Supplemental Table 1. Cardiac mitochondrial acetyl proteoforms in mouse heart.

Uniprot ID	Gene Symbol	Acetyl Proteoform
Q8BWT1	*Acaa2*	K137
Q8BWT1	*Acaa2*	K171
Q8BWT1	*Acaa2*	K234
Q8BWT1	*Acaa2*	K240
D3Z7X0	*Acad12*	K334
Q8JZN5	*Acad9*	K206
P51174	*Acadl*	K156
P51174	*Acadl*	K419
P50544	*Acadvl*	K122
P50544	*Acadvl*	K201
P50544	*Acadvl*	K240
P50544	*Acadvl*	K279
P50544	*Acadvl*	K52
Q8QZT1	*Acat1*	K171
Q8QZT1	*Acat1*	K187
Q8QZT1	*Acat1*	K220
Q8QZT1	*Acat1*	K242
Q8QZT1	*Acat1*	K248
Q8QZT1	*Acat1*	K304
Q8QZT1	*Acat1*	K335
Q8QZT1	*Acat1*	K340
Q8QZT1	*Acat1*	K80
Q99KI0	*Aco2*	K50
Q99KI0	*Aco2*	K517
Q99KI0	*Aco2*	K517|K520
Q99KI0	*Aco2*	K521
Q99KI0	*Aco2*	K523
Q99KI0	*Aco2*	K689
Q99KI0	*Aco2*	K723
Q99KI0	*Aco2*	K736
Q99KI0	*Aco2*	K739
Q9CQR4	*Acot13*	K127
Q9CQR4	*Acot13*	K27
Q9CQR4	*Acot13*	K37
Q9CQR4	*Acot13*	K43
Q9WTP7	*Ak3*	K29
Q8CG76	*Akr7a2*	K123
Q8CHT0	*Aldh4a1*	K54
Q8CHT0	*Aldh4a1*	K92
Q9EQ20	*Aldh6a1*	K117
Q9EQ20	*Aldh6a1*	K47
Q925I1	*Atad3*	K494
Q03265	*Atp5a1*	K126
Q03265	*Atp5a1*	K239
Q03265	*Atp5a1*	K498
Q03265	*Atp5a1*	K531
Q03265	*Atp5a1*	K539
P56480	*Atp5b*	K133
P56480	*Atp5b*	K485
P56480	*Atp5b*	K522
Q9DCX2	*Atp5h*	K117

Q9DCX2	*Atp5h*	K48
Q9DCX2	*Atp5h*	K63
Q9DCX2	*Atp5h*	K63|K72
Q9DCX2	*Atp5h*	K72
Q9DCX2	*Atp5h*	K78
Q9DCX2	*Atp5h*	K85
Q9DCX2	*Atp5h*	K95
Q06185	*Atp5i*	K34
Q06185	*Atp5i*	K48
P97450	*Atp5j*	K105
P97450	*Atp5j*	K41
P97450	*Atp5j*	K46
P97450	*Atp5j*	K99
Q9DB20	*Atp5o*	K162
Q9DB20	*Atp5o*	K192
Q9DB20	*Atp5o*	K53
Q9DB20	*Atp5o*	K60
Q9DB20	*Atp5o*	K70
Q9DB20	*Atp5o*	K84
Q9JLZ3	*Auh*	K80
Q91VT4	*Cbr4*	K151
Q91WS0	*Cisd1*	K68
Q6P8J7	*Ckmt2*	K292
Q6P8J7	*Ckmt2*	K344
Q8R4N0	*Clybl*	K55
Q8R4N0	*Clybl*	K80
Q8R4N0	*Clybl*	K90
P19783	*Cox4i1*	K164
P19783	*Cox4i1*	K67
P19783	*Cox4i1*	K78
P12787	*Cox5a*	K109
P56391	*Cox6b1*	K85
P56392	*Cox7a1*	K31
P56393	*Cox7b*	K75
P17665	*Cox7c*	K25
Q9CZU6	*Cs*	K321
Q9CZU6	*Cs*	K327
Q9CZU6	*Cs*	K370
Q9CZU6	*Cs*	K52
Q9D172	*D10Jhu81e*	K162
Q9D172	*D10Jhu81e*	K201
Q9D172	*D10Jhu81e*	K231
Q9CQ62	*Decr1*	K185
Q9CQ62	*Decr1*	K42
Q8BMF4	*Dlat*	K632
O08749	*Dld*	K104
O08749	*Dld*	K143
O08749	*Dld*	K155
O08749	*Dld*	K271
O08749	*Dld*	K273
O08749	*Dld*	K410
O08749	*Dld*	K420
O08749	*Dld*	K66

Q9D2G2	*Dlst*	K268
Q9D2G2	*Dlst*	K268|K273
Q9D2G2	*Dlst*	K273
Q9D2G2	*Dlst*	K278
O35459	*Ech1*	K97
Q8BH95	*Echs1*	K101
P42125	*Eci1*	K222
P42125	*Eci1*	K229
P42125	*Eci1*	K76
Q99LC5	*Etfa*	K162
Q99LC5	*Etfa*	K164
Q99LC5	*Etfa*	K69
Q99LC5	*Etfa*	K75
Q9DCW4	*Etfb*	K110
Q9DCW4	*Etfb*	K114
P26443	*Glud1*	K415
P26443	*Glud1*	K503
P26443	*Glud1*	K84
P05202	*Got2*	K122
P05202	*Got2*	K296
P05202	*Got2*	K302
P05202	*Got2*	K309
P05202	*Got2*	K363
P05202	*Got2*	K396
P05202	*Got2*	K404
P05202	*Got2*	K73
P05202	*Got2*	K90
Q61425	*Hadh*	K127
Q61425	*Hadh*	K185
Q61425	*Hadh*	K192
Q61425	*Hadh*	K212
Q61425	*Hadh*	K241
Q61425	*Hadh*	K75
Q61425	*Hadh*	K81
Q61425	*Hadh*	K87
Q8BMS1	*Hadha*	K289
Q8BMS1	*Hadha*	K334
Q8BMS1	*Hadha*	K353
Q8BMS1	*Hadha*	K386
Q8BMS1	*Hadha*	K406
Q8BMS1	*Hadha*	K519
Q8BMS1	*Hadha*	K540
Q8BMS1	*Hadha*	K569
Q8BMS1	*Hadha*	K60
Q8BMS1	*Hadha*	K728
Q99JY0	*Hadhb*	K202
Q99JY0	*Hadhb*	K273
Q99JY0	*Hadhb*	K333
Q99JY0	*Hadhb*	K73
Q99L13	*Hibadh*	K237
Q99L13	*Hibadh*	K94
Q8QZS1	*Hibch*	K352
P38647	*Hspa9*	K135

P38647	*Hspa9*	K288
P38647	*Hspa9*	K300
P38647	*Hspa9*	K612
P38647	*Hspa9*	K76
P63038	*Hspd1*	K125
P63038	*Hspd1*	K130
P63038	*Hspd1*	K202
P63038	*Hspd1*	K455
P63038	*Hspd1*	K87
Q8BIJ6	*Iars2*	K725
Q8CAK1	*Iba57*	K222
P54071	*Idh2*	K106
P54071	*Idh2*	K155
P54071	*Idh2*	K166
P54071	*Idh2*	K180
P54071	*Idh2*	K199
P54071	*Idh2*	K256
P54071	*Idh2*	K272
P54071	*Idh2*	K280
P54071	*Idh2*	K384
P54071	*Idh2*	K400
P54071	*Idh2*	K48
P54071	*Idh2*	K67
Q9D6R2	*Idh3a*	K100
Q9D6R2	*Idh3a*	K336
Q9D6R2	*Idh3a*	K343
Q9D6R2	*Idh3a*	K58
Q9D6R2	*Idh3a*	K77
Q9JHI5	*Ivd*	K76
P14152	*Mdh1*	K107
P14152	*Mdh1*	K164
P08249	*Mdh2*	K165
P08249	*Mdh2*	K185
P08249	*Mdh2*	K239
P08249	*Mdh2*	K296
P08249	*Mdh2*	K301
P08249	*Mdh2*	K307
P08249	*Mdh2*	K328|K329
Q9CQ75	*Ndufa2*	K64
Q62425	*Ndufa4*	K56
Q9CPP6	*Ndufa5*	K36
Q9CPP6	*Ndufa5*	K40
Q9CPP6	*Ndufa5*	K60
Q9CPP6	*Ndufa5*	K66
Q9DC69	*Ndufa9*	K189
Q9DC69	*Ndufa9*	K254
Q9D6J5	*Ndufb8*	K176
Q9CQJ8	*Ndufb9*	K121
Q9DCT2	*Ndufs3*	K259
P52503	*Ndufs6*	K41
Q9D6J6	*Ndufv2*	K60
Q60597	*Ogdh*	K897
Q91ZA3	*Pcca*	K146

Q91ZA3	*Pcca*	K61
P35486	*Pdha1*	K244
P35486	*Pdha1*	K267
P35486	*Pdha1*	K321
P35486	*Pdha1*	K63
P35486	*Pdha1*	K83
Q8BKZ9	*Pdhx*	K321
P20108	*Prdx3*	K254
P20108	*Prdx3*	K92
Q8K2B3	*Sdha*	K179
Q8K2B3	*Sdha*	K480
Q8K2B3	*Sdha*	K485
Q8K2B3	*Sdha*	K498
Q8K2B3	*Sdha*	K547
Q8K2B3	*Sdha*	K550
Q8K2B3	*Sdha*	K608
Q9CQA3	*Sdhb*	K269
Q9CQA3	*Sdhb*	K53
Q9CQA3	*Sdhb*	K57
Q8BH59	*Slc25a12*	K578
P51881	*Slc25a5*	K105
P51881	*Slc25a5*	K155
P09671	*Sod2*	K114
P09671	*Sod2*	K122
P09671	*Sod2*	K130
P09671	*Sod2*	K221
P09671	*Sod2*	K68
Q9WUM5	*Suclg1*	K54
Q8R1I1	*Uqcr10*	K59
Q9DB77	*Uqcrc2*	K92
Q9CR68	*Uqcrfs1*	K172
P99028	*Uqcrh*	K40
P99028	*Uqcrh*	K83
Q78IK2	*Usmg5*	K16

All identified mitochondrial acetylproteoforms are listed. Mitochondrial proteins were defined based on GOCC annotation in DAVID and MITOCARTA.

Supplemental Table 2. Mitochondrial protein acetylation sites regulated in HF mice.

Uniprot ID	Gene Symbol	Acetyl Proteoform	HF/Sham (FC)	SIRT3 Target	Regulated in CH
Q8BWT1	*Acaa2*	K137	1.56	No	Yes
D3Z7X0	*Acad12*	K334	2.08	No	No
P50544	*Acadvl*	K52	1.91	No	No
P50544	*Acadvl*	K240	1.75	Yes	No
Q8QZT1	*Acat1*	K187	1.67	No	No
Q99KI0	*Aco2*	K50	1.50	No	No
Q32MW3|Q9R0X4	*Acot10|Acot9*	K102	1.69	Yes	Yes
Q9CQR4	*Acot13*	K27	2.72	No	No
Q9Z0X1| B1AU25	*Aifm1*	K592	-1.66	No	Yes
Q8CG76	*Akr7a2*	K123	1.63	No	No
P47738|Q3U9J7| Q3U6I3|Q3UJW1| Q3TVM2	*Aldh2*	K370	1.53	Yes	Yes
P56480	*Atp5b*	K133	1.60	Yes	Yes
Q9D3D9|Q9DCZ0| Q9D0J2	*Atp5d*	K165	-1.55	No	Yes
Q8R4N0	*Clybl*	K80	1.56	Yes	No
Q8R4N0	*Clybl*	K55	1.56	Yes	No
P19783	*Cox4i1*	K67	1.77	No	No
P47934|H7BX88	*Crat*	K270	1.70	No	Yes
Q9D172	*D10Jhu81e*	K231	1.79	Yes	No
Q9D172	*D10Jhu81e*	K201	1.62	Yes	No
Q9CQ62	*Decr1*	K42	2.07	Yes	No
Q8BH95	*Echs1*	K101	1.55	Yes	No
P21550	*Eno3*	K28	-2.43	No	No
Q9DCW4	*Etfb*	K114	1.77	No	No
Q921G7|Q6PF96	*Etfdh*	K133	1.72	No	No
Q61425	*Hadh*	K87	1.60	Yes	No
Q8BMS1	*Hadha*	K406	1.68	Yes	No
Q99JY0	*Hadhb*	K73	1.92	Yes	Yes
P38647	*Hspa9*	K300	2.26	No	No
P63038	*Hspd1*	K455	2.66	No	Yes
P63038	*Hspd1*	K130	1.52	Yes	No
P63038	*Hspd1*	K125	1.51	Yes	No
Q8CAK1	*Iba57*	K222	-2.87	No	No
P54071	*Idh2*	K67	2.78	No	No
P54071	*Idh2*	K272	1.56	No	No
P54071	*Idh2*	K106	1.56	No	No
P08249	*Mdh2*	K165	1.69	No	No
P03930|A3R404| Q5GA80	*Mtatp8|mt-Atp8|ATP8*	K48	1.69	Yes	No
P09541|Q9CZ19| A2A6Q8	*Myl4*	K140	1.66	No	No
Q3UIU2|A2AP32	*Ndufb6*	K24	1.67	No	No
Q9D6J5	*Ndufb8*	K176	-1.88	No	No
P52503	*Ndufs6*	K41	2.11	No	Yes
Q8K2B3	*Sdha*	K608	1.98	No	Yes

A fold-change cut-off of ±1.5 was used for this analysis.

Supplemental Table 3. Pathway analysis of mitochondrial proteins with regulated acetylation sites in murine HF.

Ingenuity Canonical Pathways	# of genes regulated	# of genes in pathway	p-value	Acetylated Proteins
Oxidative Phosphorylation/Electron Transport Chain	**7**	**100**	7.943E-10	**SDHA,ATP5B,ATP5D,NDUFS6, NDUFB6,NDUFB8,COX4I1**
Fatty Acid β-oxidation I	**5**	**30**	2.754E-09	**HADHB,ECHS1,ACAA2,HADHA,HADH**
Glutaryl-CoA Degradation	4	11	3.802E-09	HADHB,ACAT1,HADHA,HADH
Isoleucine Degradation I	4	14	1.148E-08	HADHB,ECHS1,ACAT1,HADHA
Tryptophan Degradation III (Eukaryotic)	4	20	5.623E-08	HADHB,ACAT1,HADHA,HADH
Ketolysis	3	8	3.715E-07	HADHB,ACAT1,HADHA
Ketogenesis	3	10	7.943E-07	HADHB,ACAT1,HADHA
Mevalonate Pathway I	3	12	1.445E-06	HADHB,ACAT1,HADHA
Superpathway of Geranylgeranyldiphosphate Biosynthesis I (via Mevalonate)	3	12	3.631E-06	HADHB,ACAT1,HADHA
Valine Degradation I	3	18	5.370E-06	HADHB,ECHS1,HADHA
TCA Cycle II (Eukaryotic)	**3**	**22**	8.710E-06	**SDHA,ACO2,MDH2**
Superpathway of Cholesterol Biosynthesis	3	27	1.905E-05	HADHB,ACAT1,HADHA
Gluconeogenesis I	2	24	8.318E-04	ENO3,MDH2
Phenylethylamine Degradation I	1	4	7.762E-03	ALDH2
Aspartate Degradation II	1	7	1.148E-02	MDH2
LXR/RXR Activation	2	110	1.950E-02	ECHS1,HADH
Phenylalanine Degradation IV (Mammalian, via Side Chain)	1	14	2.512E-02	ALDH2
Histamine Degradation	1	12	2.512E-02	ALDH2
Methylglyoxal Degradation III	1	14	2.692E-02	AKR7A2
Putrescine Degradation III	1	16	3.090E-02	ALDH2
Fatty Acid α-oxidation	1	15	3.090E-02	ALDH2
Oxidative Ethanol Degradation III	1	15	3.090E-02	ALDH2
Tryptophan Degradation X (Mammalian, via Tryptamine)	1	17	3.236E-02	ALDH2
Aldosterone Signaling in Epithelial Cells	2	148	3.311E-02	HSPA9,HSPD1
Ethanol Degradation IV	1	17	3.467E-02	ALDH2
Dopamine Degradation	1	20	3.802E-02	ALDH2
Glycolysis I	1	23	4.169E-02	ENO3
Tumoricidal Function of Hepatic Natural Killer Cells	1	22	4.365E-02	AIFM1

All significantly regulated pathways as identified by Ingenuity Pathway Analysis are listed. Major energy transduction pathways are shown in bold.

Supplemental Table 4. Mitochondrial protein acetylation sites regulated in CH mice.

Uniprot ID	Gene Symbol	Acetyl Proteoform	CH/Sham (FC)	SIRT3 Target	Regulated in HF
Q8BWT1	*Acaa2*	K137	1.59	No	Yes
Q8QZT1	*Acat1*	K80	-1.50	No	No
Q8QZT1	*Acat1*	K171	-1.65	No	No
Q99KI0	*Aco2*	K739	-1.60	Yes	No
Q32MW3|Q9R0X4	*Acot10|Acot9*	K102	1.50	Yes	Yes
Q9Z0X1|B1AU25	*Aifm1*	K592	-2.08	No	Yes
P47738|Q3U9J7| Q3U6I3|Q3UJW1| Q3TVM2	*Aldh2*	K370	1.61	Yes	Yes
Q03265	*Atp5a1*	K126	-1.54	Yes	No
P56480	*Atp5b*	K133	1.96	Yes	Yes
Q9D3D9|Q9DCZ0| Q9D0J2	*Atp5d*	K165	1.75	No	Yes
Q9DCX2	*Atp5h*	K48	1.77	No	No
P97450	*Atp5j*	K99	-1.64	No	No
P97450	*Atp5j*	K41	-1.66	No	No
Q6P8J7	*Ckmt2*	K292	1.63	No	No
P19536|Q9D881	*Cox5b*	K74	1.67	No	No
P19536|Q9D881	*Cox5b*	K121	1.64	No	No
P56393	*Cox7b*	K75	1.85	No	No
P47934|H7BX88	*Crat*	K270	2.04	No	Yes
Q9D0M3|Q9D0M3-2	*Cyc1*	K177	-1.98	No	No
O08749	*Dld*	K420	1.79	No	No
Q9D2G2	*Dlst*	K278	-1.63	No	No
O35459	*Ech1*	K97	1.69	No	No
P42125	*Eci1*	K222	-2.12	No	No
Q9WUR2|Q9WUR2-2| Q3TCD4	*Eci2*	K138	3.39	No	No
Q99LC5	*Etfa*	K164	1.54	No	No
P26443	*Glud1*	K415	2.35	No	No
P26443	*Glud1*	K84	-1.82	No	No
P05202	*Got2*	K122	1.74	No	No
Q61425	*Hadh*	K127	1.52	No	No
Q8BMS1	*Hadha*	K334	1.58	Yes	No
Q8BMS1	*Hadha*	K519	1.54	No	No
Q99JY0	*Hadhb*	K73	-1.64	Yes	Yes
P63038	*Hspd1*	K455	2.46	No	Yes
P54071	*Idh2*	K400	2.32	No	No
Q9D6R2	*Idh3a*	K336	-1.57	No	No
E9Q800|Q3TEY5	*Immt*	K596	1.80	No	No
P08249	*Mdh2*	K239	1.53	Yes	No
P51667	*Myl2*	K165	1.64	No	No
Q9CPP6	*Ndufa5*	K36	1.51	No	No
Q91VD9|Q3TIU7	*Ndufs1*	K98	1.62	No	No
P52503	*Ndufs6*	K41	1.58	No	Yes
Q9JHW2	*Nit2*	K68	-2.80	No	No
Q60597	*Ogdh*	K897	-1.52	No	No
P35486	*Pdha1*	K321	1.76	No	No
P35486	*Pdha1*	K63	1.65	No	No
Q8K1R3|Q8K1R3-2| Q3TST0|Q3UNL5| Q3TN29	*Pnpt1*	K285	1.64	No	No
Q8K2B3	*Sdha*	K608	2.07	No	Yes
Q8VEM8|G5E902| Q3THU8	*Slc25a3*	K230	2.41	No	No
P51881	*Slc25a5*	K155	1.57	No	No
Q9D855|Q9CQB4	*Uqcrb*	K110	1.59	No	No
Q9D855|Q9CQB4	*Uqcrb*	K83	-1.99	No	No

A fold-change cut-off of ±1.5 was used for this analysis.

Supplemental Table 5. Mitochondrial protein acetylation sites regulated in human failing hearts.

Uniprot ID	Gene Symbol	Acetyl	DCM/NF (FC)	p-value
Q9UKU7	*ACAD8*	K144	2.22	0.055
P16219	*ACADS*	K343	2.04	0.059
A2A274	*ACO2*	K50	1.35	0.021
A2A274	*ACO2*	K138	2.03	0.022
B7Z452	*ACSL1*	K561	1.83	0.059
P30038	*ALDH4A1*	K531	2.01	0.013
P30038	*ALDH4A1*	K119	1.99	0.042
P30038	*ALDH4A1*	K93	1.52	0.169
Q8NCW5	*APOA1BP*	K148	1.62	0.030
Q6UXV4	*APOOL*	K105	2.46	0.033
P25705	*ATP5A1*	K252	2.55	0.004
P25705	*ATP5A1*	K498	-1.62	0.007
P25705	*ATP5A1*	K316	1.53	0.010
P25705	*ATP5A1*	K194	1.82	0.038
P25705	*ATP5A1*	K506	1.45	0.040
P25705	*ATP5A1*	K531	-1.62	0.186
P25705	*ATP5A1*	K230	2.09	0.074
O75947	*ATP5H*	K58	1.59	0.110
P18859	*ATP5J*	K94	1.85	0.095
Q9UII2	*ATPIF1*	K82	1.79	0.045
Q02338	*BDH1*	K97	1.88	0.045
Q02338	*BDH1*	K212	1.62	0.060
P04040	*CAT*	K237	2.29	0.023
Q03135	*CAV1*	K47	1.85	0.064
Q9NZ45	*CISD1*	K68	2.05	0.001
P12277	*CKB*	K307	3.76	0.002
P12277	*CKB*	K298	1.67	0.088
P17540	*CKMT2*	K230	1.67	0.001
Q14061	*COX17*	K40	2.45	0.003
P13073	*COX4I1*	K159	1.97	0.040
Q92523	*CPT1B*	K40	2.01	0.022
P07339	*CTSD*	K341	2.01	0.063
Q9UHQ9	*CYB5R1*	K167	-1.23	0.018
P11182	*DBT*	K295	1.60	0.255
P11182	*DBT*	K243	2.01	0.071
P11182	*DBT*	K257	2.03	0.153
P36957	*DLST*	K267/K272	1.54	0.255
P15924	*DSP*	K916	1.41	0.003
P15924	*DSP*	K1687	2.04	0.012
P15924	*DSP*	K485	1.91	0.039
P15924	*DSP*	K1099	1.84	0.126
P15924	*DSP*	K2393	1.84	0.095
P30084	*ECHS1*	K115	1.70	0.056
P13804	*ETFA*	K69	1.94	0.075
Q16134	*ETFDH*	K96	1.60	0.025
P00505	*GOT2*	K279	2.55	0.016
P00505	*GOT2*	K94	2.19	0.024
P40939	*HADHA*	K406	-2.49	0.008
P40939	*HADHA*	K353	-1.67	0.135
P40939	*HADHA*	K411	-1.63	0.072
P40939	*HADHA*	K326/K334	1.54	0.409
P40939	*HADHA*	K605	2.45	0.064
P49590	*HARS2*	K52	1.92	0.020
P31937	*HIBADH*	K56	1.89	0.103
O75874	*IDH1*	K81	2.28	0.018
P50213	*IDH3A*	K223	-1.82	0.008
O43837	*IDH3B*	K199	3.74	0.002
P83111	*LACTB*	K225	1.60	0.187
P42704	*LRPPRC*	K66	2.37	0.038

Q9BQ69	*MACROD1*	K117	1.53	0.007
P21397	*MAOA*	K469	2.36	0.058
P23368	*ME2*	K24	-2.33	0.020
P82909	*MRPS36*	K78	2.13	0.015
Q9Y3D2	*MSRB2*	K176	2.38	0.038
Q9UI09	*NDUFA12*	K114	1.70	0.005
Q9UI09	*NDUFA12*	K47	1.72	0.169
Q9P0J0	*NDUFA13*	K22	2.05	0.288
Q9P0J0	*NDUFA13*	K7	2.80	0.105
P56556	*NDUFA6*	K44	1.60	0.575
P51970	*NDUFA8*	K106	3.13	0.005
P51970	*NDUFA8*	K38	1.60	0.148
Q16795	*NDUFA9*	K163	2.17	0.006
O96000	*NDUFB10*	K121	1.86	0.078
O95298	*NDUFC2*	K114	1.59	0.002
O75489	*NDUFS3*	K109	1.84	0.000
O43920	*NDUFS5*	K38	1.63	0.008
O43920	*NDUFS5*	K101	1.32	0.012
O00217	*NDUFS8*	K88	2.00	0.037
Q13423	*NNT*	K100	2.10	0.007
Q13423	*NNT*	K331	1.58	0.009
Q13423	*NNT*	K462	1.75	0.020
Q13423	*NNT*	K453	2.32	0.030
Q13423	*NNT*	K403	1.69	0.178
E9PCR7	*OGDH*	K363	2.53	0.006
E9PCR7	*OGDH*	K402	1.58	0.033
E9PCR7	*OGDH*	K416	-1.64	0.093
E9PCR7	*OGDH*	K252	2.37	0.053
P55809	*OXCT1*	K41	2.46	0.037
P55809	*OXCT1*	K296	1.51	0.333
P30405	*PPIF*	K73	-1.81	0.018
P30405	*PPIF*	K167	1.95	0.040
P47897	*QARS*	K230	2.17	0.036
Q9Y512	*SAMM50*	K227	1.34	0.012
D6RFM5	*SDHA*	K361	1.64	0.018
E9PEF8	*SDHA*	K396	1.52	0.020
D6RFM5	*SDHA*	K179	1.84	0.130
P12235	*SLC25A4*	K163	1.67	0.003
P12235	*SLC25A4*	K33	1.81	0.013
P12235	*SLC25A4*	K96	1.53	0.051
P53597	*SUCLG1*	K54	1.88	0.012
P21980	*TGM2*	K672	2.51	0.001
P49411	*TUFM*	K297	2.13	0.015
P49411	*TUFM*	K55	1.78	0.101
P31930	*UQCRC1*	K447	1.60	0.032
P22695	*UQCRC2*	K159	1.35	0.043
P07919	*UQCRH*	K85	1.85	0.002
O14949	*UQCRQ*	K33	1.90	0.040
P21796	*VDAC1*	K224	1.20	0.018
P21796	*VDAC1*	K109	1.23	0.019
P21796	*VDAC1*	K252	1.74	0.022

A fold-change cut-off of ±1.5 or $p < 0.05$ was used for this analysis.