SUPPLEMENTARY MATERIAL

Table S1: Overview of genes included on PCR arrays*

Assay	Functional Group	Fold-Change	P-Value
18S-Hs99999901_s1	Control	-1.23	0.69
Acta2-Mm01546133_m1	Control	-1.19	0.87
Actb-Mm00607939_s1	Control	1.21	0.51
Anxa5-Mm00477537_m1	Apoptosis Signaling	1.04	0.86
Atf4-Mm00515324_m1	UPR	1.65	0.23
Atf6-Mm01295317_m1	UPR	1.06	0.79
Atm-Mm01177457_m1	DNA Damage and Repair	-1.51	0.15
Bax-Mm00432050_m1	Apoptosis Signaling	1.20	0.13
Bcl2l1-Mm00437783_m1	Apoptosis Signaling	1.46	0.31
Casp1-Mm00438023_m1	Apoptosis Signaling	1.52	0.36
Casp8-Mm00802247_m1	Apoptosis Signaling	1.05	0.89
Ccnc-Mm00443919_m1	Proliferation and Carcinogenesis	-1.11	0.50
Ccnd1-Mm00432359_m1	Proliferation and Carcinogenesis	6.28	0.02
Ccng1-Mm00438084_m1	Proliferation and Carcinogenesis	1.33	0.25
Cdh1-Mm01247357_m1	EMT	-1.30	0.85
Cdh2-Mm00483213_m1	EMT	-1.26	0.32
Cdkn1a-Mm00432448_m1	Growth Arrest and Senescence	2.31	0.13
Chek2-Mm00443844_m1	DNA Damage and Repair	1.34	0.42
Col8a2-Mm02344867_g1	Other	-1.53	0.27
Cryab-Mm00515567_m1	Oxidative and Metabolic Stress	-1.26	0.41
Cyp1a1-Mm00487218_m1	Oxidative and Metabolic Stress	1.43	0.39
Cyp1b1-Mm00487229_m1	Oxidative and Metabolic Stress	1.39	0.71
Cyp2a4;Cyp2a5-Mm00487248_g1	Oxidative and Metabolic Stress	1.06	0.93
Cyp2b10-Mm01972453_s1	Oxidative and Metabolic Stress	-2.30	0.37
Cyp2b9-Mm00657910_m1	Oxidative and Metabolic Stress	-	-
Cyp2c29-Mm00725580_s1	Oxidative and Metabolic Stress	-2.57	0.33
Cyp3a11-Mm00731567_m1	Oxidative and Metabolic Stress	-	-
Cyp4a10-Mm01622743_g1	Oxidative and Metabolic Stress	-2.54	0.31
Cyp4a14-Mm00484132_m1	Oxidative and Metabolic Stress	-	-
Cyp7a1-Mm00484152_m1	Oxidative and Metabolic Stress	-	-
Ddit3-Mm00492097_m1	UPR / Growth Arrest and Senescence	2.14	0.01
Derl2-Mm00504288_m1	UPR	1.08	0.76
Dnaja1;Smu1-Mm00787254_s1	UPR / Heat Shock	-1.79	0.08
E2f1-Mm00432936_m1	Proliferation and Carcinogenesis	3.43	0.05
Edem1-Mm00551797_m1	UPR	1.22	0.30
Edem3-Mm01295448_m1	UPR	-1.08	0.79
Egr1-Mm00656724_m1	Proliferation and Carcinogenesis	9.28	0.06
Ephx2-Mm00514706_m1	Oxidative and Metabolic Stress	-2.15	0.08
Ercc1-Mm00468337_m1	DNA Damage and Repair	1.03	0.89
Ercc4-Mm00516619_m1	DNA Damage and Repair	-1.22	0.08
Ero1lb-Mm00470754_m1	UPR	-4.22	0.25
Fasl-Mm00438864_m1	Apoptosis Signaling	2.29	0.10
Fmo1-Mm00515795_m1	Oxidative and Metabolic Stress	1.26	0.38
Fmo4-Mm00467393_m1	Oxidative and Metabolic Stress	-1.59	0.22

Fmo5-Mm00515805_m1	Oxidative and Metabolic Stress	-1.81	0.09
Gadd45a-Mm00432802_m1	Growth Arrest and Senescence	-1.08	0.88
Gapdh-Mm99999915_g1	Control	-1.21	0.59
Gclc-Mm00802655_m1	Oxidative and Metabolic Stress	1.46	0.30
Gclm-Mm00514996_m1	Oxidative and Metabolic Stress	1.19	0.17
Gpx1-Mm00656767_g1	Oxidative and Metabolic Stress	1.37	0.39
Gpx2-Mm00850074_g1	Oxidative and Metabolic Stress	-2.49	0.30
Gsr-Mm00833903_m1	Oxidative and Metabolic Stress	1.02	0.96
Gstm1-Mm00833915_g1	Oxidative and Metabolic Stress	-2.03	0.15
Gstm3-Mm00833923_m1	Oxidative and Metabolic Stress	-	-
Gusb-Mm00446953_m1	Control	-1.07	0.58
Herpud1-Mm00445600_m1	UPR	1.41	0.29
Hmox1-Mm00516005_m1	Oxidative and Metabolic Stress	5.30	0.03
Hmox2-Mm00468921_m1	Oxidative and Metabolic Stress	-	-
Hprt1-Mm00446968_m1	Control	1.09	0.53
Hsf1-Mm01201402_m1	Heat Shock	-1.10	0.74
Hsp90ab1-Mm00833431_g1	Heat Shock	1.10	0.76
Hspa1b-Mm03038954_s1	Heat Shock	1.13	0.87
Hspa1l-Mm00442854_m1	UPR / Heat Shock	-2.38	0.03
Hspa4-Mm00434038_m1	Heat Shock	-1.29	0.01
Hspa5-Mm01333323_g1	UPR / Heat Shock	1.96	0.04
Hspa8-Mm01731394_gH	Heat Shock	1.10	0.79
Hspb1-Mm00834384_g1	Heat Shock	-1.16	0.66
Hspd1-Mm00849835_g1	Heat Shock	-1.14	0.69
Hspe1-Mm00434083_m1	Heat Shock	1.00	0.99
Igfbp6-Mm00599696_m1	Growth Arrest and Senescence	1.89	0.12
Mdm2-Mm01233136_m1	Growth Arrest and Senescence	1.12	0.67
Mt2-Mm00809556_s1	Oxidative and Metabolic Stress	-1.50	0.09
Nfe2l2-Mm00477784_m1	Oxidative and Metabolic Stress	1.09	0.80
Nfkbia-Mm00477798_m1	Apoptosis Signaling	1.17	0.58
Nqo1-Mm00500821_m1	Oxidative and Metabolic Stress	-1.28	0.47
Pcna-Mm00448100_g1	Proliferation and Carcinogenesis	-1.06	0.75
Polr2k-Mm01164490_g1	Oxidative and Metabolic Stress	-1.35	0.45
Por-Mm00435876_m1	Oxidative and Metabolic Stress	-1.04	0.91
Rad23a-Mm00833569_m1	DNA Damage and Repair	1.07	0.82
Rad50-Mm00485504_m1	DNA Damage and Repair	-1.28	0.39
Snai1-Mm00441533_g1	EMT	1.12	0.77
Snai2-Mm00441531_m1	EMT	1.35	0.59
Sod1-Mm01700393_g1	Oxidative and Metabolic Stress	-1.17	0.10
Sod2-Mm00449726_m1	Oxidative and Metabolic Stress	-1.23	0.37
Tcf4-Mm00443210_m1	Other	-1.27	0.45
Tnfrsf1a-Mm00441875_m1	Apoptosis Signaling	1.33	0.17
Tnfsf10-Mm01283606_m1	Apoptosis Signaling	1.22	0.56
Tradd-Mm01251031_g1	Apoptosis Signaling	-1.11	0.52
Trp53-Mm01731287_m1	Growth Arrest and Senescence	-1.10	0.79

Twist1-Mm00442036_m1	EMT	1.36	0.06
Ugt1a2-Mm01964656_s1	DNA Damage and Repair	-1.69	0.57
Ung-Mm00449156_m1	DNA Damage and Repair	2.78	0.01
Xrcc1-Mm00494229_m1	DNA Damage and Repair	-1.04	0.87
Xrcc2-Mm00445118_m1	DNA Damage and Repair	-1.65	0.00
Xrcc4-Mm00459213_m1	DNA Damage and Repair	-1.39	0.28
Zeb1-Mm00495564_m1	EMT	-1.10	0.49

*Genes were assigned to eight functional groups or the control group as indicated in second column. Genes were marked as "other" if no special assignment to one of these groups could be made. Mean data from n=3 customized arrays per *Col8a2*$^{Q455K/Q455K}$ mutant or wildtype strain are presented. Third and fourth columns show fold-change values and p-values of gene expression in 12 month-old *Col8a2*$^{Q455K/Q455K}$ mutant compared to wildtype mice or "-" if no transcriptional expression could be detected. Fold-change >1 indicates overexpression and fold-change <-1.0 indicates underexpression in mutant compared to wild-type mice. Gene expression was normalized to the mean expression level of 18S, Actb, Gusb and Hprt1. UPR: Unfolded Protein Response, EMT: Epithelial Mesenchymal Transition.