

*Supplementary information*  
*for*

**Multi-Omics of Familial Thoracic Aortic Aneurysm  
and Dissection: Calcium Transport Impairment  
Predisposes Aortas to Dissection**

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**Supplementary Table S1.** Relative expression of genes in *Myh11*<sup>ΔK/ΔK</sup> aortas, deletion of which predisposes mice to FTAAD. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Acta2</i>	1.03	1.22E-4	0.002
<i>Col3a1</i>	0.38	0.155	0.434
<i>Fbn1</i>	1.00	1.89E-5	0.001
<i>Lox</i>	1.21	2.23E-8	2.52E-6
<i>Mylk</i>	1.08	9.46E-5	0.002
<i>Prkg1</i>	1.16	3.21E-9	5.36E-7
<i>Smad3</i>	0.15	0.398	0.700
<i>Tgfb2</i>	-0.26	0.417	0.714
<i>Tgfbr1</i>	0.52	0.022	0.128
<i>Tgfbr2</i>	0.08	0.601	0.833
<i>Efemp2</i>	0.32	0.213	0.518
<i>Eln</i>	0.63	0.030	0.155
<i>Emilin1</i>	0.34	0.127	0.389
<i>Flna</i>	0.65	0.012	0.084
<i>Mfap5</i>	-0.29	0.201	0.501

**Supplementary Table S2.** Relative expression of genes involved in the tricarboxylic acid cycle in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Aco1</i>	-0.34	0.309	0.623
<i>Aco2</i>	-0.63	0.101	0.338
<i>Cs</i>	-0.51	0.121	0.377
<i>Dld</i>	-0.20	0.517	0.784
<i>Dlst</i>	-0.48	0.147	0.423
<i>Fh1</i>	-0.37	0.236	0.545
<i>Idh1</i>	-0.60	0.025	0.140
<i>Idh2</i>	-0.67	0.006	0.052
<i>Idh3a</i>	-0.48	0.145	0.420
<i>Idh3b</i>	-0.41	0.179	0.471
<i>Idh3g</i>	-0.37	0.221	0.526
<i>Mdh1</i>	-0.28	0.142	0.413
<i>Mdh1b</i>	-1.56	0.593	NA
<i>Mdh2</i>	-0.30	0.246	0.559
<i>Ogdh</i>	-0.46	0.157	0.437
<i>Sdha</i>	-0.39	0.221	0.526
<i>Sdhaf1</i>	-0.57	0.017	0.105

<i>Sdhaf2</i>	0.08	0.595	0.830
<i>Sdhaf3</i>	-0.25	0.224	0.530
<i>Sdhaf4</i>	-0.21	0.228	0.536
<i>Sdhb</i>	-0.58	0.048	0.213
<i>Sdhc</i>	-0.13	0.561	0.813
<i>Sdhd</i>	-0.47	0.087	0.310
<i>Sucla2</i>	-0.41	0.190	0.486
<i>Suclg1</i>	-0.44	0.148	0.424
<i>Suclg2</i>	0.08	0.708	0.887

**Supplementary Table S3.** Relative expression of inflammatory cytokine genes in *Myh11*<sup>ΔK/ΔK</sup> aortas previously shown to increase in FTAAD.<sup>1,2</sup> log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild-type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Ccl3</i>	0.16	0.909	NA
<i>Ccl4</i>	0.18	0.903	NA
<i>Igf1</i>	-0.52	0.010	0.075
<i>Mmp2</i>	0.05	0.826	0.937
<i>Mmp9</i>	0.30	0.346	0.657

**Supplementary Table S4.** Relative expression of spectrin genes in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild-type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Spta1</i>	1.12	0.470	NA
<i>Sptan1</i>	0.02	0.885	0.961
<i>Sptb</i>	-1.60	0.007	0.058
<i>Sptbn1</i>	-0.20	0.079	0.291
<i>Sptbn2</i>	-7.00	0.000	0.000
<i>Sptbn4</i>	-4.27	0.000	0.003
<i>Sptbn5</i>	0.01	0.989	0.995

**Supplementary Table S5.** Relative expression of calcium channel genes in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild-type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Cacna1a</i>	-0.96	0.007	0.055
<i>Cacna1b</i>	-10.28	2.60E-7	1.72E-5

<i>Cacna1c</i>	0.52	0.034	0.169
<i>Cacna1d</i>	0.56	0.095	0.325
<i>Cacna1e</i>	-5.56	3.02E-6	1.21E-4
<i>Cacna1f</i>	3.28	0.324	NA
<i>Cacna1g</i>	0.35	0.368	0.677
<i>Cacna1h</i>	-1.20	0.007	0.054
<i>Cacna1i</i>	-0.13	0.929	NA
<i>Cacna1s</i>	-0.09	0.976	NA
<i>Cacna2d1</i>	-0.07	0.740	0.902
<i>Cacna2d2</i>	-4.40	2.35E-6	1.00E-4
<i>Cacna2d3</i>	-2.25	1.92E-7	1.37E-5
<i>Cacna2d4</i>	1.14	0.108	0.353
<i>Cacnb1</i>	-1.50	0.008	0.060
<i>Cacnb2</i>	1.44	7.53E-9	1.03E-6
<i>Cacnb3</i>	-0.58	0.086	0.307
<i>Cacnb4</i>	-2.02	1.13E-4	0.002
<i>Cacng1</i>	-1.11	0.721	NA
<i>Cacng2</i>	-8.93	0.022	0.128
<i>Cacng3</i>	-6.50	0.002	0.019
<i>Cacng4</i>	-1.42	0.060	0.247
<i>Cacng5</i>	-6.07	2.93E-7	1.91E-5
<i>Cacng6</i>	NA	NA	NA
<i>Cacng7</i>	0.06	0.798	0.928
<i>Cacng8</i>	-2.93	0.170	0.458
<i>Hcn1</i>	-2.54	0.017	0.105
<i>Hcn2</i>	-2.50	0.000	0.001
<i>Hcn3</i>	-5.91	0.000	0.006
<i>Hcn4</i>	-3.32	0.001	0.014
<i>Trpa1</i>	NA	NA	NA
<i>Trpc1</i>	0.12	0.515	0.783
<i>Trpc2</i>	NA	NA	NA
<i>Trpc3</i>	-0.09	0.871	0.956
<i>Trpc4</i>	-1.03	0.393	0.697
<i>Trpc4ap</i>	-0.07	0.621	0.841
<i>Trpc5</i>	-1.94	0.486	NA
<i>Trpc5os</i>	NA	NA	NA
<i>Trpc6</i>	-2.11	0.029	0.153
<i>Trpc7</i>	-6.91	0.077	0.288
<i>Trpd52l3</i>	NA	NA	NA
<i>Trpm1</i>	0.06	0.976	NA
<i>Trpm2</i>	-3.35	8.57E-5	0.002
<i>Trpm3</i>	-0.57	0.067	0.263
<i>Trpm4</i>	0.16	0.495	0.768
<i>Trpm5</i>	1.30	0.448	NA
<i>Trpm6</i>	-0.21	0.798	0.927

<i>Trpm7</i>	0.24	0.128	0.391
<i>Trpm8</i>	-0.29	0.920	NA
<i>Trps1</i>	0.10	0.547	0.803
<i>Trpt1</i>	-0.29	0.150	0.428
<i>Trpv1</i>	-0.63	0.276	0.588
<i>Trpv2</i>	-0.35	0.152	0.430
<i>Trpv3</i>	-1.62	0.253	0.566
<i>Trpv4</i>	0.69	0.003	0.030
<i>Trpv5</i>	-1.11	0.785	NA
<i>Trpv6</i>	-1.11	0.785	NA

**Supplementary Table S6.** Relative expression of genes related to Ca<sup>2+</sup> release from sarcoplasmic reticulum in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Atp2a1</i>	1.63	0.236	0.546
<i>Atp2a2</i>	0.52	0.002	0.023
<i>Atp2a3</i>	0.19	0.452	0.741
<i>Atp2b1</i>	0.15	0.315	0.630
<i>Atp2b2</i>	-1.54	1.31E-7	1.02E-5
<i>Atp2b3</i>	-7.10	0.001	0.007
<i>Atp2b4</i>	-0.09	0.575	0.820
<i>Orai1</i>	0.21	0.255	0.568
<i>Orai2</i>	-0.59	0.139	0.409
<i>Orai3</i>	0.36	0.046	0.206
<i>Stim1</i>	0.08	0.583	0.824
<i>Stim2</i>	0.05	0.743	0.903
<i>Itpr1</i>	0.62	0.006	0.051
<i>Itpr2</i>	-0.60	0.081	0.296
<i>Itpr3</i>	-0.10	0.575	0.820

**Supplementary Table S7.** Relative expression of ADP-ribose polymerase genes in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Parp1</i>	-0.11	0.445	0.737
<i>Parp2</i>	0.18	0.330	0.643
<i>Parp3</i>	0.10	0.564	0.814
<i>Parp4</i>	-0.36	0.043	0.200
<i>Parp6</i>	-0.57	0.005	0.042

<i>Parp8</i>	0.32	0.129	0.391
<i>Parp9</i>	-0.14	0.360	0.671
<i>Parp10</i>	-0.50	0.031	0.160
<i>Parp11</i>	-0.50	0.157	0.437
<i>Parp12</i>	-0.12	0.452	0.741
<i>Parp14</i>	-0.27	0.152	0.431
<i>Parp16</i>	-1.04	0.001	0.007
<i>Tiparp</i>	-0.51	0.036	0.177
<i>Sirt1</i>	0.22	0.187	0.482
<i>Sirt2</i>	-0.09	0.383	0.688
<i>Sirt3</i>	-0.30	0.135	0.402
<i>Sirt4</i>	0.16	0.617	0.840
<i>Sirt5</i>	-0.26	0.268	0.581
<i>Sirt6</i>	-0.06	0.798	0.927
<i>Sirt7</i>	-0.11	0.488	0.764
<i>CD38</i>	-0.48	0.138	0.407
<i>Sarm1</i>	-4.13	9.66E-8	8.13E-6
<i>Nmnat1</i>	-0.13	0.600	0.833
<i>Nmnat2</i>	-3.44	0.000	0.007
<i>Nmnat3</i>	-0.82	0.026	0.141
<i>Nampt</i>	-0.23	0.323	0.637

**Supplementary Table S8.** Relative expression of genes that convert NAD<sup>+</sup> to NADH in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Dlat</i>	-0.16	0.593	0.829
<i>Dld</i>	-0.20	0.517	0.784
<i>Dlst</i>	-0.48	0.147	0.423
<i>Gapdh</i>	0.30	0.577	0.821
<i>Idh2</i>	-0.67	0.006	0.052
<i>Mdh1</i>	-0.28	0.142	0.413
<i>Mdh1b</i>	-1.56	0.593	NA
<i>Mdh2</i>	-0.30	0.246	0.559
<i>Ogdh</i>	-0.46	0.157	0.437
<i>Pdha1</i>	-0.03	0.915	0.971
<i>Pdha2</i>	NA	NA	NA
<i>Pdhb</i>	0.24	0.427	0.724

**Supplementary Table S9.** Relative expression of genes involved in the electron transport chain in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Bcs1l</i>	−0.25	0.319	0.633
<i>Coa3</i>	−0.04	0.832	0.940
<i>Coa4</i>	−0.45	0.249	0.562
<i>Coa5</i>	−0.25	0.337	0.649
<i>Coa6</i>	0.09	0.645	0.854
<i>Coa7</i>	−0.31	0.267	0.580
<i>Cox10</i>	−0.61	0.034	0.171
<i>Cox11</i>	0.09	0.641	0.852
<i>Cox14</i>	−0.31	0.059	0.245
<i>Cox15</i>	−0.22	0.281	0.594
<i>Cox16</i>	0.10	0.770	0.917
<i>Cox17</i>	−0.26	0.265	0.577
<i>Cox18</i>	−0.21	0.356	0.667
<i>Cox19</i>	0.19	0.348	0.659
<i>Cox20</i>	0.08	0.547	0.803
<i>Cox4i1</i>	−0.43	0.060	0.246
<i>Cox4i2</i>	0.27	0.398	0.700
<i>Cox5a</i>	−0.54	0.074	0.280
<i>Cox5b</i>	−0.29	0.275	0.588
<i>Cox6a1</i>	−0.24	0.299	0.613
<i>Cox6a2</i>	2.07	0.091	0.318
<i>Cox6b1</i>	−0.46	0.076	0.285
<i>Cox6b2</i>	−0.24	0.549	0.804
<i>Cox6c</i>	−0.08	0.677	0.872
<i>Cox7a1</i>	−0.74	0.053	0.227
<i>Cox7a2</i>	−0.16	0.342	0.653
<i>Cox7a2l</i>	0.00	0.978	0.992
<i>Cox7b</i>	−0.16	0.483	0.761
<i>Cox7b2</i>	−1.11	0.785	NA
<i>Cox7c</i>	0.14	0.794	0.926
<i>Cox8a</i>	−0.26	0.256	0.569
<i>Cox8b</i>	−0.63	0.095	0.327
<i>Cox8c</i>	NA	NA	NA
<i>Cyc1</i>	−0.47	0.114	0.364
<i>mt-Co1</i>	−0.38	0.073	0.279
<i>mt-Co2</i>	NA	NA	NA
<i>mt-Co3</i>	−0.15	0.970	NA
<i>mt-Cytb</i>	−0.31	0.146	0.420
<i>Ndufa1</i>	−0.16	0.434	0.729
<i>Ndufa10</i>	−0.44	0.166	0.451
<i>Ndufa11</i>	−0.02	0.895	0.965
<i>Ndufa12</i>	−0.21	0.284	0.597
<i>Ndufa13</i>	−0.03	0.864	0.954
<i>Ndufa2</i>	0.11	0.379	0.684

<i>Ndufa3</i>	−0.24	0.263	0.576
<i>Ndufa4</i>	−0.17	0.406	0.706
<i>Ndufa4l2</i>	0.06	0.821	0.935
<i>Ndufa5</i>	−0.19	0.304	0.619
<i>Ndufa6</i>	−0.04	0.785	0.923
<i>Ndufa7</i>	−0.19	0.256	0.569
<i>Ndufa8</i>	−0.36	0.102	0.342
<i>Ndufa9</i>	−0.42	0.116	0.368
<i>Ndufab1</i>	−0.11	0.751	0.907
<i>Ndufab1-ps</i>	−1.11	0.785	NA
<i>Ndufaf1</i>	−0.42	0.060	0.246
<i>Ndufaf2</i>	0.08	0.695	0.881
<i>Ndufaf3</i>	−0.04	0.820	0.935
<i>Ndufaf4</i>	−0.08	0.631	0.847
<i>Ndufaf5</i>	−0.20	0.257	0.569
<i>Ndufaf6</i>	−0.26	0.355	0.666
<i>Ndufaf7</i>	−0.14	0.351	0.662
<i>Ndufaf8</i>	0.09	0.598	0.832
<i>Ndufb10</i>	−0.38	0.065	0.258
<i>Ndufb11</i>	−0.18	0.359	0.670
<i>Ndufb2</i>	0.04	0.798	0.927
<i>Ndufb3</i>	−0.03	0.869	0.955
<i>Ndufb4</i>	−0.28	0.204	0.505
<i>Ndufb5</i>	−0.25	0.250	0.563
<i>Ndufb6</i>	−0.25	0.319	0.633
<i>Ndufb7</i>	−0.20	0.218	0.523
<i>Ndufb8</i>	−0.22	0.371	0.679
<i>Ndufb9</i>	−0.32	0.178	0.469
<i>Ndufc1</i>	−0.22	0.271	0.583
<i>Ndufc2</i>	−0.30	0.143	0.415
<i>Ndufs1</i>	−0.29	0.324	0.637
<i>Ndufs2</i>	−0.25	0.385	0.690
<i>Ndufs3</i>	−0.35	0.192	0.489
<i>Ndufs4</i>	−0.09	0.660	0.864
<i>Ndufs5</i>	−0.03	0.917	0.971
<i>Ndufs6</i>	−0.21	0.305	0.619
<i>Ndufs7</i>	−0.51	0.036	0.175
<i>Ndufs8</i>	−0.35	0.154	0.433
<i>Ndufv1</i>	−0.47	0.144	0.419
<i>Ndufv2</i>	−0.29	0.200	0.500
<i>Ndufv3</i>	−0.28	0.160	0.443
<i>Sco1</i>	0.01	0.951	0.983
<i>Sco2</i>	−0.44	0.195	0.492
<i>Sdha</i>	−0.39	0.221	0.526
<i>Sdhaf1</i>	−0.57	0.017	0.105



<i>Sdhaf2</i>	0.08	0.595	0.830
<i>Sdhaf3</i>	-0.25	0.224	0.530
<i>Sdhaf4</i>	-0.21	0.228	0.536
<i>Sdhb</i>	-0.58	0.048	0.213
<i>Sdhc</i>	-0.13	0.561	0.813
<i>Sdhd</i>	-0.47	0.087	0.310
<i>Surf1</i>	-0.09	0.487	0.763
<i>Uqcc1</i>	-0.61	0.012	0.086
<i>Uqcc2</i>	0.03	0.842	0.944
<i>Uqcc3</i>	-0.31	0.109	0.354
<i>Uqcr10</i>	-0.16	0.454	0.742
<i>Uqcr11</i>	-0.26	0.269	0.582
<i>Uqcrb</i>	-0.01	0.956	0.985
<i>Uqcrc1</i>	-0.45	0.136	0.403
<i>Uqcrc2</i>	-0.26	0.365	0.674
<i>Uqcrfs1</i>	-0.33	0.279	0.592
<i>Uqcrh</i>	0.01	0.970	0.989
<i>Uqcrq</i>	-0.18	0.452	0.741

**Supplementary Table S10.** Relative expression of inwardly rectifying potassium channel genes in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Kcnj1</i>	NA	NA	NA
<i>Kcnj2</i>	-0.75	0.169	0.456
<i>Kcnj3</i>	-3.70	0.002	0.018
<i>Kcnj4</i>	0.06	0.959	0.986
<i>Kcnj5</i>	4.29	0.033	NA
<i>Kcnj6</i>	NA	NA	NA
<i>Kcnj8</i>	0.79	0.004	0.035
<i>Kcnj9</i>	-5.03	0.002	0.019
<i>Kcnj10</i>	-4.61	9.20E-07	4.80E-05
<i>Kcnj11</i>	-0.44	0.196	0.493
<i>Kcnj12</i>	-2.05	0.000	0.004
<i>Kcnj13</i>	-6.39	0.000	0.005
<i>Kcnj14</i>	2.15	0.426	NA
<i>Kcnj15</i>	0.32	0.268	0.580
<i>Kcnj16</i>	-6.59	0.091	0.318
<i>Kcna10</i>	NA	NA	NA

**Supplementary Table S11.** Relative expression of voltage-gated potassium channel genes in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in

wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

<b>Gene</b>	<b>log<sub>2</sub> fold change</b>	<b>p-value</b>	<b>adjusted p-value</b>
<i>Kcna1</i>	-2.03	2.98E-4	0.005
<i>Kcna2</i>	-2.00	1.05E-4	0.002
<i>Kcna3</i>	-1.29	0.275	0.588
<i>Kcna4</i>	-6.01	8.92E-4	0.011
<i>Kcna5</i>	-0.34	0.354	0.666
<i>Kcna6</i>	-3.52	9.70E-9	1.28E-6
<i>Kcna7</i>	0.78	0.801	NA
<i>Kcna10</i>	NA	NA	NA
<i>Kcnab1</i>	0.91	6.21E-4	0.008
<i>Kcnab2</i>	-3.03	7.90E-06	2.58E-4
<i>Kcnab3</i>	-0.28	0.619	0.840
<i>Kcnb1</i>	0.30	0.191	0.487
<i>Kcnb2</i>	-7.00	6.11E-5	0.001
<i>Kcnc1</i>	-5.04	0.003	0.029
<i>Kcnc2</i>	-0.32	0.642	0.853
<i>Kcnc3</i>	-1.55	0.055	0.232
<i>Kcnc4</i>	-0.58	0.215	0.520
<i>Kcnd1</i>	-1.36	0.008	0.063
<i>Kcnd2</i>	-2.11	0.001	0.016
<i>Kcnd3</i>	0.49	0.072	0.276
<i>Kcne1</i>	NA	NA	NA
<i>Kcne1l</i>	-2.10	0.057	0.237
<i>Kcne2</i>	NA	NA	NA
<i>Kcne3</i>	-0.11	0.847	0.946
<i>Kcne4</i>	0.74	0.012	0.081
<i>Kcnf1</i>	0.91	0.458	0.745
<i>Kcng1</i>	-0.55	0.765	NA
<i>Kcng2</i>	0.15	0.896	0.965
<i>Kcng3</i>	-0.15	0.970	NA
<i>Kcng4</i>	0.40	0.544	0.802
<i>Kcnh1</i>	-3.74	9.91E-8	8.24E-6
<i>Kcnh2</i>	0.11	0.662	0.865
<i>Kcnh3</i>	0.31	0.804	0.930
<i>Kcnh4</i>	0.43	0.677	0.872
<i>Kcnh5</i>	-1.92	0.635	NA
<i>Kcnh6</i>	-7.06	0.016	0.103
<i>Kcnh7</i>	-7.17	4.66E-6	1.69E-4
<i>Kcnh8</i>	-4.92	6.65E-4	0.009
<i>Kcnip1</i>	-0.13	0.959	NA
<i>Kcnip2</i>	-2.66	0.036	0.175
<i>Kcnip3</i>	-1.07	2.42E-4	0.004

<i>Kcnip4</i>	-0.82	0.08	0.31
<i>Kcns1</i>	NA	NA	NA
<i>Kcns2</i>	-6.73	0.085	0.305
<i>Kcns3</i>	-0.57	NA	NA
<i>Kcnv1</i>	-1.11	0.085	0.306
<i>Kcnv2</i>	1.73	0.009	0.067

**Supplementary Table S12.** Relative expression of voltage-gated large and small conductance calcium-activated potassium channel genes in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Kcnma1</i>	0.13	0.587	0.826
<i>Kcnmb1</i>	0.82	0.001	0.009
<i>Kcnmb2</i>	NA	NA	NA
<i>Kcnmb3</i>	NA	NA	NA
<i>Kcnmb4</i>	-8.28	2.53E-9	4.55E-7
<i>Kcnn1</i>	-0.61	0.021	0.122
<i>Kcnn2</i>	-4.76	1.24E-5	3.75E-4
<i>Kcnn3</i>	-0.74	0.035	0.172
<i>Kcnn4</i>	0.03	0.934	0.976
<i>Kcnt1</i>	-5.64	3.48E-6	1.36E-4
<i>Kcnt2</i>	0.18	0.487	0.764
<i>Kcnu1</i>	-3.72	0.009	0.068

**Supplementary Table S13.** Relative expression of genes involved in protease kinase G (PKG) pathway in *Myh11*<sup>ΔK/ΔK</sup> aortas. log<sub>2</sub> fold change = log<sub>2</sub> of relative expression normalized by expression in wild type aortas. Adjusted p-value = p-values adjusted for multiple testing, determined by the Benjamini and Hochberg method.

Gene	log <sub>2</sub> fold change	p-value	adjusted p-value
<i>Gucyl1a2</i>	0.05	0.859	0.952
<i>Gucyl1a3</i>	-0.06	0.763	0.912
<i>Gucyl1b2</i>	-1.11	0.785	NA
<i>Gucyl1b3</i>	0.18	0.342	0.653
<i>Gucy2c</i>	-0.05	0.984	NA
<i>Gucy2d</i>	-1.11	0.785	NA
<i>Gucy2e</i>	-3.74	0.219	NA
<i>Gucy2f</i>	-1.11	0.785	NA
<i>Gucy2g</i>	-0.33	0.791	0.925
<i>Guf1</i>	0.06	0.724	0.894
<i>Guk1</i>	-0.27	0.027	0.145

<i>Prkg1</i>	1.16	3.21E-9	5.36E-7
<i>Prkg2</i>	1.15	0.006	0.053

## **References**

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