

Table S1.**A) GO terms upregulated in C at 4 months**

GOID		166628			
Oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor					
Symbol	Name	ID	FC (B/C)	FDR	
<i>Dhcr24</i>	24-dehydrocholesterol reductase	Mm.133370	1.7	0.02	
<i>Ltb4dh</i>	Leucotrine B4 12-hydroxydehydrogenase	Mm.34497	4.8	0.006	
<i>Dhcr7</i>	7-dehydrocholesterol reductase	Mm.249342	1.2	0.02	
<i>Blvrb</i>	Biliverdin reductase B	Mm.24021	1.7	0.004	
<i>Fasn</i>	Fatty acid synthase	Mm.236443	1.3	0.03089	
GOID		30054			
Cell junction					
Symbol	Name	ID	FC (B/C)	FDR	
<i>Anxa2</i>	Annexin A2	Mm.238343	2.1	0.02	
<i>Fat1</i>	FAT tumor suppressor homolog 1 (Drosophila)	Mm.27365	1.7	0.007	
<i>Gja1</i>	Gap junction protein, alpha 1	Mm.378921	1.8	0.01	
<i>Pard3</i>	Par-3 (partitioning defective 3) homolog (C. elegans)	Mm.299254	1.5	0.006	
<i>Pvrl3</i>	Poliovirus receptor-related 3	Mm.328072	1.5	0.02	
<i>Jub</i>	Ajuba	Mm.100253	1.5	0.006	
<i>Sorbs3</i>	Sorbin and SH3 domain containing 3	Mm.5068	1.5	0.01	
<i>Vasp</i>	Vasodilator-stimulated phosphoprotein	Mm.9684	1.4	0.02	
<i>Rab13</i>	RAB13, member RAS oncogene family	Mm.29355	1.3	0.02	
<i>Dsg2</i>	Desmoglein 2	Mm.345891	1.7	0.03	
<i>Dsp</i>	Desmoplakin	Mm.355327	3.8	0.01	
<i>Cldn7</i>	Claudin 7	Mm.281896	2.1	0.004	
<i>F11r</i>	F11 receptor	Mm.294882	1.8	0.01	
<i>Tmem37</i>	Transmembrane protein 37	Mm.24750	1.3	0.02	
<i>Gjb5</i>	Gap junction protein, beta 5	Mm.26859	1.9	0.01	
<i>Evpl</i>	Envoplakin	Mm.293683	3	0.04	
<i>Abi2</i>	V-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gene)	Mm.329515	2.1	0.00246	
<i>Cdh1</i>	cadherin 1	Mm.35605	1.7	0.02258	
<i>Myh9</i>	Myosin, heavy polypeptide 9, non-muscle	Mm.29677	1.2	0.02848	
<i>Lasp1</i>	LIM and SH3 protein 1	Mm.271967	1.5	0.01305	
<i>Dst</i>	dystonin	Mm.336625	2.9	0.02739	
<i>Cxadr</i>	coxsackie virus and adenovirus receptor	Mm.66222	1.2	0.00511	
<i>Cldn3</i>	claudin 3	Mm.158662	2.1	0.02418	
<i>Gjb3</i>	Gap junction protein, beta 3	Mm.90003	2.2	0.00361	
<i>Inadl</i>	InaD-like (Drosophila)	Mm.90218	1.3	0.01441	
GOID		8305			
Integrin complex					
Symbol	Name	ID	FC (B/C)	FDR	
<i>30419L09I</i>	RIKEN cDNA 8430419L09 gene	Mm.34182	1.4	0.0405	

<i>Itga3</i>	Integrin alpha 3	Mm.57035	1.5	0.02
<i>Itga9</i>	Integrin alpha 9	Mm.335520	2.8	0.004
<i>Itgb4</i>	Integrin beta 4	Mm.213873	2.5	0.02
<i>Itga6</i>	integrin alpha 6	Mm.225096	1.2	0.03939
<i>Itgb1</i>	integrin beta 1	Mm.263396	1.2	0.03715
<i>Myh9</i>	Myosin, heavy polypeptide 9, non-muscle	Mm.29677	1.2	0.02848

GOID 4716

Receptor signaling protein tyrosine kinase activity

Symbol	Name	ID	FC (B/C)	FDR
<i>Egfr</i>	Epidermal growth factor receptor	Mm.8534	1.4	0.01598
<i>ErbB2</i>	V-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog	Mm.290822	1.5	0.02367
<i>ErbB3</i>	V-erb-b2 erythroblastic leukemia viral oncogene homolog 3	Mm.29023	1.8	0.01464
<i>Jak2</i>	Janus kinase 2	Mm.275839	1.4	0.01386
<i>Jak3</i>	Janus kinase 3	Mm.249645	1.5	0.00399

GOID 44420

Extracellular matrix part

Symbol	Name	ID	FC (B/C)	FDR
<i>Entpd1</i>	Ectonucleoside triphosphate diphosphohydrolase 1	Mm.2824	1.5	0.01
<i>Lamb1-1</i>	Laminin B1 subunit 1	Mm.172674	2	0.004
<i>Col4a1</i>	Collagen, type IV, alpha 1	Mm.738	1.4	0.04
<i>Lad1</i>	Ladinin	Mm.36726	2.2	0.009
<i>Nid1</i>	Nidogen 1	Mm.4691	1.5	0.006
<i>Nid2</i>	Nidogen 2	Mm.20348	1.4	0.02
<i>Col6a2</i>	Collagen, type VI, alpha 2	Mm.1949	1.7	0.02
<i>Fbn1</i>	Fibrillin 1	Mm.271644	1.2	0.02
<i>Mfap4</i>	Microfibrillar-associated protein 4	Mm.272278	1.8	0.02
<i>Lama1</i>	laminin, alpha 1	Mm.303386	1.3	0.0225
<i>Lamc1</i>	laminin, gamma 1	Mm.1249	1.2	0.02798
<i>Col5a1</i>	collagen, type V, alpha 1	Mm.7281	1.6	0.03075
<i>Col5a2</i>	Collagen, type V, alpha 2	Mm.10299	1.6	0.01888
<i>Col6a1</i>	collagen, type VI, alpha 1	Mm.66222	1.4	0.01854

GOID 16769

Transferase activity\, transferring nitrogenous groups

Symbol	Name	ID	FC (B/C)	FDR
<i>Gpt1</i>	Glutamic pyruvic transaminase 1, soluble	Mm.30130	1.9	0.008
<i>Gatm</i>	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Mm.29975	1.9	0.0003
<i>Abat</i>	4-aminobutyrate aminotransferase	Mm.259315	1.4	0.02
<i>Psat1</i>	Phosphoserine aminotransferase 1	Mm.289936	1.5	0.01
<i>Sox4</i>	SRY-box containing gene 4	Mm.240627	1.4	0.04
<i>Alas1</i>	Aminolevulinic acid synthase 1	Mm.290578	1.4	0.04188
<i>Bcat1</i>	Branched chain aminotransferase 1, cytosolic	Mm.4606	1.2	0.04947
<i>Oat</i>	Ornithine aminotransferase	Mm.13694	1.3	0.0203

GOID 45111

Intermediate filament cytoskeleton

Symbol	Name	ID	FC (B/C)	FDR
<i>Krt12</i>	Keratin 12	Mm.436651	17.2	0.01
<i>Krt5</i>	Keratin 5	Mm.451847	3.6	0.03
<i>Krt6a</i>	Keratin 6A	Mm.302399	2.6	0.03
<i>Krt7</i>	Keratin 7	Mm.289377	2.6	0.03
<i>Krt71</i>	Keratin 71	Mm.358677	3.3	0.01
<i>Eif6</i>	Eukaryotic translation initiation factor 6	Mm.271674	1.4	0.01605
<i>Krt18</i>	Keratin 18	Mm.22479	1.2	0.00747
<i>Krt20</i>	Keratin 20	Mm.28042	1.6	0.01478
<i>Krt80</i>	Keratin 80	Mm.440055	3.3	0.01072
<i>Krt86</i>	Keratin 86	Mm.383183	1.9	0.04605
<i>Lmna</i>	Lamin A	Mm.470666	1.5	0.00143

GOID 6958

Complement activation, classical pathway

Symbol	Name	ID	FC (B/C)	FDR
<i>C1qa</i>	Complement component 1, q subcomponent, alpha polypeptide	Mm.439957	1.3	0.04083
<i>C3</i>	Complement component 3	Mm.19131	1.4	0.02256
<i>Cd55</i>	CD55 antigen	Mm.101591	1.3	0.0218
<i>Cr1l</i>	Complement component (3b/4b) receptor 1-like	Mm.301652	1.4	0.02353
<i>EG317677</i>	Complement component 1, s subcomponent (C1s)	Mm.476267	1.2	0.04

GOID 42060

Wound healing

Symbol	Name	ID	FC (B/C)	FDR
<i>Fn1</i>	Fibronectin 1	Mm.193099	1.3	0.01
<i>Anxa8</i>	Annexin A8	Mm.3267	3.5	0.02
<i>Coch</i>	Coagulation factor C homolog (Limulus polyphemus)	Mm.21325	1.4	0.03
<i>Plat</i>	Plasminogen activator, tissue	Mm.154660	1.4	0.03
<i>Vwf</i>	Von Willebrand factor homolog	Mm.22339	1.4	0.04
<i>Cd9</i>	CD9 antigen	Mm.210676	1.3	0.007
<i>Entpd1</i>	Ectonucleoside triphosphate diphosphohydrolase 1	Mm.2824	1.5	0.01
<i>Anxa2</i>	Annexin A2	Mm.238343	2.1	0.02
<i>Gja1</i>	Gap junction protein, alpha 1	Mm.378921	1.8	0.01
<i>Jub</i>	Ajuba	Mm.100253	1.5	0.006
<i>Elk3</i>	ELK3, member of ETS oncogene family	Mm.4454	1.4	0.04038
<i>F3</i>	Coagulation factor III	Mm.273188	1.3	0.03249
<i>Gna13</i>	Guanine nucleotide binding protein, alpha 13	Mm.193925	1.2	0.02444

B) GO terms upregulated in B6a at 4 months

GOID 42401

Biogenic amine biosynthetic process

Symbol	Name	ID	FC (B/C)	FDR
<i>Ddc</i>	Dopa decarboxylase	Mm.12906	0.6	0.02162
<i>Hdc</i>	Histidine decarboxylase	Mm.18603	0.3	0.00264
<i>Tph2</i>	Tryptophan hydroxylase 2	Mm.31597	0.5	0.00555

<i>Atp7a</i>	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	Mm.254297	0.5	0.00295
<i>Azin1</i>	Antizyme inhibitor 1	Mm.250214	0.8	0.03106
<i>Odc1</i>	Ornithine decarboxylase, structural 1	Mm.34102	0.7	0.0073
GOID	299			
Integral to membrane of membrane fraction				
Symbol	Name	ID	FC (B/C)	FDR
<i>Mlc1</i>	Megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)	Mm.32780	0.6	0.00504
<i>Scarb1</i>	Scavenger receptor class B, member 1	Mm.282242	0.8	0.04218
<i>Atp7a</i>	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	Mm.254297	0.5	0.00295
<i>Cav1</i>	Caveolin 1, caveolae protein	Mm.28278	0.8	0.00991
GOID	42398			
Amino acid derivative biosynthetic process				
Symbol	Name	ID	FC (B/C)	FDR
<i>Ddc</i>	Dopa decarboxylase	Mm.12906	0.6	0.02162
<i>Hdc</i>	Histidine decarboxylase	Mm.18603	0.3	0.00264
<i>Tph2</i>	Tryptophan hydroxylase 2	Mm.31597	0.5	0.00555
<i>Atp7a</i>	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	Mm.254297	0.5	0.00295
<i>Azin1</i>	Antizyme inhibitor 1	Mm.250214	0.8	0.03106
<i>Odc1</i>	Ornithine decarboxylase, structural 1	Mm.34102	0.7	0.0073
GOID	7222			
Wnt receptor signaling pathway				
Symbol	Name	ID	FC (B/C)	FDR
<i>Fzd4</i>	Frizzled homolog 4 (Drosophila)	Mm.86755	0.7	0.02025
<i>Lrp6</i>	Low density lipoprotein receptor-related protein 6	Mm.321990	0.6	0.00124
<i>Slc9a3r1</i>	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Mm.27842	0.6	0.0168
<i>Sostdc1</i>	Sclerostin domain containing 1	Mm.43375	0.4	0.00338
<i>Ppap2b</i>	Phosphatidic acid phosphatase type 2B	Mm.348326	0.7	0.0337
GOID	46916			
Transition metal ion homeostasis				
Symbol	Name	ID	FC (B/C)	FDR
<i>Trf</i>	Transferrin	Mm.37214	0.6	0.04082
<i>Mt1</i>	Metallothionein 1	Mm.192991	0.4	0.00061
<i>Mt2</i>	Metallothionein 2	Mm.147226	0.5	0.00753
<i>Atp7a</i>	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	Mm.254297	0.5	0.00295
<i>Comm1d1</i>	COMM domain containing 1	Mm.259903	0.7	0.04083
<i>Pmd</i>	Prion protein dublet	Mm.180750	0.7	0.0251
<i>Tfrc</i>	Transferrin receptor	Mm.28683	0.8	0.03627
GOID	19886			
Antigen processing and presentation of exogenous peptide antigen via MHC class II				
Symbol	Name	ID	FC (B/C)	FDR
<i>Ctse</i>	Cathepsin E	Mm.230249	0.7	0.01433
<i>H2-Eb1</i>	Histocompatibility 2, class II antigen E beta	Mm.22564	0.6	0.03088

Fcεr1g Fc receptor, IgE, high affinity I, gamma polypeptide
H2-DMb2 Histocompatibility 2, class II, locus Mb2

Mm.22673 0.7 0.02424
Mm.195060 0.7 0.00769

GOID 1664

G-protein-coupled receptor binding

Symbol	Name	ID	FC (B/C)	FDR
<i>Slc9a3r1</i>	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Mm.27842	0.6	0.0168
<i>Ccl19</i>	PREDICTED: Mus musculus similar to EBI-1 ligand chemokine (LOC100039824), mRNA	Mm.258946	0.6	0.01225
<i>Cxcl10</i>	Chemokine (C-X-C motif) ligand 10	Mm.877	0.7	0.04727
<i>Ppbp</i>	Pro-platelet basic protein	Mm.293614	0.6	0.00572
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Mm.301626	0.3	0.00219
<i>Ccl25</i>	Chemokine (C-C motif) ligand 25	Mm.7275	0.7	0.03858
<i>Ccl5</i>	Chemokine (C-C motif) ligand 5	Mm.284248	0.7	0.02768

GOID 8009

Chemokine activity

Symbol	Name	ID	FC (B/C)	FDR
<i>Ccl19</i>	PREDICTED: Mus musculus similar to EBI-1 ligand chemokine (LOC100039824), mRNA	Mm.258946	0.6	0.01225
<i>Cxcl10</i>	Chemokine (C-X-C motif) ligand 10	Mm.877	0.7	0.04727
<i>Ppbp</i>	Pro-platelet basic protein	Mm.293614	0.6	0.00572
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Mm.301626	0.3	0.00219
<i>Ccl25</i>	Chemokine (C-C motif) ligand 25	Mm.7275	0.7	0.03858
<i>Ccl5</i>	Chemokine (C-C motif) ligand 5	Mm.284248	0.7	0.02768

C) GO terms upregulated in C at 8 months

GOID 3924

GTPase activity

Symbol	Name	ID	FC (B/C)	FDR
<i>Arl4c</i>	ADP-ribosylation factor-like 4C	Mm.27968	1.2	0.0017
<i>Ehd3</i>	EH-domain containing 3	Mm.18526	1.2	0.02191
<i>Gnai1</i>	Guanine nucleotide binding protein (G protein), alpha inhibiting 1	Mm.254629	1.2	0.0469
<i>Gnb1</i>	Guanine nucleotide binding protein (G protein), beta 1	Mm.2344	1.7	0.00507
<i>Gng3</i>	Guanine nucleotide binding protein (G protein), gamma 3 subunit	Mm.466502	1.3	0.02754
<i>Gnl2</i>	Guanine nucleotide binding protein-like 2 (nucleolar)	Mm.90760	1.5	0.02555
<i>Kras</i>	V-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	Mm.383182	1.6	0.00595
<i>Opa1</i>	Optic atrophy 1 homolog (human)	Mm.274285	1.4	0.03487
<i>Rab13</i>	RAB13, member RAS oncogene family	Mm.29355	2.0	0.00272
<i>Rab27a</i>	RAB27A, member RAS oncogene family	Mm.34867	1.5	0.01389
<i>Rab30</i>	RAB30, member RAS oncogene family	Mm.389966	1.4	0.013
<i>Rab38</i>	Rab38, member of RAS oncogene family	Mm.276669	1.4	0.04317
<i>Rras2</i>	Related RAS viral (r-ras) oncogene homolog 2	Mm.276572	1.8	0.00636
<i>Tuba4</i>	Tubulin, alpha 4A	Mm.1155	1.3	0.0234
<i>Arl6ip2</i>	ADP-ribosylation factor-like 6 interacting protein 2	Mm.175403	1.2	0.04487
<i>Cdc42</i>	Cell division cycle 42 homolog (S. cerevisiae)	Mm.1022	1.2	0.04577
<i>Dnm2</i>	Dynamamin 2	Mm.433257	1.6	0.02179
<i>Eef2</i>	Eukaryotic translation elongation factor 2	Mm.289431	1.2	0.02641

<i>Eif5b</i>	Eukaryotic translation initiation factor 5B	Mm.359728	1.4	0.01636
<i>Gna13</i>	Guanine nucleotide binding protein, alpha 13	Mm.193925	1.3	0.01652
<i>Nras</i>	Neuroblastoma ras oncogene	Mm.256975	1.4	0.00204
<i>Tubb2a</i>	Tubulin, beta 2A	Mm.469917	1.4	0.01084
<i>Tubb5</i>	Tubulin, beta 5	Mm.273538	1.2	0.0293
<i>Tubb6</i>	Tubulin, beta 6	Mm.181860	1.4	0.00798
<i>Gnai3</i>	Guanine nucleotide binding protein, alpha inhibiting 3	Mm.271703	1.2	0.03608
<i>Gnai2</i>	Guanine nucleotide binding protein, alpha inhibiting 2	Mm.196464	1.4	0.00787

GOID 6898

Receptor-mediated endocytosis

Symbol	Name	ID	FC (B/C)	FDR
<i>Ap1s2</i>	Adaptor-related protein complex 1, sigma 2 subunit	Mm.426783	1.3	0.00898
<i>Cap1</i>	CAP, adenylate cyclase-associated protein 1 (yeast)	Mm.8687	3.0	0.00026
<i>Cln3</i>	Ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Mm.268930	1.2	0.03413
<i>Fcgr1</i>	Fc receptor, IgG, high affinity I	Mm.150	1.2	0.01611
<i>Sor11</i>	Sortilin-related receptor, LDLR class A repeats-containing	Mm.121920	1.6	0.00229
<i>Hip1r</i>	Huntingtin interacting protein 1 related	Mm.149954	2.1	0.00474
<i>Igf2r</i>	Insulin-like growth factor 2 receptor	Mm.26553	1.6	0.03783
<i>Ppt1</i>	Palmitoyl-protein thioesterase 1	Mm.277719	1.3	0.02926

GOID 43256

Laminin-1 complex

Symbol	Name	ID	FC (B/C)	FDR
<i>Lama1</i>	Laminin, alpha 1	Mm.303386	1.5	0.0291
<i>Lamb1-1</i>	Laminin B1 subunit 1	Mm.172674	1.7	0.01413
<i>Lama5</i>	Laminin, alpha 5	Mm.4339	1.2	0.03245
<i>Lamc1</i>	laminin, gamma 1	Mm.1249	1.4	0.02634

GOID 5740

Mitochondrial envelope.

Symbol	Name	ID	FC (B/C)	FDR
<i>Bik</i>	Bcl2-interacting killer	Mm.267006	1.7	0.01911
<i>Bnip3l</i>	BCL2/adenovirus E1B interacting protein 3-like	Mm.29820	1.3	0.01858
<i>Cox6a1</i>	Cytochrome c oxidase, subunit VI a, polypeptide 1	Mm.43415	1.4	0.00134
<i>Sdhd</i>	Succinate dehydrogenase complex, subunit D, integral membrane protein	Mm.10406	1.3	0.03615
<i>Gatm</i>	Glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Mm.29975	2.0	0.01014
<i>Opa1</i>	Optic atrophy 1 homolog (human)	Mm.274285	1.4	0.03487
<i>Apex2</i>	Apurinic/apurimidinic endonuclease 2	Mm.440275	1.4	0.02551
<i>Atp5g1</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Mm.371547	1.4	0.0133
<i>Atp5j</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Mm.353	1.3	0.02276
<i>Chchd3</i>	Coiled-coil-helix-coiled-coil-helix domain containing 3	Mm.21501	1.2	0.02298
<i>Chdh</i>	Choline dehydrogenase	Mm.259916	1.2	0.04859
<i>Cul7</i>	Cullin 7	Mm.329078	1.4	0.00612
<i>Dhrs1</i>	Dehydrogenase/reductase (SDR family) member 1	Mm.21623	1.6	0.03597
<i>Etfdh</i>	Electron transferring flavoprotein, dehydrogenase	Mm.28336	1.2	0.0463

<i>Gpd2</i>	Glycerol phosphate dehydrogenase 2, mitochondrial	Mm.3711	1.3	0.01707
<i>Hadha</i>	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit	Mm.200497	1.2	0.03117
<i>Hadhb</i>	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit	Mm.291463	1.3	0.02761
<i>Hey2</i>	Hairy/enhancer-of-split related with YRPW motif 2	Mm.103573	1.5	0.00696
<i>Oclad2</i>	OCIA domain containing 2	Mm.274892	1.5	0.015
<i>Opa1</i>	Optic atrophy 1 homolog (human)	Mm.274285	1.4	0.03487
<i>Oxa1l</i>	Oxidase assembly 1-like	Mm.182340	1.4	0.01453
<i>Pcx</i>	Pyruvate carboxylase	Mm.1845	1.2	0.03576
<i>Sfxn2</i>	Sideroflexin 2	Mm.296837	1.8	0.01293
<i>Slc25a33</i>	Solute carrier family 25, member 33	Mm.41877	1.3	0.0245
<i>Sod2</i>	Superoxide dismutase 2, mitochondrial	Mm.290876	1.3	0.01273
<i>Spn</i>	SPEN homolog, transcriptional regulator (Drosophila)	Mm.299906	1.3	0.01105
<i>Bcs1l</i>	BCS1-like (yeast)	Mm.358700	1.2	0.04607
<i>Ak2</i>	Adenylate kinase 2	Mm.29460	1.2	0.01283
<i>Atp5c1</i>	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Mm.12677	1.2	0.04229
<i>Got2</i>	Glutamate oxaloacetate transaminase 2, mitochondrial	Mm.230169	1.2	0.03351
<i>Hmgcl</i>	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Mm.439940	1.2	0.01894
<i>Ndufa3</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	Mm.17851	1.2	0.03874
<i>Slc25a37</i>	Solute carrier family 25, member 37	Mm.293635	1.2	0.04901
<i>Sqrdl</i>	Sulfide quinone reductase-like (yeast)	Mm.28986	1.4	0.0169
<i>Srgap2</i>	SLIT-ROBO Rho GTPase activating protein 2	Mm.476747	1.3	0.04632
<i>Vdac1</i>	Voltage-dependent anion channel 1	Mm.3555	1.2	0.0469
<i>Vdac2</i>	Voltage-dependent anion channel 2	Mm.262327	1.2	0.04582
<i>Timm50</i>	Translocase of inner mitochondrial membrane 50 homolog (yeast)	Mm.167913	1.2	0.03862
<i>Atp5c1</i>	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	Mm.12677	1.2	0.04229
<i>Bcs1l</i>	BCS1-like (yeast)	Mm.358700	1.2	0.04607
<i>Tomm7</i>	Translocase of outer mitochondrial membrane 7 homolog (yeast)	Mm.291868	1.2	0.04906

GOID 19752

Carboxylic acid metabolic process

Symbol	Name	ID	FC (B/C)	FDR
<i>Nr1h4</i>	Nuclear receptor subfamily 1, group H, member 4	Mm.3095	2.2	0.006
<i>Cyp7b1</i>	Cytochrome P450, family 7, subfamily b, polypeptide 1	Mm.316000	1.2	0.034
<i>Adipor2</i>	Adiponectin receptor 2	Mm.291826	1.6	0.0136
<i>Agpat6</i>	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	Mm.200898	1.2	0.04273
<i>Hadha</i>	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, alpha subunit	Mm.200497	1.2	0.03117
<i>Hadhb</i>	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase, beta subunit	Mm.291463	1.3	0.02761
<i>Hao3</i>	Hydroxyacid oxidase (glycolate oxidase) 3	Mm.281874	1.5	0.03112
<i>Lpl</i>	Lipoprotein lipase	Mm.1514	2.8	0.00166
<i>Fasn</i>	Fatty acid synthase	Mm.236443	1.3	0.02554
<i>Abat</i>	4-aminobutyrate aminotransferase	Mm.259315	1.4	0.03002
<i>Pdk2</i>	Pyruvate dehydrogenase kinase, isoenzyme 2	Mm.29768	1.2	0.04975
<i>Gpd1</i>	Glycerol-3-phosphate dehydrogenase 1 (soluble)	Mm.252391	1.4	0.04886
<i>Gpd2</i>	Glycerol phosphate dehydrogenase 2, mitochondrial	Mm.3711	1.3	0.01707
<i>Gpt1</i>	Glutamic pyruvic transaminase 1, soluble	Mm.30130	1.5	0.0298
<i>Pcx</i>	Pyruvate carboxylase	Mm.1845	1.2	0.03576
<i>Acadl</i>	Acyl-Coenzyme A dehydrogenase, long-chain	Mm.2445	1.3	0.03291

<i>Gnpat</i>	Glyceronephosphate O-acyltransferase	Mm.29114	1.3	0.01744
<i>Hadh</i>	Hydroxyacyl-Coenzyme A dehydrogenase	Mm.260164	1.3	0.03981
<i>Hpgd</i>	Hydroxyprostaglandin dehydrogenase 15	Mm.18832	1.7	0.00203
<i>Pnpla8</i>	Patatin-like phospholipase domain containing 8	Mm.54126	1.2	0.04186
<i>Acot9</i>	Acyl-CoA thioesterase 9	Mm.268710	1.4	0.04529
<i>Scp2</i>	Sterol carrier protein 2, liver	Mm.379011	1.3	0.03312
<i>Ndufab1</i>	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	Mm.347976	1.2	0.0074
<i>Ptgs1</i>	Prostaglandin-endoperoxide synthase 1	Mm.275434	1.3	0.04084
<i>Elov16</i>	ELOVL family member 6, elongation of long chain fatty acids (yeast)	Mm.314113	1.7	0.0048
<i>Mapk14</i>	Mitogen-activated protein kinase 14	Mm.311337	1.2	0.00807

GOID 30865

Cortical cytoskeleton organization and biogenesis

Symbol	Name	ID	FC (B/C)	FDR
<i>Epb4.111</i>	Erythrocyte protein band 4.1-like 1	Mm.20852	2.2	0.00166
<i>Epb4.113</i>	Erythrocyte protein band 4.1-like 3	Mm.131135	1.3	0.02318
<i>Lasp1</i>	LIM and SH3 protein 1	Mm.271967	2.0	0.03689
<i>Calr</i>	Calreticulin	Mm.1971	1.6	0.02707
<i>Epb4.1</i>	Erythrocyte protein band 4.1	Mm.30038	1.2	0.02154

GOID 6778

Porphyrin metabolic process

Symbol	Name	ID	FC (B/C)	FDR
<i>Alad</i>	Aminolevulinate, delta-, dehydratase	Mm.6988	4.1	0.00058
<i>Alas1</i>	Aminolevulinic acid synthase 1	Mm.290578	1.5	0.00442
<i>Hmox1</i>	Heme oxygenase (decycling) 1	Mm.276389	1.4	0.01084
<i>Hebp1</i>	Heme binding protein 1	Mm.378937	1.4	0.00146
<i>Chd8</i>	Chromodomain helicase DNA binding protein 8	Mm.289934	1.3	0.035
<i>Sucla2</i>	Succinate-Coenzyme A ligase, ADP-forming, beta subunit	Mm.38951	1.3	0.02326

GOID 87

M phase of mitotic cell cycle

Symbol	Name	ID	FC (B/C)	FDR
<i>Cdc25a</i>	Cell division cycle 25 homolog A (S. cerevisiae)	Mm.307103	1.7	0.032
<i>Katna1</i>	Katanin p60 (ATPase-containing) subunit A1	Mm.28127	1.2	0.0396
<i>Mad111</i>	Mitotic arrest deficient 1-like 1	Mm.27250	1.3	0.019
<i>Terf1</i>	Telomeric repeat binding factor 1	Mm.4306	1.2	0.0374
<i>Mad111</i>	Mitotic arrest deficient 1-like 1	Mm.27250	1.3	0.0194
<i>Akap8</i>	A kinase (PRKA) anchor protein 8	Mm.328945	1.2	0.04576
<i>Anapc4</i>	Anaphase promoting complex subunit 4	Mm.272568	1.2	0.01892
<i>Ccnf</i>	Cyclin F	Mm.77695	1.6	0.00288
<i>Ccng1</i>	Cyclin G1	Mm.2103	1.3	0.03057
<i>Cdc20</i>	Cell division cycle 20 homolog	Mm.289747	1.3	0.02935
<i>Cdk2</i>	Cyclin-dependent kinase 2	Mm.111326	1.2	0.02355
<i>Clasp1</i>	CLIP associating protein 1	Mm.138740	1.2	0.04879

<i>Dctn2</i>	Dynactin 2	Mm.167537	1.3	0.04375
<i>Rcc1</i>	Regulator of chromosome condensation 1	Mm.255045	1.7	0.00164
<i>Rcc2</i>	Regulator of chromosome condensation 2	Mm.253	1.3	0.04719
<i>Spag5</i>	Sperm associated antigen 5	Mm.24250	1.2	0.00313
<i>Zwint</i>	ZW10 interactor	Mm.62876	1.2	0.02363
<i>Pes1</i>	Pescadillo homolog 1, containing BRCT doma	Mm.28659	1.4	0.00195
<i>Hectd3</i>	HECT domain containing 3	Mm.251420	1.4	0.01408
<i>Mad2l1bp</i>	MAD2L1 binding protein	Mm.272024	1.3	0.00975
<i>Tnfsf5ip1</i>	Tumor necrosis factor superfamily, member 5-induced protein 1	Mm.150701	1.3	0.02017
<i>Shc1</i>	Src homology 2 domain-containing transforming protein C1	Mm.86595	1.2	0.04123
<i>Tcf3</i>	Transcription factor 3	Mm.440067	1.2	0.02553

D) GO terms upregulated in D at 8 months

GOID 50880

Regulation of blood vessel size

Symbol	Name	ID	FC (B/C)	FDR
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Mm.301626	0.3	0.00053
<i>Edn1</i>	Endothelin 1	Mm.14543	0.7	0.01083
<i>Atp1a2</i>	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide	Mm.207432	0.5	0.00914
<i>Calca</i>	Calcitonin/calcitonin-related polypeptide, alpha	Mm.4361	0.6	0.04456
<i>Edn2</i>	Endothelin 2	Mm.284855	0.7	0.0383
<i>Cacna1c</i>	Calcium channel, voltage-dependent, L type, alpha 1C subunit	Mm.436656	0.8	0.03496
<i>ApoE</i>	Apolipoprotein E	Mm.305152	0.8	0.04082
<i>Ephx2</i>	Epoxide hydrolase 2, cytoplasmic	Mm.15295	0.8	0.03512

GOID 5720

Nuclear heterochromatin

Symbol	Name	ID	FC (B/C)	FDR
<i>Cbx5</i>	Chromobox homolog 5 (Drosophila HP1a)	Mm.262059	0.6	0.00379
<i>Dnmt3b</i>	DNA methyltransferase 3B	Mm.89772	0.8	0.0173
<i>Foxc1</i>	Foxc1: Forkhead box C1	Mm.12949	0.8	0.01077
<i>Suv39h2</i>	Suppressor of variegation 3-9 homolog 2 (Drosophila)	Mm.128273	0.7	0.02692
<i>Rnf2</i>	Ring finger protein 2	Mm.31512	0.9	0.04732
<i>H2afy</i>	H2A histone family, member Y	Mm.283802	0.8	0.04351

GOID 10038

Response to metal ion

Symbol	Name	ID	FC (B/C)	FDR
<i>Mt2</i>	Metallothionein 2	Mm.147226	0.5	0.0062
<i>D2hgdh</i>	D-2-hydroxyglutarate dehydrogenase	Mm.383401	0.8	0.0459
<i>Atp7a</i>	ATPase, Cu ⁺⁺ transporting, alpha polypeptide	Mm.254297	0.6	0.00577
<i>Mt1</i>	Metallothionein 1	Mm.192991	0.5	0.04487

GOID 8083

Growth factor activity

Symbol	Name	ID	FC (B/C)	FDR
<i>Gdf10</i>	Growth differentiation factor 10	Mm.432071	0.4	0.01828
<i>Gkn1</i>	Gastrokeine 1	Mm.46414	0.8	0.04778
<i>Pdgfb</i>	Platelet derived growth factor, B polypeptide	Mm.144089	0.7	0.04617
<i>Pgf</i>	Placental growth factor	Mm.4809	0.7	0.0399
<i>Spp1</i>	Secreted phosphoprotein 1	Mm.288474	0.4	0.00063
<i>Tgfb3</i>	Transforming growth factor, beta 3	Mm.307887	0.7	0.01689
<i>Cxcl12</i>	Chemokine (C-X-C motif) ligand 12	Mm.303231	0.8	0.03731
<i>Edn2</i>	Endothelin 2	Mm.284855	0.7	0.0383
<i>Rabep1</i>	Rabaptin, RAB GTPase binding effector protein 1	Mm.7087	0.7	0.00376
<i>Tgfb1</i>	Transforming growth factor, beta 1	Mm.248380	0.8	0.04228
<i>Vegfa</i>	Vascular endothelial growth factor A	Mm.282184	0.9	0.03781
<i>Il18</i>	Interleukin 18	Mm.1410	0.8	0.01171

GOID 19216

Regulation of lipid metabolic process

Symbol	Name	ID	FC (B/C)	FDR
<i>Bbs4</i>	Bardet-Biedl syndrome 4 homolog (human)	Mm.200714	0.8	0.04097
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Mm.301626	0.3	0.00053
<i>Ppargc1a</i>	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	Mm.259072	0.8	0.04458
<i>Ppara</i>	Peroxisome proliferator activated receptor alpha	Mm.212789	0.2	0.00385
<i>Edf1</i>	Endothelial differentiation-related factor 1	Mm.29945	0.8	0.03732

GOID 1664

G-protein-coupled receptor binding

Symbol	Name	ID	FC (B/C)	FDR
<i>Slc9a3r1</i>	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Mm.27842	0.7	0.03511
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Mm.301626	0.3	0.00053
<i>Edn1</i>	Endothelin 1	Mm.14543	0.7	0.01083
<i>Calca</i>	Calcitonin/calcitonin-related polypeptide, alpha	Mm.4361	0.6	0.04456
<i>Ccl19</i>	PREDICTED: Mus musculus similar to EBI-1 ligand chemokine (LOC100039824), mRNA	Mm.258946	0.6	0.01563
<i>Ccl9</i>	Chemokine (C-C motif) ligand 9	Mm.416125	0.5	0.01881
<i>Cxcl12</i>	Chemokine (C-X-C motif) ligand 12	Mm.303231	0.8	0.03731
<i>Cxcl16</i>	Chemokine (C-X-C motif) ligand 16	Mm.477542	0.7	0.03582

GOID 42773

ATP synthesis coupled electron transport

Symbol	Name	ID	FC (B/C)	FDR
<i>Ndufb2</i>	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	Mm.29415	0.8	0.01691
<i>Ndufs2</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 2	Mm.21669	0.8	0.02968

10020P15,RIKEN cDNA 1110020P15 gene

Ndufc2 NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2

Ndufs8 NADH dehydrogenase (ubiquinone) Fe-S protein 8

Mm.269736 0.7 0.01102

Mm.334031 0.7 0.03006

Mm.44227 0.8 0.01749