). In an environment in which immediate clinical survival and crisis management were paramount, the integration of emerging innovations such as genomics may have been viewed as less urgent or

feasible, potentially shaping how nurses responded to questions about relevance, confidence, or institutional support.

Conversely, it is also possible that heightened public and professional discourse around genomic concepts during the pandemic, such as PCR testing, viral sequencing, and population genomics, may have contributed to increased awareness or perceived relevance of genomics in healthcare (Park et al., 2024). These contrasting dynamics highlight the need to interpret participants' reported engagement with genomics not only in light of the systemic pressures of the pandemic, but also with sensitivity to the ways in which genomic concepts may have gained heightened salience in the zeitgeist.

More broadly, the pandemic may have reshaped participants' attitudes toward professional development and innovation adoption (Liu & Miguel-Cruz, 2022). In addition to altering clinical workload and care pathways, COVID-19 arguably shifted how nurses conceptualised change, capacity, and system-level readiness for implementing new practices (Harrington, 2020; Ziegler et al., 2024). These contextual conditions do not undermine the study's findings, but they offer important interpretive framing, particularly in light of ambivalence, disengagement, or caution among some participants.

7.4.4 Survey design and validation

The quantitative survey was based on a tool originally developed by Andrews et al. (2014b) and adapted to better reflect the contemporary Australian oncology nursing context. These adaptations included content updates, language and inclusivity improvements, and design enhancements. While these modifications strengthened the instrument's relevance and clarity, they also introduce some methodological limitations. Direct comparability with the original study is reduced, and construct validity has not been formally established for the adapted version. No full psychometric validation was undertaken, and reliability testing was limited due to the survey's wording and structure. However, Cronbach's alpha and McDonald's omega were calculated for three subscales: openness to experience (Cronbach's $\alpha = 0.75$; McDonald's $\omega = 0.78$); opinion leadership (Cronbach's $\alpha = 0.89$; McDonald's $\omega = 0.90$); and perceived influence (Cronbach's $\alpha = 0.76$; McDonald's $\omega = 0.77$). While these values fall within acceptable thresholds for internal consistency (Cronbach, 1951; McDonald, 1999), further psychometric testing, including factor analysis and assessments of construct and convergent validity, would be required to fully validate the instrument. Given the design and scope of the survey, which was intended as a descriptive, exploratory tool adapted to a specific clinical

context, extensive psychometric validation (e.g., confirmatory factor analysis or test-retest reliability) was beyond the scope of this doctoral research. Future studies with larger and more diverse samples would be well positioned to address this limitation by formally validating the instrument or developing standardised adoption metrics for use across nursing contexts.

In addition to these validation considerations, several design choices introduce limitations to the interpretation of the quantitative findings. The survey employed a fully structured, forced-choice format using five-point Likert scales. While this design enhanced internal consistency, reduced ambiguity, and supported inferential analysis, it also limited participants' ability to elaborate on their responses, particularly in relation to emerging or unfamiliar topics such as genomics. However, this decision was intentional. Unlike the original version of the instrument, which included optional free-text items, the current study deliberately adopted a fully quantitative approach in Phase 1 to reduce participant burden and maximise completion rates. Nuanced views and contextual insights were instead captured through the qualitative interviews conducted in Phase 2, which provided richer, more detailed data to complement the survey findings.

A final methodological limitation relates to the reliance on self-report measures for much of the data collected. The survey primarily assessed participants' perceived knowledge, confidence, and behaviours, and the interviews likewise relied on self-reported accounts of practice. Such measures are valuable but introduce the potential for social desirability bias, whereby participants may overstate their engagement or competence in genomics, as well as inaccuracies in self-assessment. While the survey did include several objective knowledge questions (e.g., about areas of care linked to genomics, family history taking, and available resources), these items were limited in number and scope and therefore may not fully offset the broader reliance on self-report.

7.4.5 Qualitative phase limitations

The qualitative phase of the study involved telephone interviews with nine oncology nurses who had completed the quantitative survey and expressed interest in further participation. While the interviews yielded rich, nuanced data and thematic saturation was achieved, as discussed in Section 4.7.4, the point at which qualitative data collection concluded also reflected the practical limits of participant availability and recruitment, and is acknowledged as a limitation.

Although participants represented diversity in clinical role, geographic location, and level of engagement with genomics, the modest sample size inevitably constrained the overall breadth of perspectives that could be captured. This reflects both the voluntary nature of recruitment and the specialised characteristics of the oncology nursing workforce in Australia. While this is consistent with qualitative approaches that prioritise depth and interpretive richness over generalisability, the findings should be viewed as exploratory and illustrative rather than representative of the entire nursing population.

Additionally, ethical considerations around protecting participant confidentiality required an additional step beyond standard anonymisation (see Section 4.8.3). Given the small and highly specialised nature of the genomic nursing workforce in Australia, assigning pseudonyms or participant numbers risked deductive disclosure. To address this, following consultation with the UTS HREC and the supervisory panel, interview quotes were presented without attribution to specific individuals. While this approach was ethically necessary and aligned with the principle of non-maleficence, it inevitably constrained the use of ‘thick description’ in the traditional qualitative sense. However, transferability was addressed through transparency in methodological reporting, detailed thematic presentation, and the interpretive clarity of findings. The inclusion of illustrative quotes, even without attribution, enables readers to assess the relevance and resonance of the results within other settings.

Finally, limitations relate to the analytic approach adopted in the qualitative phase. Thematic analysis was conducted within a reflexive orientation, which emphasises the active role of the researcher in generating, rather than merely discovering, themes. While this approach was appropriate for the exploratory aims of the study and enabled nuanced interpretation of participants’ accounts, it also reflects a particular epistemological stance. Different analytic choices, such as content analysis, framework analysis, or grounded theory, may have yielded alternative emphases—for example, by producing more structured categorisations, privileging frequency counts, or generating formal theory. Moreover, the interpretive lens was inevitably shaped by the researcher’s professional background and positionality, even as reflexivity and supervision were used to mitigate bias (see Section 1.12). As such, the themes presented should be understood as one possible, well-grounded interpretation rather than the only way the data might be conceptualised.

7.5 Contributions to knowledge

Despite these limitations, this study makes several original contributions to knowledge on the diffusion and adoption of genomics within the Australian oncology nursing workforce (these are also summarised in Table 7.3). It provides the first empirical examination of genomic adoption among Australian oncology nurses, establishing a foundational evidence base for workforce engagement and readiness in a context where national data were previously absent. Findings suggest that the workforce is largely situated in the early awareness and persuasion stages of adoption—nurses recognise the importance of genomics but lack the confidence and applied competencies required for consistent implementation. This baseline evidence contributes to the international nursing genomics agenda by identifying key barriers and enablers of uptake in Australia, offering the first local insights to guide the formative stages of national implementation planning.

These findings extend international evidence by demonstrating that, within an Australian oncology nursing context, adopter characteristics align with key constructs of Rogers' DOI theory. Whereas previous studies such as that of Andrews et al. (2014b) found no consistent demographic variation between adopters and non-adopters, the present research identified significant differences by age, professional experience, role, and educational attainment. This pattern suggests that professional maturity and role seniority may facilitate adoption in the Australian setting. By evidencing these relationships empirically, the study refines theoretical understanding of how demographic, professional, and personality attributes shape the diffusion of complex innovations such as genomics within nursing.

This study offers new insight into the depth and nature of nurses' genomic competence. It demonstrates that while awareness of genomics is emerging, applied competence, particularly in patient-facing and psychosocial domains, remains underdeveloped. A further contribution lies in identifying limited understanding of pharmacogenomics, which represents the first empirical indication of this gap within the Australian nursing workforce despite its critical relevance to oncology and precision healthcare. The study also exposes the magnitude of the current curriculum deficit, suggesting that some nurses may enter the workforce wholly unprepared to engage with genomics in clinical care. The findings extend existing competency frameworks by demonstrating that genomic practice requires not only technical knowledge but also the emotional and communicative skills to support patients experiencing fear, uncertainty, and familial distress. By evidencing the psychosocial complexity inherent in genomic care, this

study advances understanding of the multifaceted skill set required for genomic readiness within oncology nursing.

This research further extends the existing literature by providing empirically grounded insights into oncology nurses' preferences for, and access to, genomic education resources. In addition to identifying variation in preferred learning modalities, the findings demonstrate that nurses' engagement with genomic education may be shaped by contextual factors, including geographical location, rurality, digital literacy, and work setting. This contributes a more nuanced understanding of how accessibility and context influence uptake of genomic education, strengthening the evidence base that informs workforce development strategies.

Importantly, this study highlights nurses' preference for genomic education resources that are specifically tailored to nursing practice, easily accessible, and regularly updated. Participants expressed a clear desire for consolidated, 'one-stop' educational hubs hosted on trusted platforms already embedded within the Australian health system, such as eviQ and the HETI. This finding extends prior work by demonstrating that credibility, relevance to nursing roles, and ease of access are central to nurses' engagement with genomic education, rather than content availability alone.

The study also contributes new insights into the scope of genomic education valued by oncology nurses. Participants emphasised the importance of education that integrates foundational genomic knowledge with psychosocial and counselling-related competencies, reflecting the emotional complexity of genomic care in oncology settings. In addition, nurses consistently valued experiential and multidisciplinary learning opportunities, viewing these as particularly effective for building confidence, contextualising genomic information, and supporting translation into practice. Together, these findings advance understanding of not only *what* genomic education content nurses seek, but *how* and *where* it is most meaningfully delivered to support genomic competence in oncology nursing.

The study also contributes novel empirical evidence on the organisational determinants of genomic adoption within Australian nursing. It demonstrates that the degree to which genomics is institutionally embedded through leadership recognition, integration within clinical workflows, and proximity to genetics services directly shapes nurses' capacity and motivation to engage. When genomics is visible and valued within organisational systems, engagement is strengthened; when leaders or institutions fail to recognise its clinical relevance, nurses find it more difficult to legitimise or prioritise genomic activity within competing demands. These

findings advance understanding of diffusion by showing that organisational adoption operates not merely as a contextual backdrop but as an active driver of individual engagement. By evidencing how organisational barriers such as limited resources, workforce pressures, and the absence of protected learning time constrain diffusion, this study provides the first Australian perspective on how system-level readiness influences the pace and depth of genomic integration within nursing practice.

The study also makes a distinctive and clinically significant contribution by providing the first empirical evidence that oncology nurses in Australia are already enacting genomic care informally, despite limited structural support or defined role parameters. While some formal and informal genomic functions exist, the boundaries between them remain unclear. Nurses described acting—or recognising the potential to act—as opportunistic facilitators of genomic healthcare, often stepping into gaps in service delivery or communication between disciplines. A recurring enabler identified was the presence, or desired presence, of a genomic nurse specialist ‘on the floor’, underscoring the perceived value of accessible expertise within clinical teams. A particularly novel contribution lies in the documentation of nurses identifying patients who had ‘slipped through the cracks’, revealing the profession’s capacity to act as a genomic safety net that prevents missed opportunities for testing, referral, and appropriate care. Importantly, this directly responds to a gap highlighted in the nursing genomics literature, which notes the scarcity of evidence demonstrating how nurses’ genomic actions translate into tangible patient benefit in real-world settings (Dewell, Benzies, & Ginn, 2020; Keels et al., 2024). This observation therefore adds new empirical insight to the literature, which has acknowledged nurses’ roles in family-history collection and patient education but has rarely captured such direct examples of genomic intervention prompted by nursing vigilance and relational practice. Conversely, nurses described situations in which feeling ill-equipped to recognise or address patients’ genomic concerns contributed to missed opportunities for timely engagement, with potential implications for treatment continuation, including patients disengaging from care. Collectively, these findings legitimise nurses’ central role in facilitating genomic healthcare and demonstrate how their genomic competence and actions can directly influence the quality and continuity of care.

Finally, this study provides nationally and internationally significant evidence to inform genomic workforce development and policy. It offers the first local empirical foundation for designing nursing genomics strategies, education frameworks, and workforce reforms aligned with Australia’s transition to precision medicine. By positioning these findings within the

broader international genomics implementation agenda, the study contributes Australian evidence to global understanding of how nursing workforces adopt and integrate genomics and provides a foundation for benchmarking national progress. Collectively, these contributions extend empirical, theoretical, and practical understanding of how genomics diffuses through nursing practice. The study enriches international discourse by contextualising Australian evidence within a broader implementation landscape, clarifies the individual, organisational, and systemic conditions necessary for effective adoption, and provides an essential foundation for future research, education, and policy development to advance a genomically capable nursing workforce.

Table 7.3. Contributions to knowledge

Domain	Key contributions
Foundational evidence	• First empirical examination of genomic adoption among Australian oncology nurses. • Established a baseline of workforce engagement • Identified that the workforce is predominantly in early awareness and persuasion stages of adoption. • Identified key barriers and enablers to inform implementation efforts. • Reported the magnitude of the curriculum deficit, showing that some nurses enter practice unprepared for genomic care.
Theoretical contributions	• Extended Rogers' Diffusion of Innovations theory by demonstrating how demographic, professional, and personality traits (e.g., openness, opinion leadership) influence adoption in nursing. • Reported an adopter profile that provides an evidence base to inform targeted implementation strategies.
Competency and Education	• Provided the first evidence of limited pharmacogenomics knowledge within the Australian nursing workforce. • Highlighted underdeveloped patient-facing competence in psychosocial domains. • Emphasised that competency frameworks should include psychosocial and communicative skills. • Identified contextual influences on access to and preferences for genomic learning modalities. • Highlighted gaps in genomic education resources and the importance of experiential learning.
Organisational	• Demonstrated that organisational adoption and embedding of genomics drives individual engagement. • Provided the first empirical Australian evidence that leadership disengagement negatively impacts individual adoption of genomics. • Highlighted that organisational-level readiness is related to genomic integration.
Clinical practice	• Revealed that oncology nurses are already performing informal genomic functions despite absent role structures. • Identified nurses as opportunistic facilitators of genomic care and need/desire for on-site genomic nurse specialists.

	• Provided direct evidence of nurses acting as a genomic safety net—identifying patients who had ‘slipped through the cracks’ and preventing missed testing, referral, and follow-up that could affect patient and family health outcomes.
National Relevance	• Provided local empirical foundation to inform national nursing genomics strategies and education policy. • Established a foundation for workforce, curriculum, and system reform. • Contributed Australian evidence to the international genomics implementation agenda and precision-medicine policy development.

7.6 Recommendations

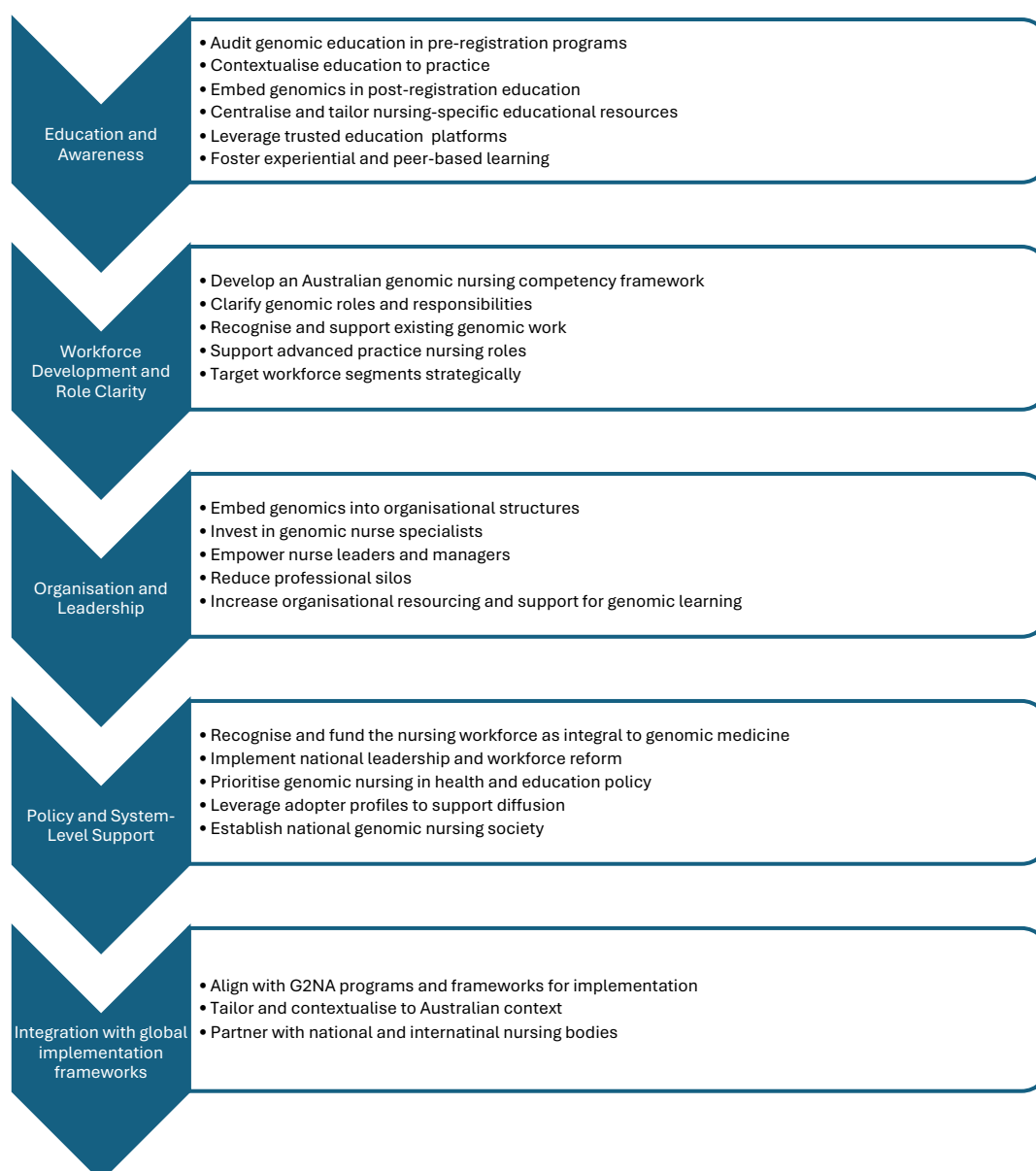


Figure 7.2. Recommendations.

7.6.1 Education and awareness

A coordinated national approach to genomic education is essential to prepare and upskill nurses for the realities of genomic healthcare. The findings of this study highlight the need for systematic evaluation and reform across both pre-registration and post-registration education. A national audit of nursing curricula would establish the current extent, depth, and mode of genomic content delivery, identifying gaps and supporting the integration of core competencies across programs. Educational content should be contextualised to practice, using clinical nursing language, case studies, and patient scenarios that reflect nurses' everyday roles to ensure relevance and application. At the post-registration level, accessible CPD opportunities, in-service training, and secondments should be expanded to enhance genomic literacy, with particular attention to pharmacogenomics and to the psychosocial dimensions of care such as communication, managing distress, and navigating family histories. Centralised, nursing-specific educational resources are also required, ideally through a national, regularly updated online hub that consolidates guidelines, learning materials, and case exemplars within existing trusted platforms such as eviQ or HETI. Finally, the importance of experiential and peer-based learning must be recognised and resourced; opportunities to observe consent discussions, participate in multidisciplinary meetings, or shadow genomic specialists can embed knowledge and build confidence, while peer-learning mechanisms can sustain engagement and normalise genomic practice within clinical teams. Promotion and dissemination of genomic education initiatives may also be strengthened by leveraging the adopter profiles identified in this study, particularly by targeting early adopters through cosmopolite channels and professional networks to accelerate awareness, uptake, and peer-to-peer diffusion within the nursing workforce.

7.6.2 Workforce development and role clarity

Developing a genomically capable nursing workforce requires formalised competencies, clear role delineation, and recognition of the genomic work already being undertaken within clinical settings. Establishing an Australian genomic nursing competency framework would align local practice with global standards while ensuring consistency with national regulation, policy, and scope of practice. Clear articulation of where genomics fits within registered nurse, advanced practice, and specialist genomic nursing roles is essential to build confidence and engagement. Importantly, many nurses are already contributing to genomic care informally, often without acknowledgment or structural support; workforce mapping and formal recognition mechanisms

are therefore required to identify, value, and resource these contributions. Integrating genomics into existing advanced practice positions and creating dedicated genomic nurse specialist roles within cancer services would further strengthen education, coordination, and advocacy across the system. Building on the adopter profile identified in this study, implementation strategies should also target workforce segments strategically leveraging the experience and influence of senior, cosmopolite nurses as opinion leaders to drive diffusion, while supporting early-career nurses through structured learning and supervised exposure that can replicate the confidence associated with professional maturity and experience.

7.6.3 Organisation and leadership

Organisational endorsement and engagement are pivotal drivers of genomic adoption and diffusion. Genomics must be embedded within the organisational structures of oncology care and positioned as a core component of routine practice rather than a specialist adjunct. Integrating genomic activities into clinical pathways and workflows can normalise genomic care and accelerate uptake at the individual level. Embedding genomic nurse specialists within teams is particularly valuable, as these roles enhance patient care, mentorship, and informal learning while facilitating diffusion through peer influence. Leadership and managerial engagement are equally critical: nurse leaders and middle managers act as gatekeepers whose endorsement legitimises genomics and supports sustained integration. Organisational culture should also prioritise collaboration across disciplines, reducing professional silos and strengthening the connection between nursing teams and genomic services to promote shared responsibility for genomic care. Achieving this integration requires tangible structural investment, protected learning time, access to current resources, and funded professional development opportunities. Creating avenues for experiential and practice-based learning, such as observing genetic consultations or participating in multidisciplinary forums, ensures that genomics is embedded within everyday nursing practice. Without such organisational commitment, individual motivation and interest are unlikely to translate into sustainable practice change, particularly in already stretched clinical environments.

7.6.4 Policy and system-level support

National coordination and policy alignment are essential to sustain progress and fully enable nursing in the genomic era. Australia's substantial investment in genomic medicine and precision-health infrastructure risks being undermined if nurses—the largest and most patient-facing component of the healthcare workforce—are not systematically included in

implementation planning and funding. Sustained national investment must therefore extend to nursing education, leadership, and workforce development to ensure that genomics delivers on its system-wide objectives. Coordinated national leadership and reform are required, supported by a dedicated governance framework to guide nursing leadership, workforce planning, and professional development across health and education sectors. In this context, establishing an Australian genomics nursing society may be beneficial, providing a dedicated professional forum to support leadership, advocacy, knowledge exchange, and the coordinated development of education and practice initiatives. Establishing a national genomic nursing strategy would align nursing initiatives with Australia's broader genomic medicine agenda and ensure consistent leadership across jurisdictions. Genomic nursing should also be embedded within national health and education policy through explicit recognition of nurses' central role in implementation. Integrating genomics into accreditation standards, curricula, and workforce policies will embed capability within the profession's regulatory and educational foundations, promoting consistency, sustainability, and equity across the system. Finally, policy initiatives should leverage the adopter profile identified in this study by engaging early adopters, who are typically senior, experienced, and cosmopolite nurses, as opinion leaders who can accelerate diffusion through mentorship and peer influence within clinical settings.

7.6.5 Integration with global implementation frameworks

Although it was beyond the scope of this study to apply the G2NA roadmap or ASIGN Maturity Matrix directly, these frameworks offer valuable structures for guiding future implementation of genomic nursing in Australia. The barriers and enablers identified in this research align closely with the domains and critical success factors articulated within the G2NA program, providing a foundation for tailoring these global frameworks to the Australian oncology nursing context and supporting future benchmarking and workforce development initiatives. Implementation planning could involve mapping the identified barriers and enablers against the six ASIGN critical success factors to identify priority areas of low readiness (e.g., education access or organisational leadership). Using the G2NA roadmap to develop targeted strategies in these areas, alongside collaboration with national nursing bodies, would enable the adaptation of the ASIGN and roadmap frameworks for the Australian context and promote alignment with global genomic nursing implementation efforts.

7.7 Future research

This study highlights several avenues for future inquiry that could build on and extend its findings. While the gender distribution of the sample closely reflected that of the Australian nursing workforce, it would be valuable to capture the perspectives of male nurses more deliberately in future research. Focused recruitment of male participants, or even male-only samples, may provide additional insights into how gender influences engagement with genomics in oncology nursing. Similarly, the absence of Aboriginal and Torres Strait Islander nurses in this study underscores the importance of centring Indigenous voices in future work. Given the unique ethical, cultural, and clinical considerations surrounding genomics in Australia, future studies should prioritise the inclusion of Indigenous nurses and communities in shaping genomic nursing practice. Geographic location should also be a focus of future work, as rural and remote nurses often face distinct structural challenges that affect access to innovation, professional networks, and continuing education. Their underrepresentation or invisibility within current data constrains the ability to comment meaningfully on these dimensions of genomic adoption.

A further direction for future research arises from this study's finding of discrepancies in adoption and perceived barriers between early- and late-career nurses. Further work is needed to examine whether early-career nurses experience the same barriers identified by their more senior counterparts, and whether targeted education and support could offset the perceived need for long-term clinical exposure. Research that explores how best to support early-career nurses—including whether structured exposure, targeted training, or early mentorship can replicate the confidence currently attributed to experience—would provide important insights for strengthening genomic capability across the career trajectory.

The survey tool adapted for this study provided a useful framework for assessing knowledge, adoption, and related characteristics, but further research is needed to refine and validate this instrument. Large-scale studies with diverse nursing populations could help to establish psychometric validity, develop standardised adoption metrics, and enable more robust comparisons across clinical contexts and international settings. Extending such work across specialties beyond oncology—for example, in primary care, paediatrics, or community health—would also help determine whether the findings reported here are unique to oncology or reflective of broader trends in nursing engagement with genomics.

In addition, research that moves beyond cross-sectional surveys is warranted. Longitudinal and intervention-based designs would provide valuable insights into how genomic adoption evolves over time and how specific strategies, such as targeted CPD modules, structured mentorship initiatives, or nursing-specific educational resources, can influence engagement and practice. Before such strategies can be evaluated, however, the development of these interventions represents an essential and substantial step in its own right—one that should be informed by empirical evidence, including the barriers and enablers identified in this study. Once developed, experimental and longitudinal designs would then be well positioned to evaluate the effectiveness of these interventions, as well as support the evaluation of system-level initiatives such as competency frameworks or policy-driven approaches in shaping workforce preparedness and organisational readiness for genomic care.

Finally, as precision oncology advances, future studies should examine how nurses engage with domains such as pharmacogenomics, biomarker-guided therapies, and personalised treatment protocols. These areas represent some of the most rapidly evolving aspects of cancer care and are increasingly central to clinical decision-making. Targeted investigation into nurses' knowledge, barriers, and educational needs in these domains would provide critical evidence to guide workforce development and ensure that nurses remain well-prepared to support patients in the era of precision medicine.

In conclusion, future research should be designed to capture the diversity of the nursing workforce, address emerging domains of genomic medicine, and rigorously test strategies that can build knowledge, confidence, and adoption over time. By broadening the scope beyond oncology, including underrepresented groups such as rural and Indigenous nurses, and embracing innovative designs and validated tools, the next generation of studies can generate the evidence needed to guide workforce development and ensure that nurses are equipped to deliver safe, equitable, and genomically informed cancer care.

7.8 Conclusion

This study set out to answer the research question: *How do oncology nurses in Australia engage with genomics, and what individual characteristics and perceived barriers or enablers influence its adoption into practice?* The research aimed to address this question through a mixed-methods design comprising a national survey and semi-structured interviews with Australian oncology nurses. Guided by Rogers' (2003) Diffusion of Innovations theory, the research sought to examine how nurses understand and engage with genomics in their clinical

practice, to identify the individual characteristics associated with adoption, and to explore the perceived barriers and enablers influencing uptake of genomics. In doing so, the study responds to a critical gap in the evidence base: despite nursing's central role in delivering genomic healthcare, little was previously known about Australian cancer nurses' genomic knowledge, attitudes, or readiness to integrate genomics into oncology care.

The findings provide a national perspective on Australian oncology nurses' genomic knowledge, confidence, and engagement in practice. Levels of knowledge among participants were variable, with limited awareness of genomic resources, initiatives, and specialist services, and low knowledge of pharmacogenomics. Confidence was similarly low, yet participants expressed positive attitudes and a strong interest in learning more. The combination of positive attitudes and limited practical readiness observed here represents an early, receptive phase of diffusion rather than established implementation. These results provide the first baseline evidence of genomic readiness within the Australian oncology nursing workforce and highlight areas of strength, uncertainty, and opportunity that can inform workforce development and implementation planning.

The study also identified a distinctive adopter profile within this workforce. Likely adopters tended to be older, more experienced, held advanced practice or postgraduate qualifications, and demonstrated higher openness to experience, opinion leadership, and cosmopolite information seeking behaviours. This profile refines understanding of the personal and professional attributes that characterise early engagement with innovation in nursing, offering an evidence base for targeted implementation strategies.

A range of barriers and enablers to genomic uptake were identified and grouped across five interrelated domains: innovation attributes, educational factors, professional factors, organisational factors, and individual factors. These domains form a layered, meso-to-micro model that reflects the contextual and interdependent nature of adoption. Barriers such as limited access to education, low confidence, and unclear role boundaries were counterbalanced by enablers including leadership support, experiential learning, and proximity to genetics services. Together, these domains illustrate how multiple influences converge to shape nurses' capacity and motivation to engage with genomics, situating adoption within a complex ecosystem of personal, professional, and organisational conditions.

Using DOI theory as an interpretive lens, this study demonstrated how each construct manifested within Australian oncology nursing. Relative advantage was evident when

genomics was seen to enhance care quality through mainstream testing, risk stratification, and multidisciplinary collaboration, but engagement declined when benefits were unclear or unsupported. Observability increased where genomics was integrated into clinical workflows or where nurses could witness visible genomic activity and outcomes, while isolation from genetics services reduced engagement. Compatibility was strengthened when genomics aligned with nursing roles in education, consent, and coordination, but weakened when perceived as being external to nursing or constrained by unclear scope or organisational support. Complexity extended beyond technical difficulty to include psychosocial and contextual dimensions, with nurses describing emotional and relational aspects of genomic care as challenging. Trialability emerged through experiential learning opportunities such as observing or assisting with genomic tasks, which enhanced confidence and understanding, whereas limited exposure restricted uptake. Finally, opinion leadership was evident among the adopter group, who were viewed by colleagues as accessible sources of guidance and learning, particularly through informal, peer-based support.

Together, these insights make several substantive contributions to knowledge. Empirically, this study provides the first evidence base for genomic adoption among Australian oncology nurses, establishing a national baseline of engagement and readiness. It highlights the magnitude of the current curriculum deficit, showing that some nurses enter practice without adequate preparation for genomic care. Theoretically, it extends the application of Rogers' DOI theory by demonstrating how demographic, professional, and personality attributes (e.g., openness to experience, opinion leadership, and cosmopolitaness) influence adoption in nursing. The identification of a distinct adopter profile offers an evidence base to inform targeted implementation strategies and the design of interventions that leverage early adopters as change agents.

This research also lays an essential foundation for workforce, education, and policy reform. By illuminating the barriers and enablers influencing adoption, it provides empirically grounded guidance for embedding genomics within nursing education, clinical governance, and organisational systems. The evidence generated here can inform the development of national strategies, competency frameworks, and leadership initiatives that align with Australia's broader genomic medicine agenda and with international implementation efforts.

In conclusion, this study demonstrates that successful integration of genomics into oncology nursing requires more than knowledge acquisition; it depends on coordinated investment in

education, organisational culture, and professional identity. Australian oncology nurses are interested in and willing to engage with genomics, yet readiness and adoption remain contingent on policy, institutional, and educational support to translate this willingness into capability. By evidencing both the challenges and the promise of genomic adoption in oncology nursing, this thesis provides a foundation for building a genomically capable workforce—one equipped not only with technical expertise but with the confidence, competence, and clinical insight to deliver equitable, person-centred genomic care within Australia’s evolving healthcare landscape.

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Appendices

Appendix A: Checklist for Reporting Of Survey Studies (CROSS)

Section/topic	Item	Item description	Reported on page #
Title and abstract			
Title and abstract	1a	State the word ‘survey’ along with a commonly used term in title or abstract to introduce the study’s design.	p. x (Abstract)
	1b	Provide an informative summary in the abstract, covering background, objectives, methods, findings/results, interpretation/discussion, and conclusions.	pp. x-xi (Abstract)
Introduction			
Background	2	Provide a background about the rationale of study, what has been previously done, and why this survey is needed.	pp. 39-40
Purpose/aim	3	Identify specific purposes, aims, goals, or objectives of the study.	pp. 40-41
Methods			
Study design	4	Specify the study design in the methods section with a commonly used term (e.g., cross-sectional or longitudinal).	p. 121
	5a	Describe the questionnaire (e.g., number of sections, number of questions, number and names of instruments used).	pp. 122-125, 135
Data collection methods	5b	Describe all questionnaire instruments that were used in the survey to measure particular concepts. Report target population, reported validity and reliability information, scoring/classification procedure, and reference links (if any).	pp. 122-143
	5c	Provide information on pretesting of the questionnaire, if performed (in the article or in an online supplement). Report the method of pretesting, number of times questionnaire was pre-tested, number and demographics of participants used for pretesting, and the level of similarity of demographics between pre-testing participants and sample population.	p. 136
	5d	Questionnaire if possible, should be fully provided (in the article, or as appendices or as an online supplement).	Appendix B
Sample characteristics	6a	Describe the study population (i.e., background, locations, eligibility criteria for participant inclusion in survey, exclusion criteria).	p. 136
	6b	Describe the sampling techniques used (e.g., single stage or multistage sampling, simple random sampling, stratified sampling, cluster sampling, convenience sampling). Specify the locations of sample participants whenever clustered sampling was applied.	pp. 136-138

Survey administration	6c	Provide information on sample size, along with details of sample size calculation.	p. 137, 165
	6d	Describe how representative the sample is of the study population (or target population if possible), particularly for population-based surveys.	p. 165
	7a	Provide information on modes of questionnaire administration, including the type and number of contacts, the location where the survey was conducted (e.g., outpatient room or by use of online tools, such as SurveyMonkey).	pp. 137-138
	7b	Provide information of survey's time frame, such as periods of recruitment, exposure, and follow-up days.	p. 138
Study preparation	8	Describe any preparation process before conducting the survey (e.g., interviewers' training process, advertising the survey).	pp. 137-138
Ethical considerations	9a	Provide information on ethical approval for the survey if obtained, including informed consent, institutional review board [IRB] approval, Helsinki declaration, and good clinical practice [GCP] declaration (as appropriate).	p. 137, 160, Appendix C
	9b	Provide information about survey anonymity and confidentiality and describe what mechanisms were used to protect unauthorized access.	pp. 160-163
Statistical analysis	10a	Describe statistical methods and analytical approach. Report the statistical software that was used for data analysis.	pp. 138-139, 165
	10b	Report any modification of variables used in the analysis, along with reference (if N/A available).	
	10c	Report details about how missing data was handled. Include rate of missing items, missing data mechanism (i.e., missing completely at random [MCAR], missing at random [MAR] or missing not at random [MNAR]) and methods used to deal with missing data (e.g., multiple imputation).	pp. 165-166
	10d	State how non-response error was addressed.	p. 165-166
	10e	For longitudinal surveys, state how loss to follow-up was addressed.	N/A
	10f	Indicate whether any methods such as weighting of items or propensity scores have been used to adjust for non-representativeness of the sample.	N/A
	10g	Describe any sensitivity analysis conducted.	N/A

Results

Respondent characteristics	11a	Report numbers of individuals at each stage of the study. Consider using a flow diagram, if possible.	p. 165
	11b	Provide reasons for non-participation at each stage, if possible.	N/A
	11c	Report response rate, present the definition of response rate or the formula used to calculate response rate.	pp. 277-278

Descriptive results	11d	Provide information to define how unique visitors are determined. Report number of unique visitors along with relevant proportions (e.g., view proportion, participation proportion, completion proportion).	N/A
	12	Provide characteristics of study participants, as well as information on potential confounders and assessed outcomes.	pp. 165-166
	13a	Give unadjusted estimates and, if applicable, confounder-adjusted estimates along with 95% confidence intervals and p-values.	pp. 138-139, 179-190
Main findings	13b	For multivariable analysis, provide information on the model building process, model fit statistics, and model assumptions (as appropriate).	N/A
	13c	Provide details about any sensitivity analysis performed. If there are considerable amount of missing data, report sensitivity analyses comparing the results of complete cases with that of the imputed dataset (if possible).	N/A
Discussion			
Limitations	14	Discuss the limitations of the study, considering sources of potential biases and imprecisions, such as non-representativeness of sample, study design, important uncontrolled confounders.	pp. 276-281
Interpretations	15	Give a cautious overall interpretation of results, based on potential biases and imprecisions and suggest areas for future research.	pp. 289-293
Generalizability	16	Discuss the external validity of the results.	pp. 277-278
Other sections			
Role of funding source	17	State whether any funding organization has had any roles in the survey's design, implementation, and analysis.	N/A
Conflict of interest	18	Declare any potential conflict of interest.	N/A
Acknowledgements	19	Provide names of organizations/persons that are acknowledged along with their contribution to the research.	p. xii

Appendix B: REDCap Survey

Australian nurses in the Genomic Era: exploring barriers and enablers to uptake of genomic innovations

Consent to participate

WHO IS CONDUCTING THIS RESEARCH?

My name is Elle Elan, and I am a PhD candidate at the University of Technology Sydney (UTS) - Faculty of Health. My supervisors are Prof Jane Maguire (jane.maguire@uts.edu.au) and Dr Deborah Debono (deborah.debono@uts.edu.au).

WHAT IS THE RESEARCH ABOUT?

As the term 'genomics' becomes more popular and genetic technologies more accessible, there is increasing demand for nurses to engage and adopt genomic innovations into practice (e.g., genetic risk assessments, family history taking, recognising need for referral to genetic services, etc).

The purpose of this research is to identify the characteristics of nurses who are genomic adopters or leaders in the cancer healthcare setting and explore the conditions that allow nurses to adopt these innovations into practice. Through understanding these individual characteristics, as well as the barriers and enablers cancer nurses face; strategies can be designed for promotion of wider engagement and ultimately uptake of genomics in this essential health workforce.

You have been invited to participate because you are an AHPRA registered nurse currently working in a cancer healthcare setting within Australia, and this puts you in an ideal position to give us valuable first-hand information from your own perspective.

WHAT DOES MY PARTICIPATION INVOLVE?

Participation in this study is voluntary. It is completely up to you whether or not you decide to take part.

If you decide to participate, I will invite you to complete a brief online survey that will contain several questions for you to answer anonymously. The survey should take no longer than 10-15 minutes to complete.

You can change your mind at any time and stop completing the survey without impacting your relationship with the researchers, the University of Technology Sydney, or your place of work. You can withdraw any time before you submit, however, once your responses are submitted, they cannot be withdrawn. This is because they are anonymous, and we will not be able to tell which one is yours.

If you wish to be involved further, at the end of the survey you will be invited to indicate your interest in taking part in an optional follow-up telephone interview which will involve a separate consent procedure. Your response to this invitation is entirely voluntary and cannot be linked to your anonymous survey responses.

ARE THERE ANY RISKS/INCONVENIENCE?

We don't expect this survey to cause any harm or discomfort.

To minimise any inconvenience, the survey has been designed to be completed online to allow you to respond at your own pace and at a time suitable to your schedule. To protect your privacy and confidentiality, the online survey is entirely anonymous and will not require you to disclose any information that could be linked to your identity.

If you experience discomfort or distress answering the questions, please contact your family doctor or physician. You can also contact the Nurse & Midwife support hotline: 1800 667 877 for free and confidential support 24/7 Australia wide, or access support resources through their website: www.nmsupport.org.au. You are also encouraged to contact the researcher for support (contact information is available at the end of this document).

WHAT WILL HAPPEN TO INFORMATION ABOUT ME?

All survey responses are anonymous, and the survey questions do not require any identifiable information. No one will be able to identify you or your answers, and no one will know whether or not you participated in the study. By submitting your survey, you consent to take part in the study. You can withdraw any time before you submit, however, once your responses are submitted, they cannot be withdrawn. This is because they are anonymous, and we will not be able to tell which one is yours.

It is anticipated that the results of this research project will be published and/or presented in a variety of forums.

Research shared in this way will always be de-identified, and will not include personal information (e.g., your name, address, date of birth etc.) and/or any contextual information that could identify you.

All research materials will be securely stored for a minimum of 5 years. On completion of the project, data will be archived and stored on approved UTS owned or recommended infrastructure. Any disposal of research data will follow UTS Records Management Policy and the General retention and disposal authority: higher and further education records (GA47 - 3.5.0) policy as approved by the State Archives and Records Authority of NSW.

WHAT IF I HAVE ANY QUERIES OR CONCERNS?

If you have any queries or concerns about the research that you think I or my supervisors can help you with, please feel free to contact us:

Elle Elan, PhD candidate: elle.elan@student.uts.edu.au

Prof Jane Maguire, supervisor: Jane.maguire@uts.edu.au

Dr Deborah Debono, supervisor: Deborah.debono@uts.edu.au

If you would like to talk to someone who is not connected with the research, or if you have any concerns or complaints about any aspect of the conduct of this research that you wish to raise independently of the research team, please contact the Ethics Secretariat on 02 9514 2478 email or Research.ethics@uts.edu.au and quote the UTS HREC reference number: ETH22-6852. Any matter raised will be treated confidentially, investigated and you will be informed of the outcome.

The researchers acknowledge the Traditional Custodians of the lands where we live, work and learn. We pay our respects to Elders past, present and emerging and acknowledge the continuation and celebration of cultural, spiritual and educational practices of Aboriginal and Torres Strait Islander peoples.

- D1 What area of nursing practice are you currently working in? _____
- D2 Please indicate the number of years you have been practicing in this role _____
- D3 How long have you been practicing as a registered nurse? _____
- At what grade are you currently practicing?
- ☐ Registered Nurse (RN)
 - ☐ Clinical Nurse Specialist (CNS)
 - ☐ Clinical Nurse Consultant (CNC)
 - ☐ Clinical Nurse Educator (CNE)
 - ☐ Nursing Unit Manager (NUM)
 - ☐ Nurse Practitioner (NP)
 - ☐ Other
- Other: _____
- D5 What is your highest level of academic achievement?
- ☐ TAFE/vocational training
 - ☐ Bachelor's degree
 - ☐ Graduate certificate/diploma
 - ☐ Master's degree
 - ☐ PhD/post-graduate research degree
- D6 What is your age?
- ☐ 18 - 24
 - ☐ 25 - 34
 - ☐ 35 - 44
 - ☐ 45 - 54
 - ☐ 55 - 64
 - ☐ 65+

D7 Please indicate your gender

- ☐ Female
- ☐ Male
- ☐ Non-binary
- ☐ I do not have a gender identity
- ☐ Prefer not to say
- ☐ Prefer to self-describe / other

Please describe

D8 Have you or anyone in your family had experience with genetic counselling or genetic testing?

- ☐ Yes
- ☐ No

D9 What is your ethnic background? (tick any that apply)

- ☐ Australian
- ☐ Indigenous Australian or Torres Strait Islander
- ☐ New Zealander
- ☐ Asian
- ☐ Indian
- ☐ Middle Eastern
- ☐ European
- ☐ Caribbean
- ☐ North American
- ☐ South American
- ☐ African
- ☐ Jewish
- ☐ Decline to answer
- ☐ Other

Please describe

Q1

Please select the relevant answer to the following statements.

I am someone who:

	Strongly Disagree	Disagree	Neither Agree or Disagree	Agree	Strongly Agree
Is original, comes up with new ideas	☐	☐	☐	☐	☐
Is curious about many different things	☐	☐	☐	☐	☐
Is ingenious, a deep thinker	☐	☐	☐	☐	☐
Has an active imagination	☐	☐	☐	☐	☐
Is inventive	☐	☐	☐	☐	☐
Values artistic, aesthetic experiences	☐	☐	☐	☐	☐
Prefers work that is routine	☐	☐	☐	☐	☐
Likes to reflect, play with ideas	☐	☐	☐	☐	☐
Has few artistic interests	☐	☐	☐	☐	☐
Is sophisticated in art, music or literature	☐	☐	☐	☐	☐

Q2 Please tick either Yes or No to each statement below

	Yes	No
I am usually successful in everything I do	☐	☐
I am rarely unsure about how I should behave	☐	☐
I like to assume responsibility	☐	☐
I like to take the lead when a group does things together	☐	☐
I enjoy convincing others of my opinions	☐	☐
I often notice that I serve as a role model for others	☐	☐
I am good at getting what I want	☐	☐
I am often a step ahead of others	☐	☐
I have many things others envy me for	☐	☐
I often give others advice and suggestions	☐	☐
I am successful at leading a team	☐	☐
I see myself as a collaborative leader	☐	☐
I lead by motivating and enabling others	☐	☐

Q3 Please rate your familiarity with the following:

	Not at all familiar	Slightly familiar	Somewhat familiar	Moderately familiar	Extremely familiar
The Australian College of Nursing (ACN) 2021 position statement: Nurses, Genomics and Clinical Practice	☐	☐	☐	☐	☐
The Australian Genomics Health Alliance	☐	☐	☐	☐	☐
Your state's health department strategic plan for genomics (e.g., NSW health)	☐	☐	☐	☐	☐
Your local specialist genetics service	☐	☐	☐	☐	☐
Centre for Genetics Education website: www.genetics.edu.au	☐	☐	☐	☐	☐
Human Genome Project	☐	☐	☐	☐	☐
International Society of Nurses in Genetics (ISONG)	☐	☐	☐	☐	☐
Global Genomics Nurses Alliance (G2NA)	☐	☐	☐	☐	☐

Q4	Please indicate your response to each statement:				
	Strongly Disagree	Disagree	Neither Agree or Disagree	Agree	Strongly Agree
Nurses should regularly keep up to date with new areas of practice	☐	☐	☐	☐	☐
Nurses should be able to decide which areas of knowledge they want to expand	☐	☐	☐	☐	☐
Taking a patient's FAMILY HISTORY is an important aspect of my role	☐	☐	☐	☐	☐
Continual professional development in genetics and genomics should be encouraged for all nurses	☐	☐	☐	☐	☐
I have a good awareness of how genetics and genomics impacts my own specialty	☐	☐	☐	☐	☐
Developments in genomics offer limited potential to improve health outcomes for all patient groups	☐	☐	☐	☐	☐

Q5

Scenario: A 43-year-old woman is admitted for symptom management and treatment of endometrial cancer. While caring for her, she mentions in passing that she had several colon polyps removed during a routine colonoscopy last year.

Based on this:

How important would it be in this situation to take a family history ?

- ☐ Not at all important
- ☐ Slightly important
- ☐ Somewhat important
- ☐ Moderately important
- ☐ Extremely important

How confident would you feel educating the person in this scenario?

- ☐ No at all confident
- ☐ Slightly confident
- ☐ Somewhat confident
- ☐ Moderately confident
- ☐ Extremely confident

How confident would you feel managing this scenario in practice?

- ☐ No at all confident
- ☐ Slightly confident
- ☐ Somewhat confident
- ☐ Moderately confident
- ☐ Extremely confident

In your opinion:

- Q6 Do you think that the application of genomics is relevant to your patient group?
- ☐ Not at all relevant
 - ☐ Slightly relevant
 - ☐ Somewhat relevant
 - ☐ Moderately relevant
 - ☐ Extremely relevant
- Q7 Which of the following areas of care are linked to genomics? (tick as many options as you like)
- ☐ People's response to medication
 - ☐ Appendicitis
 - ☐ Weight
 - ☐ Blood pressure
 - ☐ Blood volume
 - ☐ Ethnic origin
 - ☐ Cholesterol level
 - ☐ Cancer
- Q8 Would you feel confident asking patients about their genetic family history?
- ☐ No at all confident
 - ☐ Slightly confident
 - ☐ Somewhat confident
 - ☐ Moderately confident
 - ☐ Extremely confident
- Q9 Which of the following should be included when taking a genetic family history for an Adult with cancer? (tick as many as you like)
- ☐ Familial medical conditions
 - ☐ Whether the patient received treatment as a private or public patient
 - ☐ Births, pregnancy loss and deaths
 - ☐ Ages of family disease onset
 - ☐ Exposure to environmental toxins
 - ☐ Information about the patient's partner's family
 - ☐ History of road accidents
 - ☐ If partners are blood-related in any way (e.g., cousins)
 - ☐ Asking about other cancers in the family
 - ☐ Including grandparents when collecting a family history

Public clinical genetic services are available throughout Australian states and territories, providing diagnosis, screening, testing and counselling for inherited disorders. Genetic counselling is provided by a team of health professionals who work together to provide the most up-to-date information and support to people and their families who have a health condition that may have a genetic basis.

- Q10** Which statement best represents your understanding of genetic services? (tick all that apply)
- ☐ I am unaware of available genetic services
 - ☐ I am aware of genetic services
 - ☐ I know about available genetic services and have used them
 - ☐ I know about these genetic services and have recommended them to colleagues/ patients
 - ☐ I know that genetic counsellors work for genetics services
 - ☐ I know the genetic counsellor that works for my local genetic service by name
- Q11** What resources are available through your local genetic services? (Tick as many as you like)
- ☐ Genetic screening
 - ☐ Genetic risk assessment
 - ☐ Genetic counselling
 - ☐ Pregnancy terminations
 - ☐ Access to support groups
 - ☐ Access to research opportunities
 - ☐ I don't know
- Q12** In the last month, how many times have you referred a patient to genetic services?
- ☐ 0 times
 - ☐ 1-10 times
 - ☐ >10 times
- If you have not identified an individual to be referred, is it because:
(Select as many as you like)
- ☐ I have never encountered an individual who should be referred
 - ☐ Not relevant to my practice
 - ☐ I would not recognise when this was appropriate
 - ☐ I do not have the resources to do this
 - ☐ I do not have the support of my organisation to do this
 - ☐ Other
- Other _____

Q1
3

Please rate yourself on the following scales relating to your interactions with colleagues regarding clinical issues in your practice

	Never	Rarely	Sometimes	Often	Always
In general, do you talk to your colleagues about current advancements in nursing practice?	☐	☐	☐	☐	☐
How often have you given expert information to colleagues about clinical issues in your field in the past 6 months?	☐	☐	☐	☐	☐
How likely are you to be asked about current advances in nursing practice in your field compared with your colleagues?	☐	☐	☐	☐	☐
Overall, in your discussion with your colleagues about clinical issues in your field, are you often used as a source of expert advice?	☐	☐	☐	☐	☐

Q14 Please select the answer that best reflects your level of agreement/disagreement with each statement

	Never	Rarely	Sometimes	Often	Always
I use research articles for information to make practice decisions	☐	☐	☐	☐	☐
I use information I learn from conferences to guide my practice	☐	☐	☐	☐	☐
I use information learnt from continuing professional development (CPD) to make practice decisions	☐	☐	☐	☐	☐
I use scholarly database searches for information to make practice decisions	☐	☐	☐	☐	☐
I use internet sources (e.g., google search) for information to make practice decisions	☐	☐	☐	☐	☐

Q15 Which issues/problems prevent you from using genomics more in your nursing role? (select as many as you like)

- ☐ Genomics is not relevant
- ☐ I don't understand genomics
- ☐ My colleagues don't support my interests
- ☐ There are no relevant resources to help me learn
- ☐ There are too many time constraints
- ☐ My boss doesn't think it's important
- ☐ I don't like science
- ☐ There are no local study sessions
- ☐ It's the doctor's job
- ☐ Patients never talk to me about genomics
- ☐ It isn't my decision
- ☐ Other

Other

Q16	How difficult is it for you to achieve the following actions?	Very difficult	Difficult	Neutral	Easy	Very easy
	Attend study days/courses that include genomics in practice	☐	☐	☐	☐	☐
	Apply new knowledge into your nursing practice	☐	☐	☐	☐	☐
	Request access from senior management to new resources	☐	☐	☐	☐	☐
	Talk to colleagues about genomics	☐	☐	☐	☐	☐
	Seek support from senior nurses and management to include genomics in your role	☐	☐	☐	☐	☐

Q17 Scenario: A 42-year-old patient with breast cancer mentions to you her concerns about her daughter's and granddaughter's chances of developing breast cancer. The patient tells you that both her mother and sister died under the age of 40 from the disease

Bearing this in mind, please answer the following questions:

	Strongly Disagree	Disagree	Neither Agree or Disagree	Agree	Strongly Agree
It is my responsibility to highlight the possible need for more in-depth patient investigation	☐	☐	☐	☐	☐
My colleagues expect me to make sure the patient's family is followed up by genetic services	☐	☐	☐	☐	☐
It is part of my role to follow up genetic consultations for the family either directly or via my manager	☐	☐	☐	☐	☐

Q1
8

Scenario: A 20-year-old man presents with abdominal pain, unexplained weight loss and regular diarrhoea. Upon completing his family history, you discover that his mother's brother (uncle) aged 45 is recovering from bowel cancer

Based on this, please answer the following statements:

	Strongly Disagree	Disagree	Neither Agree or Disagree	Agree	Strongly Agree
Patients and relatives expect me to refer to a specialist genetics service	☐	☐	☐	☐	☐
My manager would approve of me highlighting the need for further patient investigation	☐	☐	☐	☐	☐
It is my responsibility to raise the possibility of a genetic link with this patient's doctors	☐	☐	☐	☐	☐
If I thought my actions with this patient were appropriate, I would not be influenced by my colleagues' views	☐	☐	☐	☐	☐
I would make decisions regarding this patient without seeking the opinions of others	☐	☐	☐	☐	☐

In your opinion:

Q19 How often do you speak to your colleagues about genetics/genomics?

- ☐ Never
☐ Rarely
☐ Sometimes
☐ Often
☐ Always

Q20 Would you like to incorporate more genetics/genomics as part of your everyday practice?

- ☐ Definitely not
☐ Probably not
☐ Possibly
☐ Probably
☐ Definitely

Q21 Are you interested in new areas of genetic and genomic knowledge within your practice?

- ☐ Not at all interested
☐ Slightly interested
☐ Somewhat interested
☐ Moderately interested
☐ Extremely interested

Q22 Have you ever sought genetic information for the following people?
(select as many as you like)

- ☐ Self
☐ Family
☐ Client / patient's family
☐ For a colleague
☐ Friend
☐ I have never sought genetic information
☐ Other

Other

Q23 Which of the following interventions/people encourage you to incorporate new areas of knowledge into your practice? (Please tick as many options as you like)

- ☐ Peers
☐ Heads of department (e.g. NUM)
☐ Contacts with specific professional services
☐ Other health professionals
☐ Attending study days
☐ Having a mentor
☐ Case studies
☐ Attending short presentations (e.g. lunchtime in-service)
☐ Patients

Q24 If you need advice for a particular patient or medical issue, who would you consult with first?

- ☐ I would consult a junior colleague
☐ I would consult a senior colleague
☐ I would consult a colleague practicing at my level of experience
☐ I would consult with anyone, level of experience doesn't matter

What is the reason for your answer?

Appendix C: Ethics Approval

Subject: HREC Approval Granted - ETH22-6852
Date: Wednesday, 1 June 2022 at 3:23:39 pm Australian Eastern Standard Time
From: Research.Ethics@uts.edu.au
To: Research.Ethics@uts.edu.au, Jane.Maguire@uts.edu.au, Elle.Elan@student.uts.edu.au
Attachments: Ethics Application.pdf

Dear Applicant

Re: ETH22-6852 - "Australian nurses in the Genomic Era: exploring barriers and enablers to uptake of genomic innovations"

Thank you for your response to the Committee's comments for your project. The Committee agreed that this application now meets the requirements of the National Statement on Ethical Conduct in Human Research (2007) and has been approved on that basis. You are therefore authorised to commence activities as outlined in your application.

You are reminded that this letter constitutes ethics approval only. This research project must also be undertaken in accordance with all [UTS policies and guidelines](#) including the Research Management Policy.

Your approval number is UTS HREC REF NO. ETH22-6852.

Approval will be for a period of five (5) years from the date of this correspondence subject to the submission of annual progress reports.

The following special conditions apply to your approval:

- The final interview guide should be sent to the Ethics Secretariat prior to qualitative data collection commencing.
- Evidence of support from CNSA must be provided once obtained.

The following standard conditions apply to your approval:

- Your approval number must be included in all participant material and advertisements. Any advertisements on Staff Connect without an approval number will be removed.
- The Principal Investigator will immediately report anything that might warrant review of ethical approval of the project to the [Ethics Secretariat](#).
- The Principal Investigator will notify the Committee of any event that requires a modification to the protocol or other project documents, and submit any required amendments prior to implementation. Instructions on how to submit an amendment application can be found [here](#).
- The Principal Investigator will promptly report adverse events to the Ethics Secretariat. An adverse event is any event (anticipated or otherwise) that has a negative impact on participants, researchers or the reputation of the University. Adverse events can also include privacy breaches, loss of data and damage to property.
- The Principal Investigator will report to the UTS HREC or UTS MREC annually and notify the Committee when the project is completed at all sites. The Principal Investigator will notify the Committee of any plan to extend the duration of the project past the approval period listed above.
- The Principal Investigator will obtain any additional approvals or authorisations as required (e.g. from other ethics committees, collaborating institutions, supporting organisations).

1 of 2

- The Principal Investigator will notify the Committee of his or her inability to continue as Principal Investigator including the name of and contact information for a replacement.

This research must be undertaken in compliance with the [Australian Code for the Responsible Conduct of Research](#) and [National Statement on Ethical Conduct in Human Research](#).

You should consider this your official letter of approval. If you require a hardcopy please contact the Ethics Secretariat.

If you have any queries about your ethics approval, or require any amendments to your research in the future, please don't hesitate to contact the Ethics Secretariat and quote the ethics application number (e.g. ETH20-xxxx) in all correspondence.

Yours sincerely,
The Research Ethics Secretariat

On behalf of the UTS Human Research Ethics Committees
C/- Research Office
University of Technology Sydney
E: Research.Ethics@uts.edu.au

Ref: E38

Appendix D: Survey Email invitation

**RESEARCH SURVEY**
**Australian nurses in the Genomic Era:
exploring barriers and enablers to
uptake of genomic innovations**
You're invited to participate in research to enhance the Cancer
Nursing workforce, and in turn, improve patient outcomes.

Dear,

Survey: Australian nurses in the Genomic Era: exploring barriers and enablers to uptake of genomic innovations

Can you spare 10 - 15 minutes to participate in a survey?

You're invited to participate in research exploring the use of Genetics and Genomics in Cancer Nursing.

The purpose of this research is to identify the characteristics of nurses who may or may not be genomic adopters or leaders in the cancer healthcare setting and explore the conditions that allow nurses to adopt these innovations into practice. Through understanding these individual characteristics, as well as the barriers and enablers cancer nurses face; strategies can be designed for promotion of wider engagement and ultimately uptake of genomics in this essential health workforce.

We would like to invite individuals who are members of the Cancer Nurses Society of Australia to complete a 10–15-minute anonymous online survey, with the additional opportunity to take part in a semi-structured interview.

If you would like to participate in this study, we ask that you read the Participant Information Sheet embedded at the start of the survey. Completion of the survey will be taken as implied consent.

 **Click here to take the survey**

Please note that this study has been approved by the University of Technology Sydney Human Ethics Committee (approval number ETH22-6852) and by the CNSA Research Standing Committee.

We appreciate your participation in completing this survey. Should you wish to have more information, or have any questions, please reach out to Elle Elan (elle.elan@student.uts.edu.au).

With thanks,

Elle Elan (PhD candidate)
Prof Jane Maguire (supervisor)
Dr Deborah Debono (supervisor)

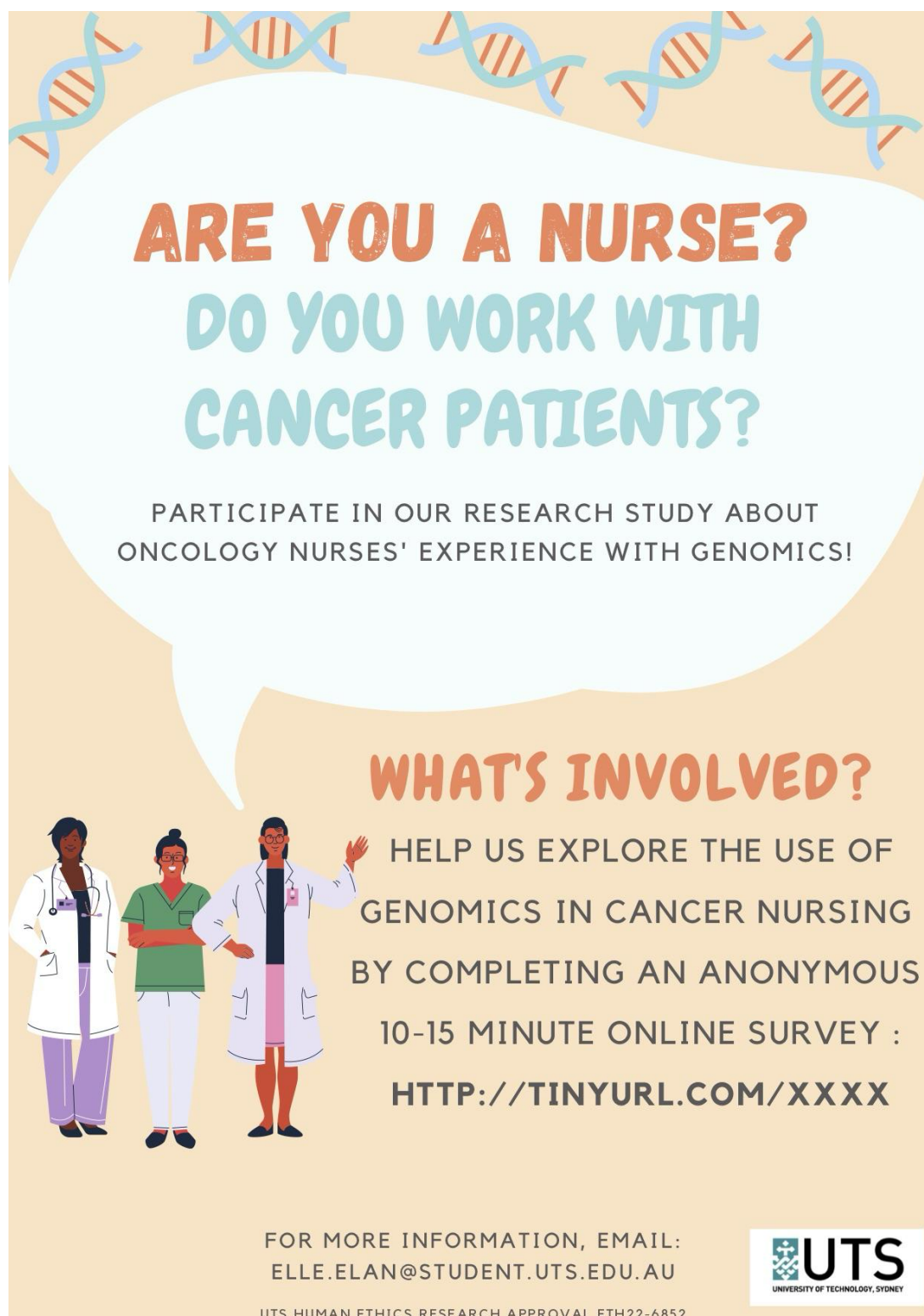
This survey has been reviewed and approved by the CNSA Research Standing Committee.



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Sent by CNSA

Appendix E: Social Media post



The graphic features a light orange background with a large white speech bubble in the center. At the top, there are five blue and orange DNA double helix icons. Inside the speech bubble, the text asks if the viewer is a nurse who works with cancer patients and invites them to participate in a research study. Below the speech bubble, three stylized illustrations of healthcare professionals (two nurses in white coats and one in green scrubs) stand on the left. To their right, the text describes the involvement: a 10-15 minute online survey. At the bottom, contact information and the UTS logo are provided.

ARE YOU A NURSE?
DO YOU WORK WITH
CANCER PATIENTS?

PARTICIPATE IN OUR RESEARCH STUDY ABOUT
ONCOLOGY NURSES' EXPERIENCE WITH GENOMICS!

WHAT'S INVOLVED?

HELP US EXPLORE THE USE OF
GENOMICS IN CANCER NURSING
BY COMPLETING AN ANONYMOUS
10-15 MINUTE ONLINE SURVEY :
[HTTP://TINYURL.COM/XXXX](http://tinyurl.com/xxxx)

FOR MORE INFORMATION, EMAIL:
ELLE.ELAN@STUDENT.UTS.EDU.AU

UTS
UNIVERSITY OF TECHNOLOGY, SYDNEY

UTS HUMAN ETHICS RESEARCH APPROVAL ETH22-6852

Appendix F: Semi-structured Interview Guide

Questions/ probes	Diffusion of Innovations concepts
Can you tell me what you know about genomics? - Have you had any experience with genomics? - Can you give me an example?	Knowledge / Trialability
What do you think is the role of a nurse in implementing and translating evidence-based practice such as genomic science? - How relevant is it to your nursing practice? - Do you think the relevance of genomics science will change overtime? How so?	Compatibility / Relative advantage
How do you think genomic evidence and concepts influences clinical practice? - Can you think of an example where genomic science has impacted patient care?	Relative Advantage / Observability
If you think about genomic science in clinical practice and advancing technology such as genomic testing and precision medicine (and others), can you think of barriers in your day-to-day practice to adopting these innovations? - How difficult would it be for you to learn more about genomics? - Do you feel there are resources to help you with this? - Can you think of any enablers to this? Is there anything that would support you adopting this innovation into practice?	Complexity / barriers and enablers
Is there anything you'd like to add, or do you have any questions for me?	

Appendix G: Telephone Interview Participant Information Sheet

ETH22-6852 – Australian nurses in the Genomic Era: exploring barriers and enablers to uptake of genomic innovations

WHO IS CONDUCTING THIS RESEARCH?

My name is Elle Elan, and I am an PhD candidate at the University of Technology Sydney (UTS) – Faculty of Health. My supervisors are Prof Jane Maguire (jane.maguire@uts.edu.au) and Dr Deborah Debono (deborah.debono@uts.edu.au).

WHAT IS THE RESEARCH ABOUT?

As the term ‘genomics’ becomes more popular and genetic technologies more accessible, there is increasing demand for nurses to engage and adopt genomic innovations into practice (e.g., genetic risk assessments, family history taking, recognising need for referral to genetic services, etc).

The purpose of this research is to identify the characteristics of nurses who are genomic adopters or leaders in the cancer healthcare setting and explore the conditions that allow nurses to adopt these innovations into practice.

WHY HAVE I BEEN INVITED?

You have been invited to participate because you are an AHPRA registered nurse currently working in a cancer healthcare setting within Australia, and because you voluntarily provided your contact details to arrange a follow-up interview as part of the online survey you recently completed.

WHAT DOES MY PARTICIPATION INVOLVE?

Participation in this study is voluntary. It is completely up to you whether or not you decide to take part. If you decide to participate, I will interview you on the telephone to understand your experience as an oncology nurse and the kinds of barriers or enablers you face engaging with genomics in practice.

The interview will be semi-structured and will last up to 60 minutes. We can arrange for this interview to be conducted at a time and date most convenient to your schedule. With your permission, the interview will be recorded and transcribed. This means written records (transcripts) of your interview will be produced, but any identifiable information (e.g., name, place of work) will be removed to protect your privacy and confidentiality. You can request a copy of your de-identified interview transcript prior to data analysis (within 14 days from completion of the interview).

At the completion of the interview, you will be offered a movie voucher (to the sum of \$25) as a token of our gratitude for agreeing to participate in this research.

ARE THERE ANY RISKS/INCONVENIENCE?

There are some risks/inconveniences. The telephone interview will take up to 60 minutes, and the researchers acknowledge this could be an inconvenience. Every effort will be made to ensure the interview is arranged for a time and date most suited to your schedule.

To protect any risk to your privacy or professional reputation, identifiable or distinguishing characteristics raised in the interview will be removed from the transcript so that you cannot be identified from the text. Your confidentiality is of priority, we will not disclose any identifiable information, unless required by law (e.g., disclosure of notifiable criminal activities, such as child abuse). You will have an opportunity to request a copy of the de-identified transcript prior to data analysis.

It is unlikely that the questions asked during this interview will incite distress or discomfort, as the subject matter is not designed to invoke emotive information. However, if you were to become distressed or fatigued, you can ask to stop the interview at any time without having to provide justification for this decision. You are encouraged to seek support through your GP or call the Nurse & Midwife support hotline: 1800 667 877 for free and confidential support 24/7 Australia-wide. You can also access this service through their website: www.nmsupport.org.au

You are also encouraged to contact me for support (contact information outlined at the end of this document).

DO I HAVE TO TAKE PART IN THIS RESEARCH PROJECT?

Participation in this study is voluntary. It is completely up to you whether or not you decide to take part.

If you decide not to participate, or to withdraw from the study, it will not affect your relationship with the researchers, the University of Technology Sydney, or your place of work.

WHAT IF I WITHDRAW FROM THIS RESEARCH PROJECT?

If you wish to withdraw from the study **before the interview** is held, you can do so at any time without having to provide a reason, by contacting the research team. Any change to your participation in the study will not impact your relationship with the researchers, the University of Technology Sydney, or your place of work.

If you wish to withdraw from the study **while the interview is being conducted**, you can do so at any time without having to provide an explanation. Any data collected up to the time you withdraw from the study (audio recording, transcript, notes) will be erased and destroyed per UTS data management policy.

If you wish to withdraw from the study **after the interview** has been completed, you will have the opportunity to request a copy of your de-identified transcript and withdraw from the study before data analysis is complete. However, it may not be possible to withdraw your data from the study results after interview data has been analysed, as the research team will not be able to link your identity to individual responses.

Any disposal of research data will follow UTS Records Management Policy and the General retention and disposal authority: higher and further education records (GA47 – 3.5.0) policy as approved by the State Archives and Records Authority of NSW.

WHAT WILL HAPPEN TO INFORMATION ABOUT ME?

By consenting to take part in this study, you consent to the research team collecting and using personal information about you for the research project. All this information will be treated confidentially. Your information will only be used for the purpose of this research project and it will only be disclosed with your permission, except as required by law.

Interview recordings will be made on a dedicated audio recording device under password protection which only the research team has access to. The interview recording will be sent to a professional transcription service, after a confidentiality agreement has been signed with the transcriber. Audio recordings will be stored on a UTS password protected cloud storage system only accessible to the approved research investigators until such time as they have been transcribed, then they will be destroyed.

It is anticipated that the results of this research project will be published and/or presented in a variety of forums. In any publication and/or presentation, information will be provided in such a way that you cannot be identified, except with your permission. Identifiable information (e.g., names, place of work) will be removed from transcripts and pseudonyms will be used to protect the anonymity of all participants.

In accordance with relevant Australian and/or NSW Privacy laws, you have the right to request access to the information about you that is collected and stored by the research team. You also have the right to request that any information with which you disagree be corrected. Please inform the research team member named at the end of this document if you would like to access your information. However, it may not be possible to withdraw or correct your data after interview data has been analysed, as the research team will not be able to link your identity to individual responses.

All research materials will be securely stored for a minimum of 5 years. On completion of the project, data will be archived and stored on approved UTS owned or recommended infrastructure. Any disposal of research data will follow UTS Records Management Policy and the General retention and disposal authority: higher and further education records (GA47 – 3.5.0) policy as approved by the State Archives and Records Authority of NSW.

WHAT IF I HAVE ANY QUERIES OR CONCERNS?

If you have any queries or concerns about the research that you think I or my supervisors can help you with, please feel free to contact us:

Elle Elan, PhD candidate: elle.elan@student.uts.edu.au

Prof Jane Maguire, supervisor: Jane.maguire@uts.edu.au

Dr Deborah Debono, supervisor: Deborah.debono@uts.edu.au

NOTE:

This study has been approved in line with the University of Technology Sydney Human Research Ethics Committee [UTS HREC] guidelines. If you have any concerns or complaints about any aspect of the conduct of this research that you wish to raise independently of the research team, please contact the Ethics Secretariat on ph.: +61 2 9514 2478 or email: Research.Ethics@uts.edu.au] and quote the UTS HREC reference number: ETH22-6852. Any matter raised will be treated confidentially, investigated and you will be informed of the outcome.

Appendix H: Thematic Table

Domain	Domain Definition	
<i>Attributes of the Innovation</i>	This domain explores how specific attributes of genomics as a clinical innovation (e.g., genomic concepts, testing, risk assessment, family history-taking, referral, genomic education) were experienced by participants and how these attributes shaped their ability to adopt and deliver genomically informed care.	
Theme	Theme Definition	Key Quotes
<i>Complexity of Genomics</i>	This theme captures nurses' perceptions of genomics as complex, abstract, and technically demanding, with scientific language, unfamiliar terminology, and conceptual depth posing barriers to comprehension and integration into practice. Participants described genomic concepts, terminology, and data as difficult to interpret and apply without specialised training, which reduced their confidence in discussing genomic information and created uncertainty about when and how genomics was relevant to their role.	<i>'I actually just feel like... it's like a foreign language to me, almost'</i> <i>'It's like me reading Chinese. I have no idea. I don't know what I'm looking at'</i> <i>'It was just like I was speaking a different language'</i>
<i>Volume and Velocity of Emerging Genomic Information</i>	This theme highlights nurses' feelings of being overwhelmed by the sheer volume of emerging genomic information and the rapid pace of change. The exponential growth in genomic discoveries and evolving practices created a sense of information overload, describing challenges keeping up with new developments which made it difficult to stay current.	<i>'It does get bigger and bigger every time I look at another paper on what the next genetic marker is... You think, 'Oh my goodness,' every time I get a new referral when I was working and I'd look at it and say, 'Well, what's this new gene in this?' It's becoming more and more a minefield... Yeah, the information is quite vast'</i> <i>'I'm finding it's actually a struggle to—it's starting to be a struggle to keep up with all of the rapid pace of knowledge and changes that are coming out'</i>
<i>Difficulty Ascertaining Clinical Relevance</i>	This theme refers to nurses' uncertainty about which aspects of genomic information were relevant to their clinical practice. The vastness of the topic, combined with a lack of clear guidance on what knowledge was necessary for their role, created confusion and was reported as a barrier to engagement. Participants described varied responses to this uncertainty: some felt discouraged or disengaged from further learning when the information seemed overwhelming, while others attempted to 'wade through it' by independently seeking resources or peer support to clarify what was most relevant.	<i>'I didn't know what I did need to know and what I didn't need to know... I kind of got lost in that for a bit'</i> <i>'Some information may be relevant, it may not be relevant, I don't know'</i>

<i>Psychosocial Complexity of Genomic Care</i>	This theme captures nurses' views of the psychosocial attributes of genomics as significant barriers to engagement and adoption. Genomics was described as increasing patient anxiety and making discussions about genetic risk and family history emotionally taxing and psychosocially complex. Some participants described reluctance to engage with genomic topics due to the potential for re-traumatisation or the unintended consequences of delving into sensitive family histories. This psychosocial burden was recognised as a barrier to providing genomic care.	
<i>Timing and Patient Readiness</i>	This theme underscores the importance of patient readiness and timing in genomic care. Nurses emphasised that genomic conversations require an appropriate emotional context, adequate time, and careful pacing, which are often difficult to accommodate within everyday clinical workflows. The emotional weight of genomic information, combined with time constraints and emotionally overwhelmed patients, was identified as a significant barrier to the adoption of genomics. Participants viewed these timing challenges as unique to genomics, describing genomic care as fundamentally different from other medical and nursing interactions due to its emotional intensity and layered implications.	<i>'It's quite time sensitive. You can't rush telling somebody about all of this. They need to take it in. In the ward, if they're just post-op, they're often overwhelmed by information, so we've just got to kind of titrate it to how they're feeling and maybe pick a time with them, with a relative there'</i> <i>'Finding when they're on the ward, are there any psychosocial barriers, getting approval from the oncologists, and making sure that they don't have anything else challenging that day—having the conversation about the study means that a whole lot of things need to align, and then me actually having time to go and do it'</i>
Domain	Domain Definition	
<i>Education Factors</i>	This domain explores how nurses' exposure to genomics through formal education, ongoing training, and access to resources shaped their engagement with genomic care.	
Theme	Theme Definition	Key Quotes
Foundational and continuing education	This theme refers to participants' reports of limited exposure to genomics during pre-registration training and minimal opportunities for continuing education post-registration. These educational gaps were identified as key barriers that contributed to ongoing uncertainty and limited confidence in genomic practice. Participants described the absence of genomics in formal nursing education as a foundational deficit and highlighted the lack of workplace-based education and training as a further barrier to	<i>'Looking back... at my degree... I don't recall ever having a thorough or comprehensive—even a single lecture slide dedicated to it. I don't recall that'</i> <i>'I mean, you learn about disease progression. Genetics component, okay, BRCA genes. We just – that's the only thing we learn. We don't learn anything else. How to approach this situation with the patient, how to – if something like this happens, how are you dealing with it? What services are available? How are you managing all these situations? You never learn all those things, and then you land in a</i>

	engagement. Conversely, continuing education opportunities, such as in-services, were viewed as valuable enablers that supported interest and confidence in genomic practice.	<i>situation like this and most of the nurses are clueless. What do we do? We don't know'</i> <i>'I think when you are working in the unit with the patients, they'll often ask questions... some of them worry about their children's future and those sorts of things; what should they do?... we need counselling training'</i> <i>'Yeah, not too many in-services like directly related to that information and how it affects patient care for nurses'</i> <i>'I really wish that, yeah, work would do a bit more in-depth in-services regarding that aspect of oncology'</i> <i>'I have had a new grad, that after my [in-service] talk come to me and be like, 'wow this is really interesting. I want to know more about this in cancer''</i>
Learning Modalities	This theme captures the diverse educational approaches participants used to build their genomic knowledge and the particular value they placed on hands-on, experiential learning. Participants described engaging with university courses, webinars, newsletters, and online self-directed study to develop their understanding of genomics. Several nurses also highlighted the impact of immersive experiences such as secondments, mentorships, and observational learning. These experiential opportunities were viewed as especially effective in building confidence and translating theoretical knowledge into clinical practice.	<i>'I started learning about this through University doing a Masters level Introduction to Genetics'</i> <i>'I think it was four online webinars... the last one, you sat in and listened to a Molecular Tumour Board discussion'</i> <i>'I subscribe to a few oncology-related newsletters... that's one way of keeping abreast of what's happening'</i> <i>'When I'm reading through a patient's history... I just do a bit of a Google search to learn a little bit more about it'</i> <i>'I would ask my educator, or I'd look at seminars, or webinars that CNSA would put on'</i> <i>'Going up to see what happens to the samples and where they go and speak to genetic counsellors is really good'</i> <i>'We arranged for her to go up to [redacted genetics service] and have a mentor up there. She sat in on about three or four interviews... now she does them herself'</i> <i>'I was seconded to [Redacted: specialist cancer centre]... It was really, really useful. It was fantastic'</i>
Genomic Education Resources	This theme explores how the accessibility, clarity, and relevance of genomic education resources shaped participants' engagement with genomics. Nurses described	<i>'I think they are not resources that are easy to understand... it's more like – they don't relate back to practice, like how do you use that day to day. I think that would discourage nurses from accessing them'</i>

	existing resources as often too complex, poorly aligned with nursing practice, and difficult to translate into clinical application, which discouraged self-directed learning. Conversely, trusted platforms such as eviQ and CNSA were identified as important sources of reliable genomic information that supported knowledge acquisition and clinical decision-making. Participants also articulated a strong need for a simplified, centralised, and nursing-specific resource to better support genomic education in practice.	<i>'it needs to be relevant and clinically appropriate and it needs to help facilitate discussion, but not necessarily get into too much of the nitty gritty as working on the floor'</i> <i>'for nurses that isn't quite as high powered but gives enough information to be useful onsite in the hospitals'</i> <i>'Like if there was a central spot that you could go and look at all the updates for ovarian cancer, that'd be great'</i> <i>'online training like HETI modules and things like that could be really valuable, or eviQ modules specific to genetic syndromes I think would be really valuable, just so that there's that consistency of knowledge'</i>
Domain	Domain Definition	
Professional Factors	This domain presents how characteristics of the nursing profession—including workforce issues such as time pressures, staffing instability, professional scope boundaries, and the nature of nurse–patient relationships—shaped participants' ability to engage with and adopt genomics in clinical practice.	
Theme	Theme Definition	Key Quotes
Workforce constraints	This theme captures how time scarcity and broader workforce instability shaped nurses' capacity to engage with genomic education and incorporate genomics into clinical practice. Participants consistently described competing clinical demands, limited protected learning time, and understaffing as key barriers to genomic integration. These constraints were seen as systemic issues across the nursing workforce, affecting both educational access and clinical application.	<i>'I think time constraint is one of them. Time and staff. Staff availability. Looking at the number of patients and the amount of work we have and the lack of resource which we have, it definitely is a time-consuming process. Staff, availability of staff'</i> <i>'With nurses these days, we are always constantly trying to upgrade and study, but it's something that gets harder and harder and harder with the hours that we work'</i> <i>'It's so hard to just cover staff for at least 20 minutes without some sort of interruption where they can just have a consolidated protected learning time'</i> <i>'You don't have time - nurses don't have time to sit down with that and engage with the person'</i> <i>'It's tricky to run in-services... getting more than two people is a win when you've only got eight, nine staff on the ward'</i> <i>'I know there's a high turnover in nursing, so our workforce is so junior at the moment, I think we've got a two or three year out of uni is the majority... they're such junior nurses leading the ward. So I think part of it is just a massive education drain'</i>

		<i>'you are more pushed to focus on your work and just do your work, that's it... Even if you have questions, this is not relevant, you can do research in your own time. Let's now focus on this work at hand. We need to do chemotherapy, we are not encouraging the curiosity I don't think. We aren't developing a very curious workforce'</i>
Scope Boundaries and Role Delineation	This theme reflects participants' varying understandings of where genomic responsibilities sit within nursing scope, with evidence of both uncertainty and professional gatekeeping. Among nurses not in formal genomic roles, there was no clear consensus. Some viewed genomics as falling outside their scope, others described a default deference to medical staff, and a few actively questioned these assumptions. In contrast, nurses in dedicated genomic roles described genomic care as routine and firmly within their clinical remit.	<i>'I can give them an overview but it's outside of my scope to go into lots of details'</i> <i>'Patients that haven't been through genetic testing but that I have suspected them needing to be referred to genetic testing, is kind of something like, you refer to the doctor. You just don't do it yourself'</i> <i>'I think some of it is what is the doctor's role versus what's the nurse's role. Generally, we would expect that it's the doctors that talk about - to patients about genomics. However, I've found that, often, it doesn't happen'</i> <i>'That's a bit of a thing that people say, 'That's the doctors job', but that's not what it is. We need to understand the disease and how it affects, because that's where we come in... How it affects them in every aspect of their life because that's where us nurses could help. That's what we need to know, and I think that [we're lacking]. Where do we come in'</i>
Nurses as Opportunistic Facilitators	This theme captures how nurses' sustained presence, relational proximity, and communication skills position them as opportunistic facilitators of genomic care. Nurses are often the first to elicit family histories, identify potential genomic red flags, and provide patient education. This intrinsic feature of nursing practice, where clinical tasks are interwoven with interpersonal connection, was described as a key workforce-level enabler of genomic engagement.	<i>'I think with training, nurses can be very useful because we're in the ward – at the coalface, if you like – and able to facilitate the testing quickly for patients'</i> <i>'Nurses are such a perfect position to be providing education and a little bit more support in those areas. Just making sure that they are aware of the risk, not only to themselves but to families. Also making sure that they do have on hand, services that they can be referred to if they do want to have further testing. Or just making sure you bridge that for them to pass that information to their relatives as well'</i> <i>'The amount of time we spend with patients. Most of the time we build a lot more rapport with them. As you're doing things with them, like giving medications, or changing their beds, you're always chatting to them. Getting to know when patients also start seeing you as a person that they have a good rapport with, that they trust and disclose a lot of information. They are very open to education coming from nurses. I think because nurses are a little bit more connected with the patients, they kind of know how to break down information in a way that they</i>

		<i>understand much easier than let's say, the doctors. It's not uncommon for a patient to be like, 'oh the doctor said this and that but I don't understand what does that mean, what does this mean?' Kind of like, they feel safe having those conversations with you'</i> <i>'I think nurses recognise in general that a doctor says something to a patient and then that's facilitated to understand with the nurse backing it up, to say 'well this is what it means in normal language''</i> <i>'I've picked up on someone who've slipped through the cracks. I've been doing my assessment of the patient and they've started telling me about their family history of different cancers and such. I thought, 'gee, that's an awful lot of cancers in one family'. I've asked the patient if anybody has spoken to them about genetics or genetic testing or anything like that and they've said no. Then I've gone to contact the genetics team at [REDACTED] and discussed the patient and their family history with them. They've then said that they feel that, yes, this person warrants having a full assessment'</i>
Compatibility with Advanced Practice Nursing	This theme identifies the perceived compatibility between genomics and advanced practice nursing roles, particularly Clinical Nurse Specialists (CNSs) and Clinical Nurse Consultants (CNCs), as an enabler for genomic integration within the nursing workforce. Participants described these roles as already encompassing leadership, coordination, complex clinical knowledge, and patient education, making them a logical and appropriate fit for genomic responsibilities.	<i>'I think there's a lot of value in having advanced practice nurses that can be champions and leaders in this area and I think there are certain positions that you need to have the navigator, coordinator, advanced practice role in. But I think everybody should have an understanding of it and every oncology nurse in particular should understand how genomics, at least at a broad level, impacts the care that we're delivering, impacts the role that cancer plays, treatment and the prognosis and the tumour genesis even. So for example, we've got oncology nurses and we also have advanced practice oncology nurses. I think the same should be done for genetics'</i> <i>'I think about the types of NUM, CNSs and CNCs. We have breast CNCs and CNSs, we have supportive care CNSs that work in our outpatient clinic for, like, massage therapy and acupuncture and things like that. So I wouldn't see why it wouldn't be relevant – it would be quite relevant, I think, to have someone to have that discussion with patients and to specialise in that area and be able to give them a better understanding as to how to communicate their illness diagnoses and their trajectory – potential trajectory with family'</i>
Support 'On the Floor' – Genomic Nurse Specialists	This theme explores participants' experiences and reflections on the value of having a genetics nurse specialist embedded within the clinical environment. Where such roles existed, they were described as highly	<i>'It's such an involved field I think that you need a specialised nurse that can be a support person for other nurses. In the past I've worked in an area where we actually had a particular nurse in that role and it was in that way we were able to ask them for support and help or even</i>

	beneficial for adoption. Participants highlighted that access to a knowledgeable, approachable resource person could improve their ability to navigate patient queries, integrate genomics into practice, and build their own genomic literacy. Even where no such specialist was available, participants suggested that introducing these roles would strengthen the adoption of genomics in nursing practice.	<i>ask them to come and help us with a patient that might have asked about the genetics in regards to their family and risk and so on. That was good'</i> <i>'At least we could have someone in our team who knows what it is. It's like me reading Chinese. I have no idea. I don't know what I'm looking at. So, at least if someone has knowledge about that – and that will really help us because that person can act as an educator. They can teach us what's happening. So, in the future if we encounter something like this, we know what we're dealing with. So, it can help us to – how to manage a patient. The patient management and patient care will be far better. The quality of care which we're going to provide is far better than what we're providing now'</i> <i>'If I have someone in the department who knows about it, a resource person or a resource where I could go and get all of the information, it would be a very good thing to have in our department. Then that'll motivate not me, everyone, even the grads, to go and get that information'</i>
Domain	Domain Definition	
Organisational Factors	This domain presents how organisational factors, including funding, leadership engagement, service integration, and multidisciplinary collaboration, were experienced by participants as shaping their ability to adopt and deliver genomically informed care in clinical practice.	
Theme	Theme Definition	Key Quotes
Organisational Resourcing	This theme captures how organisational investment shaped nurses' capacity to engage with and adopt genomics in clinical practice. Participants identified resourcing as a critical determinant of genomic integration, encompassing financial support for education and training, the creation of specialist roles, and structural provisions such as protected learning time.	<i>'There's that financial cost if your workplace is not willing to supplement or assist'</i> <i>'All these things cost, and nurses can't afford to pay for them. We're lucky at this hospital that we have a lot of scholarships offered which can pay for things like that, but it's difficult if you haven't got that to afford to pay for university things'</i> <i>'To have the hospitals recognise the need for specialists in these fields and specialists is hard with the financial side of it. I think that's probably the biggest barrier at the moment that I see... I think that they don't see the relevance as to the priority that we do. So creating a role that would be funded is hard'</i>

Managerial and Organisational Leadership Support	This theme captures participants' perceptions of limited engagement and support from managerial and senior nursing leadership in the integration of genomics into nursing practice. Participants described a lack of awareness, understanding, and prioritisation of genomic innovation among leadership. This disengagement ranged from passive disinterest to active resistance, creating organisational inertia that, in some cases, undermined nurse-led initiatives or requests for genomics training.	<i>'The educators aren't necessarily... upskilled or knowledgeable in genomics'</i> <i>'I don't think my manager quite knows what I do'</i> <i>'On paper it sounds really easy but I think because a lot of like middle and senior management doesn't see the point... it doesn't really give us room at the moment to do that... Given that middle management and senior management don't even see the applicability of this yet on our day to day. They're not really keen to help us bridge that gap'</i> <i>'It's always 'yes, but...' or 'yeah, we can – absolutely I'm supportive of an in service', but again only one person turns up, because there was a clinical priority'</i> <i>'Every attempt I have made and been like, 'oh maybe I could do a case study on the haematology patient and link it back to the genetics'. Talking a little bit about the basics so the nurses can understand this a bit better, I was shut down by my manager and education department'</i>
Organisational Adoption and Integration into Nursing Workflows	This theme captures how the integration of genomics into routine nursing workflows and the organisational adoption of genomic testing into clinical pathways functioned as key enablers of genomic practice. As genomics became embedded in some institutional protocols, particularly through initiatives such as mainstream genetic testing, nurses working in these settings reported increased engagement, comfort, and role clarity in genomic care delivery. These changes positioned genomics as a standard component of oncology care, fostering familiarity through necessity and routine exposure.	<i>'Most recent change in the last few years has probably been introduction of mainstream testing, particularly for breast cancer'</i> <i>'If there's an oncologist who's got patients coming into day oncology that wants a test here, I just go over and explain it and consent them... I provide the explanation and introduction to it and explain what it's all about to get consent for the test'</i> <i>'There's also a little bit more awareness of mainstreaming testing, which has changed quite a bit'</i>
Multidisciplinary Collaboration and Support	This theme captures how organisational structures that fostered collaboration across disciplines supported nurses' engagement with genomics. Participants highlighted the value of working alongside genetic counsellors, clinical geneticists, consultants, pathology services, and research staff. They described how embedded roles within multidisciplinary teams, regular multidisciplinary meetings, and proximity to specialised expertise contributed to skill development, increased awareness, and confidence. These collaborative environments were seen to make genomics more accessible, visible, and embedded in	<i>'Our team meetings are very much talking about patients... to build up that knowledge and kind of baseline understanding of it'</i> <i>'We run a Molecular Tumour Board once a week... that has been huge learning'</i> <i>'All the oncologists will update the staff there about the new therapies and things like that'</i> <i>'When we've had our triple negative breast cancer patients and we look at testing, genetic testing. We have terminology thrown around,</i>

	routine nursing care. Conversely, limited access to genetic services was reported as a barrier to adoption.	<i>but it's been mainly like say, consultants, medical oncologist consultants that discuss this while we do the notes'</i> <i>'The biggest one is the pathology service... [they] have a turnaround of about four days... After the multidisciplinary team meeting, the surgeons will come around and tell the patients their results and then I'm usually with them then... The enabler is the speed that we get the histopathology back and the cooperation between the surgeons, and the pathologists, and the theatre staff to get the samples over there, so it's streamlined'</i> <i>'I will often... go back to one of the genetic counsellors that I work closely with, or with the geneticist, and talk to them about it'</i> <i>'I meet with the geneticist every week, so if there are any questions, or anything coming up, we can talk about any changes. I meet with the genetic counsellor once a fortnight'</i> <i>'When you get to know the genetic counsellors and that they're passionate about their field as well, so they're more than happy to share their knowledge to help, I guess, spread the word. I guess I could see them as enablers in helping'</i> <i>'That blindness... are we aware? are we liaising with the other hospital? – which we are not – but then if we have service here with us, we know what's happening. Then we have a bit more cohesion of the care rather than people working in isolation. At the moment our department, we are working in isolation'</i> <i>'Often we would have two or three patients where we would be required by our research team to take bloods and help with them gathering as much data as possible. So the staff on the floor as such became over the months, particularly last year with some of the newer discoveries coming out, began to see the importance of why we did this particular part of the work... So I must admit our research team do a little bit of education in that area as well and involve the staff as much as they can too. So it does bring the awareness there.'</i> <i>'Because we are seeing all these new novel agents and we're trialling a whole lot of stuff... this sort of high quality care environment, where you're participating in research... And possibly a little bit of knowledge through osmosis I think'</i>

Domain	Domain Definition	
Individual Factors	This domain explores how nurses' individual characteristics, such as personal knowledge, clinical experience, baseline awareness, personal interest, and perceived relevance, shaped their engagement with genomics in cancer care.	
Theme	Theme Definition	Key Quotes
Genomic Knowledge and Confidence	This theme reflects participants' reports of limited genomic knowledge and minimal clinical experience, which contributed to a lack of confidence in engaging with genomic care. Nurses who were not in formal genomic roles consistently described knowledge and confidence as foundational barriers to adoption. Participants reported uncertainty about genomic concepts, discomfort in applying them in practice, and hesitancy in initiating patient conversations due to fear of providing incorrect or insufficient information.	<i>'I guess one of the barriers is having enough knowledge to feel confident in talking about this'</i> <i>'I think there's still a lack of, you know, even a lack of that somatic understanding of that even a cancer cell has got some genetic change in it'</i> <i>'I find that there's a lot of areas where the nurses are unsure of how to ask the questions, how to broach the more difficult topics and how to manage the patients' response'</i> <i>'Many female – specifically female patients – they come ask, 'Is my daughter going to get this disease?' Then it's a very difficult thing to answer. We don't know... we don't know how to deliver this talk'</i> <i>'We do have patients that come in and say, you know, 'I don't have a history of, say, breast or pancreatic or colorectal cancer in my family. You know, this doesn't run in my family, why is this happening?' I just genuinely don't have an explanation for them... wish I did... I just feel like I'd have a bit more in my toolkit to be able to know what to say. I just feel like I don't know what I don't know when it comes to the topic. So, when those sorts of things are raised, when, you know, you're by the bedside and someone says, 'I don't know why this is happening to me. I've been healthy all my life. Is it because of my genes, or is it because of my—like, my aunt had something like this?' I actually don't know what to say'</i> <i>'I think I wish I would have had a bit more knowledge about it. I went ahead and researched about it, but I think it was too late. She didn't turn up, she didn't come back'</i>
Clinical Experience and Seniority	This theme captures how some nurses described years of experience and clinical seniority as shaping their confidence and ability to engage with genomics in practice. Participants who held formal genomic roles or regularly facilitated mainstream testing and genomic consenting consistently framed their own longevity of	<i>'I've probably absorbed a lot of knowledge over many, many years. So for me it's not a big issue'</i> <i>'I've been nursing for a long time, so it's hard to stump me and throw me off'</i>

	experience as a key enabler of genomic adoption. These individuals emphasised how cumulative exposure over time, through observation, case familiarity, and ongoing practice, built their comfort with genomic conversations and processes.	<i>'I feel quite comfortable in having those sorts of conversations. I think there probably needs to be more education available for younger nurse'</i> <i>'You throw a junior nurse into that, they're going to walk off either half asleep or crying'</i> <i>'It's something the younger ones struggle with because they are so busy. I think it's a time-poor thing'</i>
Awareness of Genomics	This theme captures how participants framed awareness as a foundational individual-level factor shaping genomic engagement. Several nurses described general awareness of genomics as limited among their peers, noting that without visibility or promotion, genomics remained peripheral to many nurses' practice. Lack of awareness was seen not only as a barrier to knowledge acquisition but also as limiting curiosity and perceived relevance.	<i>'More awareness. Knowledge is powerful... So I think more education I think is the key. Being aware of the relevance of genetics as well. What the relevance and why it is important'</i> <i>'I think overall promotion of – genomics needs to be promoted. I mean, when we think of oncology, cancer and everything, genomics I believe is not very promoted kind of thing. So, it needs to be more – people need to be more aware of it. It's something to be more aware of. When you're more aware of it, then you try to learn more about it, try to know more about it. You have the curiosity to learn'</i>
Interest and Curiosity	This theme captures how personal interest and intrinsic curiosity were described as individual-level enablers of genomic engagement. Participants noted that interest in genomics was not uniformly distributed across the nursing workforce and was often the determining factor in whether nurses pursued further knowledge or engaged with genomic innovations.	<i>'When you're more aware of it, then you try to learn more about it, try to know more about it. You have the curiosity to learn'.</i> <i>'Interest. Personal interest in the area'</i> <i>'Well, across Australia the gynaecology clinical nurse consultants could all learn this, and all do it on the spot in their own hospitals, but it's just a matter of whether they're interested'</i> <i>'I have had a new grad, that after my [in-service] talk come to me and be like, 'wow this is really interesting. I want to know more about this in cancer''</i>
Perceived Relevance	Perceived relevance to clinical practice emerged as a critical factor influencing nurses' engagement with genomics. Participants who had adopted genomics into their roles, either through formal positions or by facilitating mainstream testing, consistently described the integration of genomics as both clinically necessary and professionally motivating. Conversely, a lack of perceived relevance was framed as a reason for resistance to genomic uptake.	<i>'I think these things [Genomic innovations] will actually motivate everyone including me to take the time out to invest in the future, because this is going to go in the long run. So, if you're going to be an oncology nurse for the next 30, 40 years this is the future of cancer nursing'</i> <i>'Like the knowledge has exploded in recent years. Especially since the human genome was done. Instead of it just being a niche area, it's now becoming an area where it really needs to be considered in almost every patient's diagnosis'</i>

		<i>'If I spoke to any of the colleagues that they still would have no idea about genomics and I'm trying to push that education, but it's not high on the agenda. You know, with febrile neutropenia and sepsis and what is leukaemia and what is daunorubicin, you know, impact their right now daily care, it's hard to push that relevance of what genomics and genetics is and how that impacts their care, particularly when they've come up in a system that doesn't mention it in their training at all'</i> <i>'I think in the early stages, the important stuff is generally around the main cancer diagnoses and the treatments and side effects of all of those and what they need to do to support patients. Looking at the deeper things, like genomics and stuff is probably, 'oh yeah, I'll do that later''</i> <i>'It is hard because like, I guess if we can make it more apparent how genomics can be applicable, cost and time efficient, we'd probably have a good case. But there will always going to be resistance on things that they don't see the applicability, like right there'</i>

Appendix I: Coding Journal Excerpt Entry

Please note: This extract is drawn from my handwritten coding journal, maintained during the data analysis phase. It has been transcribed and lightly reformatted here for clarity while retaining the original structure and wording of my notes.

Reflexive Positioning:

I come to this data with a dual professional background in nursing and genetic counselling, which inevitably shapes how I engage with these accounts. I'm already feeling a sense of familiarity when participants describe close relationships with genetic counsellors and clinical geneticists. I found myself nodding along to accounts of 'informal chats' or the reassurance of having a genetics colleague nearby. I need to be careful that this alignment doesn't lead me to overvalue positive collaboration accounts and overlook their complexities or limits. Not all collaboration is effective or equitable. I want to stay curious about counter-narratives in the data and remain alert for moments where multidisciplinary engagement may be tokenistic, one-sided, or absent.

Initial coding (descriptive, close to data):

First pass, staying mostly semantic.

- Seeking guidance from genetic counsellors when genomics issues arise
- Meeting regularly with geneticists/genetic counsellors for questions or updates
- Proximity to genetics staff enabling informal conversations
- Genetics staff providing formal training (e.g., ethics sessions)
- Genetic counsellors sharing knowledge 'passionately'
- No onsite genetics staff → minimal engagement with genomics
- Working in isolation from genetics services in private/regional settings
- Lack of communication between hospitals/departments → fragmented care
- Co-location of genetics staff as potential enabler for adoption?

Reflexive note: I'm struck by the mix of formal structures (scheduled meetings, training) and informal 'chats'. This feels like what I've experienced in practice, so much of how we communicate is in the corridor on the way to a meeting (I'll need to check I'm not overvaluing it as the 'right' way to do things).

Looking for conceptual links, thinking about what Braun and Clarke write: 'what's going on' rather than just 'what's said':

- Informal relationships as channels for genomic knowledge exchange
- Structured collaboration building confidence in practice
- 'Passion' and approachability of genetics staff as enablers
- Organisational isolation as a barrier to adoption

- Lack of integration leading to ‘blindness’ in patient care
- Co-location as an enabler for collaboration and care cohesion

Reflexive note: I’m starting to think less about the *role* and more about the *function*? what these people do for the nurses: educate, connect, support, advocate etc. and the context in which this occurs (e.g., the organisation). Also noticing how absence of these functions is experienced as isolation or disconnection. But, am I looking for this specifically? Need to chat to supervisors.

Collapsing and refining codes

- ‘Seeking guidance’ + ‘Meeting regularly’ → Liaising with genetics counsellors (covers both formal and informal interactions)
- ‘Proximity enabling conversations’ + ‘Co-location as facilitator’ → Embedded genetics support (highlights organisational integration, not just geography!)
- ‘Passion of genetics staff’ + ‘Providing training’ → Genetic counsellors as education resource (note: risk of losing the emotional drive here, so flag to revisit in theme write-up)
- Keep organisational isolation from genetics services distinct (It’s a barrier and important to show absence alongside presence as an enabler).
- Separate Limited availability of genetic counsellors from ‘no contact’ (one is complete absence, the other is scarcity. There’s also ambiguity in a couple of the interviews where it’s not clear how limited this contact is).
-

Reflexive note: Deciding to keep both the positive and negative codes in parallel feels important here (it preserves the data’s tension between enabler and barrier experiences). I can feel myself wanting to consolidate everything under ‘collaboration works!’ but that’s my bias showing. Trying to police that and letting the actual data guide me.

Working code set after refinement:

- Genetic counselling support / Embedded support
- Expertise of genetic counsellors (potential merge with education resource)
- Liaising with genetics counsellors
- Genetic counsellors as education resource
- Limited contact with genetics services or counsellors
- Limited availability of genetic counsellors (potential merge? These overlap in NVIVO)
- Isolation from genetics services

Theme development:

Going back to the interviews and trying to 'zoom in' and 'zoom out' I think what I'm noticing is contextually, a lot of this is tied to the organisation in which these nurses are working in. What links them isn't just 'working with genetics staff', it's the organisational structures that make that collaboration possible: e.g., embedded roles, regular MDT meetings, and accessible expertise etc. When these structures are present, genomics feels more visible, embedded, and approachable for nurses. When absent, participants describe isolation (that 'blindness'), lack of cohesion, and missed opportunities for knowledge-sharing.

I noticed my initial codes separated 'education' from 'collaboration,' but on reflection, in this dataset education is delivered *through* collaboration, I'm not sure this is a separate process? This feels really central to the overarching theme. The 'collaboration' and the support as the umbrella tying these codes?

From notes post-meeting with supervisors:

I keep debating on how I should layout these themes, my overarching question is about barriers and enablers. I have this dilemma about whether to split enablers and barriers into separate themes, but I think they sit together (like under an overarching theme: *Collaboration and Support of Genetics Services?*). The tension between the 'presence' and 'absence' of collaboration actually deepens the theme in my opinion, these don't exist in a vacuum. The participants are showing what is possible when collaboration exists, and what is lost when it doesn't. The organisation they practice in is what dictates the presence or absence of this.

Final theme development:

Within Domain 4: Organisational Factors, these codes fall under Theme 4: Multidisciplinary Collaboration and Support.

The interpretive shift was in recognising that participants frame collaboration not simply as 'working with genetics staff,' but as a product of organisational structures (e.g., embedded roles, MDT meetings, shared spaces etc) Enable this collaboration possible and effective. When absent, participants describe barriers: 'blindness,' isolation, and missed opportunities for learning and coordinated care.

Appendix J: Distress Protocol

Distress and safety Protocol:

The following protocol will be put in place should a participant become distressed and require either additional or on-going assistance. A range of services could be offered depending on their circumstances.

Prior to the commencement of any interview, information regarding the counselling available should it be required will be provided to all prospective and actual study participants. Researchers will provide sufficient information regarding the risks and benefits of the research so that individuals may freely accept or decline participation. This information will be made available to the participant prior to the interview commencing. An additional notification of this information will also be given to those participants should they become distressed during the actual study.

Strategies to assist those distressed during an interview.

Should a participant become uncomfortable or distressed while discussing any topic during the interview, the following actions will be taken by the interviewer:

1. The researcher will determine the severity and transience of the participant's distress through methods such as using a Subjective Units of Discomfort scale (SUDs) where a participant rates themselves on a scale of 1-10, where 0=no distress and 10=extreme distress. If the distress is transient, it is expected that the SUDs will reduce by 2-3 points within 15 minutes. When seeking to determine severity, a rating of 3/10 is considered sufficient evidence that distress is mild and that the participant is not experiencing any lingering harm, and that they could be reasonably expected to 'self-regulate' (Draucker, Martsolf & Poole, 2009).

If a participant's distress reflects imminent danger:

- Cease the interview;
- Contact Emergency Services (000), unless arrangements can be made for the participant to be transferred to appropriate services by a support person;
- Notify the Chief Investigator.

Should a participant become distressed during participation, and there is no risk of imminent danger, the following processes should be followed:

1. The researcher will suggest that it is appropriate that the interview be terminated, paused, or postponed.
2. If the participant wishes this to happen, the interview will be ceased.
3. The researcher conducting the interviews is a trained counsellor and Registered Nurse with several years of experience working with clients experiencing mental and emotional distress. The researcher will exercise sensitivity and consideration to the welfare and interests of the

participant and will spend time with the participant and provide assistance, within the scope of their abilities, to discuss their concerns and support them.

4. After seeking advice from the Chief investigator (principal supervisor), a recommendation will be made that the participant speak to a counselling professional to discuss their concerns and referred if they agree.

- Free and confidential support is available to nurses, midwives, and students 24/7 Australia wide through Nurse & Midwife Support: 1800 667 877. NM Support is a Nursing and Midwifery Board of Australia (NMBA) initiative run by Turning Point, a leading mental health organisation. Participants can access this service by phone, or through their website: www.nmsupport.org.au

- If the participant has a general practitioner (GP) involved in their care it may be more appropriate to refer them to their GP who is already familiar with their history and would provide continuity of care. In this case the options of a counsellor or extant clinician would be provided to the participant as well. A mental health care plan is available through Medicare to provide a number of free sessions of counselling every calendar year.

6. The intended outcome of the activation of this protocol will be a comprehensive assessment and the presentation of options regarding ongoing counselling or other management as appropriate.

7. A follow-up phone call (with consent from the participant) will be made by the interviewer the following day to ensure that the participant is well and to determine feasibility of a follow up interview if one is planned.

Distress and safety Protocol: Researcher (PhD student)

The following protocol will be put in place should a researcher become distressed or be at risk during field work and require emergency, additional or on going assistance. A range of services could be offered depending on her circumstances.

Strategies to assist those distressed during an interview.

1. The researcher will have regular meetings with their supervisors
2. The researcher will practice healthy reflective practices to maintain their emotional and mental health (e.g., reflective journal)
3. The researcher will be referred to a counselling professional to discuss their concerns or a referral made to their Employee Assistance Program

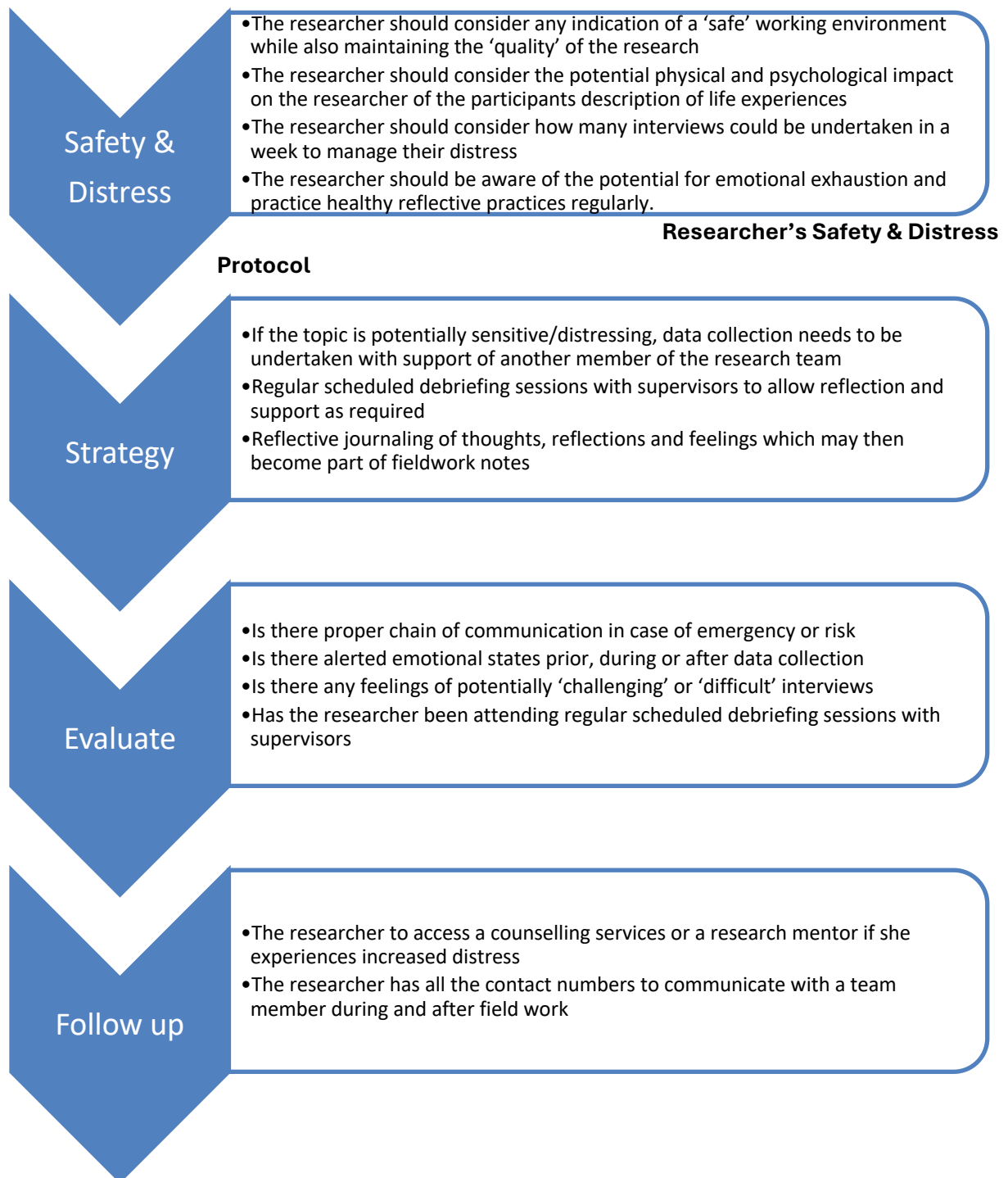
Conclusion

It is the researcher's duty of care to ensure that there is a balance consideration of the benefits against the risks. The research will ensure these strategies are put in place prior to commencing the interviews or discussions.

Below is the step-by-step guided protocol adapted from Draucker C B, Martsof D S and Poole C (2009) Developing Distress Protocols for research on Sensitive Topics. *Archives of Psychiatric Nursing* 23 (5) pp 343-350)

Participants' Safety & Distress protocol





Appendix K: Incidental Disclosure and Victimisation Protocol

Disclosure protocol

The following protocol will be put in place should a participant directly or incidentally disclose illegal activity, professional misconduct, or experience of criminal victimisation. This protocol serves to protect participants and third parties whose potential illegal activity or criminal victimisation may be recorded during the interview phase of this study. Research which records illegal activity can be subpoenaed in criminal and civil matters. This means that a researcher may be compelled to provide their research, which they have recorded confidentially, for use in legal proceedings. While not common this can place participants and others at significant risk. Participants may disclose victimisation which raises issues with respect to support for victims of crime and ethical issues with respect to reporting past crimes and addressing ongoing vulnerability.

Strategies to minimise risk of disclosure of illegal activity

1. Questions asked in the interview will not be designed to elicit information regarding illegal activities, or information not necessary for the research project.
2. Participants will be advised prior to the interview to be mindful of incidentally disclosing sensitive information that may result in litigation. Participants will be made aware of the risks and consequences of directly or incidentally disclosing illegal activities, and this information will be communicated clearly and in lay terms prior to consenting to participate in the study.
3. If participants wish to discuss a sensitive matter, participants will be asked to discuss these in abstract terms without disclosing the names and/or identifying details of those involved.
4. If the interviewer recognises information that is 'legally problematic', the recording will be paused, and the interviewer will review the sensitivity of the subject matter and advise the participant not to broach certain topics or not to provide individually-specific details.
5. If the interviewer recognises potential professional misconduct, the recording will be paused, and the interviewer will review the subject matter with the participant and chief investigator. Consultation with AHPRA mandatory notification support line (1300 419 495) will be conducted to determine steps necessary if reporting is appropriate.
6. Where mandatory reporting exists, or the disclosure is with respect to criminal acts against vulnerable third parties, for example children, the method for reporting this disclosure will be made clear and disclosed to the participant in the consent process prior to the interview.
7. Per the National Statement [4.6.4]: 'Consideration should be given to ... the removal of links between names and data, for participants whose illegal activities may be revealed or discovered in research'. Thus, interview data will be de-identified and pseudonyms

will be used if necessary. Any data (recording, transcript, field notes) containing identifying information will be removed and only stored in its de-identified form.

8. Participants may request to review a copy of their de-identified interview transcript prior to data analysis.

Strategies to minimise risk of disclosure of victimisation

1. When victimisation of the participant is being investigated, or is disclosed incidentally, a process for effectively referring the participant to relevant support services will be outlined (see below).
2. Where the participant discloses that they or another party has been a victim of crime, a process for referral to support services including services which can assist the participant with information on reporting the crime and the legal process will be provided (see below).

Referral to support services and reporting options

Victims Access Line: 1800 633 063 | Aboriginal Contact Line: 1800 019 123

Provides confidential support and information to victims of all crimes, including sexual and physical assault and family violence.

LawAccess Hotline: 1300 888 529

Provides free legal information, referrals and in some cases, advice for people who have legal problems.

Police assistance line: 131 444

For general non-emergency enquiries

Nurse & Midwife Support: 1800 667 877

Provides free and confidential support to nurses, midwives, and students 24/7 Australia wide

AHPRA mandatory notification support line: 1300 419 495

Provides advice and information regarding professional misconduct, unprofessional conduct, and mandatory reporting.

Child Protection Helpline: 13 2111

NSW Ageing and Disability Abuse Helpline: 1800 628 221

Protocol

Before Interview

- Participants will be informed of risks and consequences of directly or incidentally disclosing illegal activities.
- Participants will be asked to discuss potentially problematic incidents in abstract terms without disclosing the names and/or identifying details of those involved
- A thorough consent process will take place confirming participant's understanding of the risks and consequences of directly or incidentally disclosing illegal activities as well as options for reporting if appropriate.

During Interview

- If the researcher recognises information that is 'legally problematic', the activity will be paused, and the researcher will review the sensitivity of the subject matter and advise the participant not to broach certain topics or not to provide individually-specific details.
- The participant will be reminded of the risks and consequences of disclosing illegal activities.
- If the participant discloses illegal activities that fall under mandatory reporting guidelines, such as criminal acts against vulnerable third parties, for example children, the interview will be terminated and the participant will be notified of the process to follow (see 'After').
- If the participant discloses victimisation, the researcher (who is a health professional and trained counsellor) will pause the activity and offer immediate support.
- The researcher will assess the participants level of distress (per distress protocol) and offer to pause, terminate, or postpone the interview as appropriate
- The researcher will refer the participant to support services including services which can assist the participant with information on reporting the crime and the legal process involved.

After Interview

- All data collected (recording, transcripts, fieldnotes) will be de-identified, and only stored in its de-identified form.
- In the event of disclosure of illegal activities that fall under mandatory reporting guidelines, such as criminal acts against vulnerable third parties, for example children:
 - The supervisory team will be immediately informed, and a plan of action will be established
- If the researchers reasonably believe there is risk of serious and imminent threat to anyone's life, health, safety or welfare or a serious threat to public health, safety or welfare, emergency services will be contacted, and/or notification be made to the Department of Communities and Justice.
- If the participant has disclosed notifiable misconduct by a registered health practitioner, the researchers will contact AHPRA (mandatory notification support line 1300 419 495) for advice, and a formal notification will be lodged if deemed appropriate.
- In the event of disclosure of victimisation:
 - The supervisory team will be immediately informed and a plan of action will be established.
 - Appropriate support services will be communicated to the participant (see above), and the distress protocol will be enacted.
 - A courtesy phone call (with consent) will be made the following day to provide support and assess participant's welfare.