# Investigating Novel Caveolar Protein Interactions in Cardiovascular Redox Signalling

# Seyed Mojtaba Moosavi

Thesis submitted in fulfilment of the requirements for the degree of Doctor of Philosophy

Supervisors: Dr David van Reyk

Co-Supervisors: Dr Kristen Bubb Professor Gemma Figtree

University of Technology Sydney Faculty of Science

November 2021

### **CERTIFICATE OF ORIGINAL AUTHORSHIP**

I, *Seyed Mojtaba Moosavi*, declare that this thesis is submitted in fulfilment of the requirements for the award of *Doctor of Philosophy* in the *School of Life Sciences/of the Faculty of Science* 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.

I certify that the work in this thesis has not previously been submitted for a degree, nor has it been submitted as part of the requirements for a degree at any other academic institution except as fully acknowledged within the text. This thesis is the result of a Collaborative Doctoral Research Degree program with Kolling Medical Research Institute, University of Sydney.

This research is supported by the Australian Government Research Training Program.

Signature: Production Note: Signature removed prior to publication.

Date: 07<sup>th</sup> November 2021

#### ACKNOWLEDGEMENTS

It is a genuine pleasure to express my deep sense of thanks and gratitude to all people who decided to make this PhD possible and assisted me along the journey.

I would like to begin by sincere thanking my supervisor Dr Kristen Bubb who has been tremendously supportive throughout the project, and this thesis will not happen to be possible without her assistance, guidance, mentorship, and encouragement. She created a welcoming work environment through her enthusiasm, patience, and positive attitude. Working under her guidance was motivating and helped me achieve my goals.

I would like to extend my gratitude to Professor Gemma Figtree, who allowed me to start my PhD in her laboratory and provided guidance and feedback throughout this project. Her knowledge and achievements in and outside of the world of academia are inspiring.

I owe a deep sense of gratitude to Dr David van Reyk who offered valuable input and assistance with submitting my thesis.

I would like to thank all the team members in the lab, Dr Belinda Di Bartolo for scientific and technical guidance, Dr Own Tang for their technical assistance, Dr Marie Besnier for her comments, Dr Zara Sharane Ali and Dr Luisa Osorio for their administrative assistant. Furthermore, I would like thanks to Tom, Kat, Steve, Woody, Elijah, and Meg.

I would like to thank Prof Stuart Cordwell, Dr Melanie White and Mr Alexander Rookyard for their assistance with collecting the proteomics data and analysis; I also express my deep gratitude to Prof Marc Wilkins and Dr Matt Padula for their excellent advice for proteomics analysis.

The financial support of the University of Technology Sydney and for awarding the UTSD scholarship is greatly acknowledged. Without their support, I would not have been able to complete this project.

At a personal level, I would like to express my deep and sincere gratitude to my wife, Dr Sussan Ghassabian, for her love and support. I feel a deep sense of gratitude to my late father, mother and sister, who formed a part of my vision and taught me the good things that really matter in life. The happy memory of my father still provides endless inspiration for my journey in this life.

### ABSTRACT

**Background**: Cardiovascular disease (CVD) is a chronic disorder developing perniciously during life and usually progressing to an advanced stage by the time symptoms occur. CVD has been listed as the most common non-communicable disease globally. Notwithstanding some decline, CVD remains the principal cause of death in both developing and developed countries. Despite some recent success, current therapeutic methods are not efficient enough to prevent CVD, so it is essential to look for a novel therapeutic approach to preclude mortality and morbidity caused by CVD. FXYD1 protein is abundant in the heart and is known to protect cardiac sodium-potassium ATPase from oxidative stress. Nevertheless, little is known about the interaction of FXYD1, which is localised in caveolae, with other caveolae resident proteins in the heart or the role of the FXYD1 in other cardiovascular tissues. Our lab has recently demonstrated that FXYD1 protein, which is located in the invaginations of the plasma membrane called caveolae, protects eNOS from dysregulated redox signalling in the vasculature, making it a potential therapeutic target for vascular diseases.

Methods and Results: In this project, we first aimed to investigate the role of FXYD1 in cardiac and vascular redox signalling in several models of cardiovascular disease, including atherosclerosis, diabetes, and hypertension. For this project's aim, FXYD1 knock out mice, which exhibit enhanced oxidative stress and are prone to subtle increased cardiac dysfunction under normal conditions, were used. In the first instance, I examined the cardiac and vascular expression of redox signalling proteins by immunoblotting. Overall, there appeared to be some protection from oxidative stress by the presence of FXYD1. Heart and vascular tissues were obtained from atherosclerosis-prone apolipoprotein knockout (ApoE KO) mice crossed with FXYD1 wildtype and knockout mice to examine the role of FXYD1. ApoE KO / FXYD1KO males had lower NOX2 protein expression, while females had higher eNOS. In hypertensive mice, which was induced by chronic angiotensin 2 infusion, the expression level of Prdx6 in mesentery vascular tissues in FXYD-1 KO mice was significantly decreased. In the diabetic mice, which was induced by injection of pancreatic beta-cell toxin, streptozotocin and a longterm high-fat diet, the expression level of glutaredoxin 1 (GLRX-1) and eNOS in heart tissues in FXYD-1 KO mice was significantly increased. The only pattern emerging from these three models was a propensity for modified eNOS expression. Taken together with findings from a parallel study in the laboratory (in appendix) indicating a functional

interaction of FXYD1 with eNOS, I proceeded to focus on the caveolae subcellular region, a known hotspot for both eNOS regulation and oxidative signalling.

Firstly, I examined the impact of FXYD1 on caveolae morphology using electron microscopy analysis of sections of the heart from FXYD1 +/+ and -/- mice. The results of electron microscopic images showed the caveolae were denser in FXYD1 KO heart tissue, and the diameter and circumferences significantly decreased. I next aimed to determine the interaction of FXYD1 with other caveolae resident proteins and compared this to whole heart preparations using proteomics analysis. The results of cell and molecular biology studies showed that the protein expression of FXYD1 in mouse hearts was highest in caveolae subfractions (4-6) compared with other sub-fractions, which agrees with those studies that demonstrated the FXYD1 protein localized in caveolae. The results of whole heart unbiased proteomics showed that 11 proteins were considerably upregulated, although none of these were typical redox signalling proteins; rather they fall mainly within the haemostasis, immune system, metabolism, and transportation of small molecules groups. In addition, 61 proteins were significantly down-regulated in whole hearts of FXYD1 KO mice, including peroxiredoxin 5 (Prdx5), which acts as a cytoprotective antioxidant enzyme in inflammation and Phospholamban (Pln) which has a vital role in calcium homeostasis in the heart muscle.

Remarkably, from the isolated caveolae sub-fractions (fractions 4 and 5 combined), 139 proteins were upregulated, and 39 proteins were significantly downregulated in FXYD1 KO mice compared with WT. That these 139 proteins were upregulated in the caveolae fractions suggests a potential accumulation or translocation of these proteins to the caveolae. Of these, the most common signalling pathway affected were complex I biogenesis and respiratory electron transport. On the other hand, 39 proteins were uniquely down regulated in FXYD1 KO mice's caveolae, which may have contributed to the disease phenotype. Within the caveolae subfractions, glutathione peroxidase 1(Gpx1), which is an antioxidant enzyme counteracting oxidative stress, and apolipoprotein A-I (Apoa1), which participates in the reverse transport of cholesterol from tissues to the liver for excretion by promoting cholesterol efflux from tissues and by acting as a cofactor for the lecithin cholesterol acyltransferase, apolipoprotein C-I (ApoC I), which is an inhibitor of lipoprotein binding to LDL and catalase (Cat), which is involved in redox signalling, were significantly upregulated in FXYD1 KO mice. In addition, glutathione synthetase (GSS), a redox-signalling proteins, was upregulated in caveolae, whilst down-regulated

proteins included glutaredoxin-3 (Glrx3), a critical negative regulator of cardiac hypertrophy and thioredoxin (Txn), which has a critical role in the reversible S-nitrosylation of cysteine residues in target proteins thereby contributing to intracellular nitric oxide response.

Given the key changes to lipoprotein signalling proteins, I utilised our uniquely established mouse line of FXYD1 KO mice on the atherosclerosis-prone apolipoprotein E KO background to assess the functional impact on atherosclerosis development. Here I demonstrated that FXYD1 was involved in regulating body weight in male mice but had minimal effect on plaque development. Interestingly, FXYD1 appeared pro-inflammatory and detrimental to cholesterol metabolism, as FXYD1 KO mice had lower circulating total cholesterol and increased circulating IL-1<sup>β</sup>. This pro-inflammatory phenotype was restricted to females, hinting at a potential unique mechanism involved in the gender differences seen in our clinics' as to cardiovascular adverse events. As inflammation is a critical driver of plaque rupture, I also examined the impact of FXYD1 absence on plaque stability using the established carotid artery tandem stenosis protocol. However, no changes were evident in either necrotic core or fibrous cap thickness in FXYD1<sup>-/-</sup> vs. <sup>+/+</sup> mice on ApoE KO background. Therefore, I conclusively showed that whilst FXYD1KO mice were prone to inflammation, they were not at increased risk of plaque development or rupture.

**Conclusion:** This thesis's overall findings are that FXYD1 appears to be protective against oxidative damage and proinflammatory. Overall, cardiovascular disease's effect appears to be balanced with no change in atherosclerosis plaque development or stability, whether FXYD1 was present or absent. Some of the changes in atherosclerotic mice were sex-dependent. Future studies may investigate targeting FXYD1 in specific sub-cellular regions such as the caveolae, which are redox hotspots, to lower oxidative stress without causing inflammation.

#### **PUBLICATIONS**

Lo, C. C. W., **Moosavi, S.M.**, Bubb, K.J. (2018). "The Regulation of Pulmonary Vascular Tone by Neuropeptides and the Implications for Pulmonary Hypertension." Front Physiol 9: 1167.

Bubb, K.J., Tang, O., Gentile, C., **Moosavi, S.M.**, Hansen, T., Liu, C.C., Di Bartolo, B.A. & Figtree, G.A. 2021, 'FXYD1 Is Protective Against Vascular Dysfunction', *Hypertension*, p. HYPERTENSIONAHA12016884.

#### PRESENTATIONS

**S.M.Moosavi**, D.van Reyk, B.Di Bartolo, O.Tang, K.J.Bubb, G.A.Figtree, FXYD1 is associated with a female-specific pro-inflammatory and hypercholesterolemic environment: Implications for Atherosclerosis, American Heart Association's annual Scientific Sessions conference, Nov.13-17<sup>th</sup> 2020, Virtual (Poster Presentation)

**Seyed Mojtaba Moosavi**, Belinda Di Bartolo, Owen Tang, Kristen J Bubb and Gemma Figtree, FXYD1 may be a new signalling protein in cholesterol metabolism or handling in a mouse model of atherosclerosis, New Horizon 2019, Nov. 14-15<sup>th</sup> 2019, Sydney, Australia (Oral Presentation)

**Seyed Mojtaba Moosavi**, Belinda Di Bartolo, Owen Tang, Kristen J Bubb and Gemma Figtree, FXYD1 is associated with lower circulating cholesterol in a mouse model of atherosclerosis, Australian Society of Atherosclerosis Meeting, Oct. 16-19<sup>th</sup> 2019, Melbourne, Australia (Finalist) (Oral Presentation)

# Table of Contents

ACKNOW	LEDGEMENTSIII		
ABBREVIATIONS XVI			
SYMBOLSXVII			
UNITS OF	UNITS OF MEASUREMENTXVII		
List of Fig	guresXVIII		
List of TablesXXVI			
1.1. Intro	oduction1		
1.2. CVD	Risk Factors:		
1.2.1.Mc	odifiable Risk factors		
1.2.1.1.	Cholesterol		
1.2.2.No	n-modifiable risk factors		
1.2.2.1.	Age is an Independent Risk Factor for Cardiovascular Disease5		
1.2.2.2.	The impact of sex on CVD		
1.2.2.3.	Genetics and CVD:		
1.3. Read	ctive oxygen species (ROS)7		
1.3.1.Wh	nat is the cause of oxidative stress?		
1.3.2.Dif	fferent types and Sources of ROS		
1.3.2.1.	NADPH oxidases (NOX)		
1.3.2.2.	Mitochondria9		
1.3.2.3.	Oxidised low-density lipoprotein (ox-LDL)9		
1.3.2.4.	Angiotensin II (AngII) - Indoxyl sulphate (IS)10		
1.3.2.5.	Tetrahydrobiopterin (BH <sub>4</sub> )11		
1.3.2.6.	The Lipoxygenase (LOX) family11		
1.3.2.7.	Myeloperoxidase (MPO)11		
1.3.2.8.	Xanthine oxidoreductase (XOR)11		
1.3.2.9.	Glucose		
1.3.2.10.	The major source of ROS in CVD		
1.4. Anti	oxidants		
1.4.1.No	n-protein endogenous antioxidants14		
1.4.1.1.	Glutathione ((L-γ-glutamyl-L-cysteinyl-glycine) (GSH))14		
1.4.1.2.	Alpha-lipoic acid (ALA)14		
1.4.1.3.	Coenzyme Q (CoQ)		
1.4.1.4.	Ferritin		

1.4	4.1.5.	Bilirubin	. 16
1.4	4.1.6.	Uric acid (UA)	. 16
1.4	4.2.End	ogenous protein antioxidants	. 17
1.4	4.2.1.	Superoxide dismutase (SOD)	. 18
1.4	4.2.2.	Catalase	. 18
1.4	4.2.3.	Glutathione peroxidase (GPx)	. 19
1.5.	Role	and impacts of ROS in cardiovascular disease (CVD):	19
1.:	5.1.Ath	erosclerosis	. 21
1.:	5.1.1.	Oxidative stress and inflammatory basis of plaque development	. 22
1.:	5.1.2.	Plaque instability	. 22
1.	5.1.3.	ROS in Endothelium	. 22
1.	5.1.4.	Influence of ROS in smooth muscle cells	. 23
1.:	5.2.Hyp	pertension	. 23
1.	5.2.1.	ROS in the development of hypertension	. 24
1.	5.2.2.	Endothelial dysfunction	. 24
1.	5.3.Dia	betes	. 25
1.	5.3.1.	ROS in diabetic vascular disease	. 25
1.6.	Redo	x signalling in subcellular regions	26
1.7.	Cave	olae as a centre of cell signalling	26
1.7. 1.8.	Cave The r	olae as a centre of cell signalling ole of Caveolae in diseases	26 28
1.7. 1.8.	Cave The r	olae as a centre of cell signalling ole of Caveolae in diseases	26 28 29
1.7. 1.8.	Cave The r 8.1.eN(	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae	26 28 . 29 30
<ol> <li>1.7.</li> <li>1.8.</li> <li>1.3</li> <li>1.9.</li> </ol>	Cave The r 8.1.eN Infla	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae mmation	26 28 . 29 30
<ol> <li>1.7.</li> <li>1.8.</li> <li>1.3</li> <li>1.9.</li> <li>1.10</li> </ol>	Cave The r 8.1.eN Infla . FXYI	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae mmation D family:	26 28 . 29 30 32
<ol> <li>1.7.</li> <li>1.8.</li> <li>1.3</li> <li>1.9.</li> <li>1.10</li> <li>1.</li> </ol>	Cave The r 8.1.eNC Inflan . FXYI 10.1.	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae mmation D family: Phospholemman (PLM-FXYD1):	26 28 . 29 30 32 . 33
<ol> <li>1.7.</li> <li>1.8.</li> <li>1.3</li> <li>1.9.</li> <li>1.10</li> <li>1.</li> <li>1.</li> </ol>	Cave The r 8.1.eNC Inflan . FXYI 10.1. 10.2.	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae mmation D family: Phospholemman (PLM-FXYD1): FXYD1 in CVD	<ul> <li>26</li> <li>28</li> <li>29</li> <li>30</li> <li>32</li> <li>33</li> <li>36</li> </ul>
<ol> <li>1.7.</li> <li>1.8.</li> <li>1.3</li> <li>1.9.</li> <li>1.10</li> <li>1.</li> <li>1.11</li> </ol>	Cave The r 8.1.eNC Inflat . FXYI 10.1. 10.2. . Sumr	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae mmation D family: Phospholemman (PLM-FXYD1): FXYD1 in CVD	<ul> <li>26</li> <li>28</li> <li>29</li> <li>30</li> <li>32</li> <li>33</li> <li>36</li> <li>37</li> </ul>
<ol> <li>1.7.</li> <li>1.8.</li> <li>1.9.</li> <li>1.10</li> <li>1.</li> <li>1.11</li> <li>1.12</li> </ol>	Cave The r 8.1.eNC Inflan . FXYI 10.1. 10.2. . Sumr . Aims	olae as a centre of cell signalling role of Caveolae in diseases OS and Caveolae mmation D family: Phospholemman (PLM-FXYD1): FXYD1 in CVD nary: and Hypotheses	26 28 . 29 30 32 . 33 . 36 37 39
1.7. 1.8. 1.9. 1.10 1. 1.11 1.112 2.1.	Cave The r 8.1.eNC Inflat . FXYI 10.1. 10.2. . Sumr . Aims Mous	olae as a centre of cell signalling ole of Caveolae in diseases OS and Caveolae mmation D family: Phospholemman (PLM-FXYD1): FXYD1 in CVD nary: and Hypotheses	26 28 30 32 33 33 36 37 39 40
1.7. 1.8. 1.9. 1.10 1. 1.11 1.11 1.12 2.1. 2.	Cave The r 8.1.eNC Inflat . FXYI 10.1. 10.2. . Sumr . Aims Mous 1.1.FX	olae as a centre of cell signalling role of Caveolae in diseases OS and Caveolae mmation D family: Phospholemman (PLM-FXYD1): FXYD1 in CVD nary: and Hypotheses e models	<ul> <li>26</li> <li>28</li> <li>29</li> <li>30</li> <li>32</li> <li>33</li> <li>36</li> <li>37</li> <li>39</li> <li>40</li> <li>40</li> </ul>
1.7. 1.8. 1.9. 1.10 1. 1.11 1.12 2.1. 2. mice	Cave The r 8.1.eNC Inflat . FXYI 10.1. 10.2. . Sumr . Aims Mous 1.1.FXY 1.2.Apc 40	olae as a centre of cell signalling ole of Caveolae in diseases	26 28 30 32 33 33 36 37 39 40 .40 out
1.7. 1.8. 1.9. 1.10 1. 1.11 1.12 2.1. 2. mice 2	Cave The r 8.1.eN( Inflat . FXYI 10.1. 10.2. . Sumr . Aims Mous 1.1.FX 1.2.Apc 40	olae as a centre of cell signalling	26 28 29 30 32 33 33 36 37 39 40 .40 out
1.7. 1.8. 1.9. 1.10 1. 1.11 1.12 2.1. 2. mice 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	Cave The r 8.1.eNC Inflan . FXYI 10.1. 10.2. . Sumr . Aims Mous 1.1.FX 1.2.Apc 40 1.3.Stre 1.4.Apc	olae as a centre of cell signalling	<ul> <li>26</li> <li>28</li> <li>29</li> <li>30</li> <li>32</li> <li>33</li> <li>36</li> <li>37</li> <li>39</li> <li>40</li> <li>40</li> <li>out</li> <li>41</li> <li>41</li> </ul>
1.7. 1.8. 1.9. 1.10 1. 1.11 1.12 2.1. 2. mice 2. 2. 2.2.	Cave The r 8.1.eNC Inflan . FXYI 10.1. 10.2. . Sumr . Aims Mous 1.1.FX 1.2.Apc 40 1.3.Stre 1.4.Ang Anae	olae as a centre of cell signallingole of Caveolae in diseases	<ul> <li>26</li> <li>28</li> <li>29</li> <li>30</li> <li>32</li> <li>33</li> <li>36</li> <li>37</li> <li>39</li> <li>40</li> <li>40</li> <li>out</li> <li>41</li> <li>41</li> <li>42</li> </ul>

2.2.1.Anaesthesia for recovery	
2.2.2.Endpoint Anaesthesia	
2.3. Tissue and Organ collection	42
2.4. Detection of Proinflammatory and anti-inflammatory interleuking	ıs 43
2.4.1.Proinflammatory Cytokines	
2.4.1.1. Blood sample collection:	
2.4.1.2. Interleukin 1-β (IL-1β):	
2.4.1.3. IL-6	
2.4.1.4. TNF-α	
2.4.2.Anti-inflammatory cytokines	
2.4.2.1. IL-10	
2.5. Genotyping	
2.5.1.Crude extraction of DNA:	
2.5.2.DNA quantitation	49
2.5.3.Primer design	49
2.5.4.Polymerase Chain Reaction (PCR) and Gel Electrophoresis:	50
2.6 Metabolic Cage Measurements	
2.0. Mictabolic Cage Measurements	
<ul><li>2.0. Nictabolic Cage Nicasurements</li><li>2.7. Blood glucose</li></ul>	
<ul><li>2.7. Blood glucose</li></ul>	<b>51</b>
<ul> <li>2.7. Blood glucose</li></ul>	
<ul> <li>2.7. Blood glucose.</li> <li>2.7.1.Endpoint, non-fasted blood glucose.</li> <li>2.7.2.Regular blood glucose.</li> <li>2.8. Total cholesterol, HDL, LDL, and triglyceride</li></ul>	
<ul> <li>2.7. Blood glucose.</li> <li>2.7.1.Endpoint, non-fasted blood glucose.</li> <li>2.7.2.Regular blood glucose.</li> <li>2.8. Total cholesterol, HDL, LDL, and triglyceride</li></ul>	
<ul> <li>2.7. Blood glucose.</li> <li>2.7.1.Endpoint, non-fasted blood glucose.</li> <li>2.7.2.Regular blood glucose.</li> <li>2.8. Total cholesterol, HDL, LDL, and triglyceride</li></ul>	
<ul> <li>2.7. Blood glucose</li></ul>	<b></b>
<ul> <li>2.7. Blood glucose</li></ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b>
<ul> <li>2.7. Blood glucose.</li> <li>2.7.1.Endpoint, non-fasted blood glucose.</li> <li>2.7.2.Regular blood glucose.</li> <li>2.8. Total cholesterol, HDL, LDL, and triglyceride</li></ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b>
<ul> <li>2.7. Blood glucose</li></ul>	51 51 51 51 51 51 51 52 52 52 52 52 52 52 52 52 52 52 53
<ul> <li>2.7. Blood glucose</li></ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>53</b> <b>53</b>
<ul> <li>2.7. Blood glucose</li></ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b>
<ul> <li>2.7. Blood glucose</li></ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b>
<ul> <li>2.7. Blood glucose</li></ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>54</b> <b>54</b>
<ul> <li>2.7. Blood glucose.</li> <li>2.7.1.Endpoint, non-fasted blood glucose.</li> <li>2.7.2.Regular blood glucose.</li> <li>2.8. Total cholesterol, HDL, LDL, and triglyceride</li> <li>2.8.1.Determination of the total cholesterol concentration:</li> <li>2.8.2.Determination of the HDL and LDL/VLDL concentration.</li> <li>2.8.3.Determination of the triglyceride concentration</li> <li>2.9. Aorta collection</li> <li>2.10. Tandem Stenosis (TS) Surgery</li> <li>2.11.1. Sectioning:</li> <li>2.11.2. Staining:</li> <li>2.11.2.1. Hematoxylin and Eosin (H&amp;E) staining.</li> <li>2.11.2.3. Trichrome Stain.</li> </ul>	<b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>51</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>52</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>53</b> <b>54</b> <b>54</b> <b>54</b> <b>54</b> <b>54</b> <b>54</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>54</b> <b>55</b> <b>55</b> <b>55</b> <b>55</b> <b>55</b> <b>56</b> <b>56</b> <b>56</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b> <b>57</b>

Tissue harvesting	54
Sample Preparation:	54
NP 40 Lysis buffer preparation:	54
Lysing Tissues:	55
Quantification of the total proteins in the lysed samples	55
ontinuous Sucrose gradient ultracentrifugation	56
ein Electrophoresis & Western Blotting	56
tron Microscopy	58
TEM	58
SEM	59
Biological samples preparation	60
Samples Sectioning	61
Post-staining:	61
Analysis of electron microscopy images	62
eomics	62
Samples preparation	62
Protein Precipitation (Chloroform/Methanol)	62
Protein reduction and alkylation	63
Trypsin digest of proteins	63
Peptide's concentration and desalting (Solid Phase Extraction)	63
Isobaric labelling of peptides (total proteome)	63
Isobaric labelling of peptides (reversibly redox modified Cys)	63
Analysis of MS/MS data for protein identification and quantitation	64
Analysis of MS/MS data for redox modified Cys peptide identificati 64	on and
stical Analysis	65
THREE	66
ing FXYD1 dependent redox signalling in pre-clinical models o	f CVD
oduction:	66
od	69
velopment of mouse models	69
AngII Induced hypertension mice model	69
STZ induced diabetes mice model	69
	Tissue harvesting

3.2	.1.3.	Development of an atherosclerosis novel mouse model	69
3.2	.2.Coll	ecting Tissue	70
3.2	.3.Red	ox Enzymes Detection	70
3.2	.4.Dete	ection of plaques using oil red O	70
3.3.	Resul	ts	71
3.3.1	. A	ng II-induced hypertension	71
3.3	.1.1.	FXYD1 and blood pressure	71
3.3	.1.2.	Protein expression of Redox Enzymes in Mesentery tissues	72
3.3.2	. S	ΓZ induced diabetes	78
3.3	.2.1.	Body Mass	78
3.3	.2.2.	Blood glucose changes in FXYD1 WT and FXYD1 KO STZ induced mice	79
3.3	.2.3.	Redox Enzymes	80
3.3.3	. A	therosclerosis	90
33	31 D	etection of plaques using oil red O	90
3.3	3 1	Redox Enzymes	91
34	Summ	ary protein expression of Reday Enzyme in different disease mode	-le
0.1.	100	ary protein expression of freudx Enzyme in different discuse mou	.15
	100		
			~ •
3.5.	Discu	ssion	02
3.5. CHAI	Discu: PTER	ssion	02 05
3.5. CHAI Invest	Discus PTER tigatin	ssion	02 05 05
3.5. CHAI Invest 4.1.	Discus PTER tigatin Introc	ssion	02 05 05 05
3.5. CHAI Invest 4.1. 4.2.	Discus PTER tigatin Introc Metho	ssion	02 05 05 05 05
3.5. CHAI Invest 4.1. 4.2. 4.2.1	Discus PTER tigatin Introd Metho . E	ssion	D2 D5 D5 D5 D6 D6
<ul> <li>3.5.</li> <li>CHAI</li> <li>Invest</li> <li>4.1.</li> <li>4.2.</li> <li>4.2.1.</li> <li>4.2</li> </ul>	Discus PTER tigatin Introd Metho . E: 2.2.Quat 106	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         xtraction of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample	02 05 05 05 06 06 les
<ul> <li>3.5.</li> <li>CHAI</li> <li>Invest</li> <li>4.1.</li> <li>4.2.</li> <li>4.2</li> <li>4.2</li> <li>4.2</li> </ul>	Discus PTER tigatin Introd Metho . E: 2.2.Quas 106	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         tron Microscopy       10	02 05 05 05 06 06 les
<ul> <li>3.5.</li> <li>CHAI</li> <li>Invest</li> <li>4.1.</li> <li>4.2.</li> <li>4.2</li> <li>4.2</li> <li>4.2</li> <li>4.2</li> <li>4.2</li> <li>4.2</li> </ul>	Discus PTER tigatin Introd Metho . E: 2.2.Quas 106 2.3.Elec 2.3.1.	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         Biological sample preparation       10	02 05 05 05 06 06 06
<ul> <li>3.5.</li> <li>CHAI</li> <li>Invest</li> <li>4.1.</li> <li>4.2.</li> <li>4.2</li> </ul>	Discus PTER tigatin Introd Metho . E: 2.2.Quas 106 2.3.Elec 2.3.1. 2.3.2.	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         stron Microscopy       11         Biological sample preparation       10         Sample sectioning and placing on mesh grids       11	02 05 05 05 06 06 06 06
<ul> <li>3.5.</li> <li>CHAI</li> <li>Invest</li> <li>4.1.</li> <li>4.2.</li> <li>4.2</li> </ul>	Discus PTER tigatin Introd Metho . E: 2.2.Quas 106 2.3.Elec 2.3.1. 2.3.2. 2.3.3.	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         sample sectioning and placing on mesh grids       10         Sample post-staining and visualising       10	02 05 05 05 06 06 06 06 06
<ul> <li>3.5.</li> <li>CHAI</li> <li>Invest</li> <li>4.1.</li> <li>4.2.</li> <li>4.2</li> </ul>	Discus PTER tigatin Introd Metho . E: 2.2.Quas 106 2.3.Elec 2.3.1. 2.3.2. 2.3.3. 2.3.4.	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         sample sectioning and placing on mesh grids       10         Sample post-staining and visualising       10         Analysis of electron microscopy images       10	02 05 05 05 06 06 06 06 06 07 07
3.5. CHAI Invest 4.1. 4.2. 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4	Discus PTER tigatin Introd Metho . E: 2.2.Qua: 106 2.3.Elec 2.3.1. 2.3.2. 2.3.3. 2.3.4. 2.4.Prot	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         sample sectioning and placing on mesh grids       10         Sample post-staining and visualising       10         Analysis of electron microscopy images       10	02 05 05 05 06 06 06 06 06 07 07
3.5. CHAI Invest 4.1. 4.2. 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4	Discus PTER tigatin Introd Metho . E: .2.Qua: 106 .3.Elec .3.1. .3.2. .3.3. .3.4. .4.Prote	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome       10         luction       10         ods:       10         ods:       10         ntification of hearts from mice       10         ntification of the total proteins in the lysed and caveolae subfraction sample       10         straction and placing on mesh grids       10         Sample sectioning and placing on mesh grids       10         Analysis of electron microscopy images       10         Protein sample preparation       10         Protein sample preparation       10	02 05 05 05 06 06 06 06 06 07 07 07
3.5. CHAI Invest 4.1. 4.2. 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4.2 4	Discus PTER tigatin Introd Metho . E: .2.Qua: 106 .3.Elec .3.1. .3.2. .3.3. .3.4. .4.Prot .4.1. .4.2.	ssion       10         FOUR       10         g the role of FXYD1 in caveolae morphology and proteome	02 05 05 05 06 06 06 06 06 07 07 07 07

4.2.4.4.	Protein digestion (Trypsin)	108
4.2.4.5.	Peptide's concentration and desalting (Solid Phase extraction)	108
4.2.4.6.	Isobaric labelling of peptides (reversibly redox modified Cys)	108
4.2.4.7.	Analysis of MS/MS data for protein identification and quantitation	109
4.2.4.8.	Analysis of MS/MS data for redox modified Cys peptide identification	n and
quantitation	109	
4.3. Resu	lts	. 111
4.3.1.Qua samples 111	antification of the total proteins in the lysed tissue and caveolae subfra	action
4.3.2.Ele	ctron microscopy	111
4.3.3.Pro	teomics	116
4.3.3.1.	Whole Hearts	116
4.3.3.2.	Caveolae Subfractions Four and Five:	128
4.3.3.3.	Caveolae Subfractions Six:	142
4.4. Discu	ission:	. 152
СПАРТЕР	EIVE	156
	. FIVE	. 150
I ne Impaci	t of FAYDI on development of Atheroscierosis	. 150
5.1. Intro	duction:	. 156
5.2. Meth	od:	. 159
<b>5.2. Meth</b> 5.2.1.Mo	od:	<b>. 159</b> 159
<b>5.2. Meth</b> 5.2.1.Mo 5.2.1.1.	od: use Model: Development of a novel mouse model	<b>. 159</b> 159 159
<b>5.2. Meth</b> 5.2.1.Mo 5.2.1.1. 5.2.1.2.	od: use Model: Development of a novel mouse model Development of atherosclerosis	<b>. 159</b> 159 159 159
<b>5.2. Meth</b> 5.2.1.Mo 5.2.1.1. 5.2.1.2. 5.2.1.3.	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass	<b>. 159</b> 159 159 159 159
<b>5.2. Meth</b> 5.2.1.Mo 5.2.1.1. 5.2.1.2. 5.2.1.3. 5.2.1.4.	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose	<b>. 159</b> 159 159 159 159 160
<b>5.2. Meth</b> 5.2.1.Mo 5.2.1.1. 5.2.1.2. 5.2.1.3. 5.2.1.4. 5.2.1.5.	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements	<b>. 159</b> 159 159 159 159 160 160
<b>5.2. Meth</b> 5.2.1.Mo 5.2.1.1. 5.2.1.2. 5.2.1.3. 5.2.1.4. 5.2.1.5. 5.2.1.6.	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride	. 159 159 159 159 159 160 160 160
<b>5.2.</b> Meth 5.2.1.Mo 5.2.1.1. 5.2.1.2. 5.2.1.3. 5.2.1.4. 5.2.1.5. 5.2.1.6. 5.2.1.7.	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride Circulating inflammatory markers	. 159 159 159 159 159 160 160 160
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> </ul>	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride Circulating inflammatory markers Plaque formation	. 159 159 159 159 160 160 160 160 160
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> </ul>	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride Circulating inflammatory markers Plaque formation	. 159 159 159 159 160 160 160 160 160 160
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> <li>5.2.1.8.2.</li> </ul>	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride Circulating inflammatory markers Plaque formation Aorta collection Detection of plaques using oil red O	. 159 159 159 159 160 160 160 160 160 160 160
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> <li>5.2.1.8.2.</li> <li>5.2.1.9. T</li> </ul>	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride Circulating inflammatory markers Plaque formation Aorta collection Detection of plaques using oil red O Tandem Stenosis (TS)	. 159 159 159 159 160 160 160 160 160 160 160 160 160
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> <li>5.2.1.8.2.</li> <li>5.2.1.9. T</li> </ul>	od:	. 159 159 159 159 160 160 160 160 160 160 160 160 160
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> <li>5.2.1.8.2.</li> <li>5.2.1.9. T</li> <li>5.2.1.9.1.</li> <li>5.2.1.9.1.</li> </ul>	od:	. 159 159 159 159 160 160 160 160 160 160 160 161 161
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> <li>5.2.1.8.2.</li> <li>5.2.1.9. T</li> <li>5.2.1.9.1.</li> <li>5.2.1.9.2.</li> <li>5.2.1.9.2.</li> <li>5.2.1.9.3</li> </ul>	od: use Model: Development of a novel mouse model Development of atherosclerosis Body Mass Endpoint non-fasted blood glucose Metabolic Cage Measurements Total cholesterol, HDL-cholesterol, LDL-cholesterol, and triglyceride Circulating inflammatory markers Plaque formation Aorta collection Detection of plaques using oil red O Surgery Tissue Collection Histochemistry	. 159 159 159 159 160 160 160 160 160 160 161 161 161
<ul> <li>5.2. Meth</li> <li>5.2.1.Mo</li> <li>5.2.1.1.</li> <li>5.2.1.2.</li> <li>5.2.1.3.</li> <li>5.2.1.4.</li> <li>5.2.1.5.</li> <li>5.2.1.6.</li> <li>5.2.1.7.</li> <li>5.2.1.8. P</li> <li>5.2.1.8.1.</li> <li>5.2.1.8.2.</li> <li>5.2.1.9. T</li> <li>5.2.1.9.1.</li> <li>5.2.1.9.2.</li> <li>5.2.1.9.3.</li> <li>5.3. Persult</li> </ul>	od:	. 159 159 159 159 160 160 160 160 160 160 161 161 161 161 162 162

5.3.1.	Atherosclerosis 162
5.3.1.1	. Body Mass
5.3.1.2	. Non-fasted blood glucose
5.3.1.3.	Metabolic Cage study 164
5.3.1.4.	Total cholesterol, HDL, LDL-cholesterol, and triglyceride 165
5.3.1.5.	Circulating inflammatory markers168
5.3.1.6.	Plaque Formation 169
5.3.2.	Results, Tandem Stenosis (ApoE KO/ FXYD1KO and WT) 171
5.3.2.1	. Body Mass
5.3.2.2	. Histochemistry
5.4. Dis	cussion
СНАРТИ	ER SIX
Discussio	on 182
Referenc	es: 190
Appendi	x 1
Appendi	x 2
Appendi	x 3

# ABBREVIATIONS

5-LO	5-lipoxygenase
ALA	Alpha-lipoic acid
AGEs	Advanced glycation end-products
Akt	Protein Kinases B
AngII	Angiotensin II
ANOVA	Analysis of variance
ApoE	apolipoprotein E
BH <sub>4</sub>	Tetrahydrobionterin
CAT	Catalase
Cav-1	Caveolin 1
Cav-2	Caveolin ?
Cav-2	Caveolin 3
CHD	Coronary Heart Disease
CKD	Chronic Kidney Disease
CRD	Campune Q
C0Q	Coenzyme Q
CoQIU	Coenzyme Q10
CVD	Cardiovascular Disease
DALYS	Disability Adjusted Life Years
DHLA	Dihydrolipoic acid
DNA	Deoxyribonucleic Acid
eNOS	endothelial Nitric Oxide Synthetase
EDRF	Endothelium-Derived Relaxing Factor
EGF	Epidermal growth factor
FDR	False Discovery Rate
FH	Familial Hypercholesterolaemia
GPX	Glutathione Peroxidase
GSH	Glutathione
GSS	Glutathione synthetase
HDL	High-Density Lipoprotein
H&E	Hematoxylin and eosin
НТ	Hypertension
IP	Intraperitoneal
IS	Indoxyl sulphate
IHD	Ischemic Heart Disease
IDI	Low-Density Linoprotein
	Low-Density Lipoprotein cholesterol
	Lipoyugenase
	Mitagan activated protain kinasa
MALK Ma SOD	Mangangag gungnovide digmutage
MII-SOD	Mulanese superoxide distilutase
MPU	Myeloperoxidase
MURC	Muscle-restricted colled-coll
NADPH	Nicotinamide adenine dinucleotide phosphate
NO	Nitric oxide
NOS	Nitric oxide synthase
NOX	NADPH oxidase
ox-LDL	Oxidized low-density lipoprotein
T1DM	Type 1 diabetes mellitus
T2DM	Type 2 diabetes mellitus
TGF <b>-</b> β	Transforming growth factor beta
TM	Melting Temperature
RAS	Renin-Angiotensin System

RNS	Reactive Nitrogen Species
ROS	Reactive Oxygen Species
SDS	Sodium Dodecyl Sulfate
SDPR	Serum deprivation-response protein
SFK	Src family kinase F
STZ	Streptozotocin
SOD	Superoxide dismutase
PCR	Polymerase chain reaction
PAH	Pulmonary arterial hypertension
РКА	Protein Kinases A
РКС	Protein Kinases C
PLM	Phospholemman
PLN	Phospholamban
PTRF	Polymerase I and transcript release factor
UA	Uric acid
VSMCs	Vascular smooth muscle cells
WHO	World Health Organisation
XDH	Xanthine dehydrogenase
XO	Xanthine oxidase
XOR	Xanthine oxidoreductase

# SYMBOLS

>	greater than
<	less than
α	alpha
β	beta
Δ	delta, change in
↑	increase
$\downarrow$	decrease
$\leftrightarrow$	no change

## UNITS OF MEASUREMENT

d	day
g	gram
hr	hour
L	litre
М	molar
m	milli
Min	minutes
mol	moles
n	nano
Pa	Pascal
Sec	second
V	volts
°C	degrees Celsius
%	percent
μ	micro

## List of Figures

Figure 1.1: ALA oxidisation process, in an interconvertible process NADPH reduces ALA to DHLA by
giving an electron and NADP <sup>+</sup> oxidase DHLA to ALA by taking an electron
Figure 1.2: Oxygen free radical formation via Fenton Reaction
Figure 1.3: Enzymatic degradation of purine in humans (Maiuolo et al. 2016) 17
Figure 1.4: Dismutation reaction
Figure 1.5: The figure shows how catalase converts $H_2O_2$ to water and molecular oxygen
Figure 1.6: GPx reduction process
Figure 1.7: Mechanism of Na/K ATPase, the enzyme pumps three Na <sup>+</sup> ions out and two K <sup>+</sup> ions into the cells
Figure 2.1: a) Serial dilution of IL-1 $\beta$ standards for standard curve, b) IL-1 $\beta$ standard curve obtained 44
Figure 2.2: a) Serial dilution of IL-6 standards for standard curve, b) IL-6 standard curve obtained 45
Figure 2.3: a) Serial dilution of TNF-a standards for standard curve, b) TNF-a standard curve obtained
Figure 2.4: a) Serial dilution of IL-10 standards for standard curve, b) IL-10 standard curve obtained 48
Figure 2.5: The standard curve obtained from the Pierce <sup>™</sup> BCA protein assay
Figure 2.6 :a) Shows schematic caveolae subfractions, b) shows tube containing sample before centrifugation, c) shows fractioned sample after 20 hours centrifugation
Figure 2.7: The schematic show how proteins transferred to the membrane
Figure 2.8: The Optics of a basic transmission electron microscope (TEM)
Figure 2.9: The optics of a basic scanning electron microscope (SEM)
Figure 2.10: The samples were immersed in a serial dilution of EPON resin at RT on the rotor, the resin infiltrates into the sample and hardens it, the EPON resin polymerised at 60°C overnight
Figure 3.1: Figure A shows the pathways and enzymes that contribute to ROS production in mammalian cells and are important in hypertension (Harrison & Gongora 2009). AngII activates the NADPH oxidase (B)(Sirker et al. 2007)
Figure 3.2: SBP(A), DBP (B), MABP (C) in WT and FXYD1 AngII induced hypertension mice ( $n=8-14$ ). Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO, (** $P<0.001$ , **** $P<0.0001$ )
Figure 3.3: HR in WT and FXYD1 AngII induced hypertension mice ( $n=8-14$ ). Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO, (* $P<0.05$ )

Figure 3.4: Protein expression level of NOX2 in FXYD1 WT and FXYD1 KO male (A, $N=4$ ) in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.5: Protein expression level of NOX4 in FXYD1 WT and FXYD1 KO male $(n=4)$ in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.6: Protein expression level of PRDX6 in FXYD1 WT and FXYD1 KO male ( $n=3-4$ ) in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA to determine differences between FXYD1 WT and FXYD1 KO, (* $P<0.05$ )
Figure 3.7: Protein expression level of GLRX-1 in FXYD1 WT and FXYD1 KO male $(n=3-4)$ in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed two-way ANOVA to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.9: Weight changes in WT and FXYD1 KO male and female (A, $n=14-19$ ) male (B, $n=8-10$ ), female (C, $n=6-9$ ). Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO, (*P<0.05, **P<0.01)
Figure 3.10: The endpoint blood glucose data are shown as mean $\pm$ SEM in all samples (A, n=14-19), male (B, n = 8-10) and female mice (C, n=6-9), statistical analysis was performed by two-way ANOVA, (** P<0.01, ****P<0.0001)
Figure 3.11: Protein expression level of NOX2 in FXYD1 WT and FXYD1 KO male and female (A, $n=6-12$ , male (B, $N=3-5$ ) and female (C, $n=3-7$ ) in mouse heart. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO, (* $p<0.05$ ** $p<0.01$ )
Figure 3.12: Protein expression of NOX4 in FXYD1 WT and FXYD1 KO male and female (A, $n=7-13$ ), male (B, $N=3-6$ ) and female (C, $n=3-6$ ) in mouse heart. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO. (* $p<0.05$ , ** $p<0.01$ , *** $p<0.001$ )
Figure 3.13: Protein expression of PRDX6 in FXYD1 WT and FXYD1 KO male and female (A, $n=6-13$ ), male (B, $n=3-6$ ) and female (C, $n=3-7$ ) in mouse heart. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO.
Figure 3.14: Protein expression of GLRX-1 in FXYD1 WT and FXYD1 KO male and female (A, $n=8-12$ ), male (B, $N=4-6$ ) and female (C, $n=3-7$ ) in mouse heart. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between WT and FXYD1 KO.
Figure 3.15: Protein expression of eNOS in FXYD1 WT and FXYD1 KO male and female (A, $n=8-13$ ),

male (B, N=5-6) and female (C, n=3-7) in mouse heart. Data are presented as mean  $\pm$  SEM. Statistical

analysis was performed by ordinary one-way ANOVA test to determine differences between WT and FXYD1 KO
Figure 3.16: Western blot analysis of the expression levels of NOX2, NOX4, PRDX6, GLRX1 and eNOS in HEART of STZ-induced Diabetes WT control, FXYD1 KO control, STZ WT and STZ FXYD1 KO 85
Figure 3.17: Protein expression level of NOX2 in FXYD1 WT and FXYD1 KO male ( $n=4-6$ ) in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.18: Protein expression level of NOX4 in FXYD1 WT and FXYD1 KO male $(n=5-7)$ in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.19: Protein expression level of GLRX-1 in FXYD1 WT and FXYD1 KO male ( $n=4-6$ ) in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.20: Protein expression level of eNOS in FXYD1 WT and FXYD1 KO male ( $n=4-6$ ) in mouse mesentery. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by two-way ANOVA to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.21: Western blot analysis of the expression levels of NOX2, NOX4, GLRX1 and eNOS in Mesentery of STZ-induced Diabetes WT control, FXYD1 KO control, STZ WT and STZ FXYD1 KO 89
Figure 3.22: Plaque detection in aorta of C57BL/6 WT and FXYD1 KO by Oil Red O and compare with the Oil red O stained aorta from ApoE KO/FXYD1 KO and ApoE KO/ FXYD1 WT mice that were on high fat/high cholesterol diet for 16 weeks. The samples are representative of a total number of 91 samples
Figure 3.23: Protein expression of NOX2 in FXYD1 WT and FXYD1 KO male and female (A, $n=10$ , male (B, $N=4-5$ ) and female (C, $n=5$ ) in mouse heart. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO (*P<0.05)
Figure 3.24: Protein expression of NOX4 in FXYD1 WT and FXYD1 KO male and female, $A$ , $n=10$ ), male (B, $N=5$ ) and female (C, $n=5$ ) in mouse heart. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.25: Protein expression of PRDX6 in FXYD1 WT and FXYD1 KO male and female A, $n=10$ ), male (B, $N=5$ ) and female (C, $n=5$ ) in mouse heart. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.26: Protein expression of GLRX-1 in FXYD1 WT and FXYD1 KO male and female (A, $n=9-10$ , male (B, $N=5$ ) and female (C, $n=5$ ) in mouse heart. All mice are ApoE KO. Data are presented as mean

± SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.27: Protein expression of eNOS in FXYD1 WT and FXYD1 KO male and female, (A, $n=9-10$ , male (B, $n=5$ ) and female (C, $n=5$ ) in mouse heart. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO (* $p<0.05$ )
Figure 3.28: Western blot analysis of the expression levels of NOX2, NOX4, PRDX6, GLRX1 and eNOS in Heart of ApoE KO/ FXYD1 KO and ApoE KO/ FXYD1 WT
Figure 3.29: Protein expression of NOX2 in FXYD1 WT and FXYD1 KO male and female, $A$ , $n=11-12$ , male (B, $N=5-6$ ) and female (C, $n=5-7$ ) in mouse mesentery. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.30: Protein expression of NOX4 in FXYD1 WT and FXYD1 KO male and female, $(A, n=9-12)$ , male $(B, N=5-6)$ and female $(C, n=5-7)$ in mouse mesentery. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.31: Protein expression of PRDX6 in FXYD1 WT and FXYD1 KO male and female (A, $n=10-12$ , male (B, $N=5-6$ ) and female (C, $n=5$ ) in mouse mesentery. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.32: Protein expression of GLRX-1 in FXYD1 WT and FXYD1 KO male and female (A, $n=10-11$ ), male (B, $N=5$ ) and female (C, $n=4-5$ ) in mouse mesentery. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by the Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.33: Protein expression of eNOS in FXYD1 WT and FXYD1 KO male and female, $(A, n=10-13)$ , male $(B, N=5-6)$ and female $(C, n=5)$ in mouse mesentery. All mice are ApoE KO. Data are presented as mean $\pm$ SEM. Statistical analysis was performed by Mann-Whitney non-parametric test to determine differences between FXYD1 WT and FXYD1 KO
Figure 3.34: Western blot analysis of the expression levels of NOX2, NOX4, PRDX6, GLRX1 and eNOS in Mesentery of ApoE KO/ FXYD1 KO and ApoE KO/ FXYD1 WT
Figure 4.1: Total protein concentration in FXYD1 WT and FXYD1 KO lysed heart tissues male mice (A, $n=14$ ), and total protein concentration in caveolae subfractions (4-5-6) FXYD1 WT and FXYD1 KO male mice (B, $n=6$ ). Data <sup>are</sup> presented as mean $\pm$ SEM. Mann-Whitney was used to determine differences between FXYD1 WT and FXYD1 KO for heart tissues and nonparametric one-way ANOVA for caveolae subfractions
Figure 4.2: Representative image of caveolae imaging in the hearts of A) FXYD1 WT and B) FXYD1 KO MICE

Figure 4.3: The number of caveolae per  $\mu$ m of the plasma membrane for FXYD1 knockout and wild type littermates. Data are shown as mean  $\pm$  SEM, and statistical analysis was performed by nonparametric Mann-Whitney test, the biological number N=5, with 2-10 images analysed per sample. \*\*p<0.01....114

Figure 4.4: The diameter of caveolae (nm) of the plasma membrane for FXYD1knock out and wild type littermates. Data are shown as mean  $\pm$  SEM, and statistical analysis was performed by nonparametric Mann-Whitney test, the biological number N=5, with 2-10 images analysed per sample. \*p<0.05 ......114

 Figure 4.6: Network nods represent proteins, which were significantly increased in FXYD1 KO whole
 117

 hearts mice
 117

Figure 5.2: Body mass changes on the high-fat diet. Male and female ApoE KO, FXYD1 WT and KO mice were fed a high-fat diet for 16 weeks, and mice were weighed fortnightly. Data are shown as mean  $\pm$  SEM, N= 21-27 and statistical analysis was performed by two-way ANOVA, \*\*\*\*p<0.0001............163

Figure 5.3: Weight changes in WT and FXYD1 KO male (A, n=21-27) and female (B, n=21-22) mice. All mice are ApoE KO. Data are presented as mean  $\pm$  SEM. Statistical analysis was performed by the Mann-Whitney non-parametric test to determine differences between WT and FXYD1 KO (\*P<0.05). 163

Figure 5.5: Water (A) and Food (B) intake in mice inhabiting metabolic cages, data are shown as mean  $\pm$  SEM (n = 6-7), all mice are ApoE KO, statistical analysis was performed by two-way ANOVA......165 Figure 5.6: Urinary (A) and Faecal (B) excretion in mice inhabiting metabolic cages, data are shown as mean  $\pm$  SEM (n = 6-7), all mice are ApoE KO, statistical analysis was performed by two-way ANOVA Figure 5.7: Total cholesterol concentration in FXYD1 WT and FXYD1 KO male and female mice (A, n=25-38), male (B) and female(C) mice (n=11-21, all mice are ApoE KO. Data are presented as mean  $\pm$ SEM. Mann-Whitney was used to determine differences between FXYD1 WT and FXYD-1 KO mice (\* Figure 5.8: Levels of HDL-C in FXYD1 WT and FXYD1 KO male and female mice (A, n=23-31), male (B) and female(C) mice (N=9-16) All mice are ApoE KO. Data are presented as mean  $\pm$  SEM. Mann-Whitney was used to determine differences between FXYD1 WT and FXYD-1 KO mice (\*\* P < 0.01)...166 Figure 5.9: Levels of LDL-C in FXYD1 WT and FXYD1 KO male and female mice (A, n=17-18), male and female (B) mice (n=6-11). All mice are ApoE KO. Data are presented as mean  $\pm$  SEM. Mann-Whitney (A) and two-way ANOVA (B) were used to determine differences between FXYD1 WT and *FXYD-1 KO mice*, \*\*\**p*<0.001, \*\*\*\**p*<0.0001......167 Figure 5.10: Levels of triglyceride in FXYD1 WT and FXYD1 KO male and female mice (A, n=35-41), male (B) and female (C) mice (n=18-22). All mice are ApoE KO. Data are presented as mean  $\pm$  SEM. Mann-Whitney was used to determine differences between FXYD1 WT and FXYD-1 KO mice......167 Figure 5.11: Levels of IL-1 $\beta$  in FXYD1 WT and FXYD1 KO male and female mice (A, n=11-12), male and female (B) mice (N=5-6). All mice are ApoE K.O Data are presented as mean  $\pm$  SEM. Mann-Whitney (A) and two-way ANOVA (B) were used to determine differences between FXYD1 WT and Figure 5.12: Collected aorta from WT and FXYD1 KO mice stained with Oil Red O procedure, all mice are ApoE KO. (A) Male FXYD-1 WT, (B) Male FXYD-1 KO, (C) Female WT, (D) Female FXYD-1 KO Figure 5.13: Percentage of the aorta covered by plaques in FXYD-1 WT and FXYD-1 KO male and female (A, n=35-46) mice, male (B, n=15-20) and female (C, n=20-26) mice. All mice are ApoE KO. Data are presented as mean  $\pm$  SEM. Mann-Whitney test was used to determine differences between Figure 5.14: Body mass changes on the high-fat diet. Male and female ApoE KO, FXYD1 WT and KO mice were fed a high-fat diet for 9 weeks, and mice were weighed fortnightly. TS surgery performed at week 10 and the high-fat diet continued for 7 more weeks. Data are shown as mean  $\pm$  SEM, N=6-12, and statistical analysis was performed by two-way ANOVA......171 Figure 5.15: Section 1 of collected carotids from WT and FXYD1 KO mice stained with H&E procedure, all mice are ApoE<sup>-/-</sup> and TS surgery performed. (A) Male FXYD-1 KO, (B) Male FXYD-1 WT (C)Female 

Figure 5.16: Figure shows the ratio of plaques to the whole section area in section 1 in FXYD1 WT and FXYD1 KO male and female (A, n=10-15), male (B, N=5-9) and female (C, n=5-6) mouse carotid All mice are ApoE KO and TS surgery performed. Data are presented as mean  $\pm$  SEM. Statistical analysis was performed by Mann-Whitney test to determine differences between FXYD1 WT and FXYD1 KO ...173

Figure 5.17: Figure shows the ratio of media to the whole section area in section 1 in FXYD1 WT and FXYD1 KO male and female (A, n=10-15), male (B, N=5-9) and female (C, n=5-6) mouse carotid. All mice are ApoE KO and TS surgery performed. Data are presented as mean  $\pm$  SEM. Statistical analysis was performed by Mann-Whitney test to determine differences between FXYD1 WT and FXYD1 KO ...173

Figure 5.20: Figure shows the ratio of plaques to the whole section area in section 2 in FXYD1 WT and FXYD1 KO male and female (A, n=11-17), male (B, N=6-11) and female (C, n=5-6) mouse carotid. All mice are ApoE KO and TS surgery performed. Data are presented as mean  $\pm$  SEM. Statistical analysis was performed by Mann-Whitney test to determine differences between FXYD1 WT and FXYD1 KO ...176

Figure 5.21: Figure shows the ratio of media to the whole section area in section 2 in FXYD1 WT and FXYD1 KO male and female (A, n=11-17), male (B, N=6-11) and female (C, n=5-6) mouse carotid. All mice are ApoE KO and TS surgery performed. Data are presented as mean  $\pm$  SEM. Statistical analysis was performed by Mann-Whitney test to determine differences between FXYD1 WT and FXYD1 KO ...176

Figure 5.24: Figure shows the ratio of medial to the whole section area in section 4 in FXYD1 WT and FXYD1 KO male and female (A, n=15-17), male (B, N=9-11) and female (C, n=6) mouse carotid. All mice are ApoE KO and TS surgery performed. Data are presented as mean  $\pm$  SEM. Statistical analysis was performed by Mann-Whitney test to determine differences between FXYD1 WT and FXYD1 KO ...179

Figure 6.1; A) shows the results of Tsutsumi 2008 study and B) the results of this study. The number of
caveolae in both condition increased, but absence of FXYD1 reduces the Cav 3 concentration and the
size of caveolae

# List of Tables

Table 1.1: Clinical trials Summary    20
Table 1.2: The details of 7 FXYD family members    32
Table 1.3: Mouse FXYD1 amino acid compositions (Gasteiger E. 2005)
Table 2.1: Details of primers that were used for genotyping of the mice       49
Table 3.1: Summary of protein expression change inFXYD1 KO male mice's heart tissues of disease         models (NA=Not available)         100
Table 3.2: Summary of protein expression change in FXYD1 KO female mice's heart tissues of disease         models (NA=Not available)
Table 3.3: Summary of protein expression changes in FXYD1 KO male mice's mesentery tissues of       101         disease models (NA=Not available)       101
Table 3.4: Summary of protein expression changes in FXYD1 KO female mice's mesentery tissues of         disease models (NA=Not available)         101
Table 4.1: The list of proteins that are significantly up-regulated in FXYD1 KO hearts
Table 4.2: The 25 most relevant pathways related to the proteins which significantly up-regulated inFXYD1 KO heart tissue sorted by p-value
Table 4.3: List of proteins significantly downregulated in FXYD1 KO mice    122
Table 4.4: The 25 most relevant pathways related to the proteins which significantly decreased inFXYD1 KO mice sorted by p-value
Table 4.5: List of proteins significantly up-regulated in caveolae subfraction 4 and 5 FXYD1 KO mice
Table 4.6: The 25 most relevant pathways sorted by p-value caveolae (upregulate subfractions 4 and 5)
Table 4.7: List of proteins significantly downregulated in caveolae subfraction 4 and 5 FXYD1 KO mice
Table 4.8: The 25 most relevant pathways sorted by p-value, (downregulated in caveolae subfractions 4 and 5)
Table 4.9: List of proteins significantly up-regulated in caveolae subfraction 6 FXYD1 KO mice142
Table 4.10: The 25 most relevant and significant pathways sorted by p-value, up-regulated in caveolaesubfraction 6
Table 4.11: List of proteins significantly downregulated in caveolae subfraction 6 FXYD1 KO mice147
Table 4.12: The 25 most relevant pathways sorted by p-value, for proteins which significantlydownregulated in caveolae subfraction 6

Table 5.1: Details of the mice were used in atherosclerosis study	162
Table 5.2: Details of mice used in the TS study	171