

**Bioinformatic analysis of membrane and associated proteins in murine
cardiomyocytes and human myocardium**

Shin-Haw Lee^{1,2,†}, Sina Hadipour-Lakmehsari^{1,2,†}, Da Hye Kim^{1,2}, Michelle Di Paola^{1,2}, Uros
Kuzmanov^{1,2}, Saumya Shah^{3,4}, Joseph Jong-Hwan Lee^{1,2}, Thomas Kislinger^{5,6}, Parveen
Sharma^{2,7}, Gavin Y. Oudit^{3,4}, Anthony O. Gramolini^{1,2}

SUPPLEMENTARY INFORMATION

TABLE OF CONTENTS

Supplemental Figure 1.....2

Supplemental Figure 2.....4

Supplemental Figure 3.....6

Supplemental Figure 4.....8

Supplemental Figure 5.....10

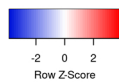
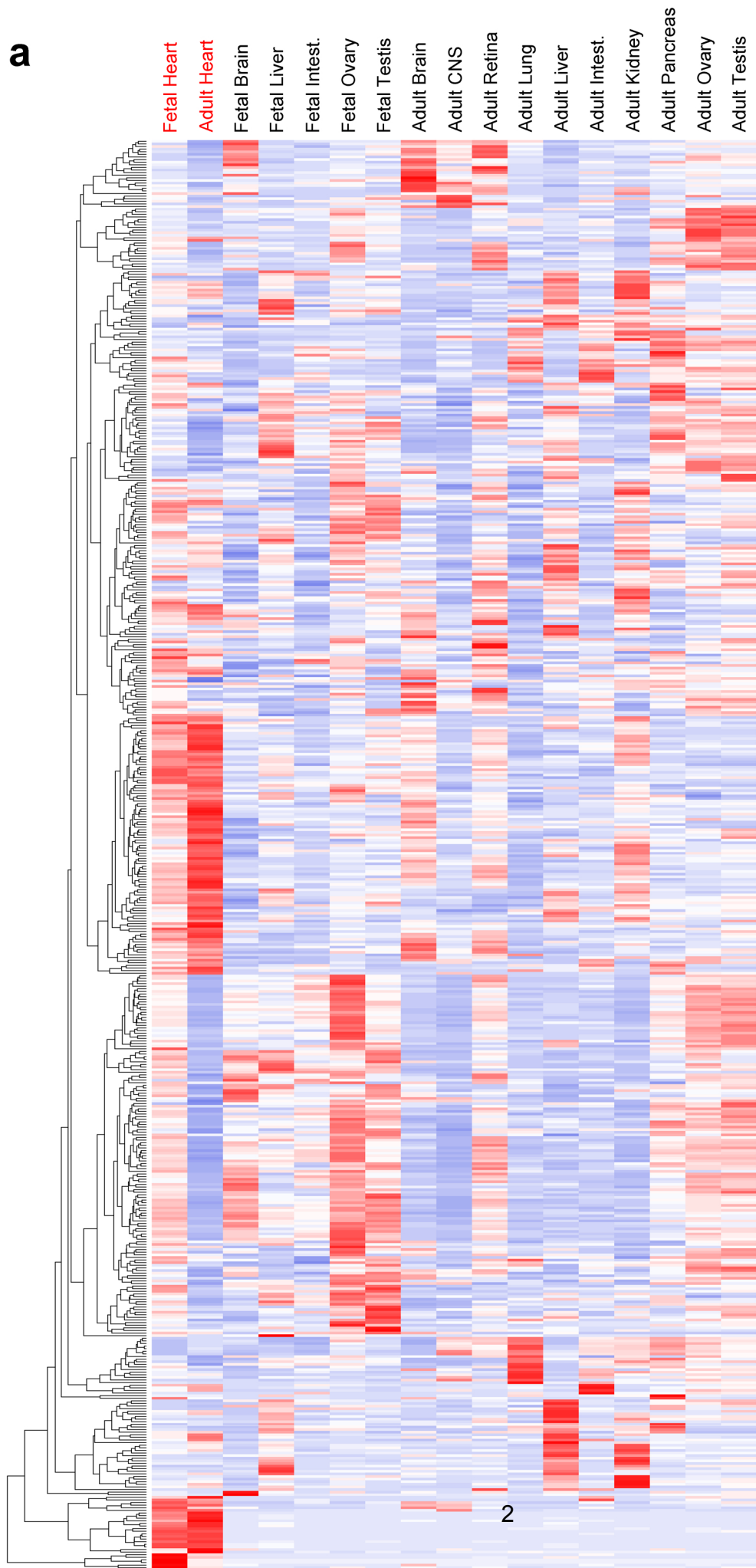
Supplemental Figure 6.....12

Supplemental Figure 7.....14

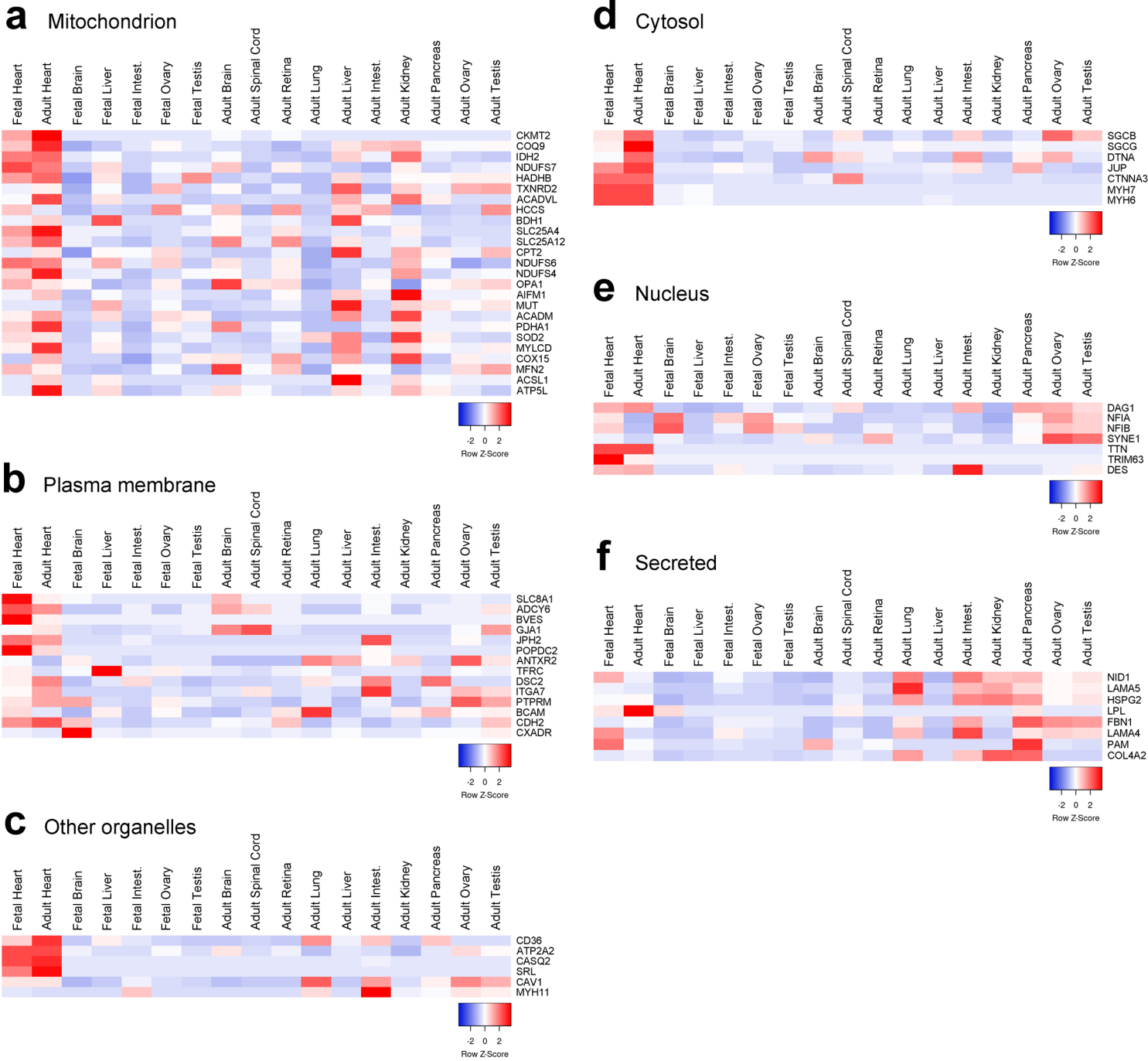
Supplemental Figure 8.....16

Supplemental Figure 9.....18

a

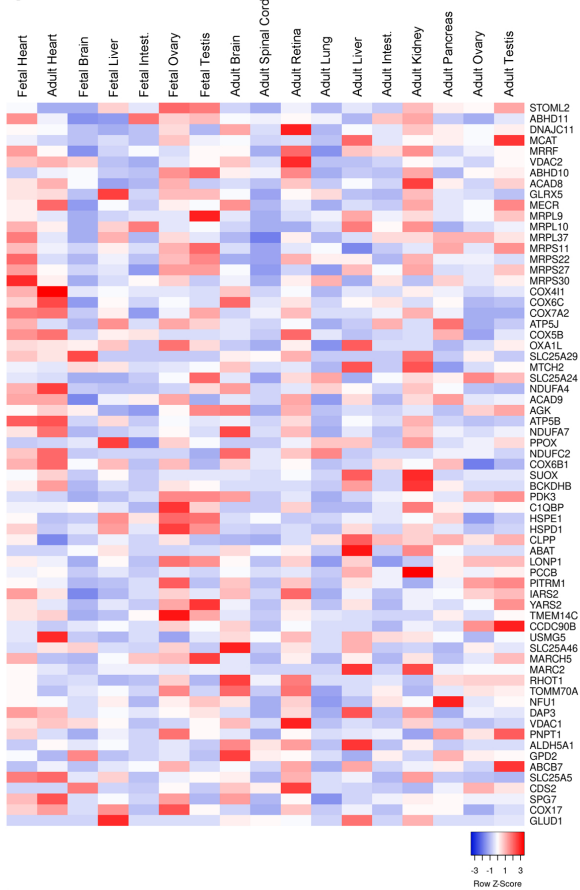
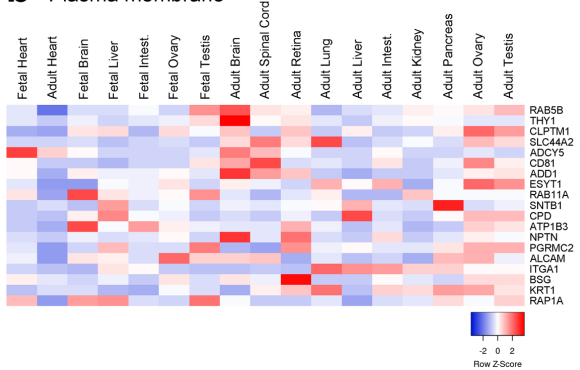
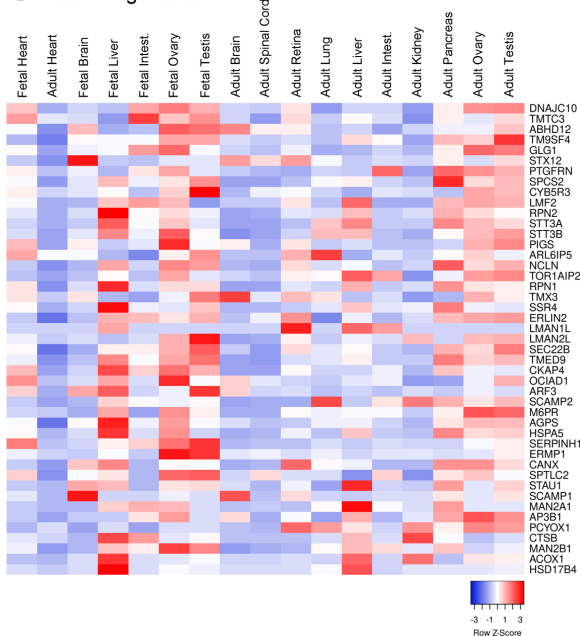
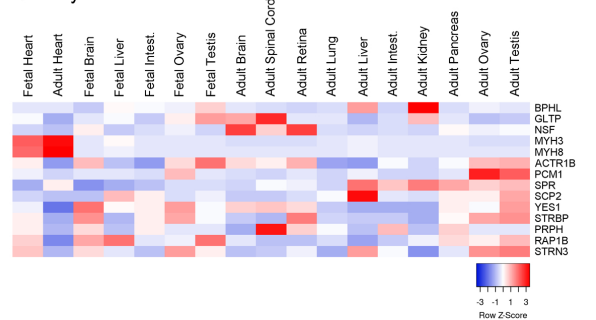
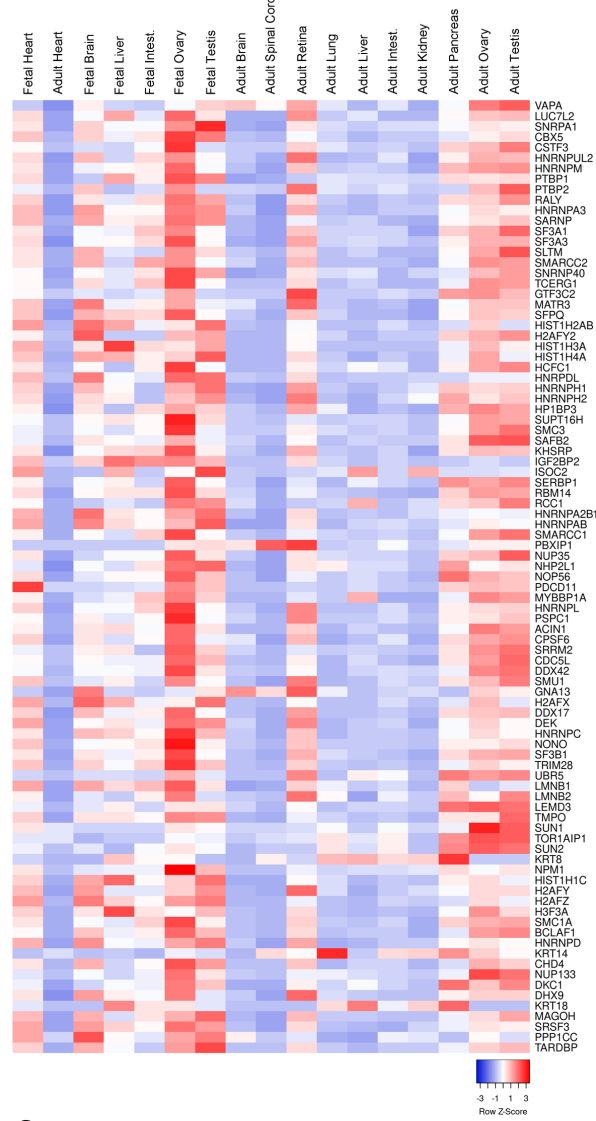
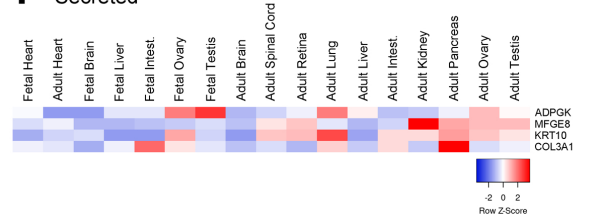


Supplemental Figure 1. **Transcriptomic analysis of the 550 membrane and membrane-associated protein clusters across various tissues.** (a) Heatmap showing unsupervised clustering of mRNA transcripts of the 550 membrane-associated proteins identified across clinically defined healthy human tissues; mRNA transcript data were obtained from Human Proteome Map. All source data input and normalized output files were uploaded to figshare (<https://doi.org/10.6084/m9.figshare.11844972.v12>).



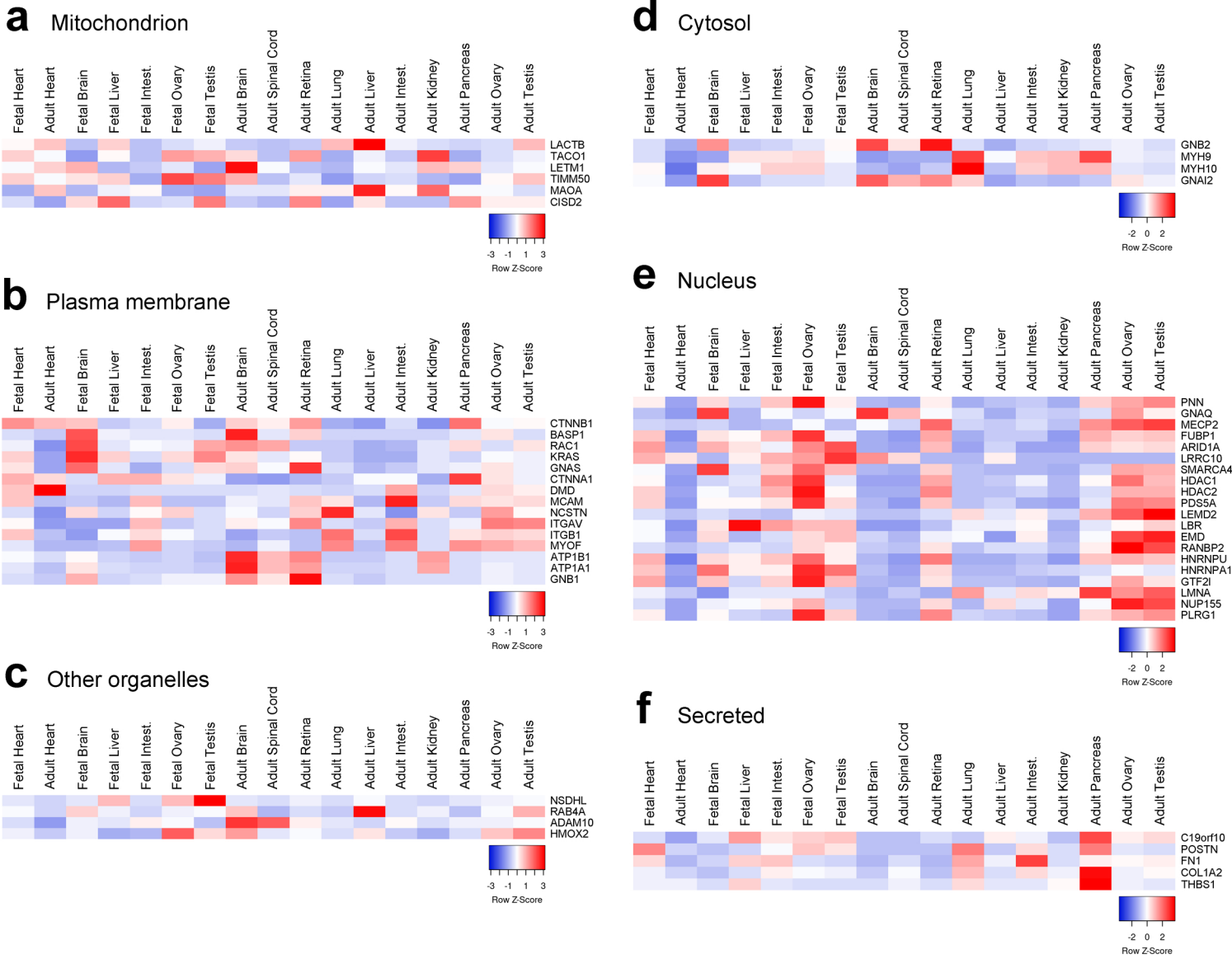
Supplemental Figure 2. **Transcriptomic analysis of cardiomyocyte-enriched membrane associated proteins with previous cardiac MGI phenotype.**

Heatmaps showing mRNA transcript levels of 67 cardiomyocyte-enriched membrane proteins with previously identified cardiac MGI phenotype across clinically defined healthy human tissues; mRNA transcript data were obtained from Human Proteome Map and are presented according to their subcellular classifications in (a) mitochondrion, (b) plasma membrane, (c) other organelles (ER, golgi apparatus, peroxisomes, lysosomes), (d) cytosol, (e) nucleus, and (f) the secretory pathway. All source data input and normalized output files were uploaded to figshare (<https://doi.org/10.6084/m9.figshare.11844972.v12>).

a Mitochondrion**b** Plasma membrane**c** Other organelles**d** Cytosol**e** Nucleus**f** Secreted

Supplemental Figure 3. **Transcriptomic analysis of non-cardiomyocyte-enriched membrane associated proteins with no previous cardiac MGI phenotype.**

Heatmaps showing mRNA transcript levels of 241 non-cardiomyocyte-enriched membrane proteins with no previously identified cardiac MGI phenotype across clinically defined healthy human tissues; mRNA transcript data were obtained from Human Proteome Map and are presented according to their subcellular classifications in (a) mitochondrion, (b) plasma membrane, (c) other organelles (ER, golgi apparatus, peroxisomes, lysosomes), (d) cytosol, (e) nucleus, and (f) the secretory pathway. All source data input and normalized output files were uploaded to figshare (<https://doi.org/10.6084/m9.figshare.11844972.v12>).



Supplemental Figure 4. **Transcriptomic analysis of non-cardiomyocyte-enriched membrane associated proteins with previous cardiac MGI phenotype.**

Heatmaps showing mRNA transcript levels of 54 non-cardiomyocyte-enriched membrane proteins with previously identified cardiac MGI phenotype across clinically defined healthy human tissues; mRNA transcript data were obtained from Human Proteome Map and are presented according to their subcellular classifications in (a) mitochondrion, (b) plasma membrane, (c) other organelles (ER, golgi apparatus, peroxisomes, lysosomes), (d) cytosol, (e) nucleus, and (f) the secretory pathway. All source data input and normalized output files were uploaded to figshare (<https://doi.org/10.6084/m9.figshare.11844972.v12>).

a

FAM162A Human MGSLSGLRLAAGSCFRLCERDVSSSLRLTRSSDLKRINGFCTKPKQESPGAPSRT--YNRV 58
 FAM162A Rat MWSLRGLRLAAGHCFLRCERNVSSPLRLTRNTDLKRINGFCTKPKQESPKAPTQ--SYRHRV 59
 FAM162A Mouse MWSLGLRLAAGHCLRLYERNASSSLRFRNTDLKRINGFCTKPKQESPKTPTQ--SYRHV 59
 FAM162A Chicken MWG-----RADKAVKLEERNIPSLRMSRGVGPVSRRLCSKPKQESSVQPRGRPVLRV 54
 FAM162A Cow MGSRLGLRLVAGSCFRSCERDAFSSSLRLTRNSDLKRTNGFCCKPKQESPKPPDQHTYSHRV 60
 FAM162A Horse MGSRLGLRLAAGSCFRLCERDASSSLRLTRNSDLKRINGFCTKPKQESPKAPS--HTYSHRV 59
 FAM162A Monkey MGTLRGLLLAAGSCFRLCERDVSSSLRLTRSSDLKINGFCIKPKQESPRAPSR--TYSHRV 59
 FAM162A Chimpanzee MGSLSGLRLAAGSCFRLCERDVSSSLRLTRSSDLKRINGFCTKPKQESPGAPSRT--YNRV 58

10 20 30 40 50 60

TM1

FAM162A Human PLHKPTDWQKILIWGRFKKEDEIPETVSEMLDAAKNKMRVKISYLMIALTVVGCIFM 118
 FAM162A Rat PLHKPTDFEKKILLWSGRFKKEEIPETISFEMLDAAKNKIRVKVSYLMIALTVAGCVYM 119
 FAM162A Mouse PLHKPTDFEKKILLWSGRFKKEEIPETISFEMLDAAKNKIRVKVSYLMIALTVAGCIYM 119
 FAM162A Chicken PGHKPTDWEKKILLWAGHFKKPEDIEPVVSDITIRAAQTLLRVKFSYVMIALTVIGCIYM 114
 FAM162A Cow PLHKPTDWEKKILIWGRFKKEDEIPETVSFEMLDAAKNKVRVKISYVMIALTVAGCVLM 120
 FAM162A Horse PLHKPTDWERKILIWGRFKKEDEIPETVSFEMLDAAKNKIRVKISYLMIALTVAGCIYM 119
 FAM162A Monkey PLHKPTDWQKMLIWGRFKKEDEIPETVSEMLDAAKNKMRVKICYLMIALTVIGCIAM 119
 FAM162A Chimpanzee PLHKPTDWQKILIWGRFKKEDEIPETVSEMLDAAKNKMRVKISYLMIALTVVGCIFM 118

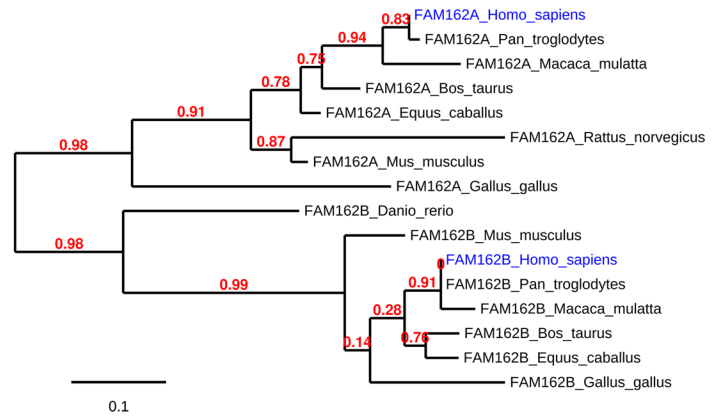
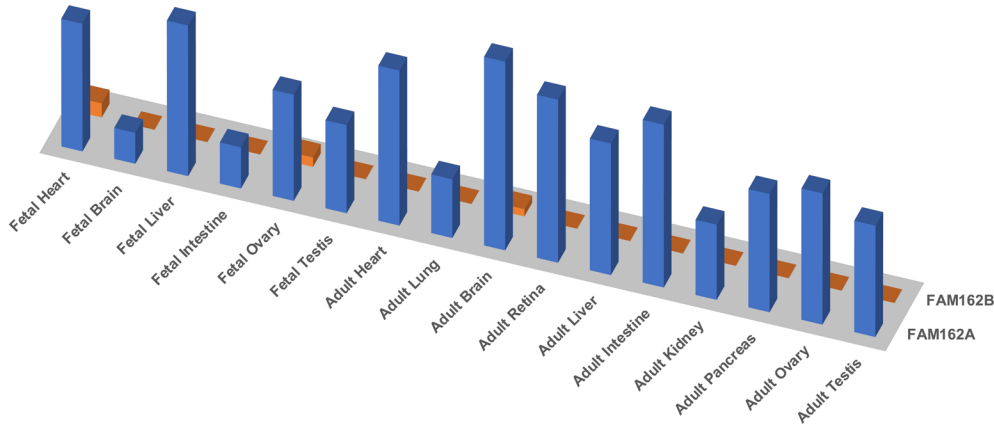
70 80 90 100 110 120

TM1

FAM162A Human VIEGKKAQRHETLTSLN-----LEKKARLKEEAAMKAKE----- 154
 FAM162A Rat VIEGKLEPRKESPSERGSGSYEGQGLDVFLDLLEKPGIFQKPSGKAIERERTVQG 178
 FAM162A Mouse VIEGKKAQRHESLTSLN-----LEKKARLKEEAAMKAKE----- 155
 FAM162A Chicken VIRGQKAWKRHESLTSLN-----LEKKAQWKEEATQSTSAKP----- 151
 FAM162A Cow VIEGKKAQRHETLTSLN-----LEKKARLKEEAAMKAKE----- 156
 FAM162A Horse VIEGKKAQRHESLTSLN-----LEKKARLKEEAAMKAKE----- 155
 FAM162A Monkey IIDGKKAQRNQTTLTRLN-----LEKKARLKEEAAMKAKE----- 155
 FAM162A Chimpanzee VIEGKKAQRHETLTSLN-----LEKKARLKEEAAMKAKE----- 154

130 140 150 160 170

RED indicates positions which have a single, fully conserved residue.

b**c****d**

COX20 Human MAAPPEGEPEERKSLKLLGLDVENTPCARHSILYGLSVVAGFGHFLTSRIRRS 60
 COX20 Rat MAAASEPHEP-EKKPFKLLGILDVENTPCARESILYGLSVIVTGLGHFLVTSRIRRS 59
 COX20 Mouse MAAAPPHET-EKKPFKLLGILDVENTPCARESILYGLSVIVTGLGHFLVTSRIRRS 59
 COX20 Chicken ---MAGEGDSEPEKSFLLGLFDVKNVPCARESIVLYGLSVLVGLGHFLATSRRVRS 57
 COX20 Cow -----MAA-APEPFKLLGILDVENIPCARDSVLYGLSVVAGLGHFLTSRIRRS 52
 COX20 Monkey MAAAPPEGEPEERKAFKLLGLDVENIPCARDSVLYGLSVIVAGFGHFLTSRIKRS 60
 COX20 Chimpanzee MAAAPPEGEPEERKSVKLLGLDVENTPCARHSILYGLSVAAGFGHFLTSRIRRS 60
 COX20 Frog --MAGQEGEVVKEKSFLLGIIDVQNTPCARESILYGTVGLSVLVGLGHFLATSRRVRS 58
 COX20 Zebrafish -----MTEEDGKTQGMKVLGILDINHNTPCAREAILHGAAGSVAAGLLHFLATSRRVRS 55

10 20 30 40 50 60

TM1 TM2

COX20 Human VGVGGFVLVTLCWFHCRYNFAKQRIQERAREEIKKILYEGTHLDPERKHNGSSN-- 118
 COX20 Rat VGVGGFVLVTLCWFHCRYNFAKQRIQERAREEIKKILYESTHLDPERKTKSSNSS-- 117
 COX20 Mouse VGVGGFVLVTLCWFHCRYNFAKQRIQERAREEIKKILYESTHLDPERKMTNNS-- 117
 COX20 Chicken FAVGGFICTMLGYWFCRYNLAQQRIQRMLEKGMKNMLFEGSSFDPEKKQTGNERSNS 117
 COX20 Cow VGVGGFIVVTLCWFHCRYNFAKQRIQERAREEIKKILYESTHLDPARKQTNGSSSS 112
 COX20 Monkey VGVGGFVLVTLCWFHCRYNFAKQRIQERAREEIKKILYEGTHLDPERKHNSNSS-- 118
 COX20 Chimpanzee VGVGGFVLVTLCWFHCRYNFAKQRIQERAREEIKKILYEGTHLDPERKHNGSSN-- 118
 COX20 Frog VAVGGYLLTTLGCWMCRYNNAKVRIOQKMLQEGIKNRILFEGSSIDPNTRKNTTDSKT- 117
 COX20 Zebrafish VGVAGFMITTLGSWFYCRYNNAKLRFOQRIIQEGLKNKVFYEGTDLDPTLKKTGDK--- 111

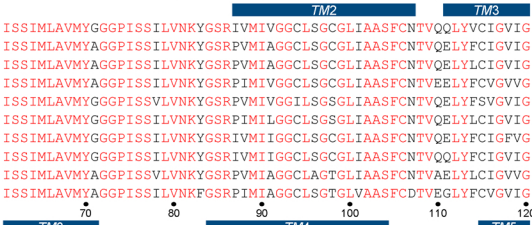
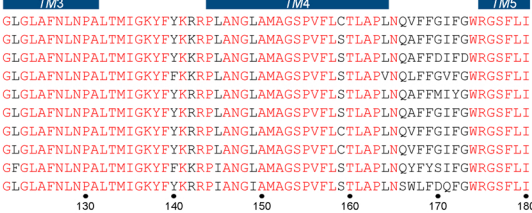
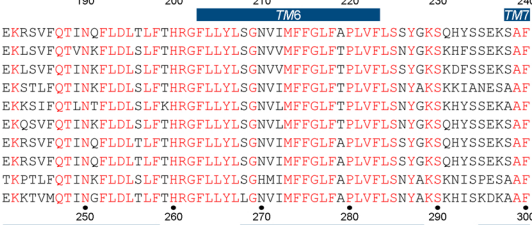
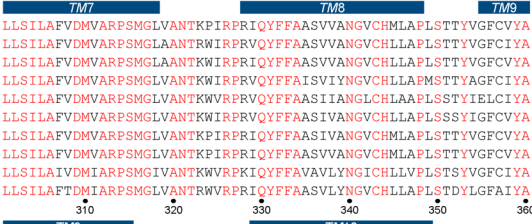
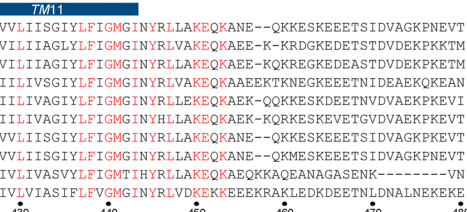
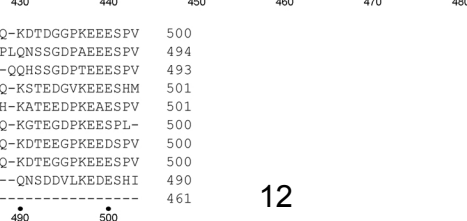
70 80 90 100 110 120

TM2

RED indicates positions which have a single, fully conserved residue.

Supplemental Figure 5. **FAM162A and COX20 share high degrees of homology throughout evolution.** (a) A multi-species alignment of FAM162A from selected vertebrates shows 65% peptide conservation throughout evolution. (b) Phylogenetic analysis of the FAM162 family of proteins displays clustering of mammalian taxa with conservation throughout multiple species. (c) mRNA transcript levels of FAM162A and FAM162B obtained from Human Proteome Map across various healthy human organ tissues in transcriptomic analyses. (d) A multi-species alignment of COX20 from vertebrates demonstrates 69% peptide conservation throughout evolution. TM indicates the transmembrane domains identified. All source data input and normalized output files were uploaded to figshare (<https://doi.org/10.6084/m9.figshare.11844972.v12>).

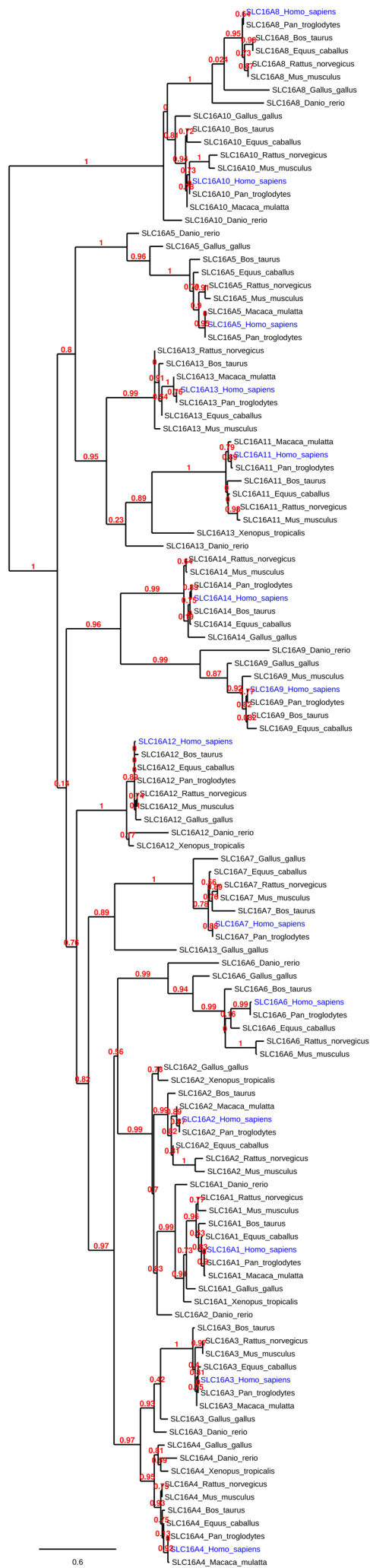
a

MCT1/SLC16AHuman	MPPAVGGPVGYTPPDGGGWAVVIGAFISIGFSYAFPKSITVFFKEIEIGIFHATTSEVSW	60
MCT1/SLC16ARat	MPPAIGGPVGYTPPDGGGWAVVVGAFISIGFSYAFPKSITVFFKEIEIIFSATTSEVSW	60
MCT1/SLC16AMouse	MPPAIGGPVGYTPPDGGGWAVLVGAFISIGFSYAFPKSITVFFKEIEIVFSATTSEVSW	60
MCT1/SLC16AChicken	MPPAIGGPVGYTPPDGGGWAVVVGAFISIGFSYAFPKSITVFFKEIEIVFNASSKVS	60
MCT1/SLC16ACow	MPPAVGGPVGYTPPDGGGWAVVIGAFISIGFSYAFPKSITVFFKEIEIGFNATTSEVSW	60
MCT1/SLC16AHorse	MPPAVGGPVGYTPPDGGGWAVVVGAFISIGFSYAFPKSITVFFKEIESIFNATTSEVSW	60
MCT1/SLC16AMonkey	MPPAVGGPVGYTPPDGGGWAVVIGAFISIGFSYAFPKSITVFFKEIESIFHATTSEVSW	60
MCT1/SLC16AChimpanzee	MPPAVGGPVGYTPPDGGGWAVVIGAFISIGFSYAFPKSITVFFKEIEIGIFHATTSEVSW	60
MCT1/SLC16AFrog	MPPAVGGPVGYTPPDGGGWVAVVAFVSIIGFSYAFPKSITVFFKDIEAIFGATSEVSW	60
MCT1/SLC16AZebrafish	MPPATGGPVGYTPPDGGGWAVVVGAFISIGFSYAFPKSITVFFKEIEIVFNATSSQVSW	60
		
MCT1/SLC16AHuman	ISSIMLAVMYGGPISSILVNKYGSRPVMIVGGCLSGCGLIAASFCNTVQQLYVCIGVIG	120
MCT1/SLC16ARat	ISSIMLAVMYAGGPISILVNKYGSRPVMIVGGCLSGCGLIAASFCNTVQQLYFCIGVIG	120
MCT1/SLC16AMouse	ISSIMLAVMYAGGPISILVNKYGSRPVMIVGGCLSGCGLIAASFCNTVQQLYLCIGVIG	120
MCT1/SLC16AChicken	ISSIMLAVMYAGGPISILVNKYGSRPIMIVGGCLSGCGLIAASFCNTVEELYFCVGVIG	120
MCT1/SLC16ACow	ISSIMLAVMYGGGPISILVNKYGSRPVMIVGGCLSGCGLIAASFCNTVQQLYFSVGVIG	120
MCT1/SLC16AHorse	ISSIMLAVMYGGGPISILVNKYGSRPIMIVGGCLSGCGLIAASFCNTVQQLYLCIGVIG	120
MCT1/SLC16AMonkey	ISSIMLAVMYGGGPISILVNKYGSRPVMIVGGCLSGCGLIAASFCNTVQQLYFCIGVIG	120
MCT1/SLC16AChimpanzee	ISSIMLAVMYGGGPISILVNKYGSRPVMIVGGCLSGCGLIAASFCNTVQQLYFCIGVIG	120
MCT1/SLC16AFrog	ISSIMLAVMYAGGPISILVNKYGSRPVMIVGGCLAGTGLIAASFCNTVQQLYLCIGVIG	120
MCT1/SLC16AZebrafish	ISSIMLAVMYAGGPISILVNKYGSRPIMIVGGCLSGTGLVAAASFCNTVEGLYFCVGVIG	120
		
MCT1/SLC16AHuman	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLCTAPLNQVFFGIFGWRGSFLI	180
MCT1/SLC16ARat	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLSTAPLNQAFFGIFGWRGSFLI	180
MCT1/SLC16AMouse	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLSTAPLNQAFFDIFDWRGSFLI	180
MCT1/SLC16AChicken	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLSTAPLNQVFFGIFGWRGSFLI	180
MCT1/SLC16ACow	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLSTAPLNQAFFMIYFWRGSFLI	180
MCT1/SLC16AHorse	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLSTAPLNQAFFGIFGWRGSFLI	180
MCT1/SLC16AMonkey	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLCTAPLNQVFFGIFGWRGSFLI	180
MCT1/SLC16AChimpanzee	GLGLAFNLNPAITMIGKYFYKRRPLANGLAMAGSPVFLCTAPLNQVFFGIFGWRGSFLI	180
MCT1/SLC16AFrog	GLGLAFNLNPAITMIGKYFYKRRPIANGLAMAGSPVFLSTAPLNQYFYSIFGWRGSFLI	180
MCT1/SLC16AZebrafish	GLGLAFNLNPAITMIGKYFYKRRPIANGLAMAGSPVFLSTAPLNSWLFQDQFWRGSFLI	180
		
MCT1/SLC16AHuman	LGGLLLNCCVAGALMRPIGPKPTKAGDKSKASLEKAGKSGVKKDLHDANTDLIGRHPKQ	240
MCT1/SLC16ARat	LGGLLLNCCVAGSLMRPIGPKQGGKVEKLSKESLQEAQK-----SDANTDLIGGSPKG	233
MCT1/SLC16AMouse	LGGLLLNCCVAGSLMRPIGPEQVKLEKLSKESLQEAQK-----SDANTDLIGGSPKG	233
MCT1/SLC16AChicken	LGGLLLNCCVAGSLMRPIGPKPDQLKKEPTKEVLQEAQK-VKKGDGDTSTDLIGGKTKK	239
MCT1/SLC16ACow	LGGLLLNCCVAGALMRPIGPKPTTAEKEKSKGSLQEAQKYETKKGASDANTDLIGGNPKR	240
MCT1/SLC16AHorse	LGGFLNCCVAGALMRPIGPKPTNAKERSKESLQEAQKPDQAGKAGDANTDLIGGYPKR	240
MCT1/SLC16AMonkey	LGGLLLNCCVAGALMRPIGPKPTKAGDKSKASLQKAGKSGVKKGRHDANTDLIGRHPKR	240
MCT1/SLC16AChimpanzee	LGGLLLNCCVAGALMRPIGPKPTKAGKNKSKASLEKAGKSGVKKDLHDANTDLIGRHPKQ	240
MCT1/SLC16AFrog	LGGLLFNCCVAGSLMRPIGPKPEDTKKVKTEVLEEAGKCV-SKEDGDAHKDLIEGKAK-	238
MCT1/SLC16AZebrafish	LGGALLNCCVAGSLMRPIGPKQPAIPKEDA-----EIKPKQ	216
		
MCT1/SLC16AHuman	EKRSVFQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFAPLVFLSSYQKSQHSSEKSAF	300
MCT1/SLC16ARat	EKLSVFQTVNKFLLDLTLFTHRGFLLYLGSNVIMFFGLFTPLVFLSNYKSKHFSSEKSAF	293
MCT1/SLC16AMouse	EKLSVFQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFTPLVFLSNYKSKDFSSEKSAF	293
MCT1/SLC16AChicken	EKSTLFQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFTPLVFLSNYAKSKKIANESAAF	299
MCT1/SLC16ACow	EKKSIFQTLNFTLTLFTHRGFLLYLGSNVIMFFGLFTPLVFLSNYKSKHYSSEKSAF	300
MCT1/SLC16AHorse	EKQSVFQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFTPLVFLSNYKSKHYSSEKSAF	300
MCT1/SLC16AMonkey	EKRSVFQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFAPLVFLSSYQKSQHSSEKSAF	300
MCT1/SLC16AChimpanzee	EKRSVFQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFAPLVFLSSYQKSQHSSEKSAF	300
MCT1/SLC16AFrog	TKPTLFQTIHQFLDLTLFTHRGFLLYLGSNHIMFFGLFAPLVFLSNYAKSKNISPESEAF	298
MCT1/SLC16AZebrafish	EKKTVMTQTIHQFLDLTLFTHRGFLLYLGSNVIMFFGLFAPLVFLSNYAKSKHISKDAAF	276
		
MCT1/SLC16AHuman	LLSILAFVDMVARPSMGLVANTKPIRPRIQYFFAASVAVGVCHLAPLSTTYVGFVCVIA	360
MCT1/SLC16ARat	LLSILAFVDMVARPSMGLAANTRWIRPRVQYFFAASVAVGVCHLAPLSTTYVGFVCVIA	353
MCT1/SLC16AMouse	LLSILAFVDMVARPSMGLAANTKWIIRPRIQYFFAASVAVGVCHLAPLSTTYVGFVCVIA	353
MCT1/SLC16AChicken	LLSILAFVDMVARPSMGLVANTKWIIRPRVQYFFAASVAVGVCHLAPMSTTYAGFCVIA	359
MCT1/SLC16ACow	LLSILAFVDMVARPSMGLVANTKWIIRPRVQYFFAASVAVGVCHLAPLSTTYIELCVIA	360
MCT1/SLC16AHorse	LLSILAFVDMVARPSMGLVANTKWIIRPRVQYFFAASVAVGVCHLAPLSSSYIGFCVIA	360
MCT1/SLC16AMonkey	LLSILAFVDMVARPSMGLVANTKPIRPRIQYFFAASVAVGVCHLAPLSTTYVGFVCVIA	360
MCT1/SLC16AChimpanzee	LLSILAFVDMVARPSMGLVANTKPIRPRIQYFFAASVAVGVCHLAPLSTTYVGFVCVIA	360
MCT1/SLC16AFrog	LLSILAFVDMVARPSMGLVANTKWIIRPRVQYFFAASVAVGVCHLAPLSTTYVGFVCVIA	358
MCT1/SLC16AZebrafish	LLSILAFVDMVARPSMGLVANTRWIRPRVQYFFAASVAVGVCHLAPLSTTYLGFVIA	336
		
MCT1/SLC16AHuman	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	420
MCT1/SLC16ARat	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	413
MCT1/SLC16AMouse	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	413
MCT1/SLC16AChicken	GFFGFAGWLSSVLFETLMDLVGAQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	419
MCT1/SLC16ACow	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	420
MCT1/SLC16AHorse	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	420
MCT1/SLC16AMonkey	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	420
MCT1/SLC16AChimpanzee	GFFGFAGWLSSVLFETLMDLVGPQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	420
MCT1/SLC16AFrog	GFFGFAGWLSSVLFETLMDLVGAQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYGDYK	418
MCT1/SLC16AZebrafish	VFFGFAGWLSSVLFETLMDLVGAQRFSSAVGLVTIVECCPVLLGPPLLGRLNDMYDYK	396
		
MCT1/SLC16AHuman	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKANE--QKESKEETSIDVAGKPNEVT	478
MCT1/SLC16ARat	YTYWACGVLIISGIYLFIMGINRYRLVAKEQKAEK-K-KRDGDETSIDVDEKPKKTM	471
MCT1/SLC16AMouse	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKAEK-KQKREGKEASTDVEKPKETM	472
MCT1/SLC16AChicken	YTYWACGVLIISGIYLFIMGINRYRLVAKEQKAEK-KQKREGKEASTDVEKPKETM	479
MCT1/SLC16ACow	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKAEK-KQKESKEETSIDVAGKPKEVI	479
MCT1/SLC16AHorse	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKAEK-KQKESKEETSIDVAGKPKEVI	479
MCT1/SLC16AMonkey	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKANE--QKESKEETSIDVAGKPNEVT	478
MCT1/SLC16AChimpanzee	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKANE--QKESKEETSIDVAGKPNEVT	478
MCT1/SLC16AFrog	YTYWACGVLIISGIYLFIMGINRYRLLAKEQKAEKQKAEANAGASENK-----VN	470
MCT1/SLC16AZebrafish	YTYWACGVLIISGIYLFIMGINRYRLVAKEQKAEKKEEKRKLEKDEETNLDALEKEKE	456
		
MCT1/SLC16AHuman	KAAESPDQ-KDTEGGPKKEESPV 500	
MCT1/SLC16ARat	KETQSPAPLQNSGDPAAEESPV 494	
MCT1/SLC16AMouse	KAAQSP--QHSDDGDPTEESPV 493	
MCT1/SLC16AChicken	NDVATLPQ-KSTEDGVKEEESHM 501	
MCT1/SLC16ACow	DAAESPEH-KATEEDPKAEESPV 501	
MCT1/SLC16AHorse	NAAGSPQ-KGTEGDPKEESPL- 500	
MCT1/SLC16AMonkey	KAAESPDQ-KDTEEGPKKEESPV 500	
MCT1/SLC16AChimpanzee	KAAESPDQ-KDTEGGPKKEESPV 500	
MCT1/SLC16AFrog	ELSVLP--QNSDDVLKEDESHI 490	
MCT1/SLC16AZebrafish	ADGVV----- 461	
		

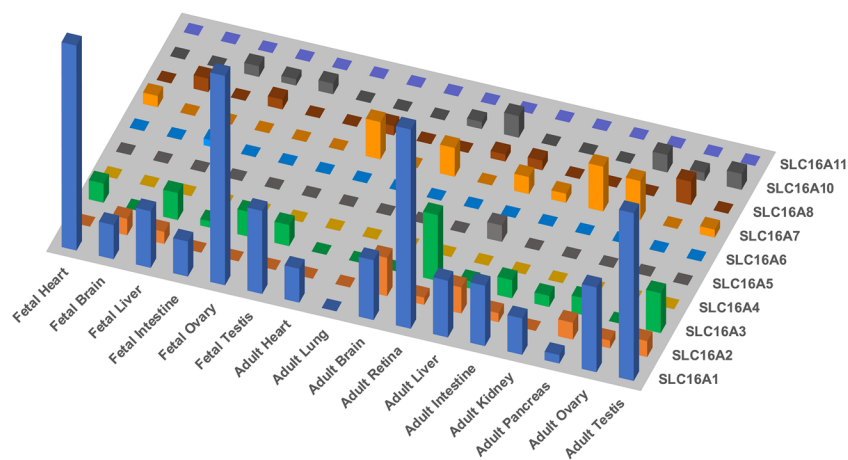
RED indicates positions which have a single, fully conserved residue.

Supplemental Figure 6. (a) A multi-species alignment of MCT1 from selected vertebrates demonstrates 78% peptide conservation throughout evolution. TM indicates the transmembrane domains identified.

a



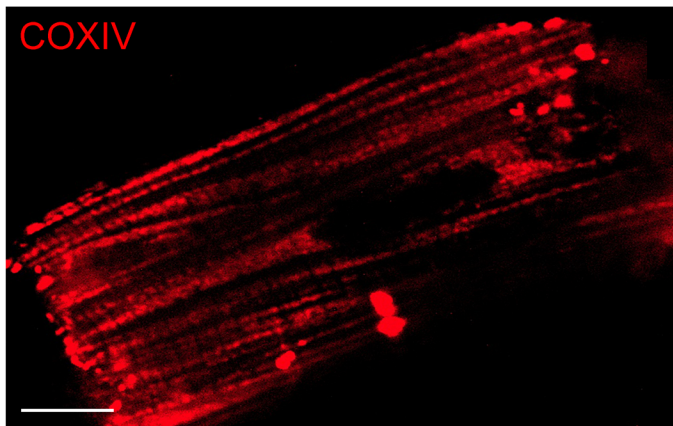
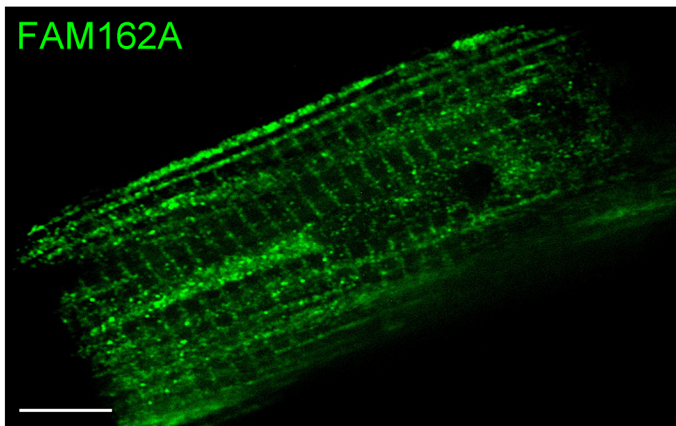
b



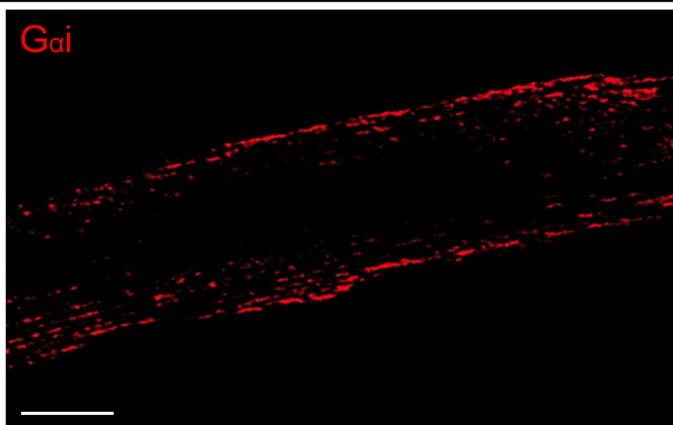
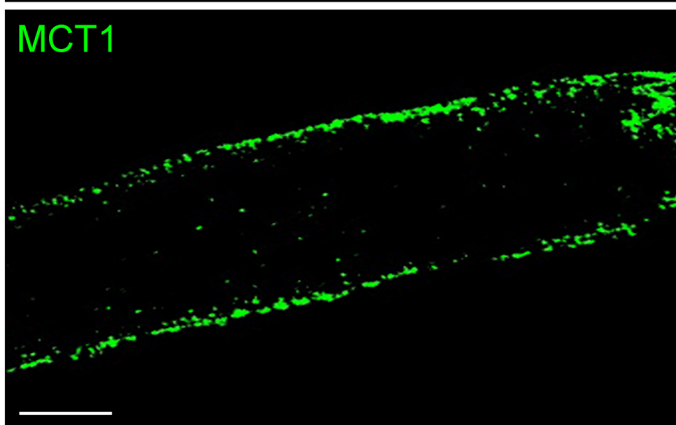
Supplemental Figure 7. **Transcriptomic and phylogenetic analyses of the SLC16A/MCT family of proteins.** (a) Phylogenetic analysis of the SLC16A/MCT family of proteins identifies phylogenetically distinct groups and shows evolutionary conservation within clustered mammalian taxa. (b) mRNA transcript levels of SLC16A/MCT family of proteins obtained from Human Proteome Map demonstrates dominant expression of SLC16A1/MCT1 across various healthy human organ tissues in transcriptomic analyses. All source data input and normalized output files were uploaded to figshare (<https://doi.org/10.6084/m9.figshare.11844972.v12>).

a

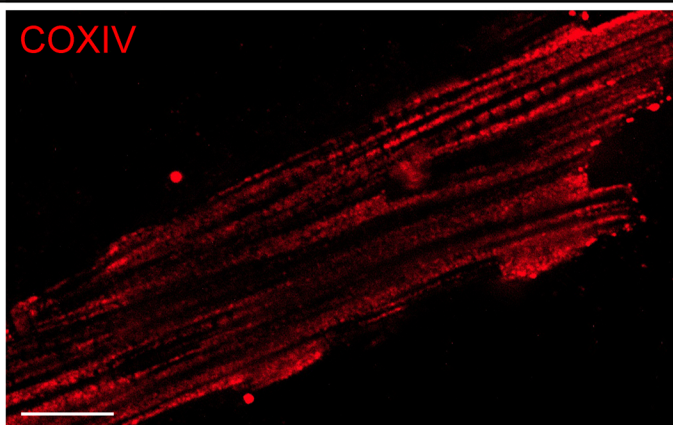
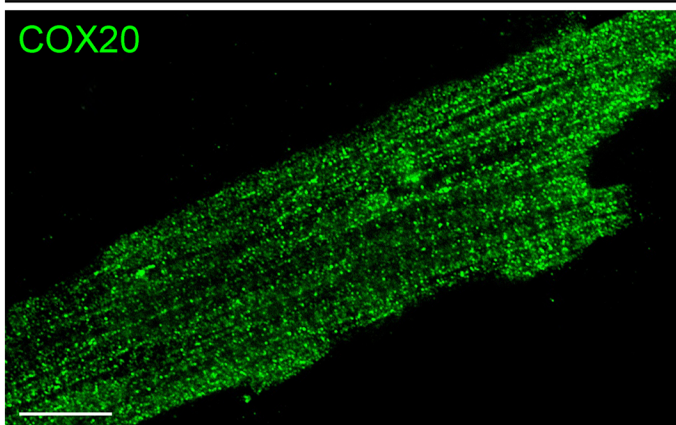
Isolated adult mouse ventricular cardiomyocytes

**b**

Isolated adult mouse ventricular cardiomyocytes

**c**

Isolated adult mouse ventricular cardiomyocytes



Supplemental Figure 8. Co-immunofluorescence analysis of FAM162A, MCT1, and COX20 with known mitochondrial marker, COXIV and known plasma membrane protein, Gai in isolated adult mouse cardiomyocytes. (a)

Immunofluorescence analysis of FAM162A (green) co-stained with mitochondrial protein, COXIV (red) in acutely isolated adult mouse cardiomyocytes. Scale, 10 μ m.

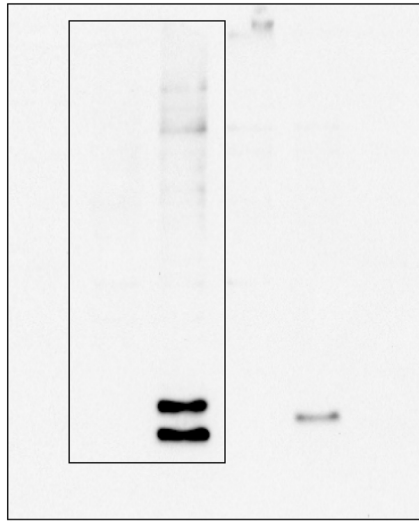
(b) Immunofluorescence analysis of MCT1 (green) co-stained with known plasma membrane protein, Gai (red) in acutely isolated adult mouse cardiomyocytes. Scale, 10 μ m.

(c) Immunofluorescence analysis of COX20 (green) co-stained with mitochondrial protein, COXIV (red) in acutely isolated adult mouse cardiomyocytes. Scale, 10 μ m.

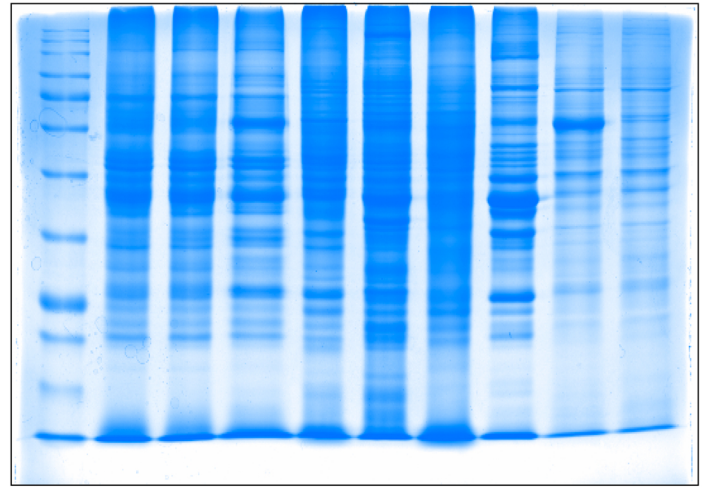
All images shown are representative of approximately 30-40 total images captured per condition, n=3 independent biological replicates. All original uncropped microscopy images were uploaded to figshare

(<https://doi.org/10.6084/m9.figshare.11844972.v12>).

Fig. 5a

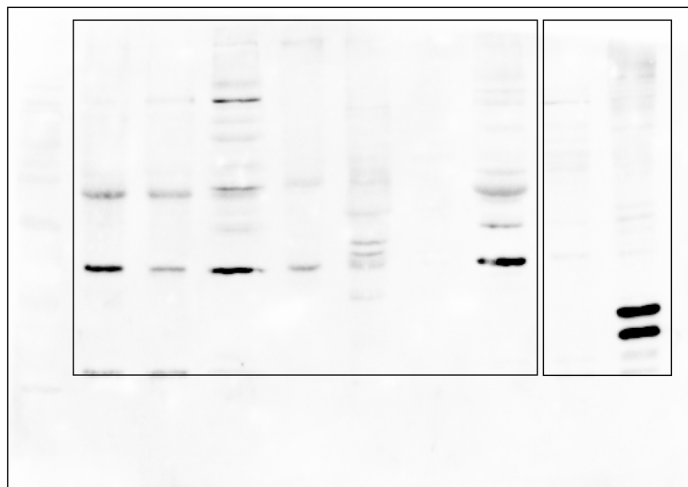


IB:DDK

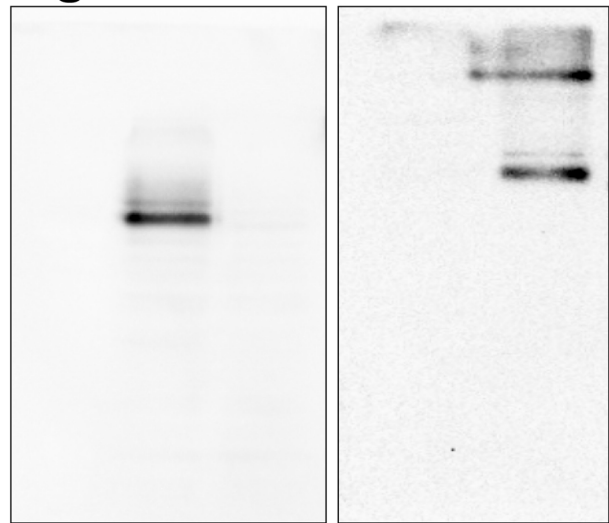


Coomassie Blue

Fig. 5b

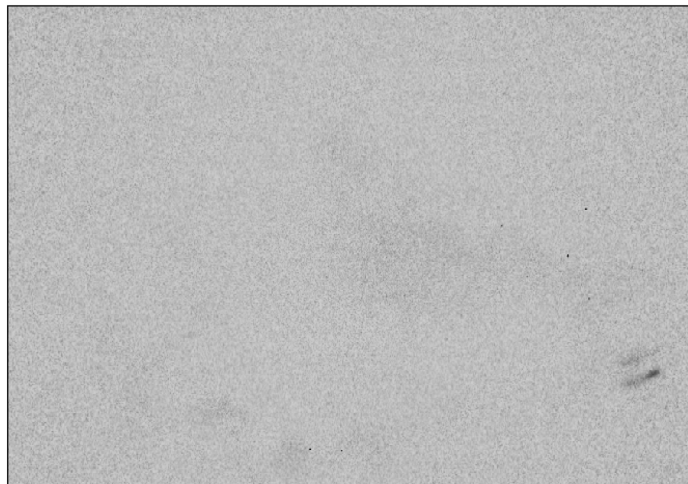


IB:FAM162A

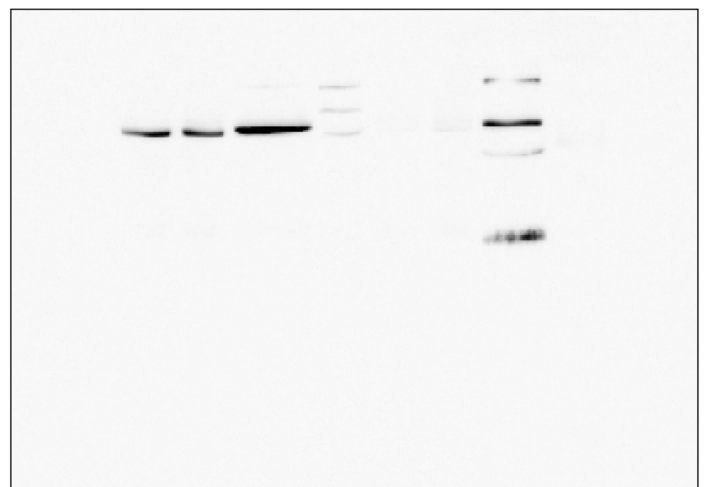


IB:DDK

IB:MCT1

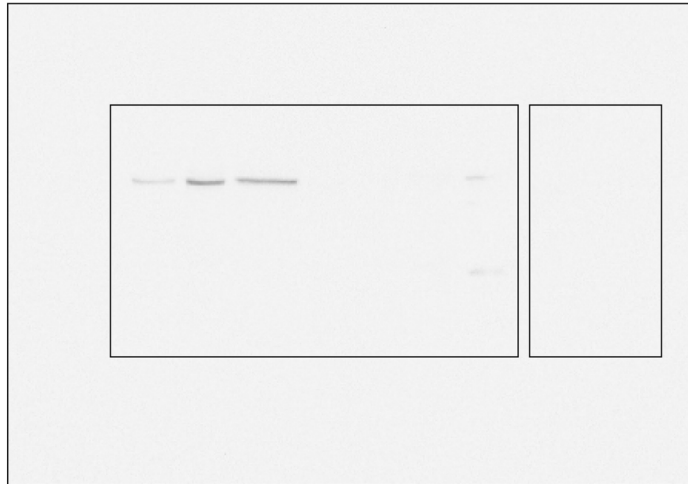


IB:FAM162 Immunodepletion

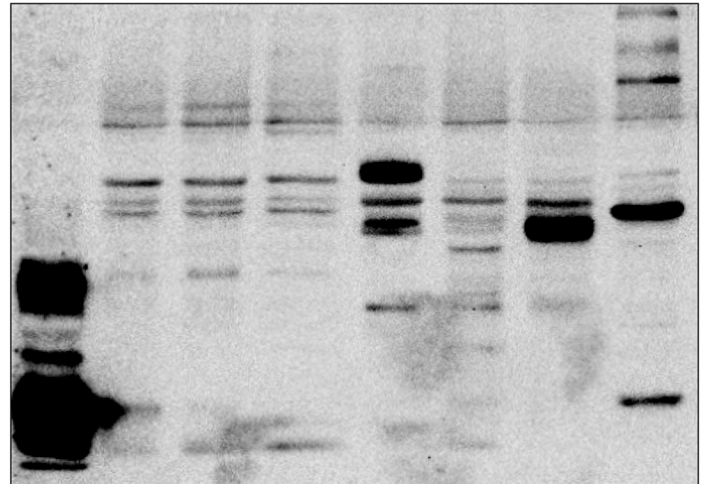


IB:MCT1

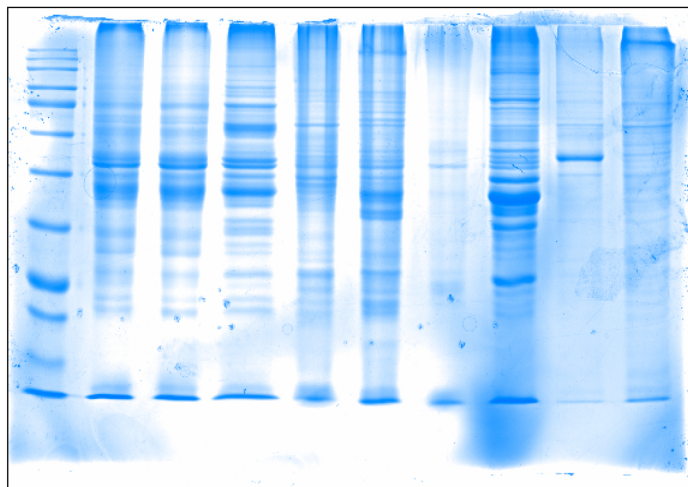
Fig. 5b cont.



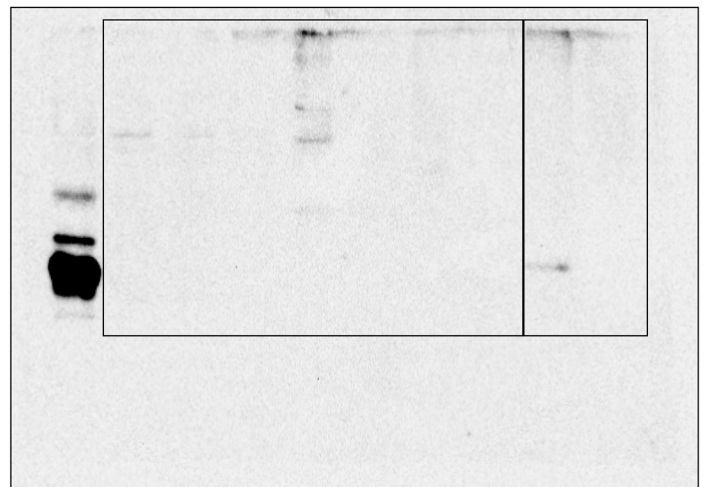
IB:MCT1 Immunodepletion



IB:COX20

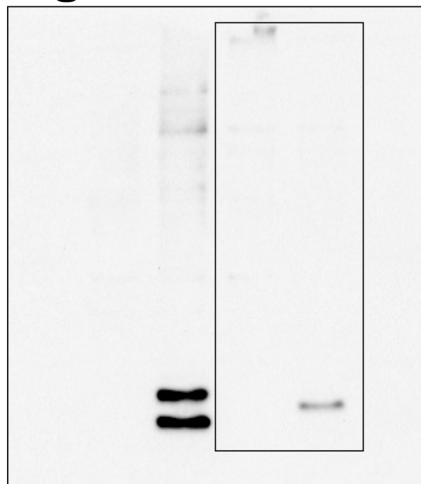


Coomassie Blue

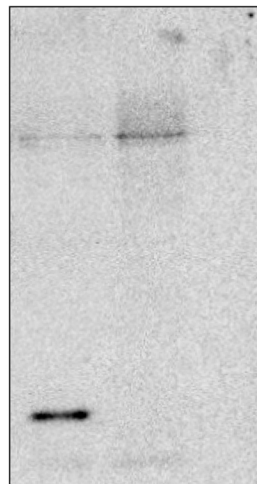


IB:COX20 Immunodepletion

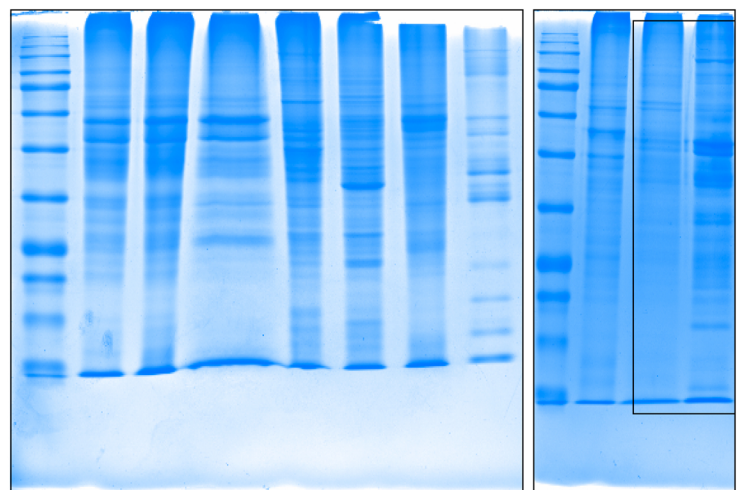
Fig. 5c



IB:DDK

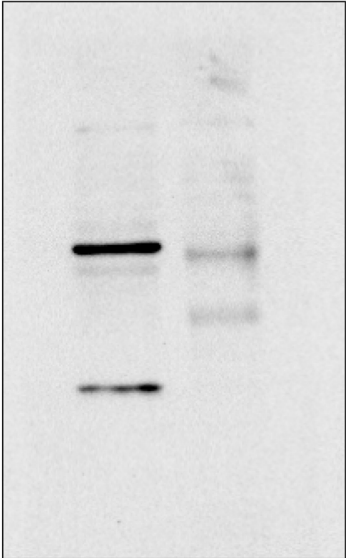


IB:COX20

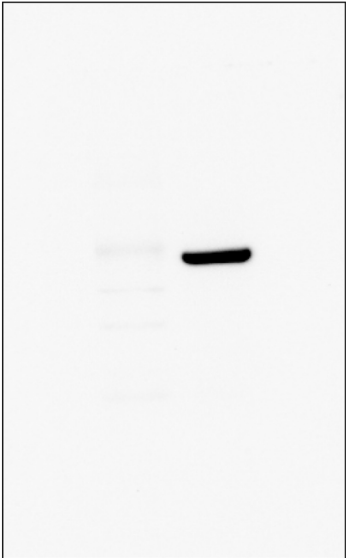


Coomassie Blue

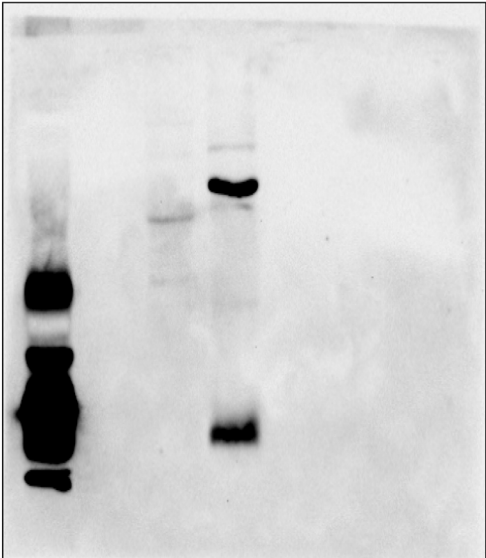
Fig. 5d



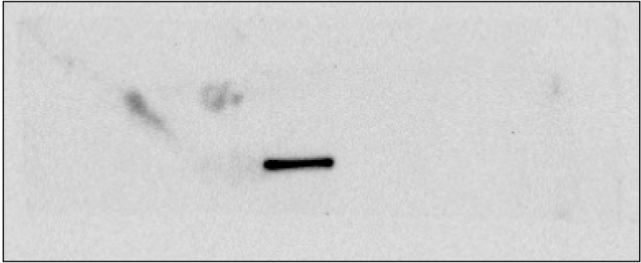
IB:FAM162A



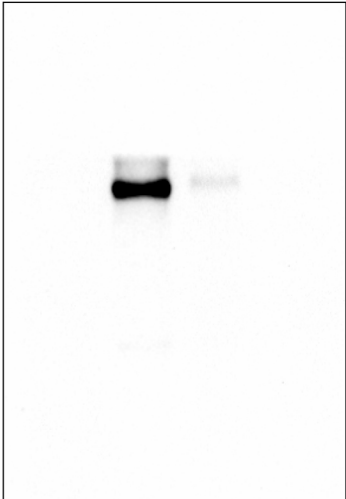
IB:MCT1



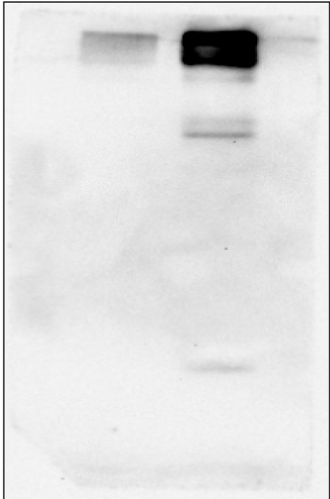
IB:COX20



IB:Calnexin



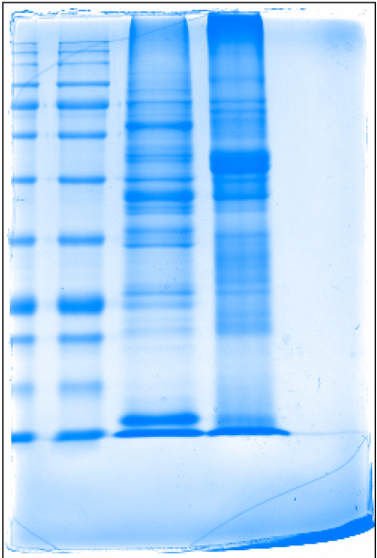
IB:α-Tubulin



IB:NCX1

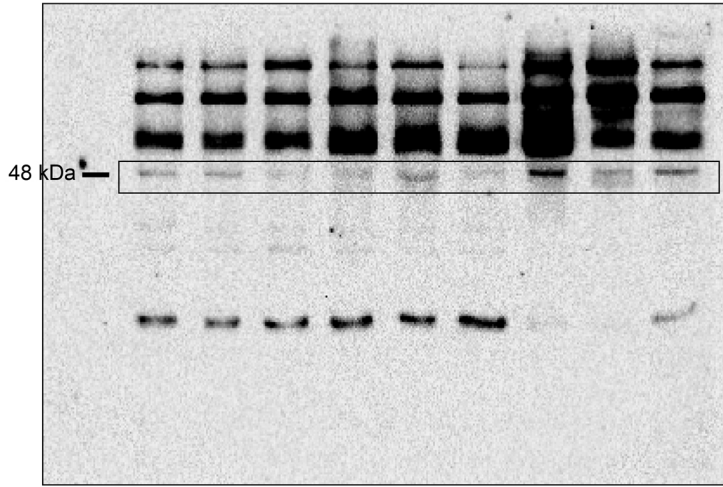


IB:COXIV

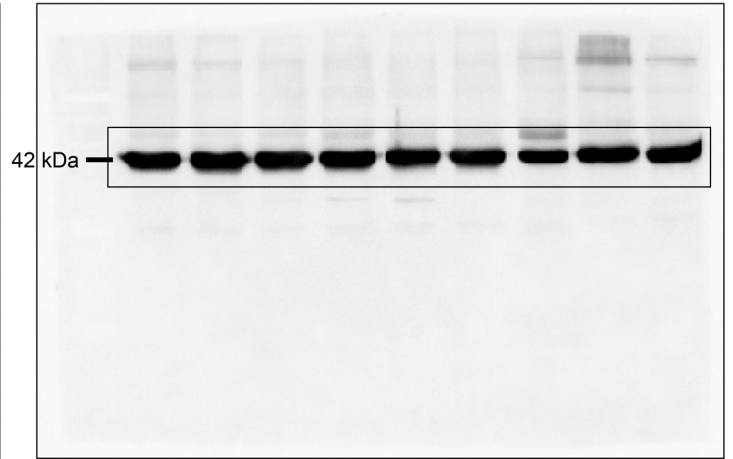


Coomassie Blue

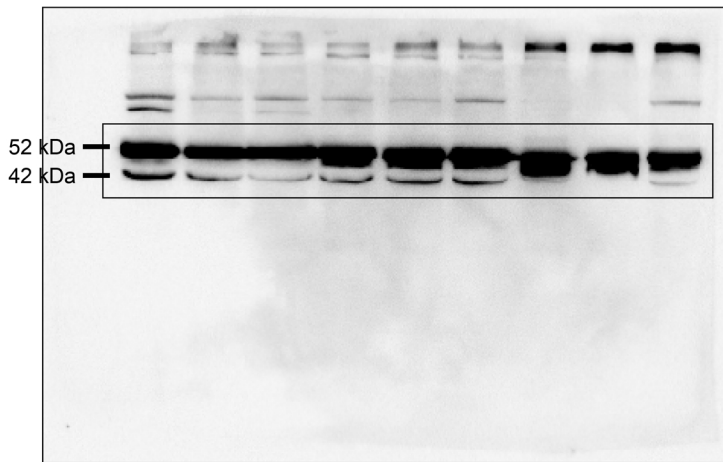
Fig. 10a



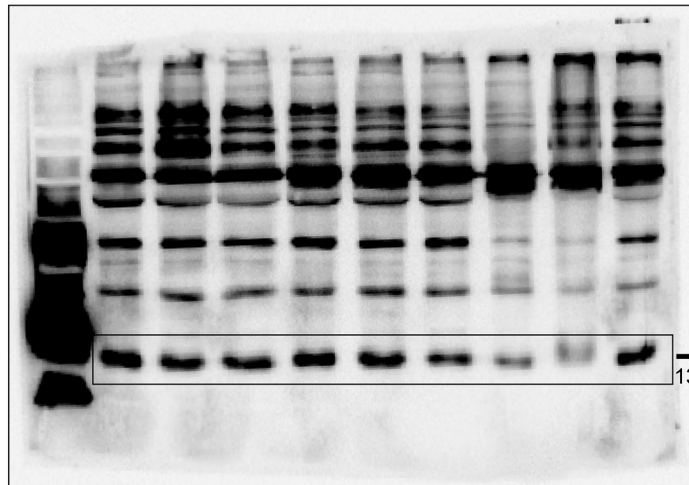
IB: FAM162A



IB: α -actin

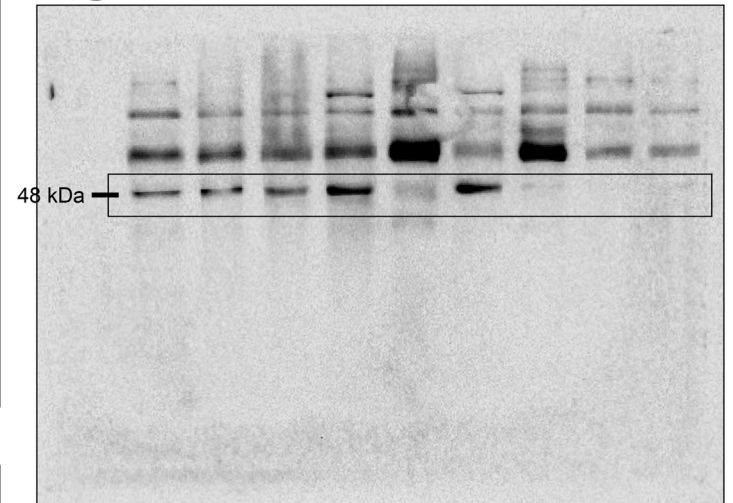


IB: MCT1

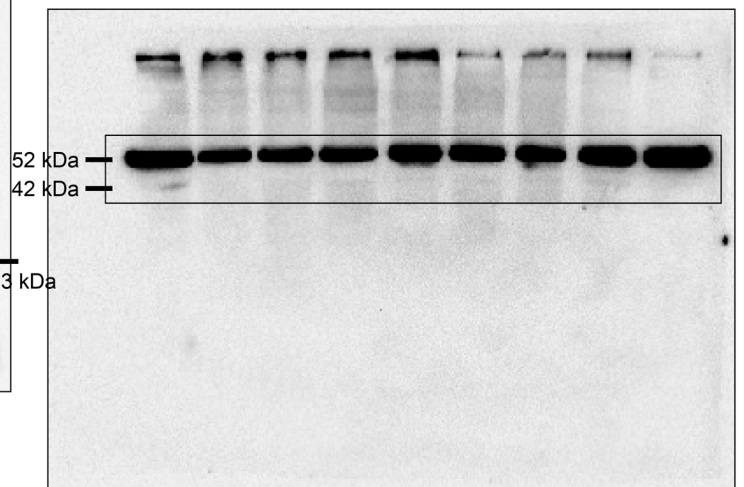


IB: COX20

Fig. 10b

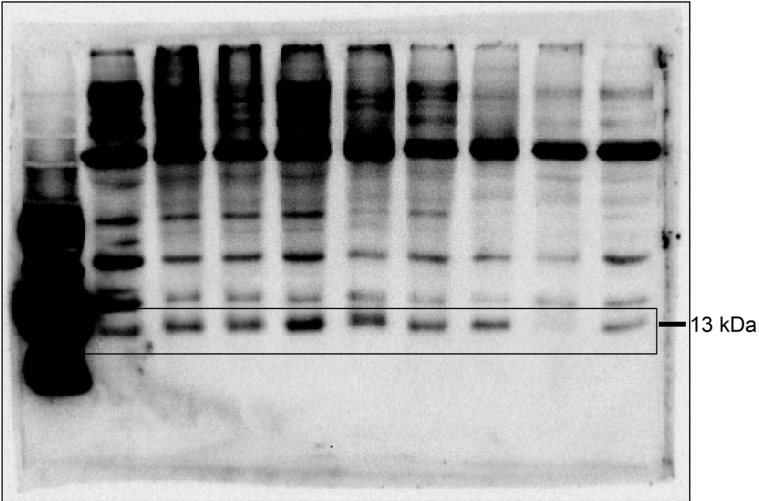


IB: FAM162A

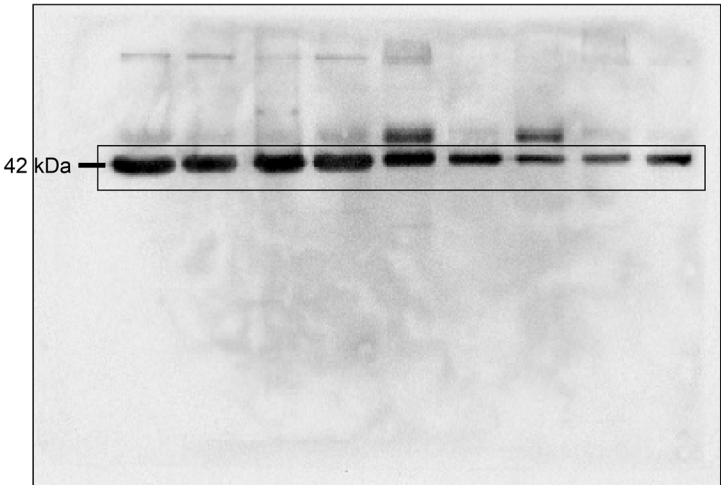


IB: MCT1

Fig. 10b cont.



IB: COX20



IB: α -actin

Supplemental Figure 9. Original uncropped immunoblots.