

**S4 Table**

Chow - CTRL vs. NiPKO – Down-regulated genes					
#term	Term name	p-value	Adjusted p-value	-log(p)	Positive ids
mmu05012	Parkinson's disease (PD)	8.75E-36	1.65E-33	<b>32.78</b>	Cox7a1,ND6,LOC100046079,Atp5h,Atp5e,Uqcrfs1,Cycs,Ndufc1,Atp5g3,Cox5a,Ndufs1,Cox4i1,Uqcrh,Ndufa8,Ndufa4,Uqcrc1,Cyc1,Ndufv2,BC002163,Ndufs6,Sdhd,Cox7a2,Ndufa1,Ndufb8,Ndufa9,Uqcrb,Ndufs8,Cox7b,Uqcrq,Atp5d,Vdac2,Slc25a4,Ndufa6,Ndufs3,Atp5f1,Vdac3,Ndufb2,Sdhc,Ndufb5,Sdha,Ndufs2
mmu00190	Oxidative phosphorylation	2.39E-35	2.26E-33	<b>32.65</b>	Cox7a1,Cox10,ND6,LOC100046079,Atp5h,Atp5e,Uqcrfs1,Ndufc1,Atp5g3,Cox5a,Ndufs1,Cox4i1,Uqcrh,Ndufa8,Ndufa4,Atp5l,Uqcrc1,Cyc1,Atp4a,Ndufv2,BC002163,Ndufs6,Sdhd,Cox7a2,Ndufa1,Ndufb8,Ndufa9,Uqcrb,Ndufs8,Cox7b,Uqcrq,Atp5d,Ndufa6,Ndufs3,Atp5f1,Ndufb2,Sdhc,Ndufb5,Sdha,Ndufs2
mmu05016	Huntington disease (HD)	4.71E-31	2.97E-29	<b>28.53</b>	Cox7a1,LOC100046079,Atp5h,Atp5e,Uqcrfs1,Cycs,Ndufc1,Atp5g3,Cox5a,Ndufs1,Cox4i1,Uqcrh,Ndufa8,Ndufa4,Uqcrc1,Cyc1,Ndufv2,BC002163,Ndufs6,Sdhd,Cox7a2,Ndufa1,Ndufb8,Ndufa9,Uqcrb,Ndufs8,Cox7b,Uqcrq,Atp5d,Vdac2,Slc25a4,Ndufa6,Ndufs3,Atp5f1,Vdac3,Ndufb2,Sdhc,Polr2h,Ndufb5,Sdha,Ndufs2
mmu05010	Alzheimer's disease (AD)	2.11E-26	9.97E-25	<b>24.00</b>	Cox7a1,LOC100046079,Atp5h,Atp5e,Uqcrfs1,Cycs,Ndufc1,Atp5g3,Cox5a,Ndufs1,Cox4i1,Uqcrh,Ndufa8,Ndufa4,Uqcrc1,Cyc1,Ndufv2,BC002163,Ndufs6,Sdhd,Cox7a2,Ndufa1,Ndufb8,Ndufa9,Uqcrb,Ndufs8,Cox7b,Uqcrq,Atp5d,Ndufa6,Ndufs3,Atp5f1,Ndufb2,Sdhc,Ndufb5,Sdha,Ndufs2
mmu00020	The citrate cycle	9.63E-15	3.64E-13	<b>12.44</b>	Idh3a,Pdha1,Dlst,Dlat,Sdhd

	(TCA cycle, Krebs cycle)				,Pdhb,Cs,Fh1,Mdh2,Dld,Sdhc,Sdha,Idh3b
mmu04260	Cardiac muscle contraction	6.99E-08	2.2E-06	<b>5.66</b>	Cox7a1,LOC100046079,Uqc rfs1,Cox5a,Cox4i1,Uqcrh,U qcrc1,Cyc1,Cox7a2,Uqcrb,C ox7b,Uqcrq
mmu00010	Glycolysis	8.17E-08	2.21E-06	<b>5.66</b>	Pfk, Pfkp, Pgam1, Ldhb, Pdh a1, Pgam2, Dlat, Pgk1, Hk1, Pd hb, Dld
mmu00620	Pyruvate metabolism	1.50E-05	0.000354	<b>3.45</b>	Me3, Ldhb, Pdha1, Dlat, Pdhb ,Mdh2, Dld
mmu00250	Alanine, aspartate and glutamate metabolism	3.02E-04	0.006348	<b>2.20</b>	Got1, Gpt2, Adssl1, GluL, Ddo

### Chow - CTRL vs. NiPKO – Up-regulated genes

#term	Term name	p-value	Adjusted p-value	-log(p)	Positive ids
mmu00511	Other glycan degradation	0.00002377	0.004493	2.35	Hexa, Sox10, Foxi1, Neu4, Man2b2

### HFD - CTRL vs. NiPKO – Down-regulated genes

#term	Term name	p-value	Adjusted p-value	-log(p)	Positive ids
mmu00190	Oxidative phosphorylation	2.19E-20	4.1363E-18	<b>17.38</b>	Ndufa9, Cox7a1, Atp5h, Uqcr c1, Cox5a, Cox7a2, Ndufa4, N dufs3, Ndufs8, Uqcrfs1, Atp5 g3, Ndufa8, Cyc1, Uqcrh, Atp5 k, Ndufc1, Cox10, Atp5f1, Uqc rq, LOC100046079, Atp5c1, A tp5e, Atp5g1, Ndufa1, Cox5b, Uqcrb
mmu05012	Parkinson's disease (PD)	7.45E-20	7.04477E-18	<b>17.15</b>	Ndufa9, Cox7a1, Atp5h, Uqcr c1, Cox5a, Cox7a2, Ndufa4, N dufs3, Ndufs8, Uqcrfs1, Atp5 g3, Ndufa8, Cyc1, Uqcrh, Ndu fc1, Atp5f1, Uqcrq, LOC1000 46079, Atp5c1, Atp5e, Cycs, S lc25a4, Atp5g1, Ndufa1, Cox5 b, Uqcrb
mmu05010	Alzheimer's disease (AD)	3.26E-18	1.80054E-16	<b>15.74</b>	Ndufa9, Cox7a1, Atp5h, Uqcr c1, Cox5a, Cox7a2, Ndufa4, N dufs3, Ndufs8, Uqcrfs1, Atp5 g3, Ndufa8, Cyc1, Uqcrh, Ndu fc1, Atp5f1, Uqcrq, LOC1000 46079, Atp5c1, Atp5e, Cycs, A tp5g1, Ndufa1, Atp2a1, Cox5 b, Gapdh, Uqcrb

mmu05016	Huntington disease (HD)	3.81E-18	1.80054E-16	<b>15.74</b>	Ndufa9,Cox7a1,Atp5h,Uqcr c1,Cox5a,Cox7a2,Ndufa4,N dufs3,Ndufs8,Uqcrfs1,Atp5 g3,Ndufa8,Cyc1,Uqcrh,Ndu fc1,Atp5f1,Uqcrq,LOC1000 46079,Atp5c1,Atp5e,Cycts, Ic25a4,Atp5g1,Ndufa1,Cox5 b,Uqcrb,Creb3l3
mmu04260	Cardiac muscle contraction	7.95E-08	3.00472E-06	<b>5.52</b>	Cox7a1,Uqcrc1,Cox5a,Cox7 a2,Uqcrfs1,Cyc1,Uqcrh,Uqc rq,LOC100046079,Cox5b,U qcrb
mmu00010	Glycolysis	1.16E-06	3.65533E-05	<b>4.44</b>	Tpi1,Ldhb,Pfkkm,Dlat,Pgk1,G 6pc,Pgam1,Pfkp,Gapdh
mmu00020	The citrate cycle	1.39E-04	0.00375555	<b>2.43</b>	Mdh2,Idh3a,Dlst,Fh1,Dlat
mmu00071	Fatty acid degradation	8.26E-04	0.0195103	<b>1.71</b>	Acaa2,Acsl3,Acadl,Acadvl,H adha
mmu00030	The pentose phosphate pathway	1.21E-03	0.0254251	<b>1.59</b>	Pfkkm,Pgls,Pfkp,G6pd2

<b>HFD - CTRL vs. NiPKO – Up-regulated genes</b>					
#term	Term name	p-value	Adjusted p-value	-log(p)	Positive ids
mmu05322	Systemic lupus erythematosus (SLE)	1.89E-05	0.00356441	<b>2.45</b>	C2,Hist1h2bn,Hist2h3b,Actn1,Hist2h3c2,Hist2h2be,C8a,Hist1h4i,C9,H2-DMb2,H2afj
mmu00260	Glycine, serine and threonine metabolism	2.10E-04	0.0198883	<b>1.70</b>	Gamt,Psat1,Cbs,Maoa,Mao b
mmu00531	Glycosaminoglycan degradation	5.79E-04	0.036507	<b>1.44</b>	Hexb,Hexa,Hpse2,Galns