

**Supplemental table 1: Primers used for real-time RT-PCR validation**

Gene ID	NCBI accession number	Forward (5'-3')	Reverse (5'-3')	Annealing temperature (°C)	Amplicon length (bp)
Aatk	NM_001168703.1	GGGCCCCGATACTCTGCTCTC	CAGGGCCAAAGTTGGGTTTCG	60	115
Aif1	NM_017196.3	CCACCTAAGGCCACCAGCGT	AGTGCTTGTTGATCCCATCCAACC	60	121
C1qa	NM_001008515.1	CGGAGGCAGGAACATCATGGA	AATTCCTGCAACCCCGTCCT	58	130
C4b	NM_031504.3	TCAGGGTTACAGCCTCCGAA	TGGTTTGTCTGCACAGCCTCTA	58	111
Cd74	NM_013069.2	CAAACCTGTGAGCCCCGATGC	ACGGGTCCAGACTTCGTAAGC	60	153
Dnajb1	NM_001108441.1	CCAAGGAAGGGGACCAGACC	CCACAGAGAGCCTCCCGAAG	60	139
Fos	NM_022197.2	AGTAGAGCAGCTATCTCCTG	GGGCTGCCAAAATAAACTCC	56	215
Gapdh	NM_017008.3	AGGGCTGCCTTCTCTTGAC	TGGGTAGAATCATACTGGAACATGTAG	58	101
Ghrhr	NM_012850	CTGCTGTCTTCCAGGGTGAT	TAGGAGATGTGGAGGCCAAC	58	159
Glr1	NM_022278.1	TCCTCAGTCAACTGCCTTTC	TCCGCCTATGCAGTCTTTAC	58	152
Gpx2	NM_183403.2	TCGACATCAGGAGAACTGT	GTAGGGCAGCTTGCTTTCA	60	164
HLA-dra	NM_001008847.2	GCGGAAGCACTGGGAGTTTG	CGACGACGATGCCTACCAGA	58	104
Hspb7	NM_031607.1	ATCTCAGCCTAGGCCCCAGT	ATGTTGCTCCCCAAGTGGCT	60	167
Igfbp3	NM_012588.1	CGTCTCCTGGAAACACCACT	AGTTCTGGGTGTCTGTGC	60	204
Jun	NM_021835.3	ATCGACATGGAGTCTCAGGA	GTTTAAGCTGTGCCACCTGT	58	196
Nol3	NM_053516.2	GGAACACTGCGCTGTGCCC	GCCCAGGACATGTGGTCCCT	60	158
Nupr1	NM_053611.1	TATGTCGTCGGTGAGGTCG	TCCATTGCTGGGTGTGGTGT	60	188
Reg3b	S77413	TCCTGCCTGATGCTCTTATC	GCCAGTTCTGCATCAAACCA	58	155
Sstr3	NM_133522.1	TCTCTGGGTACCTGGTGGT	AGACGACACATGAGAGAGCC	60	212
Tradd	NM_001100480.1	AGCTCATAGTGAACCGGCCA	ATCCCTCAGTGCTCGACAGC	58	119
Xpa	NM_001106656.1	TTCATGAACCAGGGCCCGTCA	AGCATCTCTGCAGCTATCGCATG	58	125

**Supplemental table 2: List of genes regulated by aging in the anterior pituitary**

Gene Symbol	Gene Title	RefSeq Transcript ID	Fold change	Gene Ontology Biological Process
<b>Up-regulated</b>				
<i>Reg3b</i>	regenerating islet-derived 3 beta	NM_053289	<b>5,77</b>	acute-phase response
<i>Igha</i>	immunoglobulin heavy chain, alpha	---	<b>5,41</b>	
<i>Calcr</i>	calcitonin receptor	NM_001034015 /// NM_053816	<b>4,91</b>	signal transduction
<i>IgG-2a</i>	gamma-2a immunoglobulin heavy chain	XM_002726773	<b>3,88</b>	
<i>C4-2 /// C4b</i>	complement component 4, gene 2 /// complement component 4B	NM_001002805 /// NM_031504	<b>3,51</b>	inflammatory response
<i>Pcsk2</i>	proprotein convertase subtilisin/kexin type 2	NM_012746	<b>3,42</b>	proteolysis
<i>Slc6a15</i>	solute carrier family 6 (neutral amino acid transporter), member 15	NM_172321	<b>3,33</b>	transport
<i>Olfm3</i>	olfactomedin 3	NM_145777	<b>3,32</b>	eye photoreceptor cell development
<i>Esm1</i>	endothelial cell-specific molecule 1	NM_022604	<b>3,28</b>	regulation of cell growth
<i>Krt25</i>	keratin 25	NM_001008822	<b>3,22</b>	hair follicle morphogenesis
<i>Apod</i>	apolipoprotein D	NM_012777	<b>3,19</b>	transport
<i>Sez6</i>	seizure related 6 homolog (mouse)	NM_001105754 /// XM_001080832 /// XM_239260	<b>2,96</b>	
<i>Igfbp3</i>	insulin-like growth factor binding protein 3	NM_012588	<b>2,89</b>	regulation of cell growth
<i>Reg3a</i>	regenerating islet-derived 3 alpha	NM_001145846 /// NM_172077	<b>2,68</b>	acute-phase response
<i>Id3</i>	inhibitor of DNA binding 3	NM_013058	<b>2,67</b>	negative regulation of transcription from RNA polymerase II promoter
<i>Klk1b3</i>	kallikrein 1-related peptidase b3	NM_031523	<b>2,64</b>	proteolysis
<i>Tagln3</i>	transgelin 3	NM_001035236 /// NM_031676	<b>2,56</b>	muscle organ development
<i>Gpx2</i>	glutathione peroxidase 2	NM_183403	<b>2,56</b>	temperature homeostasis
<i>Akr1c19</i>	aldo-keto reductase family 1, member C19	NM_001100576	<b>2,50</b>	oxidation reduction
<i>Syn2</i>	synapsin II	NM_001034020 /// NM_019159	<b>2,44</b>	neurotransmitter secretion
<i>Cldn7</i>	claudin 7	NM_031702	<b>2,40</b>	calcium-independent cell-cell adhesion
<i>C1qa</i>	complement component 1, q subcomponent, A chain	NM_001008515	<b>2,37</b>	complement activation, classical pathway
<i>Nol3</i>	nucleolar protein 3 (apoptosis repressor with CARD domain)	NM_053516	<b>2,36</b>	response to hypoxia
<i>Igf1</i>	insulin-like growth factor 1	NM_001082477 /// NM_001082478 /// NM_001082479 /// NM_178866	<b>2,32</b>	osteoblast differentiation
<i>Cpxm2</i>	carboxypeptidase X (M14 family), member 2	NM_001106306	<b>2,29</b>	proteolysis
<i>Rasd1</i>	RAS, dexamethasone-induced 1	XM_001077321 /// XM_340809	<b>2,28</b>	signal transduction
<i>Serping1</i>	serine (or cysteine) peptidase inhibitor, clade G, member 1	NM_199093	<b>2,28</b>	negative regulation of complement activation, lectin pathway
<i>Trhr</i>	thyrotropin releasing hormone receptor	NM_013047	<b>2,26</b>	signal transduction
<i>Ascl1</i>	achaete-scute complex homolog 1 (Drosophila)	NM_022384	<b>2,23</b>	neuron migration
<i>Lix1</i>	Lix1 homolog (chicken)	NM_001106214	<b>2,22</b>	
<i>Ngb</i>	neuroglobin	NM_033359	<b>2,21</b>	transport
<i>Gpnmb</i>	glycoprotein (transmembrane) nmb	NM_133298	<b>2,20</b>	osteoblast differentiation
<i>Snca</i>	synuclein, beta	NM_080777	<b>2,19</b>	dopamine metabolic process
<i>Fmo5</i>	flavin containing monooxygenase 5	NM_144739	<b>2,19</b>	oxidation reduction
<i>Rgs5</i>	regulator of G-protein signaling 5	NM_019341	<b>2,16</b>	signal transduction

<i>Lrrc4c</i>	leucine rich repeat containing 4C	NM_001107753	<b>2,15</b>	regulation of axonogenesis
<i>C1qc</i>	complement component 1, q subcomponent, C chain	NM_001008524	<b>2,14</b>	complement activation, classical pathway
<i>Xdh</i>	xanthine dehydrogenase	NM_017154	<b>2,12</b>	lactation
<i>Nefh</i>	neurofilament, heavy polypeptide	NM_012607	<b>2,11</b>	microtubule cytoskeleton organization
<i>Nol4</i>	nucleolar protein 4	NM_001107401	<b>2,11</b>	
<i>Tmem229a</i>	transmembrane protein 229A	NM_001109480	<b>2,10</b>	
<i>Gfra3</i>	GDNF family receptor alpha 3	NM_053398	<b>2,09</b>	neuron migration
<i>Gucy1a3</i>	guanylate cyclase 1, soluble, alpha 3	NM_017090	<b>2,08</b>	cGMP biosynthetic process
<i>Lgals1</i>	lectin, galactoside-binding, soluble, 1	NM_019904	<b>2,06</b>	negative regulation of cell-substrate adhesion
<i>Cys1</i>	cystin 1	NM_001109597	<b>2,01</b>	
<i>Nt5dc1</i>	5'-nucleotidase domain containing 1	NM_001106393	<b>1,99</b>	
<i>Fcgr2a</i>	Fc fragment of IgG, low affinity IIa, receptor (CD32) /// Fc gamma receptor II b	NM_001135992 /// NM_053843	<b>1,99</b>	antibody-dependent cellular cytotoxicity
<i>Htra1</i>	HtrA serine peptidase 1	NM_031721	<b>1,97</b>	regulation of cell growth
<i>Apoe</i>	apolipoprotein E	NM_138828	<b>1,95</b>	negative regulation of endothelial cell proliferation
<i>Suds3</i>	Suppressor of defective silencing 3 homolog (S. cerevisiae)	XM_001080131 /// XM_341092	<b>1,95</b>	negative regulation of transcription
<i>Pcdh19</i>	protocadherin 19	NM_001169129	<b>1,95</b>	cell adhesion
<i>Myo1b</i>	myosin Ib	NM_053986	<b>1,93</b>	nervous system development
<i>Rnf180</i>	ring finger protein 180	NM_001134986	<b>1,93</b>	positive regulation of proteasomal ubiquitin-dependent protein catabo
<i>Gabra1</i>	gamma-aminobutyric acid (GABA) A receptor, alpha 1	NM_183326	<b>1,93</b>	transport
<i>Ptp4a3</i>	protein tyrosine phosphatase 4a3	NM_001114405	<b>1,93</b>	protein dephosphorylation
<i>Crtac1</i>	cartilage acidic protein 1	NM_134401	<b>1,92</b>	
<i>Mtmr1</i>	Myotubularin related protein 1	NM_001191725 /// XM_001059230 /// XM_228644	<b>1,91</b>	dephosphorylation
<i>Gabrg2</i>	gamma-aminobutyric acid (GABA) A receptor, gamma 2	NM_183327	<b>1,91</b>	transport
<i>Rhobtb3</i>	Rho-related BTB domain containing 3	NM_001107645	<b>1,90</b>	retrograde transport, endosome to Golgi
<i>Ccdc88b</i>	coiled-coil domain containing 88B	NM_001108517	<b>1,90</b>	protein phosphorylation
<i>Plekhhb1</i>	pleckstrin homology domain containing, family B (evectins) member 1	NM_172033	<b>1,89</b>	regulation of cell differentiation
<i>Cdcp1</i>	CUB domain containing protein 1	NM_001106869	<b>1,87</b>	
<i>Retsat</i>	retinol saturase (all trans retinol 13,14 reductase)	NM_145084	<b>1,87</b>	retinol metabolic process
<i>Brunol5</i>	bruno-like 5, RNA binding protein (Drosophila)	NM_001135603	<b>1,87</b>	
<i>Efh1</i>	EF-hand domain family, member D1	NM_001109310	<b>1,86</b>	neuron projection development
<i>Gria4</i>	glutamate receptor, ionotropic, AMPA4	NM_001113184 /// NM_001113185 /// NM_017263	<b>1,86</b>	transport
<i>Myo1d</i>	myosin ID	NM_012983	<b>1,84</b>	transport
<i>Lppr5</i>	lipid phosphate phosphatase-related protein type 5	NM_001107720	<b>1,84</b>	
<i>Ahcyl2</i>	adenosylhomocysteinase-like 2	NM_001173510 /// XM_001062287 /// XM_231564	<b>1,84</b>	one-carbon metabolic process
<i>Arsb</i>	arylsulfatase B	NM_033443	<b>1,83</b>	autophagy
<i>Vegfa</i>	vascular endothelial growth factor A	NM_001110333 /// NM_001110334 /// NM_001110335 /// NM_001110336 /// NM_031836	<b>1,82</b>	angiogenesis
<i>Adipoq</i>	adiponectin, C1Q and collagen domain containing	NM_144744	<b>1,82</b>	response to hypoxia
<i>Agtr1b</i>	angiotensin II receptor, type 1b	NM_031009	<b>1,82</b>	blood vessel development

<i>Cdkn1c</i>	cyclin-dependent kinase inhibitor 1C	NM_001033757 /// NM_001033758 /// NM_182735	<b>1,81</b>	negative regulation of transcription from RNA polymerase II promoter
<i>Kitlg</i>	KIT ligand	NM_021843 /// NM_021844	<b>1,80</b>	ovarian follicle development
<i>Gulp1</i>	GULP, engulfment adaptor PTB domain containing 1	NM_001013171	<b>1,79</b>	transport
<i>Atp2b3</i>	ATPase, Ca++ transporting, plasma membrane 3	NM_133288	<b>1,79</b>	neural retina development
<i>Cadps2</i>	Ca++-dependent secretion activator 2	XM_001060172 /// XM_002726328 /// XM_002726329 /// XM_002726330 /// XM_002726331	<b>1,78</b>	positive regulation of exocytosis
<i>Accn4</i>	amiloride-sensitive cation channel 4, pituitary	NM_022234	<b>1,77</b>	transport
<i>Khdrbs2</i>	KH domain containing, RNA binding, signal transduction associated 2	NM_133318	<b>1,77</b>	transcription
<i>Aqp1</i>	aquaporin 1	NM_012778	<b>1,77</b>	glomerular filtration
<i>Glrx1</i>	glutaredoxin 1	NM_022278	<b>1,77</b>	transport
<i>Sox4</i>	SRY (sex determining region Y)-box 4	XM_001068302 /// XM_344594	<b>1,77</b>	response to hypoxia
<i>Rimkb</i>	ribosomal modification protein rimK-like family member B	XM_001060530 /// XM_342749	<b>1,76</b>	protein modification process
<i>Plch2</i>	Phospholipase C, eta 2	XM_001077247 /// XM_233728	<b>1,76</b>	lipid metabolic process
<i>Ifitm1</i>	interferon induced transmembrane protein 1	NM_001106314	<b>1,76</b>	response to biotic stimulus
<i>Fcgrt</i>	Fc fragment of IgG, receptor, transporter, alpha	NM_033351	<b>1,75</b>	immune response
<i>Gpr162</i>	G protein-coupled receptor 162	NM_001108646	<b>1,74</b>	G-protein coupled receptor protein signaling pathway
<i>Gabrd</i>	gamma-aminobutyric acid (GABA) A receptor, delta	NM_017289	<b>1,74</b>	transport
<i>Myh14</i>	myosin, heavy chain 14	NM_001100690	<b>1,73</b>	ATP catabolic process
<i>Dync1i1</i>	dynein cytoplasmic 1 intermediate chain 1	NM_019234	<b>1,71</b>	transport
<i>Zbtb4</i>	zinc finger and BTB domain containing 4	XM_001079524 /// XM_220612	<b>1,71</b>	
<i>Bend5</i>	BEN domain containing 5	NM_001108672	<b>1,71</b>	
<i>Ssfa2</i>	sperm specific antigen 2	NM_001107738	<b>1,70</b>	
<i>Ap1s2</i>	adaptor-related protein complex 1, sigma 2 subunit	NM_001127531	<b>1,69</b>	transport
<i>Pgcp</i>	plasma glutamate carboxypeptidase	NM_031640	<b>1,68</b>	proteolysis
<i>Stmn2</i>	stathmin-like 2	NM_053440	<b>1,68</b>	negative regulation of microtubule depolymerization
<i>Igf2</i>	insulin-like growth factor 2	NM_001190162 /// NM_001190163 /// NM_031511	<b>1,68</b>	ossification
<i>Dgkb</i>	diacylglycerol kinase, beta	NM_019304	<b>1,68</b>	activation of protein kinase C activity by G-protein coupled receptor
<i>Ccdc30</i>	coiled-coil domain containing 30	XM_001073839 /// XM_342899	<b>1,68</b>	cell-matrix adhesion
<i>Fam151b</i>	family with sequence similarity 151, member B	NM_001134748	<b>1,67</b>	
<i>Cgnl1</i>	cingulin-like 1	NM_001108164	<b>1,67</b>	
<i>Kcnq2</i>	potassium voltage-gated channel, KQT-like subfamily, member 2	NM_133322	<b>1,66</b>	transport
<i>C1qb</i>	complement component 1, q subcomponent, B chain	NM_019262	<b>1,66</b>	immune response
<i>Pah</i>	phenylalanine hydroxylase	NM_012619	<b>1,65</b>	L-phenylalanine metabolic process
<i>Fos</i>	FBJ osteosarcoma oncogene	NM_022197	<b>1,65</b>	conditioned taste aversion
<i>Cndp2</i>	CNDP dipeptidase 2 (metallopeptidase M20 family)	NM_001010920	<b>1,65</b>	proteolysis
<i>Sept_4</i>	septin 4	NM_001011893	<b>1,64</b>	cell cycle
<i>Sh3kbp1</i>	SH3-domain kinase binding protein 1	NM_053360	<b>1,64</b>	endocytosis
<i>Anxa4</i>	annexin A4	NM_024155	<b>1,64</b>	exocytosis
<i>Lgals3bp</i>	lectin, galactoside-binding, soluble, 3 binding protein	NM_139096	<b>1,64</b>	cell adhesion
<i>Cirbp</i>	cold inducible RNA binding protein	NM_031147	<b>1,63</b>	response to stress
<i>Atp5s</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	NM_001007749	<b>1,63</b>	ATP biosynthetic process

<i>Hspb8</i>	heat shock protein B8	NM_053612	1,63	response to stress
<i>Ubxn8</i>	UBX domain protein 8	NM_001106086	1,63	
<i>Palmd</i>	palmdelphin	NM_001025688	1,62	regulation of cell shape
<i>Ptpd</i>	protein tyrosine phosphatase, receptor type, D	XM_001067936 /// XM_233065	1,62	protein dephosphorylation
<i>Amn1</i>	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	NM_001008333	1,62	
<i>Map2k6</i>	mitogen-activated protein kinase kinase 6	NM_053703	1,62	MAPKKK cascade
<i>Rbbp9</i>	retinoblastoma binding protein 9	NM_019219	1,62	regulation of cell proliferation
<i>Nup54</i>	nucleoporin 54	NM_017361	1,62	protein targeting
<i>Pde1a</i>	phosphodiesterase 1A, calmodulin-dependent	NM_030871	1,62	cAMP catabolic process
<i>Gphn</i>	gephyrin	NM_022865	1,62	protein targeting
<i>F2r</i>	coagulation factor II (thrombin) receptor	NM_012950	1,61	activation of MAPKK activity
<i>Ttyh1</i>	tweety homolog 1 (Drosophila)	NM_001106225	1,61	transport
<i>Ccnd1</i>	cyclin D1	NM_171992	1,61	G1/S transition of mitotic cell cycle
<i>Cmb1</i>	carboxymethylenebutenolidase homolog (Pseudomonas)	NM_001008770	1,61	
<i>Mlc1</i>	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)	NM_001108105	1,61	
<i>Ctss</i>	cathepsin S	NM_017320	1,60	proteolysis
<i>Ptgr1</i>	prostaglandin reductase 1	NM_138863	1,60	metabolic process
<i>Flot1</i>	flotillin 1	NM_022701	1,60	
<i>Cebpd</i>	CCAAT/enhancer binding protein (C/EBP), delta	NM_013154	1,60	transcription
<i>Krt18</i>	keratin 18	NM_053976	1,59	apoptosis
<i>Pdxp</i>	pyridoxal (pyridoxine, vitamin B6) phosphatase	NM_001135819	1,59	metabolic process
<i>Ddx41</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	NM_001108046	1,59	
<i>Mmg2</i>	membrane magnesium transporter 2	NM_001013967	1,59	transport
<i>Pex5l</i>	peroxisomal biogenesis factor 5-like	NM_173152	1,59	regulation of membrane potential
<i>Tapbp</i>	TAP binding protein	NM_033098	1,58	MHC class I protein complex assembly
<i>Skap2</i>	src kinase associated phosphoprotein 2	NM_130413	1,58	negative regulation of cell proliferation
<i>Tnr</i>	tenascin R	NM_013045	1,58	cell adhesion
<i>Npas2</i>	neuronal PAS domain protein 2	NM_001108214	1,58	regulation of transcription, DNA-dependent
<i>S100a6</i>	S100 calcium binding protein A6	NM_053485	1,58	
<i>Gpm6a</i>	glycoprotein m6a	NM_178105	1,58	
<i>Khl13</i>	kelch-like 13 (Drosophila)	XM_001061200 /// XM_002727661 /// XM_002730180 /// XM_233297	1,57	cytokinesis
<i>Soat1</i>	sterol O-acyltransferase 1	NM_031118	1,57	lipid metabolic process
<i>Tgfb1</i>	transforming growth factor, beta induced	NM_053802	1,57	chondrocyte differentiation
<i>Znf521</i>	zinc finger protein 521	NM_001107403	1,57	
<i>Ppp4r2</i>	protein phosphatase 4, regulatory subunit 2	NM_001106613	1,57	
<i>Lrrc23</i>	leucine rich repeat containing 23	NM_001013165	1,57	
<i>Evl</i>	Enah/Vasp-like	NM_024147	1,57	cellular component movement
<i>Camta1</i>	similar to KIAA0833 protein	NM_001195559 /// NM_001195560 /// XM_002726619 /// XM_002729575	1,57	
<i>Pcbp3</i>	poly(rC) binding protein 3	NM_001011945	1,56	
<i>Zbtb22</i>	zinc finger and BTB domain containing 22	NM_001009172	1,56	
<i>Syne1</i>	spectrin repeat containing, nuclear envelope 1	NM_001029909	1,55	Golgi organization
<i>Vipr2</i>	vasoactive intestinal peptide receptor 2	NM_017238	1,55	signal transduction
<i>Nosip</i>	nitric oxide synthase interacting protein	NM_001106260	1,55	negative regulation of catalytic activity
<i>Fchsd2</i>	FCH and double SH3 domains 2	NM_001107539	1,55	

<i>Kcnip4</i>	Kv channel interacting protein 4	NM_181365	1,55	transport
<i>Pir</i>	pirin (iron-binding nuclear protein)	NM_001009474	1,55	
<i>Xpa</i>	xeroderma pigmentosum, complementation group A	NM_001106656	1,54	nucleotide-excision repair, DNA damage removal
<i>Cdo1</i>	cysteine dioxygenase, type I	NM_052809	1,54	cysteine metabolic process
<i>Rprm</i>	represso, TP53 dependent G2 arrest mediator candidate	NM_001044276	1,54	cell cycle arrest
<i>Caly</i>	calcyon neuron-specific vesicular protein	NM_001190399 /// NM_138915	1,54	endocytosis
<i>Ehd3</i>	EH-domain containing 3	NM_138890	1,54	
<i>Kcnd3</i>	potassium voltage-gated channel, Shal-related subfamily, member 3	NM_031739	1,54	transport
<i>Rrm1</i>	ribonucleotide reductase M1	NM_001013236	1,53	DNA replication
<i>Traf3ip2</i>	Traf3 interacting protein 2	NM_001044248	1,53	B cell apoptosis
<i>Eid2b</i>	EP300 interacting inhibitor of differentiation 2B	XM_002725600 /// XM_574407	1,53	
<i>Id2</i>	inhibitor of DNA binding 2	NM_013060	1,53	negative regulation of transcription from RNA polymerase II promoter
<i>Raph1</i>	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	NM_001108798	1,53	signal transduction
<i>Wfdc2</i>	WAP four-disulfide core domain 2	NM_173109	1,53	
<i>Tcf20</i>	transcription factor 20	NM_001130574	1,53	positive regulation of gene-specific transcription from RNA polymeras
<i>Tspan8</i>	tetraspanin 8	NM_133526	1,53	negative regulation of blood coagulation
<i>Tspo</i>	translocator protein	NM_012515	1,53	steroid biosynthetic process
<i>Etv1</i>	Ets variant 1	NM_001108709 /// NM_001163156	1,53	regulation of transcription, DNA-dependent
<i>Pcdhb9</i>	protocadherin beta 9	NM_001109390	1,53	cell adhesion
<i>Hist2h2be</i>	histone cluster 2, H2be	XM_001061909 /// XM_227459	1,52	nucleosome assembly
<i>Sorbs2</i>	sorbin and SH3 domain containing 2	NM_053770	1,52	
<i>Nfix</i>	nuclear factor I/X (CCAAT-binding transcription factor)	NM_030866	1,52	DNA replication
<i>Cpne5</i>	copine V	NM_001107616	1,52	
<i>Tox3</i>	TOX high mobility group box family member 3	NM_001106171	1,52	
<i>Zfhx4</i>	zinc finger homeobox 4	NM_001191702 /// XM_001058915 /// XM_226964	1,52	regulation of transcription, DNA-dependent
<i>Galm</i>	galactose mutarotase (aldose 1-epimerase)	NM_001007704	1,52	carbohydrate metabolic process
<i>Rpa2</i>	replication protein A2	NM_021582	1,52	nucleotide-excision repair, DNA damage removal
<i>Klc3</i>	kinesin light chain 3	NM_138520	1,52	metabolic process
<i>Fam172a</i>	family with sequence similarity 172, member A	NM_001106401	1,52	
<i>Csgalnact1</i>	chondroitin sulfate N-acetylgalactosaminyltransferase 1	NM_001107309	1,51	UDP-N-acetylgalactosamine metabolic process
<i>Slc12a5</i>	solute carrier family 12 (potassium-chloride transporter), member 5	NM_134363	1,51	transport
<i>Gstz1</i>	glutathione transferase zeta 1	NM_001109445	1,51	aromatic amino acid family metabolic process
<i>Chchd6</i>	coiled-coil-helix-coiled-coil-helix domain containing 6	NM_001106608	1,51	
<i>Pex7</i>	peroxisomal biogenesis factor 7	NM_001034147	1,51	neuron migration
<i>Fam117b</i>	family with sequence similarity 117, member B	NM_001108797	1,50	
<i>Agtrap</i>	angiotensin II receptor-associated protein	NM_001007654	1,50	response to hypoxia
<i>Tipi</i>	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	NM_001177321 /// NM_017200	1,50	blood coagulation
<i>Ppap2b</i>	phosphatidic acid phosphatase type 2B	NM_138905	1,50	blood vessel development
<i>Gpsm1</i>	G-protein signaling modulator 1 (AGS3-like, C. elegans)	NM_001145469 /// NM_144745	1,50	signal transduction

<i>Dpp6</i>	dipeptidylpeptidase 6	NM_022850	1,50	proteolysis
<i>Vangl1</i>	vang-like 1 (van gogh, Drosophila)	NM_001109584	1,49	multicellular organismal development
<i>Rab34</i>	RAB34, member RAS oncogene family	NM_001012140	1,49	GTP catabolic process
<i>Ati1</i>	atlastin GTPase 1	NM_001009831	1,49	endoplasmic reticulum organization
<i>H2afj</i>	H2A histone family, member J	NM_001109610	1,49	nucleosome assembly
<i>Capn1</i>	calpain 1	NM_019152	1,49	proteolysis
<i>Fam110c</i>	family with sequence similarity 110, member C	NM_001025051	1,49	
<i>Srbd1</i>	S1 RNA binding domain 1	XM_001059624 /// XM_237474	1,49	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process DNA replication
<i>Rfc4</i>	replication factor C (activator 1) 4	NM_001105869	1,49	
<i>Fam173a</i>	family with sequence similarity 173, member A	NM_001127447	1,49	
<i>Cd82</i>	Cd82 molecule	NM_031797	1,49	
<i>Med30</i>	mediator complex subunit 30	NM_001130539	1,48	transcription initiation from RNA polymerase II promoter
<i>Pcgf6</i>	polycomb group ring finger 6	NM_001013154	1,48	transcription
<i>Apbb1</i>	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	NM_080478	1,48	neuron migration
<i>Dnlz</i>	DNL-type zinc finger	NM_001130990 /// NR_024073	1,48	
<i>Jun</i>	Jun oncogene	NM_021835	1,48	angiogenesis
<i>Efcab4a</i>	EF-hand calcium binding domain 4A	NM_001127541	1,47	store-operated calcium entry
<i>Pbxip1</i>	pre-B-cell leukemia homeobox interacting protein 1	NM_001100976	1,47	
<i>Cpt1a</i>	carnitine palmitoyltransferase 1a, liver	NM_031559	1,47	long-chain fatty acid metabolic process
<i>Eef2k</i>	eukaryotic elongation factor-2 kinase	NM_012947	1,47	protein phosphorylation
<i>Ntan1</i>	N-terminal asparagine amidase	NM_001025124	1,47	memory
<i>Bat5</i>	HLA-B associated transcript 5	NM_212531	1,47	
<i>Pde6d</i>	phosphodiesterase 6D, cGMP-specific, rod, delta	NM_001108806	1,47	visual perception
<i>Cadm1</i>	cell adhesion molecule 1	NM_001012201	1,47	liver development
<i>Ift81</i>	intraflagellar transport 81 homolog (Chlamydomonas)	NM_199120	1,47	multicellular organismal development
<i>Rtn1</i>	reticulon 1	NM_053865	1,47	neuron differentiation
<i>Kcnc2</i>	potassium voltage gated channel, Shaw-related subfamily, member 2	NM_139216 /// NM_139217	1,47	transport
<i>Tradd</i>	TNFRSF1A-associated via death domain	NM_001100480	1,47	apoptosis
<i>Tmem106a</i>	transmembrane protein 106A	NM_001024967	1,47	
<i>Cfb</i>	complement factor B	NM_212466	1,46	proteolysis
<i>Rab3c</i>	RAB3C, member RAS oncogene family	NM_133536	1,46	transport
<i>Slc43a2</i>	solute carrier family 43, member 2	NM_001105812	1,46	amino acid transmembrane transport
<i>Pcca</i>	propionyl-coenzyme A carboxylase, alpha polypeptide	NM_019330	1,46	metabolic process
<i>Rsbn1</i>	round spermatid basic protein 1	NM_001191710 /// XM_001065582 /// XM_227540	1,46	
<i>Blcap</i>	bladder cancer associated protein homolog (human)	NM_133582	1,46	apoptosis
<i>Pm20d2</i>	peptidase M20 domain containing 2	NM_001107922	1,45	metabolic process
<i>Amigo2</i>	adhesion molecule with Ig like domain 2	NM_182816	1,45	anti-apoptosis
<i>Pcmt2</i>	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	NM_001107810	1,45	protein modification process
<i>Rgs10</i>	regulator of G-protein signaling 10	NM_019337	1,45	regulation of G-protein coupled receptor protein signaling pathway
<i>Rbmx</i>	RNA binding motif protein, X-linked	NM_001025663	1,45	mRNA splice site selection
<i>Ubxn6</i>	UBX domain protein 6	NM_001108812	1,45	
<i>Nsbp1</i>	nucleosomal binding protein 1	NM_001134706	1,45	transcription
<i>Prkcz</i>	protein kinase C, zeta	NM_022507	1,45	microtubule cytoskeleton organization

<i>Calhm2</i>	calcium homeostasis modulator 2	NM_001008306	1,45	
<i>Meis1</i>	Meis homeobox 1	NM_001134702	1,45	angiogenesis
<i>Ccl11</i>	chemokine (C-C motif) ligand 11	NM_019205	1,45	positive regulation of endothelial cell proliferation
<i>Ccdc90b</i>	coiled-coil domain containing 90B	NM_001024885	1,44	
<i>Apc2</i>	adenomatosis polyposis coli 2	NM_001106769	1,44	Wnt receptor signaling pathway
<i>Dnajc12</i>	DnaJ (Hsp40) homolog, subfamily C, member 12	NM_001034032	1,44	
<i>Klc4</i>	kinesin light chain 4	NM_001009601	1,44	
<i>Fcho2</i>	FCH domain only 2	NM_001191632 /// XM_002728999 /// XM_219503	1,44	
<i>Aldh16a1</i>	aldehyde dehydrogenase 16 family, member A1	NM_001033706	1,44	metabolic process
<i>St18</i>	suppression of tumorigenicity 18	NM_153310	1,44	negative regulation of transcription from RNA polymerase II promoter
<i>Ifitm3</i>	interferon induced transmembrane protein 3	NM_001136124	1,44	negative regulation of cell proliferation
<i>Rsrc1</i>	arginine/serine-rich coiled-coil 1	NM_001014172	1,44	alternative nuclear mRNA splicing, via spliceosome
<i>Syngr2</i>	synaptogyrin 2	NM_053553	1,43	protein targeting
<i>Gpr149</i>	G protein-coupled receptor 149	NM_138891	1,43	signal transduction
<i>Ncor1</i>	Nuclear receptor co-repressor 1	XM_001077495 /// XM_577103	1,43	negative regulation of transcription from RNA polymerase II promoter
<i>Znf467</i>	zinc finger protein 467	NM_001024327	1,43	transcription
<i>Odf2l</i>	outer dense fiber of sperm tails 2-like	NM_001134708	1,43	
<i>Ebna1bp2</i>	EBNA1 binding protein 2	NM_001008721	1,43	
<i>Mettl7a</i>	methyltransferase like 7A	NM_001037355	1,43	metabolic process
<i>Cnnm3</i>	cyclin M3	NM_001106901	1,43	
<i>Tspan33</i>	tetraspanin 33	NM_001109227	1,43	
<i>Tob1</i>	transducer of ErbB-2.1	NM_133317	1,43	SMAD protein nuclear translocation
<i>Ctnnbl1</i>	catenin, beta like 1	NM_001024870	1,43	apoptosis
<i>Klc1</i>	kinesin light chain 1	NM_001081972 /// NM_001081973 /// NM_001081974	1,43	axon cargo transport
<i>Suclg2</i>	succinate-CoA ligase, GDP-forming, beta subunit	NM_001100750	1,43	tricarboxylic acid cycle
<i>Cd151</i>	CD151 molecule (Raph blood group)	NM_022523	1,43	hemidesmosome assembly
<i>Sh3bgrl3</i>	SH3 domain binding glutamic acid-rich protein-like 3	NM_001106688	1,43	cell redox homeostasis
<i>Gcnt2</i>	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	NM_001001511	1,42	metabolic process
<i>Hes1</i>	hairy and enhancer of split 1 (Drosophila)	NM_024360	1,42	negative regulation of transcription from RNA polymerase II promoter
<i>Ltbp3</i>	latent transforming growth factor beta binding protein 3	NM_001191561 /// XM_002725776 /// XM_002728859	1,42	skeletal system development
<i>L1cam</i>	L1 cell adhesion molecule	NM_017345	1,42	cell adhesion
<i>Arse</i>	arylsulfatase E (chondrodysplasia punctata 1)	NM_001047885	1,42	metabolic process
<i>Rassf6</i>	Ras association (RalGDS/AF-6) domain family member 6	NM_001025671	1,42	apoptosis
<i>Aif1</i>	allograft inflammatory factor 1	NM_017196	1,42	positive regulation of protein phosphorylation
<i>Eif5a2</i>	eukaryotic translation initiation factor 5A2	NM_001100697 /// XM_001063995 /// XM_226974	1,42	translational frameshifting
<i>Ryr2</i>	ryanodine receptor 2, cardiac	NM_001191043 /// NM_032078	1,42	detection of calcium ion
<i>B3galnt1</i>	beta-1,3-N-acetylgalactosaminyltransferase 1	NM_001013158	1,42	protein glycosylation
<i>Rundc3b</i>	RUN domain containing 3B	NM_001047116	1,42	
<i>Ctbp2</i>	C-terminal binding protein 2	NM_053335	1,42	transcription
<i>Gpx4</i>	glutathione peroxidase 4	NM_001039849 /// NM_017165	1,42	chromatin organization



<i>Fbxl4</i>	F-box and leucine-rich repeat protein 4	NM_001107919	1,41	
<i>Slco3a1</i>	Solute carrier organic anion transporter family, member 3a1	NM_177481	1,41	transport
<i>Bcap29</i>	B-cell receptor-associated protein 29	NM_001006980	1,41	intracellular protein transport
<i>Ctsz</i>	cathepsin Z	NM_183330	1,41	proteolysis
<i>Exoc2</i>	exocyst complex component 2	NM_134414	1,41	transport
<i>Camk2d</i>	calcium/calmodulin-dependent protein kinase II delta	NM_012519	1,41	G1/S transition of mitotic cell cycle
<i>Msl1</i>	male-specific lethal 1 homolog (Drosophila)	NM_001107048	1,41	
<i>St6gal1</i>	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	NM_001113344 /// NM_147205	1,41	protein glycosylation
<i>Aarsd1</i>	alanyl-tRNA synthetase domain containing 1	NM_001034109	1,41	translation
<i>Nme4</i>	non-metastatic cells 4, protein expressed in	NM_001109478	1,41	GTP biosynthetic process
<i>Lmo4</i>	LIM domain only 4	NM_001009708	1,41	neural tube closure
<i>Cadps</i>	Ca++-dependent secretion activator	NM_013219	1,41	transport
<i>Lman2l</i>	lectin, mannose-binding 2-like	NM_001106900	1,41	protein transport
<i>Pnpla2</i>	patatin-like phospholipase domain containing 2	NM_001108509	1,41	lipid metabolic process
<i>Nrxn1</i>	neurexin 1	NM_021767	1,41	cell adhesion
<i>Lrg1</i>	leucine-rich alpha-2-glycoprotein 1	NM_001009717	1,41	brown fat cell differentiation
<i>Znf292</i>	zinc finger protein 292	NM_001008879	1,40	
<i>Camk1</i>	calcium/calmodulin-dependent protein kinase I	NM_134468	1,40	protein phosphorylation
<i>Vwc2</i>	von Willebrand factor C domain containing 2	NM_001109312	1,40	positive regulation of cell-substrate adhesion
<i>Ublcp1</i>	ubiquitin-like domain containing CTD phosphatase 1	NM_001014117	1,40	
<i>Mlh3</i>	mutL homolog 3 (E. coli)	NM_001108043	1,40	mismatch repair
<i>Gstp1</i>	glutathione S-transferase pi 1	NM_012577	1,40	glutathione metabolic process
<i>Chrac1</i>	chromatin accessibility complex 1	NM_001134880	1,39	
<i>Hopx</i>	HOP homeobox	NM_133621	1,39	negative regulation of transcription from RNA polymerase II promoter
<i>Fancl</i>	Fanconi anemia, complementation group L	NM_001191684 /// XM_001064256 /// XM_223701	1,39	gamete generation
<i>Nudt14</i>	nudix (nucleoside diphosphate linked moiety X)-type motif 14	NM_001106760	1,39	
<i>Gtpbp10</i>	GTP-binding protein 10 (putative)	NM_001100815	1,39	
<i>Dlg3</i>	discs, large homolog 3 (Drosophila)	NM_031639	1,39	
<i>Grk6</i>	G protein-coupled receptor kinase 6	NM_001112712 /// NM_001112713 /// NM_031657	1,39	protein phosphorylation
<i>Mdga2</i>	MAM domain containing glycosylphosphatidylinositol anchor 2	NM_199269	1,39	spinal cord motor neuron differentiation
<i>Pdpf</i>	pancreatic progenitor cell differentiation and proliferation factor homolog (zeb	NM_001009316	1,39	multicellular organismal development
<i>Fam60a</i>	family with sequence similarity 60, member A	NM_001134711 /// NM_001134712	1,39	
<i>Sec16a</i>	SEC16 homolog A (S. cerevisiae)	XM_002726072 /// XM_002729145	1,39	lipid metabolic process
<i>Acn9</i>	ACN9 homolog (S. cerevisiae)	NM_001047914	1,39	
<i>Inpp1</i>	inositol polyphosphate-1-phosphatase	NM_001012131	1,39	
<i>Six1</i>	SIX homeobox 1	NM_053759	1,39	ureteric bud development
<i>Zc4h2</i>	zinc finger, C4H2 domain containing	NM_001126374	1,38	
<i>Hbxip</i>	hepatitis B virus x interacting protein	NM_001106462	1,38	anti-apoptosis
<i>Snn</i>	stannin	NM_001034083	1,38	
<i>Amigo1</i>	adhesion molecule with Ig like domain 1	NM_206881	1,38	cell adhesion
<i>Znrf2</i>	zinc and ring finger 2	NM_001108628	1,38	
<i>Cenpv</i>	centromere protein V	XM_002724504 /// XM_577104	1,38	metabolic process

<i>Hmgb3</i>	high mobility group box 3	NM_001173341 /// XM_001067329 /// XM_002727293 /// XM_002730310 /// XM_223440	<b>1,38</b>	negative regulation of B cell differentiation
<i>Nap1l3</i>	nucleosome assembly protein 1-like 3	NM_133402	<b>1,38</b>	nucleosome assembly
<i>Nubp1</i>	nucleotide binding protein 1	NM_001009619	<b>1,38</b>	cellular iron ion homeostasis
<i>Lrsam1</i>	leucine rich repeat and sterile alpha motif containing 1	NM_001107833	<b>1,38</b>	protein polyubiquitination
<i>Xrcc5</i>	X-ray repair complementing defective repair in Chinese hamster cells 5	NM_177419	<b>1,38</b>	double-strand break repair
<i>Ccdc124</i>	coiled-coil domain containing 124	NM_001106071	<b>1,37</b>	
<i>Tmem206</i>	transmembrane protein 206	NM_001007679	<b>1,37</b>	
<i>Pcgf2</i>	polycomb group ring finger 2	NM_001105836	<b>1,37</b>	negative regulation of transcription from RNA polymerase II promoter
<i>Lrrc20</i>	leucine rich repeat containing 20	NM_001109171	<b>1,37</b>	
<i>Dazap2</i>	DAZ associated protein 2	NM_001013107	<b>1,37</b>	
<i>Hmg20b</i>	high mobility group 20 B	NM_001108731	<b>1,37</b>	
<i>Mrpl44</i>	mitochondrial ribosomal protein L44	NM_001031650	<b>1,37</b>	RNA processing
<i>Sts</i>	steroid sulfatase	NM_012661	<b>1,37</b>	lipid metabolic process
<i>Calmod3</i>	calmodulin 3	NM_012518	<b>1,37</b>	muscle contraction
<i>Mllt6</i>	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	XM_001081378 /// XM_239329	<b>1,37</b>	
<i>Ier3</i>	immediate early response 3	NM_212505	<b>1,37</b>	
<i>Ptgr2</i>	prostaglandin reductase 2	NM_001015009	<b>1,37</b>	metabolic process
<i>Aatk</i>	apoptosis-associated tyrosine kinase	NM_001168703	<b>1,37</b>	apoptosis
<i>Abcc3</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	NM_080581	<b>1,37</b>	transport
<i>Jmjd5</i>	jumonji domain containing 5	NM_001037196	<b>1,37</b>	G2/M transition of mitotic cell cycle
<i>Mfng</i>	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	NM_199110	<b>1,37</b>	pattern specification process
<i>Ccdc52</i>	coiled-coil domain containing 52	NM_001008285	<b>1,37</b>	cell cycle
<i>Cast</i>	calpastatin	NM_001033715 /// NM_001033716 /// NM_053295	<b>1,37</b>	myoblast fusion
<i>Lias</i>	lipoic acid synthetase	NM_001012037	<b>1,37</b>	inflammatory response
<i>Ccl2</i>	chemokine (C-C motif) ligand 2	NM_031530	<b>1,37</b>	response to hypoxia
<i>Tubb3</i>	tubulin, beta 3	NM_139254	<b>1,37</b>	neuron migration
<i>Plscr3</i>	phospholipid scramblase 3	NM_001012139	<b>1,36</b>	glucose homeostasis
<i>Fuca2</i>	fucosidase, alpha-L- 2, plasma	NM_001004218	<b>1,36</b>	carbohydrate metabolic process
<i>Prkcq</i>	protein kinase C, theta	XM_001064127 /// XM_341553	<b>1,36</b>	response to hypoxia
<i>Arrdc2</i>	arrestin domain containing 2	NM_001107303	<b>1,36</b>	signal transduction
<i>Grik2</i>	glutamate receptor, ionotropic, kainate 2	NM_019309	<b>1,36</b>	behavioral fear response
<i>Aip</i>	aryl-hydrocarbon receptor-interacting protein	NM_172327	<b>1,36</b>	protein folding
<i>Pdzd4</i>	PDZ domain containing 4	NM_001135836	<b>1,36</b>	
<i>Rab71</i>	RAB7, member RAS oncogene family-like 1	NM_133590	<b>1,36</b>	transport
<i>Banf1</i>	barrier to autointegration factor 1	NM_053631	<b>1,36</b>	DNA integration
<i>Epc2</i>	enhancer of polycomb homolog 2 (Drosophila)	NM_001108581	<b>1,36</b>	
<i>Atp6ap2</i>	ATPase, H+ transporting, lysosomal accessory protein 2	XM_001060853 /// XM_217592	<b>1,36</b>	angiotensin maturation
<i>Nek7</i>	NIMA (never in mitosis gene a)-related kinase 7	NM_001108346	<b>1,36</b>	protein phosphorylation
<i>Acot2</i>	Acyl-CoA thioesterase 2	NM_138907	<b>1,36</b>	very long-chain fatty acid metabolic process

<i>Rnf123</i>	ring finger protein 123	NM_001191580 /// XM_002727136 /// XM_002729963	1,35	
<i>Tmem147</i>	transmembrane protein 147	NM_001038494	1,35	
<i>Podxl2</i>	podocalyxin-like 2	NM_001106607	1,35	
<i>Manbal</i>	mannosidase, beta A, lysosomal-like	NM_001173380 /// XM_001067976 /// XM_002726286 /// XM_002729245 /// XM_575279	1,35	
<i>Atp6v1e1</i>	ATPase, H+ transporting, lysosomal V1 subunit E1	NM_198745	1,35	ATP catabolic process
<i>Ankrd40</i>	ankyrin repeat domain 40	NM_001134699	1,35	
<i>Rab25</i>	RAB25, member RAS oncogene family	NM_001107687	1,35	small GTPase mediated signal transduction
<i>Nacc2</i>	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	NM_001100533	1,35	
<i>Fbxo23</i>	F-box only protein 23	NM_001013138	1,35	
<i>Kctd13</i>	potassium channel tetramerisation domain containing 13	NM_198736	1,35	DNA replication
<i>Qsox2</i>	quiescin Q6 sulfhydryl oxidase 2	NM_001109434	1,35	cell redox homeostasis
<i>Tysnd1</i>	trypsin domain containing 1	NM_001108932	1,35	proteolysis
<i>Mrpl54</i>	mitochondrial ribosomal protein L54	NM_001106770	1,35	
<i>Reep6</i>	receptor accessory protein 6	NM_001013218	1,34	
<i>Timp2</i>	TIMP metalloproteinase inhibitor 2	NM_021989	1,34	spermatogenesis
<i>Igfbp1</i>	immunoglobulin (CD79A) binding protein 1	NM_031624	1,34	response to biotic stimulus
<i>Ergic3</i>	ERGIC and golgi 3	NM_001106533	1,34	
<i>Pold4</i>	polymerase (DNA-directed), delta 4	NM_001013195	1,34	positive regulation of endothelial cell proliferation
<i>Bloc1s1</i>	biogenesis of lysosomal organelles complex-1, subunit 1	NM_001105941	1,34	post-Golgi vesicle-mediated transport
<i>Ocl1</i>	occludin/ELL domain containing 1	NM_001106065	1,34	
<i>Aplp2</i>	amyloid beta (A4) precursor-like protein 2	XM_001056214 /// XM_343513	1,34	suckling behavior
<i>Bdh1</i>	3-hydroxybutyrate dehydrogenase, type 1	NM_053995	1,34	liver development
<i>Gba</i>	glucosidase, beta, acid	NM_001127639	1,34	carbohydrate metabolic process
<i>Mrps18a</i>	mitochondrial ribosomal protein S18A	NM_198756	1,34	translation
<i>Gle1</i>	GLE1 RNA export mediator homolog (yeast)	NM_001025731	1,34	transport
<i>Pnkd</i>	paroxysmal nonkinesigenic dyskinesia precursor)	NM_001134750 /// NM_001134751 /// NM_001134753	1,34	
<i>Clpb</i>	ClpB caseinolytic peptidase B homolog (E. coli)	NM_022947	1,34	cellular response to heat
<i>Stxbp1</i>	syntaxin binding protein 1	NM_013038	1,34	platelet degranulation
<i>Ift81</i>	intraflagellar transport 81 homolog (Chlamydomonas)	NM_199120	1,34	multicellular organismal development
<i>Snca</i>	synuclein, alpha (non A4 component of amyloid precursor)	NM_019169	1,34	microglial cell activation
<i>Tspan14</i>	Tetraspanin 14	NM_001169127	1,34	
<i>Lactb2</i>	lactamase, beta 2	NM_001024247	1,33	
<i>Pnpt1</i>	polynucleotide nucleotidyltransferase 1	NM_001142371	1,33	RNA processing
<i>Tpp1</i>	tripeptidyl peptidase I	NM_031357	1,33	proteolysis
<i>Gstm1</i>	glutathione S-transferase mu 1	NM_017014	1,33	glutathione metabolic process
<i>Coro1a</i>	coronin, actin binding protein 1A	NM_130411	1,33	phagolysosome assembly
<i>Vtn</i>	vitronectin	NM_019156	1,33	immune response
<i>Dhx16</i>	DEAH (Asp-Glu-Ala-His) box polypeptide 16	NM_212496	1,33	
<i>Rsp9</i>	radial spoke head 9 homolog (Chlamydomonas)	NM_001108205	1,33	cilium movement
<i>Setd8 /// Setd8-ps1</i>	SET domain containing (lysine methyltransferase) 8 /// SET domain containing (ly	XM_001072149 /// XM_002724818 /// XM_573394	1,33	negative regulation of transcription

<i>Cdkn2c</i>	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	NM_131902	1,33	regulation of cyclin-dependent protein kinase activity
<i>Clns1a</i>	chloride channel, nucleotide-sensitive, 1A	NM_031719	1,33	spliceosomal snRNP assembly
<i>Sqstm1</i>	sequestosome 1	NM_175843 /// NM_181550	1,33	positive regulation of protein phosphorylation
<i>Atrx</i>	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, <i>S. cerevi</i>	NM_001105757	1,33	DNA repair
<i>Atp9a</i> /// <i>Atp9b</i>	ATPase, class II, type 9A /// ATPase, class II, type 9B	NM_001106130 /// XM_002726282	1,33	ATP biosynthetic process
<i>Sepp1</i>	selenoprotein P, plasma, 1	NM_001083911 /// NM_019192	1,33	selenium metabolic process
<i>Jmjd8</i>	jumonji domain containing 8	NM_001014116	1,33	
<i>Tmem192</i>	transmembrane protein 192	NM_001014141	1,33	
<i>Polr2g</i>	polymerase (RNA) II (DNA directed) polypeptide G	NM_053948	1,33	transcription
<i>Tm7sf3</i>	transmembrane 7 superfamily member 3	NM_001011970	1,33	
<i>Bsn</i>	bassoon	NM_019146	1,33	cytoskeleton organization
<i>Vrk1</i>	vaccinia related kinase 1	NM_001012194	1,33	protein phosphorylation
<i>Hsd17b12</i>	hydroxysteroid (17-beta) dehydrogenase 12	NM_032066	1,32	steroid biosynthetic process
<i>Camk2n1</i>	Calcium/calmodulin-dependent protein kinase II inhibitor 1	NM_173337	1,32	synaptic transmission
<i>Dnajc27</i>	DnaJ (Hsp40) homolog, subfamily C, member 27	NM_206845	1,32	small GTPase mediated signal transduction
<i>Rnf44</i>	Ring finger protein 44	NM_001024795	1,32	
<i>Gfm1</i>	G elongation factor, mitochondrial 1	NM_053625	1,32	translation
<i>Dctn6</i>	dynactin 6	NM_001106085	1,32	
<i>Cenpq</i>	centromere protein Q	NM_001014215	1,32	
<i>Chid1</i>	chitinase domain containing 1	NM_001047854	1,32	carbohydrate metabolic process
<i>Cep70</i>	centrosomal protein 70kDa	NM_001017470	1,32	
<i>Adh5</i>	alcohol dehydrogenase 5	NM_001126120	1,32	retinoid metabolic process
<i>Igfbp7</i>	insulin-like growth factor binding protein 7	NM_001013048	1,32	regulation of cell growth
<i>Bin3</i>	bridging integrator 3	NM_001013186	1,32	barrier septum formation
<i>Smyd4</i>	SET and MYND domain containing 4	NM_001105810	1,32	
<i>Cspg5</i>	chondroitin sulfate proteoglycan 5	NM_019284 /// NM_133652	1,32	multicellular organismal development
<i>Rabac1</i>	Rab acceptor 1 (prenylated)	NM_031774	1,32	vesicle-mediated transport
<i>Plekhhg5</i>	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	NM_201272	1,32	apoptosis
<i>Pcna</i>	proliferating cell nuclear antigen	NM_022381	1,32	DNA replication
<i>Gltscr2</i>	glioma tumor suppressor candidate region gene 2	NM_207591	1,32	
<i>Crbn</i>	cereblon	NM_001015003	1,32	proteolysis
<i>Nsg2</i>	neuron specific gene family member 2	NM_001034152	1,32	dopamine receptor signaling pathway
<i>Mapkapk5</i>	mitogen-activated protein kinase-activated protein kinase 5	NM_001025761 /// NM_001164043	1,32	protein phosphorylation
<i>Tmem59l</i>	transmembrane protein 59-like	XM_001067996 /// XM_224729	1,32	
<i>Cnot8</i>	CCR4-NOT transcription complex, subunit 8	NM_001008382	1,32	
<i>Commf7</i>	COMM domain containing 7	NM_001030029	1,32	negative regulation of transcription
<i>Phf20</i>	PHD finger protein 20	NM_001107795	1,32	
<i>Cdk5rap2</i>	CDK5 regulatory subunit associated protein 2	NM_173134 /// XM_001059116 /// XM_575844	1,31	microtubule cytoskeleton organization
<i>Lxn</i>	latexin	NM_031655	1,31	negative regulation of endopeptidase activity
<i>Mtus1</i>	mitochondrial tumor suppressor 1	NM_178093	1,31	cell cycle
<i>Mex3b</i>	mex3 homolog B ( <i>C. elegans</i> )	NM_001191626 /// XM_001068105 /// XM_218846	1,31	

<i>Cyth2</i>	cytohesin 2	NM_053911	1,31	dendrite development
<i>Tmpo</i>	thymopoietin	NM_012887	1,31	nuclear envelope reassembly
<i>Eif2b3</i>	eukaryotic translation initiation factor 2B, subunit 3 gamma	NM_133609	1,31	translation
<i>Tcf19</i>	transcription factor 19	NM_213561	1,31	
<i>H3f3b</i>	H3 histone, family 3B	NM_053985	1,31	nucleosome assembly
<i>Tusc2</i>	tumor suppressor candidate 2	NM_001109297	1,31	
<i>Rnf208</i>	ring finger protein 208	NM_001109195	1,31	
<i>Tmem176a</i>	transmembrane protein 176A	NM_001039008	1,31	
<i>Tspan6</i>	tetraspanin 6	NM_001100672	1,31	positive regulation of I-kappaB kinase/NF-kappaB cascade
<i>Exoc7</i>	exocyst complex component 7	NM_022691	1,31	transport
<i>Ephx1</i>	epoxide hydrolase 1, microsomal	NM_001034090 /// NM_012844	1,31	cellular aromatic compound metabolic process
<i>Zfp91</i>	zinc finger protein 91	NM_001169120	1,31	
<i>Wdr8</i>	WD repeat domain 8	NM_001014262	1,31	
<i>Prdm2</i>	PR domain containing 2, with ZNF domain	NM_001077648	1,31	transcription
<i>Alkbh2</i>	alkB, alkylation repair homolog 2 (E. coli)	NM_001126273	1,31	DNA dealkylation involved in DNA repair
<i>Sil1</i>	SIL1 homolog, endoplasmic reticulum chaperone (S. cerevisiae)	NM_199376	1,31	transport
<i>Morn1</i>	MORN repeat containing 1	NM_001005544	1,31	
<i>Spata6</i>	spermatogenesis associated 6	NM_134392	1,31	multicellular organismal development
<i>Stmn1</i>	stathmin 1	NM_017166	1,31	microtubule depolymerization
<i>Tnfrsf12</i>	tumor necrosis factor ligand superfamily member 12	NM_001001513	1,31	immune response
<i>Slpi</i>	secretory leukocyte peptidase inhibitor	NM_053372	1,31	
<i>Snx9</i>	sorting nexin 9	NM_001127637	1,31	cell communication
<i>Abhd8</i>	abhydrolase domain containing 8	NM_001107301	1,30	
<i>Ddx20</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	NM_001191711 /// XM_001066705 /// XM_227558	1,30	negative regulation of transcription from RNA polymerase II promoter
<i>Mllt4</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	NM_013217	1,30	cell adhesion
<i>Parl</i>	presenilin associated, rhomboid-like	NM_001035249	1,30	
<i>Decr2 /// Rab11fip3</i>	2,4-dienoyl CoA reductase 2, peroxisomal /// RAB11 family interacting protein 3	NM_171996 /// XM_001062691 /// XM_002724662 /// XM_002727755 /// XM_220262	1,30	cytokinesis
<i>Evi2a</i>	ecotropic viral integration site 2A	NM_001044287	1,30	
<i>Sirt5</i>	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	NM_001004256	1,30	chromatin silencing
<i>Slit2</i>	slit homolog 2 (Drosophila)	NM_022632	1,30	luteolysis
<i>Bace2</i>	beta-site APP-cleaving enzyme 2	NM_001002802	1,30	proteolysis
<i>Asmtl</i>	acetylserotonin O-methyltransferase-like	NM_001105915	1,30	
<i>Pmp22</i>	peripheral myelin protein 22	NM_017037	1,30	cell cycle
<i>Hn1</i>	hematological and neurological expressed 1	NM_001005876	1,30	
<i>Plod1</i>	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	NM_053827	1,30	response to hypoxia
<i>Pola1</i>	polymerase (DNA directed), alpha 1	NM_053479 /// XM_001064735 /// XM_242396	1,30	S phase of mitotic cell cycle
<b>Down-regulated</b>				
<i>Mybpc1</i>	myosin binding protein C, slow type	NM_001100758 /// XM_001076591 /// XM_343196	-7,42	muscle contraction

<i>Hspb7</i>	heat shock protein family, member 7 (cardiovascular)	NM_031607	<b>-4,50</b>	response to stress
<i>Fgl2</i>	fibrinogen-like 2	NM_053455	<b>-4,04</b>	signal transduction
<i>Bean</i>	brain expressed, associated with Nedd4	XM_001057606 /// XM_341638	<b>-3,59</b>	
<i>Pycr1</i>	pyrroline-5-carboxylate reductase 1	NM_001105857	<b>-3,10</b>	proline biosynthetic process
<i>Enpep</i>	glutamyl aminopeptidase	NM_022251	<b>-2,97</b>	proteolysis
<i>RT1-Ba</i>	RT1 class II antigen, Ba chain	NM_001008831	<b>-2,96</b>	antigen processing and presentation of peptide
<i>Rbp4</i>	retinol binding protein 4, plasma	NM_013162	<b>-2,74</b>	eye development
<i>Ptprz1</i>	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	NM_001170685 /// NM_013080	<b>-2,68</b>	protein dephosphorylation
<i>Sstr2</i>	somatostatin receptor 2	NM_019348	<b>-2,66</b>	regulation of muscle contraction
<i>Clcnkb</i>	chloride channel Kb	NM_173103	<b>-2,60</b>	transport
<i>Gpc3</i>	glypican 3	NM_012774	<b>-2,60</b>	branching involved in ureteric bud morphogenesis
<i>Dlk1</i>	delta-like 1 homolog (Drosophila)	NM_053744	<b>-2,57</b>	embryo development
<i>Colec11</i>	collectin sub-family member 11	XM_002726687 /// XM_002729610	<b>-2,49</b>	
<i>Grb10</i>	growth factor receptor bound protein 10	NM_001109093	<b>-2,43</b>	signal transduction
<i>Abcc8</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	NM_013039	<b>-2,40</b>	transport
<i>Es1</i>	esterase 1 /// microsomal carboxylesterase E1-like	NM_017004 /// XM_002725379	<b>-2,35</b>	metabolic process
<i>Ntrk2</i>	neurotrophic tyrosine kinase, receptor, type 2	NM_001163168 /// NM_001163169 /// NM_012731	<b>-2,35</b>	vasculogenesis
<i>Nckap1l</i>	NCK associated protein 1 like	NM_001108119	<b>-2,31</b>	B cell homeostasis
<i>Ccnd2</i>	cyclin D2	NM_022267	<b>-2,28</b>	G1/S transition of mitotic cell cycle
<i>Ppm1j</i>	protein phosphatase 1J	NM_001005540	<b>-2,10</b>	protein dephosphorylation
<i>Rem2</i>	RAS (RAD and GEM) like GTP binding 2	NM_022685	<b>-2,09</b>	regulation of transcription, DNA-dependent
<i>Slc16a1</i>	solute carrier family 16, member 1 (monocarboxylic acid transporter 1)	NM_012716	<b>-2,08</b>	transport
<i>Rab3d</i>	RAB3D, member RAS oncogene family	NM_080580	<b>-2,05</b>	transport
<i>H2-Ea</i>	MHC class II RT1D alpha chain antigen	NM_001008847	<b>-2,04</b>	antigen processing and presentation of peptide or polysaccharide anti
<i>Amigo3</i>	adhesion molecule with Ig like domain 3	NM_178144	<b>-2,02</b>	cell adhesion
<i>Ndn</i>	neccin homolog (mouse)	NM_001008558	<b>-2,01</b>	neuron migration
<i>Vldlr</i>	very low density lipoprotein receptor	NM_013155	<b>-1,98</b>	response to hypoxia
<i>Fshb</i>	follicle stimulating hormone, beta polypeptide	NM_001007597	<b>-1,97</b>	transforming growth factor beta receptor signaling pathway
<i>HLA-drb1</i>	MHC class II RT1D beta1 chain antigen	NM_001008884	<b>-1,96</b>	antigen processing and presentation of peptide or polysaccharide anti
<i>Col24a1</i>	collagen, type XXIV, alpha 1	XM_002726055 /// XM_575056	<b>-1,96</b>	cell adhesion
<i>Rcn3</i>	reticulocalbin 3, EF-hand calcium binding domain	NM_001008694	<b>-1,94</b>	
<i>Oaf</i>	OAF homolog (Drosophila)	NM_001014090	<b>-1,93</b>	
<i>Tubb6</i>	tubulin, beta 6	NM_001025675	<b>-1,93</b>	microtubule-based process
<i>Ace</i>	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	NM_012544	<b>-1,91</b>	response to hypoxia
<i>Scnn1g</i>	sodium channel, nonvoltage-gated 1, gamma	NM_017046	<b>-1,88</b>	response to hypoxia
<i>Spp1</i>	secreted phosphoprotein 1	NM_012881	<b>-1,87</b>	ossification
<i>Lhb</i>	luteinizing hormone beta	NM_001033975 /// NM_012858	<b>-1,87</b>	
<i>Kcnj11</i>	potassium inwardly rectifying channel, subfamily J, member 11	NM_031358	<b>-1,87</b>	glucose metabolic process
<i>Cd74</i>	Cd74 molecule, major histocompatibility complex, class II invariant chain	NM_013069	<b>-1,86</b>	activation of MAPK activity

<i>Elovl5</i>	ELOVL family member 5, elongation of long chain fatty acids (yeast)	NM_134382	-1,86	fatty acid biosynthetic process
<i>Mapkapk3</i>	mitogen-activated protein kinase-activated protein kinase 3	NM_001012127	-1,85	protein phosphorylation
<i>Sfxn1</i>	sideroflexin 1	NM_001012213	-1,84	transport
<i>Bcan</i>	brevican	NM_001033665 /// NM_012916	-1,83	cell adhesion
<i>Lamc2</i>	laminin, gamma 2	NM_001100640	-1,83	cell adhesion
<i>Spata1</i>	spermatogenesis associated 1	NM_001014177	-1,81	proteolysis
<i>Lepre1</i>	leucine proline-enriched proteoglycan (leprecan) 1	NM_053667	-1,80	cell growth
<i>Slc41a2</i>	Solute carrier family 41, member 2	NM_001108742	-1,80	
<i>Aldh18a1</i>	aldehyde dehydrogenase 18 family, member A1	NM_001108524	-1,79	proline biosynthetic process
<i>Htatip2</i>	HIV-1 tat interactive protein 2, homolog (human)	NM_001106263	-1,78	cellular amino acid metabolic process
<i>Fxyd6</i>	FXYD domain-containing ion transport regulator 6	NM_022005	-1,76	transport
<i>Rnd3</i>	Rho family GTPase 3	NM_001007641	-1,76	small GTPase mediated signal transduction
<i>Usp13</i>	Ubiquitin specific protease 13 (isopeptidase T-3)	NM_001107665	-1,76	ubiquitin-dependent protein catabolic process
<i>Fam114a1</i>	Family with sequence similarity 114, member A1	XM_001078310 /// XM_573600	-1,76	
<i>Ptpn3</i>	protein tyrosine phosphatase, non-receptor type 3	XM_001055793 /// XM_001059757	-1,75	protein dephosphorylation
<i>Adamtsl4</i>	ADAMTS-like 4	NM_001034012	-1,75	apoptosis
<i>Pcdh21</i>	protocadherin 21	NM_053572	-1,75	cell adhesion
<i>Ppap2c</i>	phosphatidic acid phosphatase type 2c	NM_139252	-1,74	
<i>Mx2</i>	myxovirus (influenza virus) resistance 2	NM_134350	-1,73	response to virus
<i>Rtn4r</i>	reticulon 4 receptor	NM_053613	-1,72	axonogenesis
<i>Lyz2</i>	lysozyme 2	NM_012771	-1,72	metabolic process
<i>Camk1g</i>	calcium/calmodulin-dependent protein kinase IG	NM_182842	-1,72	protein phosphorylation
<i>Gmppb</i>	GDP-mannose pyrophosphorylase B	NM_001108781	-1,71	biosynthetic process
<i>Fitm1</i>	fat storage-inducing transmembrane protein 1	NM_001106037	-1,69	positive regulation of sequestering of triglyceride
<i>Epor</i>	erythropoietin receptor	NM_017002	-1,69	signal transduction
<i>Plat</i>	plasminogen activator, tissue	NM_013151	-1,67	response to hypoxia
<i>Chpt1</i>	choline phosphotransferase 1	NM_001007750	-1,66	phosphatidylcholine biosynthetic process
<i>Dsp</i>	desmoplakin	XM_001058477 /// XM_225259	-1,66	cell-cell adhesion
<i>Dpp3</i>	dipeptidylpeptidase 3 /// similar to Dipeptidyl-peptidase 3 (Dipeptidyl-peptidas	NM_053748 /// XM_001053134	-1,66	proteolysis
<i>Heatr5a</i>	HEAT repeat containing 5A	XM_001075318 /// XM_343061	-1,65	
<i>Gga2</i>	golgi associated, gamma adaptin ear containing, ARF binding protein 2	NM_001100519	-1,64	intracellular protein transport
<i>Arhgap9</i>	Rho GTPase activating protein 9	NM_001012198 /// NM_001080789	-1,63	signal transduction
<i>Pabpc4</i>	poly(A) binding protein, cytoplasmic 4	NM_001100538	-1,63	
<i>Srm</i>	spermidine synthase	NM_053464	-1,61	spermidine biosynthetic process
<i>Scly</i>	selenocysteine lyase	NM_001007755	-1,61	metabolic process
<i>Tesc</i>	tescalcin	XM_001076953 /// XM_213790	-1,61	negative regulation of cell proliferation
<i>Sec24d</i>	SEC24 family, member D (S. cerevisiae)	NM_001107723	-1,60	transport
<i>Trim5</i>	tripartite motif-containing 5	NM_001014023	-1,60	protein trimerization
<i>Map2k3</i>	mitogen activated protein kinase kinase 3	NM_001100674	-1,59	MAPKKK cascade
<i>Gsdma</i>	gasdermin A	NM_001108297	-1,59	induction of apoptosis
<i>Prrc1</i>	proline-rich coiled-coil 1	NM_001033887	-1,59	
<i>Pelo</i>	pelota homolog (Drosophila)	NM_001007634	-1,59	translation
<i>Kcnk10</i>	potassium channel, subfamily K, member 10	NM_023096	-1,59	transport
<i>Nab1</i>	Ngfi-A binding protein 1	NM_022856	-1,58	endochondral ossification
<i>Scn5a</i>	sodium channel, voltage-gated, type V, alpha subunit	NM_001160162 /// NM_013125	-1,57	transport

<i>Trim54</i>	tripartite motif-containing 54	NM_001013217	-1,56	negative regulation of microtubule depolymerization
<i>Gltpd1</i>	glycolipid transfer protein domain containing 1	NM_001007703	-1,56	glycolipid transport
<i>Fkbp11</i>	FK506 binding protein 11	NM_001013105	-1,56	protein folding
<i>Gas5</i>	growth arrest specific 5	NR_002704	-1,55	
<i>Ifi44</i>	interferon-induced protein 44	NM_001107729	-1,55	
<i>Steap2</i>	six transmembrane epithelial antigen of the prostate 2	NM_001107846	-1,54	Golgi to plasma membrane transport
<i>Tmem165</i>	transmembrane protein 165	NM_001024802	-1,54	
<i>Spire1</i>	spire homolog 1 (Drosophila)	NM_001107381	-1,54	Golgi vesicle transport
<i>Samd4a</i>	Sterile alpha motif domain containing 4A	NM_001107254	-1,54	regulation of translation
<i>Sstr3</i>	somatostatin receptor 3	NM_133522	-1,54	signal transduction
<i>Itsn1</i>	intersectin 1 (SH3 domain protein)	NM_001136096 /// NM_019227	-1,54	exocytosis
<i>Rcn1</i>	reticulocalbin 1, EF-hand calcium binding domain	NM_001108586	-1,54	
<i>Rtn4r</i>	reticulon 4 receptor	NM_053613	-1,53	axonogenesis
<i>Slc38a10</i>	solute carrier family 38, member 10	XM_001081798 /// XM_001081800 /// XM_002724582 /// XM_002727846 /// XM_002727847	-1,53	
<i>Mtmr2</i>	myotubularin related protein 2	NM_001108123	-1,53	dephosphorylation
<i>Acs1</i>	acyl-CoA synthetase long-chain family member 1	NM_012820	-1,52	lipid metabolic process
<i>Rps6ka1</i>	ribosomal protein S6 kinase polypeptide 1	NM_031107	-1,52	protein phosphorylation
<i>Fkbp14</i>	FK506 binding protein 14	NM_001013210	-1,52	protein folding
<i>Golt1b</i>	golgi transport 1 homolog B (S. cerevisiae)	NM_001113783	-1,51	vesicle-mediated transport
<i>St8sia3</i>	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	NM_013029	-1,50	protein glycosylation
<i>Pfkfb4</i>	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	NM_019333	-1,50	fructose metabolic process
<i>Ltbp4</i>	latent transforming growth factor beta binding protein 4	NM_001170336	-1,50	transforming growth factor beta receptor signaling pathway
<i>Tmem150a</i>	transmembrane protein 150A	NM_139107	-1,49	catabolic process
<i>Iqsec3</i>	IQ motif and Sec7 domain 3	NM_207617	-1,48	regulation of ARF protein signal transduction
<i>Ednra</i>	endothelin receptor type A	NM_012550	-1,48	patterning of blood vessels
<i>Mlec</i>	malectin	NM_001013983	-1,47	carbohydrate metabolic process
<i>Abcc5</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	NM_053924	-1,47	transport
<i>Oasl</i>	2'-5'-oligoadenylate synthetase-like	NM_001009681	-1,47	immune response
<i>Grb14</i>	growth factor receptor bound protein 14	NM_031623	-1,47	signal transduction
<i>Cnih</i>	cornichon homolog (Drosophila)	NM_001106029	-1,46	intracellular signaling pathway
<i>Ptpnk</i>	protein tyrosine phosphatase, receptor type, K, extracellular region	NM_001029902	-1,46	protein dephosphorylation
<i>Ap2a2</i>	adaptor-related protein complex 2, alpha 2 subunit	NM_031008	-1,46	transport
<i>Hr</i>	hairless	NM_024364	-1,46	transcription
<i>Otud7a</i>	OTU domain containing 7A	XM_001058176 /// XM_219703	-1,46	
<i>Degs1</i>	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)	NM_053323	-1,46	lipid metabolic process
<i>Plcg2</i>	phospholipase C, gamma 2	NM_017168	-1,46	follicular B cell differentiation
<i>Gcs1</i>	glucosidase 1	NM_031749	-1,46	metabolic process
<i>Plxna3</i>	plexin A3	NM_001107581	-1,46	signal transduction
<i>Nrsn1</i>	neurensin 1	NM_001106109	-1,45	nervous system development
<i>Ivns1abp</i>	influenza virus NS1A binding protein	NM_001047085	-1,44	



<i>Camk2b</i>	calcium/calmodulin-dependent protein kinase II beta	NM_001042354 /// NM_001042356 /// NM_021739	-1,44	G1/S transition of mitotic cell cycle
<i>Slc35e1</i>	solute carrier family 35, member E1	NM_001109107	-1,44	transport
<i>Tmem185a</i>	transmembrane protein 185A	NM_001135712	-1,44	
<i>Homer2</i>	homer homolog 2 (Drosophila)	NM_053309	-1,44	
<i>Iars</i>	isoleucyl-tRNA synthetase	NM_001100572	-1,44	translation
<i>Igsf1</i>	immunoglobulin superfamily, member 1	NM_175763	-1,43	signal transduction
<i>Chka</i>	choline kinase alpha	NM_017127	-1,43	phosphatidylethanolamine biosynthetic process
<i>Csgalnact2</i>	chondroitin sulfate N-acetylgalactosaminyltransferase 2	NM_001106616	-1,43	proteoglycan biosynthetic process
<i>Cad</i>	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	NM_001105710	-1,43	'de novo' pyrimidine base biosynthetic process
<i>Col2a1</i>	collagen, type II, alpha 1	NM_012929	-1,43	skeletal system development
<i>Doc2b</i>	double C2-like domains, beta	NM_031142	-1,43	transport
<i>Copb2</i>	coatamer protein complex, subunit beta 2 (beta prime)	NM_021765	-1,42	transport
<i>Rab2b</i>	RAB2B, member RAS oncogene family	NM_001037645	-1,42	small GTPase mediated signal transduction
<i>Tmem39a</i>	transmembrane protein 39a	NM_001013865	-1,42	
<i>Isg20</i>	interferon stimulated exonuclease gene 20	NM_001008510	-1,42	DNA catabolic process, exonucleolytic
<i>Dnajb5</i>	DnaJ (Hsp40) homolog, subfamily B, member 5	NM_001108004	-1,42	negative regulation of transcription from RNA polymerase II promoter
<i>Col1a1</i>	collagen, type I, alpha 1	NM_053304	-1,42	skeletal system development
<i>Synm</i>	synemin, intermediate filament protein	NM_001134858	-1,42	
<i>Hdlbp</i>	high density lipoprotein binding protein	NM_172039	-1,42	lipid metabolic process
<i>Ppfibp1</i>	PTPRF interacting protein, binding protein 1 (liprin beta 1)	NM_001107896	-1,42	
<i>Pdyn</i>	prodynorphin	NM_019374	-1,41	neuropeptide signaling pathway
<i>Ddx25</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	NM_031630	-1,41	ATP catabolic process
<i>Srp72</i>	signal recognition particle 72	NM_001170601 /// XM_001066751 /// XM_001074215	-1,41	SRP-dependent cotranslational protein targeting to membrane
<i>Sez6l2</i>	seizure related 6 homolog (mouse)-like 2	NM_001107550	-1,41	
<i>Fndc3b</i>	fibronectin type III domain containing 3B	NM_001191704 /// XM_001057133 /// XM_226988	-1,41	positive regulation of fat cell differentiation
<i>Slc2a4</i>	solute carrier family 2 (facilitated glucose transporter), member 4	NM_012751	-1,41	transport
<i>Slc35e3</i>	solute carrier family 35, member E3	NM_001134687	-1,41	
<i>Uba5</i>	ubiquitin-like modifier activating enzyme 5	NM_001009669	-1,40	metabolic process
<i>Golga3</i>	golgi autoantigen, golgin subfamily a, 3	NM_001107847	-1,40	
<i>Marveld1</i>	MARVEL domain containing 1	NM_001107590	-1,40	
<i>Cobl</i>	cordon-bleu homolog (mouse)	NM_001107236	-1,40	neural tube closure
<i>Txndc11</i>	thioredoxin domain containing 11	NM_001127532	-1,40	cell redox homeostasis
<i>Syncrip</i>	Synaptotagmin binding, cytoplasmic RNA interacting protein	NM_001047916	-1,40	mRNA processing
<i>Fam107a</i>	family with sequence similarity 107, member A /// downregulated in renal cell ca	NM_001025129 /// XM_002725042 /// XM_002725043	-1,39	regulation of cell growth
<i>Fam98a</i>	family with sequence similarity 98, member A	NM_001014073	-1,39	
<i>Oxnad1</i>	oxidoreductase NAD-binding domain containing 1	NM_001107295	-1,39	oxidation reduction
<i>Mark1</i>	MAP/microtubule affinity-regulating kinase 1	NM_053947	-1,39	microtubule cytoskeleton organization
<i>Ppapdc1b</i>	phosphatidic acid phosphatase type 2 domain containing 1B	NM_001109411	-1,39	

<i>Ostc</i>	oligosaccharyltransferase complex subunit	NM_001108566	-1,39	
<i>Gramd1b</i>	GRAM domain containing 1B	NM_001191616 /// XM_001059472 /// XM_217113	-1,39	
<i>Icam5</i>	intercellular adhesion molecule 5, telencephalin	NM_001172079 /// XM_001077293 /// XM_233737	-1,39	phagocytosis
<i>Lynx1</i>	Ly6/neurotoxin 1	NM_001130546	-1,38	pathogenesis
<i>Nlgn3</i>	Neuroigin 3	NM_134336	-1,38	regulation of respiratory gaseous exchange by neurological system pro
<i>Adamts12</i>	ADAMTS-like 2	XM_001078833 /// XM_231125	-1,38	
<i>Cnih2</i>	cornichon homolog 2 (Drosophila)	NM_001025132	-1,38	intracellular signaling pathway
<i>Pcp4</i>	Purkinje cell protein 4	NM_013002	-1,38	
<i>Aldh1l2</i>	aldehyde dehydrogenase 1 family, member L2	NM_001191778 /// XM_001079663 /// XM_235005	-1,38	one-carbon metabolic process
<i>Ubash3b</i>	ubiquitin associated and SH3 domain containing, B	NM_001191792 /// XM_001065047 /// XM_236104	-1,38	
<i>Bzw1</i>	basic leucine zipper and W2 domains 1	NM_198789	-1,38	transcription
<i>Zcchc12</i>	zinc finger, CCHC domain containing 12	NM_001014065	-1,37	transcription
<i>Zfp853</i>	zinc finger protein 853	XM_002724787 /// XM_221915	-1,37	
<i>Cables1</i>	Cdk5 and Abl enzyme substrate 1	NM_001107404	-1,37	nervous system development
<i>Ptk7</i>	PTK7 protein tyrosine kinase 7	NM_001106889	-1,37	neural tube closure
<i>Ttyh3</i>	tweety homolog 3 (Drosophila)	NM_001107124	-1,37	
<i>Man1b1</i>	mannosidase, alpha, class 1B, member 1	XM_001077558 /// XM_575086	-1,37	metabolic process
<i>Glb1l2</i>	galactosidase, beta 1-like 2	NM_001192018 /// XM_001053731 /// XM_578717	-1,37	carbohydrate metabolic process
<i>Fam98a</i>	family with sequence similarity 98, member A	NM_001014073	-1,37	
<i>Dgkz</i>	diacylglycerol kinase zeta	NM_031143	-1,36	activation of protein kinase C activity by G-protein coupled receptor
<i>Aldh1a2</i>	aldehyde dehydrogenase 1 family, member A2	NM_053896	-1,36	blood vessel development
<i>Ddx39</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	NM_053563	-1,35	nuclear mRNA splicing, via spliceosome
<i>Alox15</i>	arachidonate 15-lipoxygenase	NM_031010	-1,35	ossification
<i>Ppargc1b</i>	peroxisome proliferator-activated receptor gamma, coactivator 1 beta	NM_176075	-1,35	transcription
<i>Znf536</i>	zinc finger protein 536	XM_001077206 /// XM_218522	-1,35	
<i>Atg9a</i>	ATG9 autophagy related 9 homolog A (S. cerevisiae)	NM_001014218	-1,35	autophagic vacuole assembly
<i>Epas1</i>	endothelial PAS domain protein 1	NM_023090	-1,35	angiogenesis
<i>Eprs</i>	glutamyl-prolyl-tRNA synthetase	NM_001024238	-1,35	translation
<i>Ap3m1</i>	adaptor-related protein complex 3, mu 1 subunit	NM_133593	-1,35	transport
<i>Zyx</i>	zyxin	NM_053761	-1,35	regulation of inflammatory response
<i>Ggct</i>	gamma-glutamyl cyclotransferase	NM_001108629	-1,35	
<i>Fhdc1</i>	FH2 domain containing 1	NM_001106437	-1,35	cellular component organization
<i>Myl9</i>	myosin, light chain 9, regulatory	NM_001100885	-1,35	muscle contraction
<i>Rab27a</i>	RAB27A, member RAS oncogene family	NM_017317	-1,34	protein targeting
<i>Hyou1</i>	hypoxia up-regulated 1	NM_001034028 /// NM_138867	-1,34	response to hypoxia
<i>Atf5</i>	activating transcription factor 5	NM_172336	-1,34	transcription
<i>Hcfc2</i>	host cell factor C2	NM_001008357	-1,34	
<i>Tram1</i>	translocation associated membrane protein 1	NM_001007701	-1,34	transport
<i>Ln timer</i>	ligand of numb-protein X 2	NM_001108329	-1,34	protein homooligomerization
<i>Nos1ap</i>	nitric oxide synthase 1 (neuronal) adaptor protein	NM_138922	-1,34	neurotransmitter secretion
<i>Umps</i>	uridine monophosphate synthetase	NM_001025402	-1,34	'de novo' pyrimidine base biosynthetic process

<i>Dgka</i>	diacylglycerol kinase, alpha	NM_080787	-1,34	activation of protein kinase C activity by G-protein coupled receptor
<i>Ehd4</i>	EH-domain containing 4	NM_139324	-1,34	pinocytosis
<i>Trabd</i>	TraB domain containing	NM_001106788	-1,33	
<i>Prdx4</i>	peroxiredoxin 4	NM_053512	-1,33	cell redox homeostasis
<i>Fig4</i>	FIG4 homolog (S. cerevisiae)	NM_001047096	-1,33	vacuole organization
<i>Ipo4</i>	importin 4	NM_001106038	-1,33	intracellular protein transport
<i>Ddx19a</i> /// <i>Ddx19b</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a /// DEAD (Asp-Glu-Ala-As) box polypep	NM_001005381 /// NM_001005895 /// XM_001075251 /// XM_002725392	-1,32	induction of apoptosis
<i>Psmc5</i>	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	NM_001106569	-1,32	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent
<i>Mxra8</i>	matrix-remodelling associated 8	NM_001007002	-1,32	
<i>Necab3</i>	N-terminal EF-hand calcium binding protein 3	NM_001098724	-1,32	antibiotic biosynthetic process
<i>Ccdc28b</i>	coiled coil domain containing 28B	NM_001134689	-1,32	
<i>Mier2</i>	mesoderm induction early response 1, family member 2	NM_001108737	-1,32	
<i>Slc20a2</i>	solute carrier family 20 (phosphate transporter), member 2	NM_017223	-1,32	transport
<i>Tmem57</i>	transmembrane protein 57	NM_001025699	-1,31	
<i>Pdp2</i>	pyruvate dehydrogenase phosphatase catalytic subunit 2	NM_145091	-1,31	protein dephosphorylation
<i>Fam101b</i>	family with sequence similarity 101, member B	NM_001007611	-1,31	
<i>Galnt1</i>	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	NM_024373	-1,31	protein O-linked glycosylation
<i>Ctdspl</i>	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatas	NM_001106865	-1,31	
<i>Cdc42bpa</i>	CDC42 binding protein kinase alpha	NM_053657	-1,31	microtubule cytoskeleton organization
<i>Arfgap1</i>	ADP-ribosylation factor GTPase activating protein 1	NM_145090	-1,31	transport
<i>Tmem164</i>	transmembrane protein 164	NM_001109014	-1,31	
<i>Dopey2</i>	dopey family member 2	NM_001191660 /// XM_001055500 /// XM_002724703 /// XM_002727866 /// XM_221640	-1,30	
<i>Batf3</i>	basic leucine zipper transcription factor, ATF-like 3	NM_021865	-1,30	transcription
<i>Dad1</i>	defender against cell death 1	NM_138910	-1,30	blastocyst development
<i>Diaph1</i>	Diaphanous homolog 1 (Drosophila)	NM_001107393	-1,30	cellular component organization
<i>Fam20c</i>	family with sequence similarity 20, member C	NM_001012238	-1,30	

\* P value = 0.029, was obtained by permutation analysis. Fold change  $\geq 1.3$ .

Supplemental table 3: List of genes regulated by aging, classified by biological functions

A- Anterior Pituitary

Category	# of genes	P value	Genes
Cell Death	186	1,84E-04-2,32E-02	<i>Ier3, Gstm5, Rassf6, Clns1a, Ascl1, Ptpkr, Cdc42bpa, Gstp1, Calcr, Prkcz, Tradd, Bcap29, Ace, Cdh1, Camk1g, Igf2, Cdkn1c, Adamts14, Pmp22, Fcgr2a, Itsn1, Ccl11, Appb1, Plscr3, Spp, Ctnnb1, Nol3, Alox15, Soat1, Igfbp1, Adipoq, Pcsk2, Atrx, Exoc2, Chka, Rtn, Cadm1, Lgals3bp, Ehd4, Rgs5, Grb10, Id3, Htra1, Zyx, Inpp1, Fgl2, Meis1, Ryr2, Stmn1, Gpc3, Plat, Sqstm1, Sh3bgrl3, L1cam, Stxbp1, Blcap, Lyz1/Lyz2, Hes1, Snca, Grik2, Gabrg2, Dpp3, Ephx1, Igfbp7, Tnfsf12, Cdkn2c, Xrcc5, Vtn, F2r, Abcc3, Tpp1, Cd82, Sli2, Epor, Camk2b, Gfra3, Ccnd1, Gsdma, Dad1, Snn, Prdm2, Atp6ap2, Jun, Ddx19a, Gria4, Ctbp2, Cdc1, Capn1, Ap2a2, Ddx41, Gpx2, Pdyn, Reg3g, Kitlg, Sh3kbp1, Aldh1a2, Tubb3, Lgals1, Traf3ip2, Sstr3, Ccnd2, Pnpt1, Klk1, Cables1, Htatip2, Cast, Pcgf2, Six1, Gabrd, Glrx, Fos, Pcnal, Krt18, Prkcz, Cebpd, Cadps2, Ddx20, Nckap11, Vegfa, Hspb8, Map2k6, Ccl13, Mtmr1, Dgkz, C1qa, Gpx4, Nek7, Ndn, Ednra, Sox4, Aatk, Apoe, S100a6, Banf1, Gpm6a, Xdh, Tgfb1, Plcg2, Camk2n1, Aif1, Igfbp3, Copb2, Ivns1abp, Rab25, Mx1, Camk2d, Rps6ka1, Sstr2, Rasd1, Id2, Ctss, Vipr2, Dsp, Agtr1b, Igf1, St6gal1, Anxa4, Tspo, Tmem57, Map2k3, Dgka, Eef2k, Ptgr1, Abcc5, Epas1, Ptpzr1, Rnd3, Aqp1, Cd74, Xpa, Hyou1, Ngb, Col2a1, Dlk1, Rab27a, Hbxip, Hla-Drb1, Amigo2, Timp2, Rgs10, Setd8, Snca, Ntrk2, Atf5, Isg20, Atp5s</i>
Cellular Growth and Proliferation	127	1,93E-04-2,32E-02	<i>Ier3, Ctdspl, Ltp4, Rem2, Ascl1, Calcr, Gstp1, Prkcz, Igf2, Cd151, Cdkn1c, Pmp22, Dgkz, Ptp4a3, Lepre1, Ccl11, Appb1, Degs1, Spp1, Alox15, Igfbp1, Adipoq, Chka, Cadm1, Grb10, Id3, Htra1, Zyx, Meis1, Stmn1, Gpc3, Plat, Coro1a, Gfm1, Col1a1, Gltsr2, Etv1, Hes1, Myl9, Flot1, Igfbp7, Tnfsf12, Agtrap, Cdkn2c, Xrcc5, Vtn, F2r, Cd82, Epor, Sli2, Smyd4, Scn5a, Ccnd1, Mltf6, Pold4, Jun, Cdc1, Capn1, Rbbp9, Kitlg, Aldh1a2, Tubb3, Lgals1, Tusc2, Ccnd2, Pnpt1, Cables1, Cast, Six1, Pcgf2, Fos, C20orf191, Eif5a2, Ltp4, Cebpd, Vegfa, Hspb8, Map2k6, Ccl13, Nubp1, Gpx4, Ndn, Ednra, Rtn4r, Apoe, Nfix, Ptpn3, Xdh, Bin3, Camk2n1, Aif1, Igfbp3, Ivns1abp, Mx1, Fshb, Rps6ka1, Sstr2, Id2, Rasd1, Ctss, Hopx, Dsp, Rbp4, Igf1, Map2k3, Dgka, Kcnk10, Eef2k, Igh2, Abcc5, Epas1, Aqp1, Tob1, Cd74, Xpa, Diaph1, Vldlr, Col2a1, Dlk1, Steap2, Prdx4, Gga2, Ttpi, Cirbp, Timp2, Atf5, Ntrk2</i>
Cellular Function and Maintenance	117	4,85E-04-2,27E-02	<i>Cdc42bpa, Prkcz, Igf2, Scnn1g, Cadps, Cd151, Dgkz, Fcgr2a, Itsn1, Ccl11, Plscr3, Nol3, Spp1, Alox15, Adipoq, Slc2a4, Exoc2, Dopey2, Id3, Ryr2, Stmn1, Coro1a, Sqstm1, Plat, Nefh, L1cam, Stxbp1, Klk1, Ttyh1, Snca, Grik2, Evi, Gabrg2, Krt25, Pex5l, Xrcc5, Vtn, F2r, Tpp1, Rab3c, Abcc3, Stmn2, Cd82, Epor, Sli2, Scn5a, Ccnd1, Tapbp, Capn1, Ap2a2, Rab3d, Atg9a, Mark1, Kitlg, Tesc, Tubb3, Lgals1, Cdk5rap2, Pcgf2, Cast, Tnr, Kctd13, Krt18, Prkcz, Cadps2, Nckap11, Vegfa, Hspb8, Ccl13, Slc20a2, C1qa, Nubp1, Ndn, Nlgn3, Kcnj11, Rtn4r, Sox4, Apoe, Aatk, Cnih2, Xdh, Hla-Qa1, Gpm6a, Plcg2, Copb2, Rab2b, Camk2d, Aplp2, Id2, Ctss, Dsp, Rbp4, Igf1, Fcgrt, Gabra1, Dgka, Eef2k, Trim54, Arsb, Epas1, Ptpzr1, Rnd3, Aqp1, Lrrc23, Fam101b, Cd74, Diaph1, Slc16a1, Slc12a5, Rab27a, Plxna3, Steap2, Atf1, Cyth2, Exoc7, Ntrk2, Syne1</i>
Cellular Assembly and Organization	82	6,59E-04-2,47E-02	<i>Mark1, Kitlg, Tubb3, Ascl1, Cdc42bpa, Cdk5rap2, Cast, Prkcz, Tnr, Igf2, Cadps, Kctd13, Krt18, Prkcz, Pmp22, Fcgr2a, Cadps2, Ptp4a3, Lppr5, Nckap11, Ccl11, Vegfa, Spp1, Gphn, Nol3, Adipoq, Ccl13, C1qa, Ndn, Nlgn3, Dopey2, Rtn4r, Ehd4, Aatk, Apoe, Gpm6a, Plcg2, Igfbp3, Copb2, Stmn1, Sqstm1, Coro1a, Plat, Nefh, L1cam, Ctss, Klk1, Ttyh1, Snca, Dsp, Igf1, Mtmr2, Evi, Krt25, Trim54, Amigo1, Vtn, Arsb, Epas1, F2r, Ptpzr1, Tpp1, Stmn2, Rab3c, Rnd3, Aqp1, Cd82, Sli2, Fam101b, Cd74, Diaph1, Rab27a, Plxna3, Atf1, Gga2, Cyth2, Exoc7, Snca, Ntrk2, Rab3d, Lrrc4c, Syne1</i>
Cellular Development	79	1,93E-04-2,47E-02	<i>Ier3, Kitlg, Tubb3, Aldh1a2, Lgals1, Rem2, Ascl1, Tusc2, Ccnd2, Pnpt1, Calcr, Six1, Cast, Prkcz, Ace, Igf2, Fos, Cd151, Cdkn1c, Cebpd, Dgkz, Pmp22, Fcgr2a, Ptp4a3, Cadps2, Ccl11, Vegfa, Degs1, Hspb8, Spp1, Alox15, Map2k6, Ccl13, Adipoq, Lhb, Pcsk2, Chka, Fig4, Ndn, Cadm1, Apoe, Id3, Plcg2, Aif1, Igfbp3, Ivns1abp, Stmn1, Grb14, Plat, Sqstm1, Col1a1, L1cam, Rasd1, Id2, Hes1, Hopx, Igf1, Vwc2, Map2k3, Dgka, Tnfsf12, Trim54, Abcc5, F2r, Epor, Smyd4, Gfra3, Ccnd1, Mltf6, Vldlr, Tapbp, Pold4, Dlk1, Steap2, Jun, Ttpi, Cdc1, Timp2, Ntrk2</i>
Cell-To-Cell Signaling and Interaction	76	3,75E-04-2,47E-02	<i>Kitlg, Mltf4, Lgals1, Ascl1, Ccnd2, Cast, Prkcz, Gabrd, Tnr, Ace, Fos, Igf2, Cd151, Cdkn1c, Bcan, Pmp22, Fcgr2a, Ptp4a3, Grk6, Ccl11, Vegfa, Gphn, Spp1, Alox15, Adipoq, Ccl13, Syn2, Nlgn3, Cadm1, Lgals3bp, Apoe, Vangl1, Cnih2, Id3, Gpm6a, Xdh, Cspg5, Igfbp3, Bsn, Serping1, Gpc3, Plat, Col1a1, L1cam, Id2, Stxbp1, Hes1, Snca, Grik2, Agtr1b, Mtmr2, Igf1, St6gal1, Esm1, Nrxn1, Amigo3, Gabrg2, Kcnk10, Trim54, Agtrap, Vtn, Amigo1, F2r, Cd82, Sli2, Cd74, Ccnd1, Lamc2, Diaph1, Slc12a5, Col2a1, Gria4, Cdc1, Amigo2, Snca, Ntrk2</i>
Cellular Movement	72	8,97E-04-2,41E-02	<i>Ier3, Kitlg, Lgals1, Hdllbp, C4b, Htatip2, Cast, Prkcz, Tnr, Igf2, Fos, Cd151, Prkcz, Bcan, Fcgr2a, Itsn1, Ptp4a3, Grk6, Nckap11, Ccl11, Vegfa, Batf3, Spp1, Igfbp1, Adipoq, Ccl13, Cfb, Ednra, Cadm1, Apoe, S100a6, Vangl1, Xdh, Nfix, Zyx, Igfbp3, Serping1, Stmn1, Mx1, Plat, Coro1a, Fshb, Col1a1, Aplp2, Sstr2, L1cam, Etv1, Id2, Ctss, Igf1, Esm1, Podxl2, Tnfsf12, Lmo4, Vtn, F2r, Epas1, Ptpzr1, Rnd3, Cd82, Sli2, Scn5a, Cd74, Ccnd1, Diaph1, Jun, Ctbp2, Capn1, Timp2, Cyth2, Ntrk2, Cldn7</i>
Molecular Transport	64	4,85E-04-2,3E-02	<i>Kitlg, Lgals1, Calcr, Cast, Cpt1a, Prkcz, Fos, Igf2, Elovl5, Cadps, Pmp22, Fcgr2a, Cadps2, Itsn1, Grk6, Ccl11, Vegfa, Spp1, Alox15, Soat1, Ccl13, Adipoq, Slc2a4, Exoc2, Trhr, Ednra, Kcnj11, Apoe, Ppargc1b, Xdh, Plcg2, Rab2b, Ryr2, Aco2, Camk2d, L1cam, Sstr2, Stxbp1, Lyz1/Lyz2, Snca, Atp2b3, Agtr1b, Igf1, Fcgrt, Dgka, Igfbp7, Agtrap, Apod, Pex5l, F2r, Epas1, Rab3c, Pde6d, Epor, Hyou1, Vldlr, Abcc8, Dlk1, Pnpla2, Rab27a, Steap2, Acsl1, Exoc7, Rab3d</i>
Small Molecule Biochemistry	53	4,85E-04-2,41E-02	<i>Sh3kbp1, Kitlg, Plch2, Htatip2, Prkcz, Cpt1a, Igf2, Fos, Elovl5, Pex7, Fcgr2a, Ccl11, Vegfa, Spp1, Soat1, Alox15, Adipoq, Ccl13, Csgalnact1, Mtmr1, Slc2a4, Gpx4, Chka, Fig4, Ednra, Trhr, Apoe, Ppargc1b, Xdh, Csgalnact2, Plcg2, Aco2, Sstr2, Snca, Agtr1b, Mtmr2, Igf1, Dgka, Igfbp7, Agtrap, Apod, Ppap2b, Vtn, Epas1, F2r, Ptgr2, Cd74, Vldlr, Chpt1, Dlk1, Pnpla2, Ppapdc1b, Acsl1</i>
Cell Cycle	50	2,2E-04-2,38E-02	<i>Kitlg, Lgals1, Tusc2, Ccnd2, Pnpt1, Calcr, Cables1, Cast, Fos, Igf2, Tmpo, Cdkn1c, Cebpd, Dgkz, Appb1, Vegfa, Degs1, Rprm, Alox15, Adipoq, Map2k6, Chka, Apoe, Grb10, Id3, Camk2n1, Igfbp3, Ppap2c, Camk2d, Sstr2, Pola1, Id2, Hes1, Igf1, Map2k3, Igfbp7, Cdkn2c, Xrcc5, Epor, Camk2b, Ccnd1, Xpa, Babam1, Pold4, Jun, Camk1, Timp2, Ap2a2, Setd8, Atf5</i>

Lipid Metabolism	44	2,71E-03-2,41E-02	<i>Sh3kbp1, Kitlg, Acot2, Sstr2, Plch2, Snca, Cpt1a, Mtmr2, Igf1, Igf2, Elovl5, Igfbp7, Apod, Fcgr2a, Pex7, Vtn, Ppap2b, F2r, Epas1, Ccl11, Vegfa, Soat1, Ptgr2, Alox15, Adipoq, Ccl13, Cd74, Mtmr1, Slc2a4, Vldlr, Chpt1, Chka, Gpx4, Fig4, Trhr, Ednra, Dlk1, Pnpla2, Ppapdc1b, Apoe, Ppargc1b, Acs11, Xdh, Plcg2</i>
Cell Morphology	35	2,25E-03-2,36E-02	<i>Kitlg, Plat, Coro1a, L1cam, Snca, Cast, Tnr, Igf1, Evi, Krt18, Map2k3, Cdkn1c, Tnfrsf12, Pmp22, Fcgr2a, Vtn, Lppr5, F2r, Stmn2, Ccl11, Vegfa, Cd82, Slt2, Ccl13, Diaph1, Ndn, Nlgn3, Rtn4r, Jun, Apoe, Sncb, Rab3d, Xdh, Plcg2, Igfbp3</i>
Cell Signaling	31	1,25E-02-1,25E-02	<i>Ryr2, Lgals1, Camk2d, L1cam, Lys1/Lyz2, Calcr, Cast, Atp2b3, Agtr1b, Igf1, Igf2, Fos, Igfbp7, Pmp22, Fcgr2a, Grk6, F2r, Ccl11, Pde6d, Vegfa, Epdr, Spp1, Ccl13, Hyou1, Abcc8, Trhr, Ednra, Kcnj11, Apoe, Xdh, Plcg2</i>
Vitamin and Mineral Metabolism	31	1,25E-02-1,25E-02	<i>Ryr2, Lgals1, Camk2d, L1cam, Lys1/Lyz2, Calcr, Cast, Atp2b3, Agtr1b, Igf1, Igf2, Fos, Igfbp7, Pmp22, Fcgr2a, Grk6, F2r, Ccl11, Pde6d, Vegfa, Epdr, Spp1, Ccl13, Hyou1, Abcc8, Trhr, Ednra, Kcnj11, Apoe, Xdh, Plcg2</i>
Carbohydrate Metabolism	28	4,85E-04-2,3E-02	<i>Sh3kbp1, Plch2, Htatip2, Cpt1a, Prkcz, Agtr1b, Igf1, Mtmr2, Igf2, Dgka, Mfng, Fcgr2a, Vtn, Vegfa, Spp1, Alox15, Ccl13, Adipoq, Csgalnact1, Mtmr1, Slc2a4, Chpt1, Chka, Gpx4, Fig4, Trhr, Plcg2, Csgalnact2</i>
Post-Translational Modification	22	2,52E-03-7,3E-03	<i>Tpp1, Vegfa, Ltbp4, Plat, Bace2, Alox15, C4b, Pcsk2, Diaph1, Ctss, Cndp2, Wfdc2, Prkcz, Gpx4, Igf1, Ace, Apoe, Enpep, Dpp3, Capn1, Timp2, Xdh</i>
Cellular Compromise	20	5,84E-03-2,41E-02	<i>Stmn2, Pdyn, Epdr, Spp1, Sqstm1, Plat, Adipoq, Plod1, Nefh, Snca, Six1, Igf1, Cadm1, Igf2, Apoe, Krt18, Acs11, Exoc7, Ntrk2, Xrcc5</i>
Protein Degradation	18	6,87E-03-6,87E-03	<i>Tpp1, Ltbp4, Plat, Bace2, Alox15, C4b, Pcsk2, Diaph1, Cndp2, Ctss, Wfdc2, Ace, Igf1, Apoe, Enpep, Dpp3, Capn1, Timp2</i>
Protein Synthesis	18	6,87E-03-6,87E-03	<i>Tpp1, Ltbp4, Plat, Bace2, Alox15, C4b, Pcsk2, Diaph1, Cndp2, Ctss, Wfdc2, Ace, Igf1, Apoe, Enpep, Dpp3, Capn1, Timp2</i>
Antigen Presentation	16	7,3E-03-2,36E-02	<i>Epas1, Nckap11, Vegfa, Slt2, Spp1, Coro1a, Cd74, Ccl13, Adipoq, Ccnd1, Tnr, Ednra, Apoe, Cd151, Fcgr2a, Vtn</i>
Drug Metabolism	8	6,48E-04-7,07E-03	<i>Gstm5, Glrx, Agtr1b, Fos, Xdh, Agtrap, Gstp1, Snca</i>
Gene Expression	5	7,3E-03-2,27E-02	<i>Jun, Ccnd1, Id3, Id2, Cdkn2c</i>
Protein Folding	2	7,3E-03-7,3E-03	<i>Prkcz, Vegfa</i>
DNA Replication, Recombination, and Repair	2	2,27E-02-2,27E-02	<i>Pcna, Xrcc5</i>

## B- Hypothalamus

Category	# of genes	P value	Genes
Cell Death	78	7,08E-11-7,58E-03	<i>Cd48, Calcb, Pdyn, S100a9, Kitlg, Uba7, Ccnd2, Gadd45b, Ndp, Cd38, Nts, Casp4, Ptpn6, Egr4, Timp4, Cd4, Sst, Ctse, Scd, Slc40a1, Alb, Fcgr3a, Fcgr2a, Gja1, Ghrh, Hla-C, Cfh, Mtmr1, Gsta1, C1qa, Hck, Gal, Sox4, C3, Bst2, Psmb8, Dcx, Acer2, Igfbp3, Aif1, Csf1r, Cd53, B2m, Wnt4, Ptprc, Dusp6, Col1a1, Zfp36, Hspb1, Fcgr2b, Dsp, Ednrb, Slc1a2, Anxa4, Tspo, Grm2, Nptx1, Ephx1, Pycard, F2r, Anxa11, Aqp1, Sp110, Icam1, Serpina3, Rac2, Fcer1g, Cidea, Irf9, Six4, Dlk1, Rras2, Rab27a, Tyrobp, Stat1, Hcrr1, Nlk, Blnk</i>
Cellular Growth and Proliferation	71	9,46E-08-7,26E-03	<i>Cd48, Calcb, Kitlg, S100a9, Ccnd2, Gadd45b, Ndp, Cd38, Ptpn6, Nts, Egr4, Timp4, Sst, Cd4, Alb, Hmgcr, Clec7a, Gpnmb, Fcgr3a, Gja1, Ghrh, Psmb9, Fads2, Gbp2, Tmeff1, Hck, Sash3, Htr1a, Gal, Fads1, Sox4, C3, Bst2, Psmb8, Dcx, Acer2, Igfbp3, Aif1, Csf1r, B2m, Wnt4, Ptprc, Dusp6, Col1a1, Ifit3, Ube2l6, Ctss, Nrarp, Plagl1, Zfp36, Dsp, Fcgr2b, Ednrb, Slc1a2, Tspo, Lcp1, Cd37, Pycard, F2r, Anxa11, Aqp1, Icam1, Rac2, Fcer1g, Six4, Dlk1, Stat1, Tyrobp, Hcrr1, Cdh23, Blnk</i>
Cell-To-Cell Signaling and Interaction	57	1,54E-12-7,26E-03	<i>Cd48, Calcb, Kitlg, S100a9, Mlt4, Ccnd2, C4b, Ndp, Cd38, Nts, Ptpn6, Plek, Slc1a6, Cd4, Sst, Clec7a, Fcgr2a, Fcgr3a, Gja1, Ghrh, Hla-C, Psmb9, Cfh, Sash3, Hck, C1qa, Htr1a, Tnfaiip82, Gal, Fzd2, Sv2b, Lgals3bp, C3, Bst2, Psmb8, Igfbp3, Csf1r, B2m, Wnt4, Ptprc, Ctss, Ube2l6, Fcgr2b, Slc1a2, Grm2, Lcp1, Nptx1, Pycard, F2r, Icam1, Rac2, Fcer1g, Rras2, Rab27a, Tyrobp, Stat1, Hcrr1</i>
Small Molecule Biochemistry	57	5,37E-07-7,06E-03	<i>Calcb, Kitlg, Mlt4, S100a9, C4b, Cd38, Npc2, Nts, Plek, Cyp4f8, Slc1a6, Cd4, Sst, Clec7a, Hmgcr, Alb, Scd, Fcgr2a, Ghrh, Cfh, Fads2, Gsta1, Htr1a, Cyp27a1, Fzd2, Gal, Fads1, C3, Acss2, Igfbp3, Aif1, Csf1r, B2m, Wnt4, Thrsp, Ptprc, Arhgdib, Ctss, Slc7a10, Fcgr2b, Ednrb, Slc1a2, Cyp2d6, Tspo, Grm2, Ephx1, Crym, F2r, Cyp51a1, Icam1, Pnlp, Fcer1g, Dlk1, Rab27a, Tyrobp, Stat1, Cp</i>
Cellular Function and Maintenance	52	2,25E-07-7,74E-03	<i>Calcb, Kitlg, S100a9, Cd38, Ptpn6, Nts, Plek, Cenpj, Slc1a6, Sst, Cd4, Alb, Clec7a, Slc40a1, Fcgr2a, Fcgr3a, Gja1, Ghrh, Hck, C1qa, Htr1a, Gal, Sox4, C3, Bst2, Anxa3, Dcx, Csf1r, B2m, Wnt4, Ptprc, Arhgdib, Iqgap1, Ctss, Nrarp, Hspb1, Fcgr2b, Dsp, Pygl, Ednrb, Grm2, Lcp1, Pycard, F2r, Aqp1, Icam1, Rac2, Fcer1g, Rras2, Stat1, Tyrobp, Cp</i>
Cellular Development	49	2,15E-06-7,26E-03	<i>Calcb, Kitlg, Ccnd2, Gadd45b, Cd38, Ptpn6, Cd4, Sst, Ctse, Sept11, Alb, Scd, Clec7a, Fcgr2a, Gja1, Fads2, Fzd2, Sox4, C3, Dcx, Igfbp3, Csf1r, B2m, Wnt4, Ptprc, Plagl1, Nrarp, Zfp36, Fcgr2b, Dsp, C1qc, Slc1a2, Ednrb, Lcp1, Grxcr1, Cyp51a1, Icam1, Metrn, Rac2, Fcer1g, Dlk1, Rras2, Rab27a, Stat1, Tyrobp, Asb1, Cdh23, Nlk, Blnk</i>
Cell Signaling	48	4,39E-08-7,72E-03	<i>Cd48, Calcb, S100a9, Csf1r, Kitlg, B2m, Wnt4, Ptprc, C4b, Gadd45b, Cd38, Casp4, Nts, Hspb1, Zfp36, Ptpn6, Fcgr2b, Ednrb, Tspo, Grm2, Cd4, Sst, Clec7a, Alb, Fcgr3a, Fcgr2a, Pycard, F2r, Gja1, Ghrh, Icam1, Hla-C, Hck, Rac2, Htr1a, Fcer1g, Fzd2, Gal, Irf9, Tyrobp, Stat1, C3, Bst2, Wnk1, Nlk, Aif1, Blnk, Igfbp3</i>
Cellular Movement	47	1,97E-10-7,26E-03	<i>Cd48, Kitlg, Csf1r, S100a9, Ptprc, Iqgap1, Arhgdib, C4b, Col1a1, Ndp, Ctss, Cd38, Ptpn6, Nts, Fcgr2b, Slc1a2, Ednrb, Tspo, Lcp1, Nptx1, Sst, Cd4, Ctse, C2, Hmgcr, Alb, Fcgr3a, Fcgr2a, Pycard, F2r, Gja1, Aqp1, Icam1, Cfh, Serpina3, Hck, Rac2, Fcer1g, Six4, Rras2, Tyrobp, Stat1, C3, Anxa3, Dcx, Igfbp3, Aif1</i>
Molecular Transport	47	4,39E-08-7,72E-03	<i>Calcb, Csf1r, Kitlg, S100a9, B2m, Wnt4, Ptprc, C4b, Ctss, Cd38, Slc7a10, Ptpn6, Nts, Fcgr2b, Ednrb, Slc1a2, Grm2, Sst, Cd4, Crym, Slc40a1, Scd, Hmgcr, Alb, Clec7a, Fcgr3a, Fcgr2a, F2r, Ghrh, Icam1, Hla-C, Cfh, Fads2, Gsta1, Hck, Rac2, Htr1a, Cyp27a1, Fcer1g, Fzd2, Gal, Dlk1, Rab27a, Tyrobp, Cp, C3, Blnk</i>

Vitamin and Mineral Metabolism	37	4,39E-08-7,72E-03	<i>Calcb, Csf1r, Kitlg, S100a9, B2m, Wnt4, Ptprc, C4b, Cd38, Nts, Ptpn6, Fcgr2b, Ednrb, Tspo, Grm2, Sst, Cd4, Scd, Hmgcr, Alb, Clec7a, Fcgr3a, Fcgr2a, F2r, Cyp51a1, Ghrh, Hla-C, Icam1, Hck, Rac2, Htr1a, Cyp27a1, Fcer1g, Fzd2, Gal, C3, Blink</i>
Lipid Metabolism	35	3E-05-7,06E-03	<i>Kitlg, Csf1r, Wnt4, Thrsp, Ctss, Cd38, Nts, Npc2, Fcgr2b, Slc1a2, Cyp2d6, Cyp4f8, Ednrb, Tspo, Cd4, Ephx1, Alb, Hmgcr, Clec7a, Scd, Fcgr2a, F2r, Cyp51a1, Ghrh, Icam1, Fads2, Gsta1, Pnlip, Fcer1g, Cyp27a1, Gal, Dlk1, Fads1, C3, Acss2</i>
Antigen Presentation	31	1,36E-07-7,06E-03	<i>Cd48, Csf1r, Kitlg, S100a9, Ptprc, C4b, Ube2l6, Ctss, Cd38, Ptpn6, Fcgr2b, Ednrb, Cd4, Ctse, Clec7a, Fcgr2a, F2r, Icam1, Hla-C, Psmb9, Cfh, Serpina3, C1qa, Rac2, Hck, Fcer1g, Rab27a, Stat1, Tyrobp, C3, Psmb8</i>
Post-Translational Modification	22	1,2E-06-1,73E-04	<i>F2r, Cd48, Csf1r, Kitlg, Ptprc, Dusp6, Ccnd2, Hck, Fcer1g, Ptpn6, Phkg1, Fcgr2b, Ednrb, Cp, Tyrobp, Cd4, Wnk1, Alb, Fcgr2a, Nlk, Igfbp3, Aif1</i>
Cellular Assembly and Organization	22	8,78E-04-7,74E-03	<i>F2r, Gja1, S100a9, Aqp1, Csf1r, Kitlg, Icam1, Arhgdib, Iqgap1, Pls1, Rac2, C1qa, Ctss, Htr1a, Dsp, Gal, Plek, Cenpj, Lcp1, Bst2, Dcx, Fcgr2a</i>
Cell Morphology	22	1,34E-03-7,26E-03	<i>F2r, Kitlg, S100a9, Ghrh, B2m, Icam1, Hck, Hspb1, Ptpn6, Nts, Dsp, Plek, Dlk1, Ednrb, Grm2, Bst2, Sst, Cd4, Fcgr2a, Pycard, Blink, Igfbp3</i>
Cellular Compromise	21	5,61E-08-6,41E-03	<i>Gja1, Kitlg, S100a9, Icam1, Wnt4, Cfh, Ptprc, C4b, Hck, Rac2, Cd38, Fcer1g, Fcgr2b, Rab27a, Tyrobp, Cd4, Bst2, C3, Anxa3, Alb, Fcgr2a</i>
Carbohydrate Metabolism	19	2,26E-04-5,8E-03	<i>F2r, Kitlg, Csf1r, Icam1, Ptprc, Dusp6, Htr1a, Cd38, Fcer1g, Nts, Phkg1, Fcgr2b, Plek, Pygl, Gal, Dlk1, Scd, Fcgr2a, Igfbp3</i>
Nucleic Acid Metabolism	14	1E-03-5,86E-03	<i>F2r, Calcb, Mlt4, Ghrh, Icam1, Cfh, Ptprc, Arhgdib, Htr1a, Nts, Gal, Grm2, Cd4, Sst</i>
Free Radical Scavenging	13	1,59E-03-2,37E-03	<i>F2r, Pdyn, Icam1, Cfh, Arhgdib, Iqgap1, Hck, Rac2, Hspb1, Ptpn6, Fcer1g, Alb, Fcgr2a</i>
Amino Acid Metabolism	9	1,73E-04-3,48E-03	<i>Nts, Ednrb, Slc1a2, Cp, Slc1a6, Sst, Crym, Alb, Slc7a10</i>
Cell Cycle	8	5,15E-04-5,23E-03	<i>Fcgr2b, Kitlg, Stat1, Cd37, Col1a1, Fcgr2a, Blink, Cd38</i>
Protein Trafficking	3	5,23E-03-5,23E-03	<i>Ednrb, Icam1, C3</i>
Energy Production	2	1,73E-04-1,73E-04	<i>Cp, Alb</i>
Drug Metabolism	2	5,15E-04-5,15E-04	<i>Cyp2d6, Alb</i>

**Supplemental table 4: List of canonical pathways significantly represented by genes regulated with aging**

**A- Anterior Pituitary**

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>Ratio</b>	<b>Genes</b>
Complement System	2,48	0,188	<i>C1qc, Serping1, C4b, C1qb, C1qa, Cfb</i>
Antigen Presentation Pathway	2,30	0,179	<i>Hla-Drb1, Cd74, Hla-Dqa1, Hla-Dra, Tapbp</i>
Chemokine Signaling	2,85	0,147	<i>Ccl11, Camk1g, Fos, Jun, Camk2b, Camk1, Ccl13, Camk2d, Calm1, Plcg2</i>
Glutathione Metabolism	2,12	0,137	<i>Gpx4, Glrx, Gpx2, Gstm5, Ggct, Gstm1, Gstm2</i>
Growth Hormone Signaling	2,59	0,134	<i>Prkcz, Igf1, Igf2, Fos, Prkcg, Slc2a4, Rps6ka1, Plcg2, Igfbp3</i>
Melatonin Signaling	2,40	0,132	<i>Prkcz, Camk2b, Map2k3, Map2k6, Prkcg, Camk2d, Calm1, Plch2, Plcg2</i>
Glioma Signaling	3,02	0,122	<i>Prkcz, Camk1g, Igf1, Igf2, Camk2b, Camk1, Ccnd1, Prkcg, Camk2d, Calm1, Cdkn2c, Plcg2</i>
Neuropathic Pain Signaling In Dorsal Horn Neurons	2,55	0,118	<i>Prkcz, Kcnq2, Camk1g, Fos, Camk2b, Camk1, Gria4, Prkcg, Camk2d, Plch2, Ntrk2, Plcg2</i>
B Cell Development	1,52	0,115	<i>Hla-Drb1, Hla-Dqa1, Hla-Dra</i>
Calcium-induced T Lymphocyte Apoptosis	1,42	0,107	<i>Prkcz, Hla-Drb1, Prkcg, Calm1, Hla-Dqa1, Hla-Dra</i>
Aryl Hydrocarbon Receptor Signaling	2,49	0,102	<i>Aldh18a1, Gstm5, Hspb7, Aldh1a2, Ccnd1, Ccnd2, Aldh16a1, Pola1, Gstm1, Aldh1l2, Aip, Fos, Jun, Nfix</i>
Glycerolipid Metabolism	1,70	0,099	<i>Ppap2c, Pnpla2, Aldh1a2, Ppapdc1b, Dgka, Adh5, Dgkb, Dgkz, Ppap2b</i>
Phospholipid Degradation	1,77	0,099	<i>Ppap2c, Ppapdc1b, Dgka, Dgkb, Plch2, Dgkz, Plcg2, Ppap2b</i>
Cdc42 Signaling	2,41	0,092	<i>Prkcz, Apc2, Myl9, Fos, Jun, Hla-Drb1, Cdc42bpa, Exoc7, Hla-Dqa1, Diaph1, Hla-Dra, Exoc2</i>
14-3-3-mediated Signaling	1,57	0,090	<i>Prkcz, Tubb3, Fos, Jun, Tubb6, Prkcg, Rps6ka1, Plch2, Plcg2, Snca</i>
Glycerophospholipid Metabolism	1,55	0,084	<i>Chka, Ppap2c, Ppapdc1b, Dgka, Dgkb, Plch2, Dgkz, Plcg2, Chpt1, Ppap2b</i>
p38 MAPK Signaling	1,30	0,081	<i>Tradd, Hspb7, Mapkapk3, H3f3c, Map2k3, Map2k6, Eef2k, Mapkapk5</i>
PKCθ Signaling in T Lymphocytes	1,41	0,074	<i>Fos, Jun, Hla-Drb1, Camk2b, Prkcg, Camk2d, Hla-Dqa1, Plcg2, Hla-Dra</i>
Xenobiotic Metabolism Signaling	1,90	0,074	<i>Aldh18a1, Ces1c, Abcc3, Gstm5, Aldh1a2, Camk2b, Map2k6, Aldh16a1, Camk2d, Ppm1j, Gstm1, Prkcz, Aldh1l2, Aip, Camk1g, Camk1, Map2k3, Prkcg, Fmo5</i>

**B- Hypothalamus**

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>Ratio</b>	<b>Molecules</b>
Complement System	7,01	0,22	<i>C1QC, CFH, C3, C4B, C2, C1QB, C1QA</i>
Antigen Presentation Pathway	4,98	0,18	<i>B2m, Hla-C, Psmb9, Psmb8, Tap2</i>
Lipid Antigen Presentation by CD1	2,06	0,15	<i>Fcer1g, B2m</i>
Interferon Signaling	3,46	0,14	<i>Irf9, Stat1, Psmb8, Ifit3</i>
Primary Immunodeficiency Signaling	3,46	0,10	<i>Cd4, Ptprc, Tap2, Blnk</i>
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	1,59	0,09	<i>Ptpn6, Stat1</i>
Natural Killer Cell Signaling	4,13	0,08	<i>Fcer1g, Ptpn6, Rras2, Tyrobp, Fcgr3a, Fcgr2a, Rac2</i>
Dendritic Cell Maturation	5,76	0,07	<i>Fcer1g, Fcgr2b, B2m, Hla-C, Stat1, Tyrobp, Icam1, Col1a1, Fcgr3a, Fcgr2a</i>
Linoleic Acid Metabolism	3,08	0,07	<i>Cyp51a1, Fads1, Cyp2d6, Cyp4f8, Fads2</i>

Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses	3,11	0,07	<i>C1qc,C3,C1qb,Clec7a,C1qa</i>
OX40 Signaling Pathway	2,69	0,07	<i>Fcer1g,B2m,Hla-C,Cd4</i>
Allograft Rejection Signaling	2,11	0,06	<i>Fcer1g,B2m,Hla-C</i>
Autoimmune Thyroid Disease Signaling	1,31	0,06	<i>Fcer1g,Hla-C</i>
Communication between Innate and Adaptive Immune Cells	2,44	0,06	<i>Fcer1g,B2m,Hla-C,Cd4</i>
TREM1 Signaling	1,93	0,06	<i>Fcgr2b,Tyrobp,Icam1</i>
FcγRIIB Signaling in B Lymphocytes	1,93	0,06	<i>Fcgr2b,Rras2,Blnk</i>
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	1,93	0,06	<i>Fcer1g,B2m,Hla-C</i>
Activation of IRF by Cytosolic Pattern Recognition Receptors	1,62	0,06	<i>Irf9,Stat1,Ift2</i>
Caveolar-mediated Endocytosis Signaling	2,12	0,06	<i>Cd48,B2m,Hla-C,Alb</i>
Glioma Invasiveness Signaling	1,60	0,06	<i>F2r,Rras2,Timp4</i>
Glutamate Receptor Signaling	1,49	0,05	<i>Slc1a2,Grm2,Slc1a6</i>
B Cell Receptor Signaling	2,98	0,05	<i>Ptpn6,Fcgr2b,Rras2,Ptpnc,Fcgr2a,Rac2,Blnk</i>
JAK/Stat Signaling	1,44	0,05	<i>Ptpn6,Rras2,Stat1</i>
GM-CSF Signaling	1,42	0,05	<i>Rras2,Stat1,Hck</i>
Virus Entry via Endocytic Pathways	1,78	0,05	<i>Rras2,B2m,Hla-C,Rac2</i>
Systemic Lupus Erythematosus Signaling	3,47	0,05	<i>Fcer1g,Ptpn6,Fcgr2b,Rras2,Hla-C,Ptpnc,Fcgr3a,Fcgr2a</i>
Role of JAK1 and JAK3 in γc Cytokine Signaling	1,51	0,05	<i>Rras2,Stat1,Blnk</i>
Antiproliferative Role of Somatostatin Receptor 2	1,42	0,05	<i>Ptpn6,Rras2,Sst</i>
Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes	1,65	0,05	<i>Fcgr3a,Fcgr2a,Hck,Rac2</i>
Growth Hormone Signaling	1,37	0,04	<i>Ptpn6,Stat1,Igf1bp3</i>
LXR/RXR Activation	2,04	0,04	<i>C3,C4B (Includes Others),HMGCR,ALB,SCD</i>
Acute Phase Response Signaling	2,46	0,04	<i>Rras2,Cp,C3,Serpina3,C4b,Alb</i>
Role of NFAT in Regulation of the Immune Response	2,61	0,04	<i>Fcer1g,Fcgr2b,Rras2,Cd4,Fcgr3a,Fcgr2a,Blnk</i>
Metabolism of Xenobiotics by Cytochrome P450	1,64	0,04	<i>Cyp51a1,Cyp2d6,Cyp4f8,Gsta1</i>
PI3K Signaling in B Lymphocytes	1,77	0,04	<i>Fcgr2b,Rras2,C3,Ptpnc,Blnk</i>
Hepatic Fibrosis / Hepatic Stellate Cell Activation	1,64	0,04	<i>Ednrb,Stat1,Icam1,Col1a1,Igf1bp3</i>
CD28 Signaling in T Helper Cells	1,48	0,04	<i>Fcer1g,Ptpn6,Cd4,Ptpnc</i>
Germ Cell-Sertoli Cell Junction Signaling	1,56	0,03	<i>Milt4,Rras2,Iqgap1,Pls1,Rac2</i>
PKCθ Signaling in T Lymphocytes	1,49	0,03	<i>Fcer1g,Rras2,Cd4,Rac2</i>
Wnt/β-catenin Signaling	1,40	0,03	<i>Fzd2,Gja1,Sox4,Wnt4,Nlk</i>
Cdc42 Signaling	1,38	0,03	<i>Fcer1g,B2m,Hla-C,Iqgap1</i>
Protein Ubiquitination Pathway	1,63	0,03	<i>Hspb1,B2m,Hla-C,Psmb9,Psmb8,Ube2l6,Tap2</i>
ERK/MAPK Signaling	1,30	0,03	<i>Hspb1,Rras2,Stat1,Dusp6,Rac2</i>



**Supplemental table 5: List of genes regulated by aging in the hypothalamus**

Gene Symbol	Gene Title	RefSeq Transcript ID	Fold change	Gene Ontology Biological Process
<b>Up-regulated</b>				
<i>C3</i>	complement component 3	NM_016994	<b>5,39</b>	positive regulation of type IIa hypersensitivity
<i>C4-2 /// C4b</i>	complement component 4, gene 2 /// complement component 4B (Chido blood group)	NM_001002805 /// NM_031504	<b>3,58</b>	inflammatory response
<i>RT1-A2 /// RT1-A3 /// RT1-EC2</i>	RT1 class Ia, locus A2 /// RT1 class I, locus A3 /// RT1 class Ib, locus EC2	NM_001008829 /// NM_001008830 /// NM_012645	<b>3,47</b>	positive regulation of T cell mediated cytotoxicity
<i>Psmb8</i>	proteasome (prosome, macropain) subunit, beta type 8 (large multifunctional pept	NM_080767	<b>2,54</b>	antigen processing and presentation
<i>Gpnmb</i>	glycoprotein (transmembrane) nmb	NM_133298	<b>2,52</b>	osteoblast differentiation
<i>Fcgr2a /// Fcgr2b</i>	Fc fragment of IgG, low affinity IIa, receptor (CD32) /// Fc fragment of IgG, lo	NM_053843 /// NM_175756	<b>2,50</b>	antibody-dependent cellular cytotoxicity
<i>Bst2</i>	bone marrow stromal cell antigen 2	NM_198134	<b>2,37</b>	positive regulation of I-kappaB kinase/NF-kappaB cascade
<i>Rsad2</i>	radical S-adenosyl methionine domain containing 2	NM_138881	<b>2,12</b>	ossification
<i>Psmb9</i>	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional pept	NM_012708	<b>2,11</b>	antigen processing and presentation
<i>Fcgr3a</i>	Fc fragment of IgG, low affinity IIIa, receptor	NM_207603	<b>2,00</b>	NK T cell proliferation
<i>Cp</i>	ceruloplasmin	NM_012532	<b>1,96</b>	liver development
<i>Lgals3bp</i>	lectin, galactoside-binding, soluble, 3 binding protein	NM_139096	<b>1,95</b>	cell adhesion
<i>Emr1</i>	EGF-like module containing, mucin-like, hormone receptor-like 1	NM_001007557	<b>1,95</b>	signal transduction
<i>Igfbp3</i>	insulin-like growth factor binding protein 3	NM_012588	<b>1,90</b>	regulation of cell growth
<i>Icam1</i>	intercellular adhesion molecule 1	NM_012967	<b>1,89</b>	ovarian follicle development
<i>Anxa4</i>	annexin A4	NM_024155	<b>1,86</b>	exocytosis
<i>RT1-CE12</i>	RT1 class I, locus CE12	NM_001008835	<b>1,85</b>	antigen processing and presentation of peptide antigen via MHC class
<i>Hspb1</i>	heat shock protein 1	NM_031970	<b>1,85</b>	anti-apoptosis
<i>C1qa</i>	complement component 1, q subcomponent, A chain	NM_001008515	<b>1,84</b>	complement activation, classical pathway
<i>Lcp1</i>	lymphocyte cytosolic protein 1	NM_001012044	<b>1,82</b>	T cell activation involved in immune response
<i>Gbp2</i>	guanylate binding protein 2	NM_133624	<b>1,77</b>	
<i>Pqlc3</i>	PQ loop repeat containing 3	NM_001034952	<b>1,76</b>	
<i>Aif1</i>	allograft inflammatory factor 1	NM_017196	<b>1,76</b>	positive regulation of protein phosphorylation
<i>Dusp6</i>	Dual specificity phosphatase 6	NM_053883	<b>1,75</b>	inactivation of MAPK activity
<i>Grm2</i>	glutamate receptor, metabotropic 2	NM_001105711	<b>1,73</b>	signal transduction
<i>Cd4</i>	Cd4 molecule	NM_012705	<b>1,71</b>	cytokine production
<i>Acer2</i>	alkaline ceramidase 2	NM_001107943	<b>1,70</b>	negative regulation of cell-matrix adhesion
<i>Cyp27a1</i>	cytochrome P450, family 27, subfamily a, polypeptide 1	NM_178847	<b>1,68</b>	steroid catabolic process
<i>Crym</i>	crystallin, mu	NM_053955	<b>1,68</b>	negative regulation of transcription from RNA polymerase II promoter
<i>C2</i>	complement component 2	NM_172222	<b>1,67</b>	proteolysis
<i>Cenpj</i>	centromere protein J	NM_001107265	<b>1,66</b>	centriole replication
<i>Cml3</i>	camello-like 3	XM_001074100 /// XM_575585	<b>1,64</b>	gastrulation with mouth forming second

<i>Ms4a6b</i>	membrane-spanning 4-domains, subfamily A, member 6B	NM_001006975	<b>1,63</b>	
<i>Tyrobp</i>	Tyrosine protein tyrosine kinase binding protein	NM_212525	<b>1,63</b>	intracellular signaling pathway
<i>RT1-EC2</i>	RT1 class Ib, locus EC2	NM_012645	<b>1,63</b>	antigen processing and presentation of peptide antigen via MHC class
<i>Ctsz</i>	cathepsin Z	NM_183330	<b>1,63</b>	proteolysis
<i>Cfh</i>	complement factor H	NM_130409	<b>1,62</b>	complement activation
<i>Plek</i>	pleckstrin	NM_001025750	<b>1,62</b>	hemopoietic progenitor cell differentiation
<i>Rab27a</i>	RAB27A, member RAS oncogene family	NM_017317	<b>1,61</b>	protein targeting
<i>Fam189a2</i>	family with sequence similarity 189, member A2	XM_001078764 /// XM_219909	<b>1,61</b>	
<i>Smagp</i>	small trans-membrane and glycosylated protein	NM_182817	<b>1,61</b>	
<i>Fcgr1g</i>	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	NM_001131001	<b>1,60</b>	positive regulation of type IIa hypersensitivity
<i>C1qc</i>	complement component 1, q subcomponent, C chain	NM_001008524	<b>1,59</b>	complement activation, classical pathway
<i>Pycard</i>	PYD and CARD domain containing	NM_172322	<b>1,58</b>	proteolysis
<i>Pcdhb9</i>	protocadherin beta 9	NM_001109390	<b>1,56</b>	cell adhesion
<i>Ifit3</i>	interferon-induced protein with tetratricopeptide repeats 3	NM_001007694	<b>1,55</b>	
<i>Pbld</i>	phenazine biosynthesis-like protein domain containing	NM_138530	<b>1,54</b>	biosynthetic process
<i>Tspo</i>	translocator protein	NM_012515	<b>1,53</b>	steroid biosynthetic process
<i>Tmc4</i>	transmembrane channel-like 4	NM_001034104	<b>1,52</b>	
<i>Stat1 /// Stat4</i>	signal transducer and activator of transcription 1 /// signal transducer and act	NM_001012226 /// NM_001034164 /// NM_032612	<b>1,52</b>	transcription
<i>Tmem176a</i>	transmembrane protein 176A	NM_001039008	<b>1,51</b>	
<i>Adpgk</i>	ADP-dependent glucokinase	NM_001100723	<b>1,50</b>	carbohydrate metabolic process
<i>Aadat</i>	aminoadipate aminotransferase	NM_017193	<b>1,49</b>	2-oxoglutarate metabolic process
<i>Ube2l6</i>	ubiquitin-conjugating enzyme E2L 6	NM_001024755	<b>1,49</b>	modification-dependent protein catabolic process
<i>Cd53</i>	Cd53 molecule	NM_012523	<b>1,48</b>	regulation of growth
<i>Uba7</i>	ubiquitin-like modifier activating enzyme 7	NM_001106856	<b>1,48</b>	protein modification process
<i>Anxa3</i>	Annexin A3	NM_012823	<b>1,47</b>	phagocytosis
<i>Clec7a</i>	C-type lectin domain family 7, member a	NM_001173386 /// XM_001067977 /// XM_578404	<b>1,47</b>	response to yeast
<i>Serpina3n</i>	serine (or cysteine) peptidase inhibitor, clade A, member 3N	NM_031531	<b>1,47</b>	inflammatory response
<i>C1qb</i>	complement component 1, q subcomponent, B chain	NM_019262	<b>1,47</b>	immune response
<i>Grxcr1</i>	glutaredoxin, cysteine rich 1	NM_001191935 /// XM_001077572 /// XM_573590	<b>1,46</b>	sensory perception of sound
<i>Alb</i>	albumin	NM_134326	<b>1,45</b>	transport
<i>Blnk</i>	B-cell linker	NM_001025767	<b>1,44</b>	intracellular signaling pathway
<i>Ptpn6</i>	protein tyrosine phosphatase, non-receptor type 6	NM_053908	<b>1,44</b>	negative regulation of humoral immune response mediated by circulating
<i>Rac2</i>	ras-related C3 botulinum toxin substrate 2	NM_001008384	<b>1,44</b>	GTP catabolic process
<i>Irf9</i>	interferon regulatory factor 9	NM_001012041	<b>1,43</b>	transcription
<i>Npc2</i>	Niemann-Pick disease, type C2	NM_173118	<b>1,42</b>	response to virus
<i>Calca</i>	calcitonin-related polypeptide alpha	NM_001033955 /// NM_001033956 /// NM_017338	<b>1,41</b>	endothelial cell proliferation
<i>Rnaset2</i>	ribonuclease T2	NM_001106210	<b>1,41</b>	
<i>Dsp</i>	desmoplakin	XM_001058477 /// XM_225259	<b>1,41</b>	cell-cell adhesion
<i>Lap3</i>	leucine aminopeptidase 3	NM_001011910	<b>1,40</b>	proteolysis

<i>RT1-CE5</i>	RT1 class I, locus CE5	NM_001008843 /// NM_001033986	<b>1,40</b>	antigen processing and presentation of peptide antigen via MHC class
<i>Csf1r</i>	colony stimulating factor 1 receptor	NM_001029901	<b>1,40</b>	protein phosphorylation
<i>Tap2</i>	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	NM_032056	<b>1,40</b>	positive regulation of T cell mediated cytotoxicity
<i>Tnfaip8l2</i>	tumor necrosis factor, alpha-induced protein 8-like 2	NM_001014039	<b>1,40</b>	innate immune response
<i>Laptm5</i>	lysosomal protein transmembrane 5	NM_053538	<b>1,39</b>	transport
<i>Casp4</i>	caspase 4, apoptosis-related cysteine peptidase	NM_053736	<b>1,39</b>	proteolysis
<i>S100a9</i>	S100 calcium binding protein A9	NM_053587	<b>1,38</b>	chronic inflammatory response
<i>Cidea</i>	cell death-inducing DFFA-like effector a	NM_001170467	<b>1,37</b>	temperature homeostasis
<i>Ephx1</i>	epoxide hydrolase 1, microsomal	NM_001034090 /// NM_012844	<b>1,37</b>	cellular aromatic compound metabolic process
<i>Ptprc</i>	protein tyrosine phosphatase, receptor type, C	NM_001109887 /// NM_001109888 /// NM_001109889 /// NM_001109890 /// NM_138507	<b>1,37</b>	activation of MAPK activity
<i>Gldc</i>	glycine dehydrogenase (decarboxylating)	NM_001107583	<b>1,37</b>	cellular amino acid metabolic process
<i>Anxa11</i>	annexin A11	NM_001011918	<b>1,36</b>	phagocytosis
<i>Hck</i>	hemopoietic cell kinase	NM_013185	<b>1,36</b>	protein phosphorylation
<i>Unc93b1</i>	unc-93 homolog B1 (C. elegans)	NM_001108513	<b>1,36</b>	toll-like receptor signaling pathway
<i>Gadd45b</i>	growth arrest and DNA-damage-inducible, beta	NM_001008321	<b>1,36</b>	activation of MAPKK activity
<i>Ifit2</i>	interferon-induced protein with tetratricopeptide repeats 2	NM_001024753	<b>1,36</b>	cellular response to interferon-alpha
<i>Cd37</i>	CD37 molecule	NM_017124	<b>1,36</b>	positive regulation of immunoglobulin production
<i>Ctse</i>	cathepsin E	NM_012938	<b>1,35</b>	proteolysis
<i>Cyb5r2</i>	cytochrome b5 reductase 2	NM_001014244	<b>1,35</b>	steroid biosynthetic process
<i>Pygl</i>	phosphorylase, glycogen, liver	NM_022268	<b>1,35</b>	carbohydrate metabolic process
<i>Aqp1</i>	aquaporin 1	NM_012778	<b>1,35</b>	glomerular filtration
<i>Gsta3</i>	glutathione S-transferase A3	NM_031509	<b>1,35</b>	glutathione metabolic process
<i>Zfp36</i>	zinc finger protein 36	NM_133290	<b>1,35</b>	nuclear-transcribed mRNA catabolic process, deadenylation-dependent
<i>B2m</i>	beta-2 microglobulin	NM_012512	<b>1,35</b>	positive regulation of T cell mediated cytotoxicity
<i>Six4</i>	SIX homeobox 4	NM_001106739	<b>1,35</b>	regulation of transcription, DNA-dependent
<i>Slfn8</i>	schlafen 8	NM_001013970	<b>1,34</b>	
<i>Pls1</i>	Plastin 1 (I isoform)	NM_001108178	<b>1,34</b>	
<i>Cd48</i>	Cd48 molecule	NM_139103	<b>1,34</b>	signal transduction
<i>Cdh23</i>	cadherin 23 (otocadherin)	NM_053644	<b>1,33</b>	cell adhesion
<i>Fcn1</i>	ficolin (collagen/fibrinogen domain containing) 1	NM_031348	<b>1,33</b>	signal transduction
<i>Ctss</i>	cathepsin S	NM_017320	<b>1,33</b>	proteolysis
<i>Kitlg</i>	KIT ligand	NM_021843 /// NM_021844	<b>1,33</b>	ovarian follicle development
<i>Sash3</i>	SAM and SH3 domain containing 3	NM_001134992	<b>1,32</b>	positive regulation of immunoglobulin production
<i>Iqgap1</i>	IQ motif containing GTPase activating protein 1	NM_001108489	<b>1,32</b>	signal transduction
<i>Abca8a</i>	ATP-binding cassette, sub-family A (ABC1), member 8a	XM_001081603 /// XM_221100	<b>1,32</b>	
<i>Dctd</i>	dCMP deaminase	NM_001013882 /// NM_001161512	<b>1,32</b>	nucleotide biosynthetic process
<i>Sp110</i>	SP110 nuclear body protein	NM_001034137	<b>1,32</b>	transcription
<i>Dlk1</i>	delta-like 1 homolog (Drosophila)	NM_053744	<b>1,32</b>	embryo development
<i>Abcg3l1</i>	ATP-binding cassette, sub-family G (WHITE), member 3-like 1	NM_001004076	<b>1,32</b>	
<i>Cmtm7</i>	CKLF-like MARVEL transmembrane domain containing 7	NM_001109300	<b>1,31</b>	
<i>Arhgdib</i>	Rho, GDP dissociation inhibitor (GDI) beta	NM_001009600	<b>1,31</b>	

<i>Wnk1</i>	WNK lysine deficient protein kinase 1	NM_001002823 /// NM_053794	<b>1,30</b>	positive regulation of systemic arterial blood pressure
<i>Klhl6</i>	kelch-like 6 (Drosophila)	NM_001105867	<b>1,30</b>	germinal center formation
<i>Plagl1</i>	pleiomorphic adenoma gene-like 1	NM_012760	<b>1,30</b>	positive regulation of transcription from RNA polymerase II promoter

#### Down-regulated

<i>Ghrh</i>	growth hormone releasing hormone	NM_031577	<b>-1,99</b>	G-protein signaling, coupled to cAMP nucleotide second messenger
<i>S100g</i>	S100 calcium binding protein G	NM_012521	<b>-1,82</b>	
<i>Cd38</i>	CD38 molecule	NM_013127	<b>-1,79</b>	response to hypoxia
<i>Nts</i>	neurotensin	NM_001102381	<b>-1,76</b>	regulation of blood vessel size
<i>Ccnd2</i>	cyclin D2	NM_022267	<b>-1,72</b>	G1/S transition of mitotic cell cycle
<i>Pnlip</i>	pancreatic lipase	NM_013161	<b>-1,63</b>	lipid metabolic process
<i>Scd1</i>	stearoyl-Coenzyme A desaturase 1	NM_139192	<b>-1,57</b>	lipid metabolic process
<i>Mtmr1</i>	myotubularin related protein 1	NM_001191725 /// XM_001059230 /// XM_228644	<b>-1,56</b>	dephosphorylation
<i>Wnt4</i>	wingless-type MMTV integration site family, member 4	NM_053402	<b>-1,55</b>	metanephros development
<i>Col1a1</i>	collagen, type I, alpha 1	NM_053304	<b>-1,52</b>	skeletal system development
<i>Mfhas1</i>	malignant fibrous histiocyoma amplified sequence 1	NM_001107316	<b>-1,52</b>	
<i>Tlcd1</i>	TLC domain containing 1	NM_001013858	<b>-1,51</b>	
<i>Shisa4</i>	shisa homolog 4 (Xenopus laevis)	NM_001077826	<b>-1,48</b>	
<i>Col5a2</i>	collagen, type V, alpha 2	NM_053488	<b>-1,47</b>	skeletal system development
<i>Gal</i>	galanin prepropeptide	NM_033237	<b>-1,46</b>	response to stress
<i>Tm7sf2</i>	transmembrane 7 superfamily member 2	NM_001013071	<b>-1,45</b>	
<i>Slc7a10</i>	solute carrier family 7, (neutral amino acid transporter, y+ system) member 10	NM_053726	<b>-1,45</b>	amino acid transmembrane transport
<i>Fzd2</i>	frizzled homolog 2 (Drosophila)	NM_172035	<b>-1,44</b>	cell activation
<i>Nlk</i>	Nemo like kinase	NM_001191924 /// XM_001080888 /// XM_573152	<b>-1,43</b>	protein phosphorylation
<i>Pnma12</i>	PNMA-like 2	NM_001107481	<b>-1,42</b>	
<i>Thrsp</i>	thyroid hormone responsive	NM_012703	<b>-1,42</b>	
<i>Tmem100</i>	transmembrane protein 100	NM_001017479	<b>-1,41</b>	
<i>Hhat1</i>	hedgehog acyltransferase-like	NM_001106868	<b>-1,41</b>	negative regulation of N-terminal protein palmitoylation
<i>Pop5</i>	Processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	NM_001105752	<b>-1,41</b>	tRNA processing
<i>Egr4</i>	early growth response 4	NM_019137	<b>-1,40</b>	transcription
<i>Nptx1</i>	neuronal pentraxin 1	NM_153735	<b>-1,40</b>	
<i>Bdh1</i>	3-hydroxybutyrate dehydrogenase, type 1	NM_053995	<b>-1,40</b>	liver development
<i>Fastkd5</i>	FAST kinase domains 5	XR_085786 /// XR_086207	<b>-1,39</b>	
<i>Fads2</i>	fatty acid desaturase 2	NM_031344	<b>-1,39</b>	lipid metabolic process
<i>Sept_11</i>	septin 11	NM_001107208	<b>-1,39</b>	cell cycle
<i>Ndp</i>	Norrie disease (pseudoglioma) (human)	NM_001108814	<b>-1,38</b>	placenta development
<i>Slc40a1</i>	solute carrier family 39 (iron-regulated transporter), member 1	NM_133315	<b>-1,38</b>	transport
<i>Hcrtr1</i>	hypocretin (orexin) receptor 1	NM_013064	<b>-1,38</b>	signal transduction
<i>Rras2</i>	related RAS viral (r-ras) oncogene homolog 2	NM_001013434	<b>-1,38</b>	signal transduction
<i>Scrg1</i>	stimulator of chondrogenesis 1	NM_033499	<b>-1,37</b>	

<i>Phkg1</i>	phosphorylase kinase, gamma 1	NM_031573	-1,37	carbohydrate metabolic process
<i>Tmem90b</i>	transmembrane protein 90B	NM_001025020	-1,36	response to biotic stimulus
<i>Syt6</i>	synaptotagmin VI	NM_022191	-1,36	transport
<i>Col4a5</i>	collagen, type IV, alpha 5	XM_001055156 /// XM_343778	-1,36	
<i>YdjC</i>	YdjC homolog (bacterial)	NM_001013863	-1,36	carbohydrate metabolic process
<i>Tbl1xr1</i>	transducin (beta)-like 1 X-linked receptor 1	NM_001108941	-1,36	negative regulation of gene-specific transcription from RNA polymerase
<i>Bbox1</i>	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxyla	NM_022629	-1,36	carnitine biosynthetic process
<i>Cyp51</i>	cytochrome P450, family 51	NM_012941	-1,35	steroid biosynthetic process
<i>Sv2b</i>	synaptic vesicle glycoprotein 2b	NM_057207	-1,35	neurotransmitter uptake
<i>Fxyd7</i>	FXD domain-containing ion transport regulator 7	NM_022008	-1,35	transport
<i>Slc1a2</i>	solute carrier family 1 (glial high affinity glutamate transporter), member 2	NM_001035233 /// NM_017215	-1,34	amino acid transmembrane transport
<i>Rnf182</i>	ring finger protein 182	NM_001109117	-1,34	protein ubiquitination
<i>Tmeff1</i>	transmembrane protein with EGF-like and two follistatin-like domains 1	NM_023020	-1,34	multicellular organismal development
<i>Ednrb</i>	endothelin receptor type B	NM_017333	-1,34	neural crest cell migration
<i>Asb1</i>	ankyrin repeat and SOCS box-containing 1	NM_001108232	-1,34	intracellular signaling pathway
<i>Timp4</i>	tissue inhibitor of metalloproteinase 4	NM_001109393	-1,33	central nervous system development
<i>Slc1a6</i>	solute carrier family 1 (high affinity aspartate/glutamate transporter), member	NM_032065	-1,33	amino acid transmembrane transport
<i>Gamt</i>	guanidinoacetate N-methyltransferase	NM_012793	-1,33	creatine metabolic process
<i>Nrarp</i>	Notch-regulated ankyrin repeat protein	NM_001143750	-1,33	
<i>Sst</i>	somatostatin	NM_012659	-1,33	response to acid
<i>Nkain4</i>	Na <sup>+</sup> /K <sup>+</sup> transporting ATPase interacting 4	NM_001106550	-1,32	
<i>F2r</i>	coagulation factor II (thrombin) receptor	NM_012950	-1,32	activation of MAPKK activity
<i>Pdyn</i>	prodynorphin	NM_019374	-1,32	neuropeptide signaling pathway
<i>Hmgcr</i>	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	NM_013134	-1,32	steroid biosynthetic process
<i>Mpped1</i>	metallophosphoesterase domain containing 1	NM_001130569	-1,32	
<i>Cyp2d4</i>	cytochrome P450, family 2, subfamily d, polypeptide 4	NM_138515	-1,32	steroid metabolic process
<i>Cpxm1</i>	carboxypeptidase X (M14 family), member 1	NM_001106511	-1,31	proteolysis
<i>Metrn</i>	meteorin, glial cell differentiation regulator	NM_001009962	-1,31	multicellular organismal development
<i>Cyp4f17</i>	cytochrome P450, family 4, subfamily f, polypeptide 17	NM_001191986 /// XM_002726858 /// XM_002729769 /// XM_576190	-1,31	
<i>Mllt4</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	NM_013217	-1,31	cell adhesion
<i>Acss2</i>	acyl-CoA synthetase short-chain family member 2	NM_001107793	-1,31	acetyl-CoA biosynthetic process
<i>Fads1</i>	fatty acid desaturase 1	NM_053445	-1,30	lipid metabolic process
<i>Cyp2d4</i>	cytochrome P450, family 2, subfamily d, polypeptide 4	NM_138515	-1,30	steroid metabolic process
<i>Sox4</i>	SRY (sex determining region Y)-box 4	XM_001068302 /// XM_344594	-1,30	response to hypoxia
<i>Lrrc40</i>	Leucine rich repeat containing 40	NM_001034926	-1,30	
<i>Gja1</i>	gap junction protein, alpha 1	NM_012567	-1,30	in utero embryonic development
<i>Csrp2</i>	cysteine and glycine-rich protein 2	NM_177425	-1,30	multicellular organismal development
<i>Dcx</i>	doublecortin	NM_053379	-1,30	neuron migration
<i>Htr1a</i>	5-hydroxytryptamine (serotonin) receptor 1A	NM_012585	-1,30	signal transduction

\* P value = 0.029, was obtained by permutation analysis. Fold change  $\geq 1.3$ .

**Supplemental table 6: List of genes regulated by LTMCR in the anterior pituitary**

Gene Symbol	Gene Title	RefSeq Transcript ID	Fold change	Gene Ontology Biological Process
<b>Up-regulated</b>				
<i>Snca</i>	synuclein, gamma (breast cancer-specific protein 1)	NM_031688	<b>3,11</b>	peripheral nervous system development
<i>Pcdh10</i>	protocadherin 10	XM_001054521 /// XM_342242	<b>2,45</b>	cell adhesion
<i>Per2</i>	period homolog 2 (Drosophila)	NM_031678	<b>2,07</b>	transcription
<i>Hspa1a</i> /// <i>Hspa1b</i>	heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	NM_031971 /// NM_212504	<b>1,79</b>	telomere maintenance
<i>Dnajb1</i>	DnaJ (Hsp40) homolog, subfamily B, member 1	NM_001108441	<b>1,67</b>	protein folding
<i>Chordc1</i>	cysteine and histidine-rich domain (CHORD)-containing 1	NM_001108128	<b>1,67</b>	
<i>Usp2</i>	ubiquitin specific peptidase 2	NM_053774	<b>1,64</b>	negative regulation of transcription from RNA polymerase II promoter
<i>Adamtsl4</i>	ADAMTS-like 4	NM_001034012	<b>1,61</b>	apoptosis
<i>Lrrn3</i>	leucine rich repeat neuronal 3	NM_030856	<b>1,58</b>	positive regulation of protein phosphorylation
<i>Plk5</i>	polo-like kinase 5	NM_001170557 /// XM_001076512 /// XM_234920	<b>1,47</b>	protein phosphorylation
<i>Dnase1</i>	deoxyribonuclease I	NM_013097	<b>1,45</b>	DNA catabolic process
<i>Nr1d2</i>	nuclear receptor subfamily 1, group D, member 2	NM_147210	<b>1,44</b>	transcription
<i>Hgf</i>	hepatocyte growth factor activator	NM_053320	<b>1,43</b>	proteolysis
<i>Fkbp14</i>	FK506 binding protein 14	NM_001013210	<b>1,42</b>	protein folding
<i>Tef</i>	thyrotrophic embryonic factor	NM_019194	<b>1,41</b>	transcription
<i>Rbm3</i>	RNA binding motif (RNP1, RRM) protein 3	NM_053696	<b>1,39</b>	translation
<i>Jam2</i>	junctional adhesion molecule 2	NM_001034004	<b>1,38</b>	
<i>Bhlhe41</i>	basic helix-loop-helix family, member e41	XM_001074956 /// XM_002729454	<b>1,37</b>	transcription
<i>Dnaja1</i>	DnaJ (Hsp40) homolog, subfamily A, member 1	NM_022934	<b>1,35</b>	protein folding
<i>Hla-e</i>	Major histocompatibility complex class I E	NM_001008886	<b>1,35</b>	positive regulation of T cell mediated cytotoxicity
<i>Myh6</i>	myosin, heavy chain 6, cardiac muscle, alpha	NM_017239	<b>1,35</b>	response to reactive oxygen species
<i>Syncp</i>	Synaptotagmin binding, cytoplasmic RNA interacting protein	NM_001047916	<b>1,34</b>	mRNA processing
<i>Klf6</i>	Kruppel-like factor 6	NM_031642	<b>1,34</b>	transcription
<i>Cacybp</i>	calcyclin binding protein	NM_001004208	<b>1,34</b>	heart development
<i>Avil</i>	advillin	NM_024401	<b>1,34</b>	cytoskeleton organization

<i>Wee1</i>	wee 1 homolog (S. pombe)	NM_001012742	<b>1,34</b>	protein phosphorylation
<i>Birc3</i>	baculoviral IAP repeat-containing 3	NM_023987	<b>1,33</b>	anti-apoptosis
<i>Mettl7a</i>	methyltransferase like 7A	NM_001037355	<b>1,32</b>	metabolic process
<i>Tpsb2</i>	tryptase beta 2	NM_019180	<b>1,31</b>	proteolysis
<i>H13</i>	histocompatibility 13	NM_001107789	<b>1,31</b>	
<i>Cry2</i>	cryptochrome 2 (photolyase-like)	NM_133405	<b>1,30</b>	DNA repair
<i>Jph3</i>	junctophilin 3	NM_001107437	<b>1,30</b>	locomotion

## Down-regulated

<i>Igfbp3</i>	insulin-like growth factor binding protein 3	NM_012588	<b>-2,33</b>	regulation of cell growth
<i>Nupr1</i>	nuclear protein, transcriptional regulator, 1	NM_053611	<b>-1,93</b>	acute inflammatory response
<i>Fam171a1</i> /// <i>LOC684862</i>	family with sequence similarity 171, member A1 /// hypothetical protein LOC68486	XM_001056358 /// XM_001072231	<b>-1,93</b>	
<i>Lix1</i>	Lix1 homolog (chicken)	NM_001106214	<b>-1,92</b>	
<i>Serping1</i>	serine (or cysteine) peptidase inhibitor, clade G, member 1	NM_199093	<b>-1,76</b>	negative regulation of complement activation, lectin pathway
<i>F2r</i>	coagulation factor II (thrombin) receptor	NM_012950	<b>-1,76</b>	activation of MAPKK activity
<i>Ptp4a3</i>	protein tyrosine phosphatase 4a3	NM_001114405	<b>-1,74</b>	protein dephosphorylation
<i>Cmb1</i>	carboxymethylenebutenolidase homolog (Pseudomonas)	NM_001008770	<b>-1,74</b>	
<i>Syn2</i>	synapsin II	NM_001034020 /// NM_019159	<b>-1,73</b>	neurotransmitter secretion
<i>Xdh</i>	xanthine dehydrogenase	NM_017154	<b>-1,70</b>	lactation
<i>Chrn4</i>	cholinergic receptor, nicotinic, beta 4	NM_052806	<b>-1,68</b>	regulation of action potential
<i>Aqp4</i>	aquaporin 4	NM_001142366 /// NM_012825	<b>-1,65</b>	transport
<i>Arsb</i>	arylsulfatase B	NM_033443	<b>-1,64</b>	autophagy
<i>B4gal4</i>	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4	NM_001012018	<b>-1,64</b>	carbohydrate metabolic process
<i>Pigt</i>	phosphatidylinositol glycan anchor biosynthesis, class T	NM_001106540	<b>-1,61</b>	attachment of GPI anchor to protein
<i>Tmem98</i>	transmembrane protein 98	NM_001007672	<b>-1,57</b>	
<i>Aqp1</i>	aquaporin 1	NM_012778	<b>-1,55</b>	glomerular filtration
<i>Arntl</i>	aryl hydrocarbon receptor nuclear translocator- like	NM_024362	<b>-1,51</b>	protein import into nucleus, translocation
<i>Retsat</i>	retinol saturase (all trans retinol 13,14 reductase)	NM_145084	<b>-1,50</b>	retinol metabolic process
<i>Cbr1</i> /// <i>LOC100360507</i>	carbonyl reductase 1 /// inducible carbonyl reductase-like	NM_019170 /// XM_002727460 /// XM_002727863	<b>-1,50</b>	ovulation from ovarian follicle
<i>Slc43a2</i>	solute carrier family 43, member 2	NM_001105812	<b>-1,47</b>	amino acid transmembrane transport
<i>Carhsp1</i>	calcium regulated heat stable protein 1	NM_152790	<b>-1,47</b>	regulation of transcription, DNA-dependent
<i>H2afj</i>	H2A histone family, member J	NM_001109610	<b>-1,46</b>	nucleosome assembly
<i>Glrx1</i>	glutaredoxin 1	NM_022278	<b>-1,45</b>	transport

<i>Pvrl2</i>	poliovirus receptor-related 2	NM_001012064	-1,44	positive regulation of natural killer cell mediated cytotoxicity
<i>Tspan8</i>	tetraspanin 8	NM_133526	-1,44	negative regulation of blood coagulation
<i>Slco3a1</i>	Solute carrier organic anion transporter family, member 3a1	NM_177481	-1,44	transport
<i>Emcn</i>	endomucin	NM_001004228	-1,43	angiogenesis
<i>Flnb</i>	filamin, beta	NM_001107288	-1,43	skeletal muscle tissue development
<i>Eid2b</i>	EP300 interacting inhibitor of differentiation 2B	XM_002725600 /// XM_574407	-1,40	
<i>Trappc6a</i>	trafficking protein particle complex 6A	NM_001109410	-1,40	cGMP biosynthetic process
<i>Myh14</i>	myosin, heavy chain 14	NM_001100690	-1,39	ATP catabolic process
<i>Nup93</i>	nucleoporin 93	NM_001011925	-1,39	transport
<i>Sts</i>	steroid sulfatase	NM_012661	-1,38	lipid metabolic process
<i>Kazald1</i>	Kazal-type serine peptidase inhibitor domain 1	NM_001033064	-1,38	regulation of cell growth
<i>Tfpi</i>	tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)	NM_001177321 /// NM_017200	-1,38	blood coagulation
<i>Slc20a2</i>	solute carrier family 20 (phosphate transporter), member 2	NM_017223	-1,38	transport
<i>Klc1</i>	kinesin light chain 1	NM_001081972 /// NM_001081973 /// NM_001081974	-1,37	axon cargo transport
<i>Glx5</i>	glutaredoxin 5	NM_001108722	-1,37	cell redox homeostasis
<i>Ehd3</i>	EH-domain containing 3	NM_138890	-1,37	
<i>Nfs1</i>	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	NM_053462	-1,35	cysteine metabolic process
<i>Cenpb</i>	centromere protein B	XM_001081194 /// XM_342521	-1,35	regulation of transcription
<i>Bend5</i>	BEN domain containing 5	NM_001108672	-1,35	
<i>Chchd6</i>	coiled-coil-helix-coiled-coil-helix domain containing 6	NM_001106608	-1,35	
<i>Thumpd3</i>	THUMP domain containing 3	NM_001170546 /// NM_001170547 /// NM_001170548 /// XM_001078607 /// XM_575638	-1,35	
<i>Rrm1</i>	ribonucleotide reductase M1	NM_001013236	-1,35	DNA replication
<i>Csgalnact1</i>	chondroitin sulfate N-acetylgalactosaminyltransferase 1	NM_001107309	-1,34	UDP-N-acetylgalactosamine metabolic process
<i>Slc41a3</i>	solute carrier family 41, member 3	NM_001037492	-1,34	cation transport
<i>Gaa</i>	glucosidase, alpha, acid	NM_199118	-1,33	angiogenesis
<i>Pigy</i>	phosphatidylinositol glycan anchor biosynthesis, class Y	NM_001024370	-1,33	GPI anchor biosynthetic process
<i>Pfkfb</i>	phosphofructokinase, platelet	NM_206847	-1,33	fructose 6-phosphate metabolic process
<i>Cip98</i>	CASK-interacting protein CIP98	NM_181088	-1,33	retina homeostasis



<i>Galm</i>	galactose mutarotase (aldose 1-epimerase)	NM_001007704	-1,33	carbohydrate metabolic process
<i>Tfrc</i>	transferrin receptor	NM_022712	-1,33	response to hypoxia
<i>Bat3</i>	HLA-B-associated transcript 3	NM_001033968 /// NM_053609	-1,33	regulation of cell proliferation
<i>Pdhx</i>	Pyruvate dehydrogenase complex, component X	NM_001044242	-1,33	metabolic process
<i>Polr2l</i>	polymerase (RNA) II (DNA directed) polypeptide L	NM_001143911	-1,33	transcription, DNA-dependent
<i>Prr13</i>	proline rich 13	NM_001008379	-1,33	transcription
<i>Aloxe3</i>	arachidonate lipoxygenase 3	NM_001105793	-1,33	leukotriene metabolic process
<i>Mrpl21</i>	mitochondrial ribosomal protein L21	NM_001107567	-1,32	translation
<i>G3bp1</i>	GTPase activating protein (SH3 domain) binding protein 1	NM_133565	-1,32	transport
<i>Adck5</i>	aarF domain containing kinase 5	NM_001135798	-1,32	
<i>Mrps18a</i>	mitochondrial ribosomal protein S18A	NM_198756	-1,32	translation
<i>Thy1</i>	Thy-1 cell surface antigen	NM_012673	-1,32	angiogenesis
<i>Lgals3bp</i>	lectin, galactoside-binding, soluble, 3 binding protein	NM_139096	-1,32	cell adhesion
<i>Bat5</i>	HLA-B associated transcript 5	NM_212531	-1,32	
<i>Aig1</i>	androgen-induced 1	NM_001134425	-1,32	
<i>Elmo2</i>	engulfment and cell motility 2	NM_001134955	-1,32	phagocytosis
<i>Cd151</i>	CD151 molecule (Raph blood group)	NM_022523	-1,32	hemidesmosome assembly
<i>Ppp1r10</i>	protein phosphatase 1, regulatory subunit 10	NM_022951	-1,31	transcription
<i>Camk2d</i>	calcium/calmodulin-dependent protein kinase II delta	NM_012519	-1,31	G1/S transition of mitotic cell cycle
<i>Mcts2</i>	malignant T cell amplified sequence 2	XM_001071410 /// XM_002726252	-1,31	
<i>Bola3</i>	bolA homolog 3 (E. coli)	NM_001106601	-1,31	
<i>Atp5s</i>	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	NM_001007749	-1,31	ATP biosynthetic process
<i>Mgea5</i>	meningioma expressed antigen 5 (hyaluronidase)	NM_131904	-1,31	N-acetylglucosamine metabolic process
<i>Shbg</i>	sex hormone binding globulin	NM_012650	-1,31	primary spermatocyte growth
<i>Gmpr</i>	guanosine monophosphate reductase	NM_057188	-1,30	metabolic process
<i>Laptm4b</i>	lysosomal protein transmembrane 4 beta	NM_001013174	-1,30	transport
<i>Sorcs2</i>	sortilin-related VPS10 domain containing receptor 2	NM_001107225	-1,30	
<i>Taf10</i>	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	NM_001134735	-1,30	G1/S transition of mitotic cell cycle
<i>Asns</i>	asparagine synthetase	NM_013079	-1,30	liver development

\* *P* value = 0.029, was obtained by permutation analysis. Fold change  $\geq 1.3$ .

**Supplemental table 7: List of genes regulated by caloric restriction, classified by biological functions**

**A- Anterior Pituitary**

Category	# of genes	P value	Genes
Cell Death	35	5,22E-03-4,71E-02	<i>Snca, Prr13, Camk2d, Taf10, Dnaja1, Klif6, Asns, Pvr12, Glrx, Laptm4b, Dnajb1, Rbm3, Adamtsl4, Jph3, F2r, Bag6, Shbg, Tfr, Aqp1, Hspa1a/Hspa1b, Hla-E, Dnase1, Tpsab1/Tpsb2, Wee1, Birc3, Lgals3bp, Pigf, Cacybp, Flnb, Nupr1, Xdh, Thy1, Usp2, Igfbp3, Atp5s</i>
Cellular Function and Maintenance	21	9,35E-04-4,71E-02	<i>F2r, Myh14, Hspa1a/Hspa1b, Aqp1, Sorcs2, Tfr, Hla-E, Chmb4, Aqp4, Dnase1, Camk2d, Syn2, Dnaja1, Slc20a2, Myh6, Dnajb1, Gaa, Cd151, Nupr1, Xdh, Arst</i>
Cell-To-Cell Signaling and Interaction	18	2,6E-04-4,71E-02	<i>F2r, Serping1, Hspa1a/Hspa1b, Tfr, Snca, Chmb4, Syn2, Jam2, Pvr12, Birc3, Lgals3bp, Dfnb31, Tfp1, Cd151, Xdh, Thy1, Ptp4a3, Igfbp3</i>
Cellular Assembly and Organization	16	3,34E-03-4,71E-02	<i>F2r, Myh14, Hspa1a/Hspa1b, Snca, Dnase1, Camk2d, Syn2, Dnaja1, Klc1, Pvr12, Myh6, Dnajb1, Gaa, Flnb, Xdh, Arst</i>
Small Molecule Biochemistry	14	1,47E-04-4,71E-02	<i>F2r, Slco3a1, Serping1, Aqp1, Snca, Tef, Csgalnact1, Dnaja1, Asns, Dnajb1, Tfp1, Xdh, Arsb, Igfbp3</i>
Cell Morphology	13	3,78E-04-4,71E-02	<i>F2r, Aqp1, Snca, Aqp4, Cenpb, Klc1, Pvr12, Elmo2, Cd151, Flnb, Xdh, Nupr1, Igfbp3</i>
Cellular Compromise	11	3,34E-03-4,71E-02	<i>Pvr12, Hspa1a/Hspa1b, Aqp1, Snca, Dnajb1, Aqp4, Dnase1, Flnb, Dnaja1, Xdh, Klc1</i>
Cellular Growth and Proliferation	11	8,01E-03-4,71E-02	<i>F2r, Shbg, Hspa1a/Hspa1b, Tfr, Hla-E, Tpsab1/Tpsb2, Thy1, Klif6, Ptp4a3, Armtl, Igfbp3</i>
Molecular Transport	10	3,78E-04-4,71E-02	<i>Ppp1r10, Slco3a1, Tfr, Aqp1, Cry2, Aqp4, Dnaja1, Xdh, Igfbp3, Arst</i>
Cellular Development	9	8,01E-03-4,07E-02	<i>Pvr12, Shbg, Hspa1a/Hspa1b, Tfr, Aloxe3, Klif6, Thy1, Ptp4a3, Igfbp3</i>
Cellular Movement	9	8,01E-03-3,94E-02	<i>Pvr12, F2r, Myh14, Tfr, Snca, Cd151, Xdh, Ptp4a3, Igfbp3</i>
Lipid Metabolism	8	1,47E-04-4,71E-02	<i>F2r, Slco3a1, Serping1, Snca, Dnajb1, Tef, Dnaja1, Xdh</i>
Carbohydrate Metabolism	7	8,01E-03-4,71E-02	<i>F2r, Aqp1, Tfp1, Csgalnact1, Xdh, Pfkfb, Arsb</i>
Drug Metabolism	6	1,73E-03-4,71E-02	<i>Glrx, Snca, Dnajb1, Tfp1, Dnaja1, Xdh</i>
Protein Synthesis	5	3,78E-04-4,71E-02	<i>Tfr, Aqp4, Taf10, Ehd3, Igfbp3</i>
Protein Trafficking	5	3,78E-04-9,24E-03	<i>Ppp1r10, Tfr, Cry2, Dnaja1, Igfbp3</i>
DNA Replication, Recombination, and Repair	4	3,34E-03-4,71E-02	<i>Hspa1a/Hspa1b, Dnajb1, Dnase1, Dnaja1</i>
Cell Cycle	4	8,01E-03-4,71E-02	<i>Myh14, Hspa1a/Hspa1b, Wee1, Igfbp3</i>
Post-Translational Modification	3	5,44E-03-3,94E-02	<i>Hspa1a/Hspa1b, Dnaja1, Xdh</i>
Gene Expression	3	8,01E-03-4,71E-02	<i>Dnajb1, Taf10, Igfbp3</i>
Protein Folding	2	5,44E-03-5,44E-03	<i>Hspa1a/Hspa1b, Dnaja1</i>
Amino Acid Metabolism	2	8,01E-03-4,71E-02	<i>Asns, Igfbp3</i>
Nucleic Acid Metabolism	2	8,01E-03-1,6E-02	<i>Csgalnact1, Xdh</i>
Cell Signaling	2	2,1E-02-3,94E-02	<i>Xdh, Igfbp3</i>

**B- Hypothalamus**

Category	# of genes	P value	Genes
Cellular Growth and Proliferation	19	3,18E-04-4,79E-02	<i>Dnaja3, Nov, Apoa1, Irf2, Hspa1a/Hspa1b, Yy1, Nr1d1, Fkbp5, Cd1d, Cartpt, Tpr, Egr2, Vcan, Casp8, Calcr1, Rbm3, Nr4a3, Tgm2, Pla2g3</i>
Cell Death	19	1,43E-03-4,93E-02	<i>Dnaja3, Otud7b, Hspa1a/Hspa1b, Irf2, Apoa1, Yy1, Nr1d1, Fkbp5, Cd1d, Egr2, Camk1g, Vcan, Casp8, Calcr1, Rbm3, Nr4a3, Tgm2, Ppp1r15b, Gas2</i>
Cellular Development	15	3,66E-04-4,54E-02	<i>Dnaja3, Nov, Apoa1, Hspa1a/Hspa1b, Irf2, Yy1, Nr1d1, Cd1d, Cartpt, Egr2, Kat6a, Vcan, Casp8, Nr4a3, Tgm2</i>
Cellular Movement	15	3,26E-03-4,79E-02	<i>Dnaja3, Nov, Hspa1a/Hspa1b, Apoa1, Yy1, Nr1d1, Cd1d, Tpr, Cartpt, Egr2, Vcan, Casp8, Calcr1, Nr4a3, Tgm2</i>
Cell-To-Cell Signaling and Interaction	12	5,62E-04-4,79E-02	<i>Dnaja3, Egr2, Hspa1a/Hspa1b, Vcan, Apoa1, Irf2, Casp8, Calcr1, Tgm2, Cd1d, Cartpt, Gas2</i>
Cellular Function and Maintenance	11	3,66E-04-4,47E-02	<i>Dnaja3, Egr2, Hspa1a/Hspa1b, Apoa1, Irf2, Casp8, Syt6, Ppp1r15b, Tgm2, Cartpt, Cd1d</i>
Small Molecule Biochemistry	11	1,13E-03-4,79E-02	<i>Irf2, Vcan, Apoa1, Casp8, Calcr1, Nr4a3, Fkbp5, Pla2g3, Tgm2, Cd1d, Cartpt</i>
Gene Expression	11	9,76E-03-4,13E-02	<i>Egr2, Kat6a, Irf2, Yy1, Casp8, Nr4a3, Nr1d1, Rbm3, Per2, Tgm2, Tle1</i>
Cellular Assembly and Organization	10	1,37E-03-4,47E-02	<i>Egr2, Dnaja3, Vcan, Apoa1, Hspa1a/Hspa1b, Casp8, Syt6, Fkbp5, Tgm2, Gas2</i>
DNA Replication, Recombination, and Repair	10	3,26E-03-3,78E-02	<i>Dnaja3, Nov, Zbtb20, Kat6a, Hspa1a/Hspa1b, Irf2, Yy1, Casp8, Nr4a3, Tgm2</i>
Lipid Metabolism	8	1,13E-03-4,79E-02	<i>Irf2, Apoa1, Casp8, Nr4a3, Fkbp5, Pla2g3, Cd1d, Cartpt</i>
Cell Signaling	8	3,26E-03-3,53E-02	<i>Dnaja3, Otud7b, Apoa1, Irf2, Casp8, Calcr1, Tgm2, Cartpt</i>
Cellular Compromise	7	3,26E-03-4,47E-02	<i>Hspa1a/Hspa1b, Irf2, Yy1, Casp8, Nr4a3, Tgm2, Gas2</i>
Molecular Transport	7	3,26E-03-4,79E-02	<i>Irf2, Apoa1, Syt6, Pla2g3, Tgm2, Tpr, Cartpt</i>
Cell Morphology	6	1,66E-02-4,47E-02	<i>Egr2, Dnaja3, Vcan, Casp8, Fkbp5, Tgm2</i>
Carbohydrate Metabolism	4	3,26E-03-3,85E-02	<i>Apoa1, Pla2g3, Cd1d, Cartpt</i>
Cell Cycle	4	3,26E-03-2,58E-02	<i>Hspa1a/Hspa1b, Yy1, Nr4a3, Tpr</i>
Protein Degradation	4	1,69E-02-4,51E-02	<i>Dnaja3, Apoa1, Casp8, Tgm2</i>
Protein Synthesis	4	1,69E-02-4,51E-02	<i>Dnaja3, Apoa1, Casp8, Tgm2</i>
Antigen Presentation	3	5,62E-04-4,47E-02	<i>Apoa1, Irf2, Tgm2</i>
Energy Production	3	4,56E-03-1,63E-02	<i>Apoa1, Nr4a3, Cartpt</i>
Nucleic Acid Metabolism	3	1,96E-02-1,96E-02	<i>Apoa1, Casp8, Calcr1</i>
Vitamin and Mineral Metabolism	2	6,51E-03-3,53E-02	<i>Apoa1, Tgm2</i>
Drug Metabolism	2	1,3E-02-4,47E-02	<i>Fkbp5, Cartpt</i>
Post-Translational Modification	2	1,74E-02-4,47E-02	<i>Dnaja3, Hspa1a/Hspa1b</i>
Protein Folding	2	1,74E-02-4,47E-02	<i>Dnaja3, Hspa1a/Hspa1b</i>
Amino Acid Metabolism	2	1,94E-02-4,79E-02	<i>Vcan, Cartpt</i>

**Supplemental table 8: List of canonical pathways significantly represented by genes regulated with LTMCR**

**A- Anterior Pituitary**

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>Ratio</b>	<b>Molecules</b>
Circadian Rhythm Signaling	3,98	0,13	<i>Bhlhe41, Cry2, Per2, Arntl</i>
Androgen and Estrogen Metabolism	1,97	0,04	<i>Sts, Csgalnact1, Arsb</i>
Glycosaminoglycan Degradation	1,96	0,08	<i>Mgea5, Arsb</i>
Crosstalk between Dendritic Cells and Natural Killer Cells	1,91	0,04	<i>Pvrl2, Hla-E, Camk2d</i>
Glycolysis/Gluconeogenesis	1,71	0,04	<i>Pdhx, Galm, Pfkp</i>
Tight Junction Signaling	1,63	0,03	<i>Pvrl2, Jam2, Myh14, Myh6</i>
Coagulation System	1,57	0,06	<i>F2r, Tfp1</i>
Protein Ubiquitination Pathway	1,54	0,02	<i>Hspa1a/Hspa1b, Birc3, Dnajb1, Dnaja1, Usp2</i>
Calcium Signaling	1,50	0,02	<i>Myh14, Myh6, Chrn4, Camk2d</i>
Alanine and Aspartate Metabolism	1,50	0,05	<i>Pdhx, Asns</i>
Galactose Metabolism	1,47	0,05	<i>Gaa, Pfkp</i>

**B- Hypothalamus**

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>Ratio</b>	<b>Molecules</b>
Circadian Rhythm Signaling	3,86	0,10	<i>Cry1, Per2, Nr1d1</i>
Cytotoxic T Lymphocyte-mediated Apoptosis of Target Cells	3,67	0,06	<i>Casp8, Rt1-N2, Rt1-T24-3</i>
Allograft Rejection Signaling	2,34	0,04	<i>Rt1-N2, Rt1-T24-3</i>
OX40 Signaling Pathway	2,10	0,03	<i>Rt1-N2, Rt1-T24-3</i>
Endothelin-1 Signaling	1,97	0,02	<i>Gna14, Casp8, Pla2g3</i>
Phospholipid Degradation	1,71	0,02	<i>Gna14, Pla2g3</i>
Huntington's Disease Signaling	1,60	0,01	<i>Hspa1a/Hspa1b, Casp8, Tgm2</i>
Apoptosis Signaling	1,54	0,02	<i>Casp8, Gas2</i>
Atherosclerosis Signaling	1,48	0,02	<i>Apoa1, Pla2g3</i>
Sphingosine-1-phosphate Signaling	1,44	0,02	<i>Gna14, Casp8</i>
Neuropathic Pain Signaling In Dorsal Horn Neurons	1,42	0,02	<i>Gna14, Camk1g</i>
Cdc42 Signaling	1,38	0,02	<i>Rt1-N2, Rt1-T24-3</i>
Glycerophospholipid Metabolism	1,38	0,02	<i>Gna14, Pla2g3</i>
Synaptic Long Term Depression	1,30	0,02	<i>Gna14, Pla2g3</i>

**Supplemental table 9: List of genes regulated by LTMCR in the hypothalamus**

Gene Symbol	Gene Title	RefSeq Transcript ID	Fold change	Gene Ontology Biological Process
<b>Up-regulated</b>				
<i>RT1-N1</i> /// <i>RT1-N2</i>	RT1 class Ib, locus N1 /// RT1 class Ib, locus N2	NM_001008854 /// NM_012646	<b>2,18</b>	immune response
<i>Nr4a3</i>	nuclear receptor subfamily 4, group A, member 3	NM_017352 /// NM_031628	<b>1,69</b>	mesoderm formation
<i>Hspa1a</i> /// <i>Hspa1b</i>	heat shock 70kD protein 1A /// heat shock 70kD protein 1B (mapped)	NM_031971 /// NM_212504	<b>1,56</b>	telomere maintenance
<i>Hspa1a</i>	heat shock 70kD protein 1A	NM_031971	<b>1,56</b>	telomere maintenance
<i>Fkbp5</i>	FK506 binding protein 5	NM_001012174	<b>1,49</b>	protein folding
<i>Gas2</i>	growth arrest-specific 2	NM_001127504	<b>1,49</b>	cell cycle arrest
<i>Tpr</i>	translocated promoter region	NM_001107185	<b>1,48</b>	translation
<i>DnaJ3</i>	DnaJ (Hsp40) homolog, subfamily A, member 3	NM_001038595 /// NM_001038596	<b>1,48</b>	mitochondrial DNA replication
<i>Osgp</i>	O-sialoglycoprotein endopeptidase	NM_001100510	<b>1,47</b>	proteolysis
<i>Zbtb20</i>	zinc finger and BTB domain containing 20	NM_001105880	<b>1,47</b>	
<i>RT1-T24-3</i>	RT1 class I, locus T24, gene 3	NM_001166403	<b>1,43</b>	immune response
<i>Per2</i>	period homolog 2 (Drosophila)	NM_031678	<b>1,43</b>	transcription
<i>Rbm3</i>	RNA binding motif (RNP1, RRM) protein 3	NM_053696	<b>1,41</b>	translation
<i>Afmid</i>	arylformamidase	NM_001111366	<b>1,40</b>	metabolic process
<i>Cry1</i>	cryptochrome 1 (photolyase-like)	NM_198750	<b>1,40</b>	DNA repair
<i>Gpatch4</i>	G patch domain containing 4	NM_001024979	<b>1,38</b>	
<i>Ppp1r15b</i>	protein phosphatase 1, regulatory (inhibitor) subunit 15b	NM_001107175	<b>1,36</b>	response to stress
<i>Egr2</i>	early growth response 2	NM_053633	<b>1,35</b>	transcription
<i>Pdlim5</i>	PDZ and LIM domain 5	NM_053326	<b>1,35</b>	heart development
<i>Casp8</i>	caspase 8	NM_022277	<b>1,35</b>	angiogenesis
<i>Tmem144</i>	transmembrane protein 144	NM_001108551	<b>1,34</b>	
<i>Tle1</i>	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	NM_001173433 /// XM_001066887 /// XM_002726541 /// XM_002726542 /// XM_002726543	<b>1,34</b>	negative regulation of transcription from RNA polymerase II promoter
<i>Myst3</i>	MYST histone acetyltransferase (monocytic leukemia) 3	NM_001100570	<b>1,34</b>	nucleosome assembly
<i>Otud7b</i>	OTU domain containing 7B	NM_001107697	<b>1,34</b>	protein deubiquitination
<i>Calcl</i>	calcitonin receptor-like	NM_012717	<b>1,34</b>	regulation of muscle contraction
<i>Nhlrc3</i>	NHL repeat containing 3	XM_001054658 /// XM_227139	<b>1,33</b>	
<i>Gna14</i>	guanine nucleotide binding protein, alpha 14	NM_001013151	<b>1,33</b>	protein ADP-ribosylation
<i>Cd1d1</i>	CD1d1 molecule	NM_017079	<b>1,32</b>	positive regulation of T cell mediated cytotoxicity
<i>Syt6</i>	synaptotagmin VI	NM_022191	<b>1,32</b>	transport
<i>Pla2g3</i>	phospholipase A2, group III	NM_001106015	<b>1,32</b>	phospholipid metabolic process
<i>Camk1g</i>	calcium/calmodulin-dependent protein kinase IG	NM_182842	<b>1,31</b>	protein phosphorylation
<i>Wfdc6a</i>	WAP four-disulfide core domain 6A	XM_001062561 /// XM_002726295	<b>1,31</b>	
<i>Tctn3</i>	tectonic family member 3	XM_001053561 /// XM_220007	<b>1,31</b>	
<i>Yy1</i>	YY1 transcription factor	NM_173290	<b>1,31</b>	regulation of transcription, DNA-dependent
<i>Prpf38b</i>	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	NM_001024305	<b>1,30</b>	mRNA processing

## Down-regulated

<i>Irf2</i>	interferon regulatory factor 2	NM_001047086	<b>-1,30</b>	regulation of transcription, DNA-dependent
<i>Apoa1</i>	apolipoprotein A-I	NM_012738	<b>-1,31</b>	regulation of protein phosphorylation
<i>Cartpt</i>	CART prepropeptide	NM_017110	<b>-1,33</b>	activation of MAPKK activity
<i>Tgm2</i>	transglutaminase 2, C polypeptide	NM_019386	<b>-1,33</b>	blood vessel remodeling
<i>Lmf1</i>	lipase maturation factor 1	XM_001060521 /// XM_340769	<b>-1,35</b>	protein secretion
<i>Vcan</i>	versican	NM_001170558 /// NM_001170559 /// NM_001170560 /// NM_053663 /// XM_001058357 //	<b>-1,36</b>	ureteric bud development
<i>Nr1d1</i>	nuclear receptor subfamily 1, group D, member 1	NM_001113422 /// NM_145775	<b>-1,38</b>	transcription
<i>Opalin</i>	oligodendrocytic myelin paranodal and inner loop protein	NM_001017386	<b>-1,41</b>	
<i>Htra3</i>	HtrA serine peptidase 3	XM_001058037 /// XM_341237	<b>-1,44</b>	regulation of cell growth
<i>Nov</i>	nephroblastoma overexpressed gene	NM_030868	<b>-1,51</b>	regulation of cell growth
<i>Matn2</i>	matrilin 2	XM_001058523 /// XM_216941	<b>-1,62</b>	
<i>Vof16</i>	ischemia related factor vof-16	NM_147207	<b>-2,25</b>	

\* *P* value = 0.029, was obtained by permutation analysis. Fold change  $\geq 1.3$ .

**Supplemental table 10: List of genes regulated by soy diet in the anterior pituitary**

**A- Anterior pituitary**

Gene Symbol	Gene Title	RefSeq Transcript ID	Fold change	Gene Ontology Biological Process
<b>Up-regulated</b>				
<i>Dusp26</i>	dual specificity phosphatase 26 (putative)	NM_001012352	<b>2,61</b>	protein dephosphorylation
<i>Sncg</i>	synuclein, gamma (breast cancer-specific protein 1)	NM_031688	<b>2,16</b>	peripheral nervous system development
<i>Tspy14</i>	TSPY-like 4	NM_001012075	<b>1,69</b>	nucleosome assembly
<i>Slc16a13</i>	Solute carrier family 16, member 13 (monocarboxylic acid transporter 13)	NM_001005530	<b>1,34</b>	transport
<i>RT1-S3</i>	RT1 class Ib, locus S3	NM_001008886	<b>1,33</b>	positive regulation of T cell mediated cytotoxicity
<i>Nckap1l</i>	NCK associated protein 1 like	NM_001108119	<b>1,32</b>	B cell homeostasis
<i>Plk5</i>	polo-like kinase 5	NM_001170557 /// XM_001076512 /// XM_234920	<b>1,32</b>	protein phosphorylation
<i>Rab33a</i>	RAB33A, member of RAS oncogene family	NM_001108257	<b>1,32</b>	small GTPase mediated signal transduction
<i>Dnmt3a</i>	DNA (cytosine-5-)-methyltransferase 3 alpha	NM_001003957 /// NM_001003958	<b>1,31</b>	negative regulation of transcription from RNA polymerase II promoter
<i>Hfe</i>	hemochromatosis	NM_001173434 /// NM_001173435 /// NM_053301	<b>1,30</b>	antigen processing and presentation of peptide antigen via MHC class
<i>Fry</i>	Furry homolog (Drosophila)	NM_001170398	<b>1,30</b>	
<b>Down-regulated</b>				
<i>Robo2</i>	roundabout, axon guidance receptor, homolog 2 (Drosophila)	NM_032106	<b>-2,20</b>	luteolysis
<i>Vegfa</i>	vascular endothelial growth factor A	NM_001110333 /// NM_001110334 /// NM_001110335 /// NM_001110336 /// NM_031836	<b>-2,08</b>	angiogenesis
<i>Fam122b</i>	family with sequence similarity 122B	NM_001166586	<b>-2,07</b>	
<i>Lum</i>	lumican	NM_031050	<b>-2,06</b>	response to organic cyclic substance
<i>Nqo2</i>	NAD(P)H dehydrogenase, quinone 2	NM_001004214	<b>-1,99</b>	memory
<i>Cgln1</i>	cingulin-like 1	NM_001108164	<b>-1,75</b>	
<i>F2r</i>	coagulation factor II (thrombin) receptor	NM_012950	<b>-1,71</b>	activation of MAPKK activity
<i>Cmb1</i>	carboxymethylenebutenolidase homolog (Pseudomonas)	NM_001008770	<b>-1,66</b>	
<i>Retsat</i>	retinol saturase (all trans retinol 13,14 reductase)	NM_145084	<b>-1,59</b>	retinol metabolic process
<i>Raph1</i>	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	NM_001108798	<b>-1,58</b>	signal transduction
<i>Sec61a2</i>	Sec61 alpha 2 subunit (S. cerevisiae)	NM_001170343	<b>-1,57</b>	transport
<i>Phka1</i>	Phosphorylase kinase, alpha 1	NM_022626	<b>-1,57</b>	carbohydrate metabolic process

<i>Ehd3</i>	EH-domain containing 3	NM_138890	-1,54	cAMP catabolic process in utero embryonic development
<i>Pde10a</i>	phosphodiesterase 10A	NM_022236	-1,54	
<i>Gja1</i>	gap junction protein, alpha 1	NM_012567	-1,53	
<i>Clec16a</i>	C-type lectin domain family 16, member A	XM_002724483 /// XM_213209	-1,51	
<i>Hrsp12</i>	heat-responsive protein 12	NM_031714	-1,47	induction of apoptosis cell adhesion cation transport proteolysis protein methylation blood vessel maturation
<i>Timp3</i>	TIMP metalloproteinase inhibitor 3	NM_012886	-1,46	
<i>Dsg2</i>	desmoglein 2	XM_001054396 /// XM_226112	-1,46	
<i>Slc41a3</i>	solute carrier family 41, member 3	NM_001037492	-1,45	
<i>Npepl1</i>	aminopeptidase-like 1	NM_001107806	-1,45	
<i>MGC72974</i>	hypothetical LOC316976	NM_198772	-1,43	
<i>Reck</i>	reversion-inducing-cysteine-rich protein with kazal motifs	NM_001107954	-1,43	
<i>H2afj</i>	H2A histone family, member J	NM_001109610	-1,42	nucleosome assembly tricarboxylic acid cycle G1 phase of mitotic cell cycle cell cycle
<i>Aco1</i>	aconitase 1, soluble	NM_017321	-1,42	
<i>Cdk1</i>	cyclin-dependent kinase 1	NM_019296	-1,41	
<i>Cks2</i>	CDC28 protein kinase regulatory subunit 2	NM_001126083	-1,40	
<i>Ttc19</i>	tetratricopeptide repeat domain 19	NM_001109644	-1,40	carbohydrate metabolic process regulation of cell growth
<i>Ganab</i>	glucosidase, alpha; neutral AB	NM_001106334	-1,39	
<i>Hsd3b7</i>	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	NM_139329	-1,38	
<i>Ctps</i>	CTP synthase	NM_001134873	-1,38	pyrimidine nucleotide biosynthetic process ovulation from ovarian follicle
<i>Cbr1</i>	carbonyl reductase 1 /// inducible carbonyl reductase-like	NM_019170 /// XM_002727460 /// XM_002727863	-1,38	
<i>Syngn2</i>	synaptogyrin 2	NM_053553	-1,37	protein targeting cell morphogenesis
<i>Atp2b2</i>	ATPase, Ca++ transporting, plasma membrane 2	NM_012508	-1,36	
<i>Cbfb</i>	core-binding factor, beta subunit	NM_001013191	-1,36	ossification translation DNA replication
<i>Gfm1</i>	G elongation factor, mitochondrial 1	NM_053625	-1,36	
<i>Kctd13</i>	potassium channel tetramerisation domain containing 13	NM_198736	-1,36	
<i>Lsm12</i>	LSM12 homolog (S. cerevisiae)	NM_001105843	-1,36	regulation of cell growth
<i>Igfbp7</i>	insulin-like growth factor binding protein 7	NM_001013048	-1,35	
<i>Klc1</i>	kinesin light chain 1	NM_001081972 /// NM_001081973 /// NM_001081974	-1,35	axon cargo transport
<i>Dnajc30</i>	DnaJ (Hsp40) homolog, subfamily C, member 30	NM_001109024	-1,35	
<i>Ar</i>	androgen receptor	NM_012502	-1,35	in utero embryonic development
<i>Zfyve27</i>	zinc finger, FYVE domain containing 27	NM_199104	-1,35	
<i>Snx7</i>	sorting nexin 7	NM_001012083	-1,35	cell communication respiratory system process neuron migration protein dephosphorylation
<i>Rab3a</i>	RAB3A, member RAS oncogene family	NM_013018	-1,34	
<i>Pex7</i>	peroxisomal biogenesis factor 7	NM_001034147	-1,33	
<i>Ptpn3</i>	Protein tyrosine phosphatase, non-receptor type 3	XM_001055793 /// XM_001059757	-1,33	
<i>Pcbp3</i>	poly(rC) binding protein 3	NM_001011945	-1,32	

<i>Mtus1</i>	mitochondrial tumor suppressor 1	NM_178093	-1,32	cell cycle
<i>Cd151</i>	CD151 molecule (Raph blood group)	NM_022523	-1,32	hemidesmosome assembly
<i>Polr2g</i>	polymerase (RNA) II (DNA directed) polypeptide G	NM_053948	-1,31	transcription
<i>Vdac1</i>	voltage-dependent anion channel 1	NM_031353	-1,31	behavioral fear response
<i>Mthfd1</i>	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrof	NM_022508	-1,30	histidine biosynthetic process
<i>Racgap1</i>	Rac GTPase-activating protein 1	NM_001108112	-1,30	cytokinesis
<i>Mcart1</i>	mitochondrial carrier triple repeat 1	NM_001024785	-1,30	transport
<i>Rbm18</i>	RNA binding motif protein 18	NM_001107838	-1,30	
<i>Mrps18a</i>	mitochondrial ribosomal protein S18A	NM_198756	-1,30	translation
<i>Znrf2</i>	zinc and ring finger 2	NM_001108628	-1,30	
<i>Fktn</i>	fukutin	NM_001108667	-1,30	
<i>Cib2</i>	calcium and integrin binding family member 2	NM_001015010	-1,30	

## B-Hypothalamus

Gene Symbol	Gene Title	RefSeq Transcript ID	Fold change	Gene Ontology Biological Process
<b>Up-regulated</b>				
<i>Ero1l</i>	ERO1-like (S. cerevisiae)	NM_138528	1,49	protein folding
<i>Fitm2</i>	fat storage-inducing transmembrane protein 2	NM_001107799	1,48	regulation of triglyceride biosynthetic process
<i>Rexo4</i>	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	NM_001033884	1,42	
<i>Tspyl4</i>	TSPY-like 4	NM_001012075	1,42	nucleosome assembly
<i>Rprd1a</i>	Regulation of nuclear pre-mRNA domain containing 1A	XM_001056597 /// XM_214609	1,39	
<i>Myst3</i>	MYST histone acetyltransferase (monocytic leukemia) 3	NM_001100570	1,38	nucleosome assembly
<i>Tmem144</i>	transmembrane protein 144	NM_001108551	1,37	
<i>Cit</i>	Citron	NM_001029911	1,35	mitotic sister chromatid segregation
<i>Pdyn</i>	prodynorphin	NM_019374	1,34	neuropeptide signaling pathway
<i>Pop5</i>	Processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	NM_001105752	1,33	tRNA processing
<i>Nf1</i>	neurofibromin 1	NM_012609	1,31	MAPKKK cascade
<i>Susd2</i>	sushi domain containing 2	NM_001106381	1,30	immune response
<b>Down-regulated</b>				
<i>Coq10b</i>	coenzyme Q10 homolog B (S. cerevisiae)	NM_001009671	-1,31	



<i>Ston2</i>	Stonin 2	NM_001135874	<b>-1,39</b>	intracellular protein transport
<i>Tnnc2</i>	troponin C type 2 (fast)	NM_001037351	<b>-1,41</b>	skeletal muscle contraction
<i>Fmod</i>	fibromodulin	NM_080698	<b>-1,47</b>	wound healing
<i>RT1-EC2</i>	RT1 class Ib, locus EC2	NM_012645	<b>-1,49</b>	antigen processing and presentation of peptide antigen via MHC class

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\* *P* value = 0.029, was obtained by permutation analysis. Fold change  $\geq 1.3$ .

**Supplemental table S11: List of genes regulated by soy, classified by biological functions**

**A- Anterior Pituitary**

Category	# of genes	P value	Genes
Cellular Growth and Proliferation	19	3,28E-04-2,02E-02	<i>Cbfb, F2r, Gja1, Timp3, Cks2, Vegfa, Sncg, Gfm1, Reck, Cdk1, Mthfd1, Mtus1, Vdac1, Ar, Cd151, Igfbp7, Lum, Ptpn3, Hsd3b7</i>
Cellular Assembly and Organization	17	1,49E-04-2,24E-02	<i>Cbfb, F2r, Nckap1l, Gja1, Timp3, Vegfa, Sncg, Rab3a, Gfm1, Reck, Cdk1, Klc1, Vdac1, Robo2, Kctd13, Ar, Lum</i>
Small Molecule Biochemistry	16	1,6E-03-2,34E-02	<i>F2r, Aco1, Gja1, Vegfa, Sncg, Dnmt3a, Hfe, Cdk1, Mthfd1, Ctps, Vdac1, Ar, Igfbp7, Pex7, Atp2b2, Pde10a</i>
Cellular Movement	15	1,49E-04-2,43E-02	<i>F2r, Cbfb, Nckap1l, Gja1, Timp3, Vegfa, Sncg, Reck, Cdk1, Nqo2, Robo2, Ar, Cd151, Lum, Pex7</i>
Cellular Function and Maintenance	14	1,52E-04-2,31E-02	<i>F2r, Gja1, Aco1, Timp3, Vegfa, Hla-E, Rab3a, Hfe, Cdk1, Vdac1, Ar, Cd151, Dsg2, Atp2b2</i>
Cell Morphology	14	2,02E-04-2E-02	<i>F2r, Cbfb, Gja1, Timp3, Vegfa, Sncg, Racgap1, Reck, Robo2, Ar, Cd151, Igfbp7, Lum, Atp2b2</i>
Cell-To-Cell Signaling and Interaction	10	1,31E-03-2E-02	<i>F2r, Timp3, Gja1, Vegfa, Sncg, Ar, Cd151, Rab3a, Dsg2, Vdac1</i>
Molecular Transport	8	3,24E-03-2E-02	<i>F2r, Gja1, Aco1, Hfe, Rab3a, Pde10a, Atp2b2, Vdac1</i>
Cellular Development	7	1,37E-03-2E-02	<i>Timp3, Gja1, Vegfa, Ar, Gfm1, Igfbp7, Lum</i>
Nucleic Acid Metabolism	7	1,6E-03-2,06E-02	<i>F2r, Gja1, Cdk1, Ctps, Pde10a, Atp2b2, Vdac1</i>
Cell Cycle	7	2,52E-03-2,36E-02	<i>Cks2, Vegfa, Ar, Igfbp7, Racgap1, Ttc19, Cdk1</i>
Cell Signaling	7	5,04E-03-1,63E-02	<i>Nckap1l, Gja1, Vegfa, Hfe, Cdk1, Atp2b2, Vdac1</i>
Gene Expression	7	5,04E-03-2E-02	<i>Cbfb, Aco1, Dnmt3a, Ar, Hrsp12, Cdk1, Dusp26</i>
Cellular Compromise	6	4,48E-03-1,5E-02	<i>Gja1, Vegfa, Sncg, Ar, Hfe, Racgap1</i>
Cell Death	5	5,04E-03-2E-02	<i>F2r, Gja1, Vegfa, Lum, Vdac1</i>
Lipid Metabolism	4	2,87E-03-1,5E-02	<i>F2r, Vegfa, Igfbp7, Pex7</i>
Energy Production	4	3,24E-03-2,06E-02	<i>F2r, Gja1, Cdk1, Vdac1</i>
Vitamin and Mineral Metabolism	4	5,04E-03-1,18E-02	<i>Gja1, Vegfa, Atp2b2, Vdac1</i>
Protein Synthesis	4	1E-02-1,63E-02	<i>Nckap1l, Hrsp12, Hfe, Cdk1</i>
Antigen Presentation	4	1,46E-02-1,5E-02	<i>F2r, Nckap1l, Vegfa, Cd151</i>
Post-Translational Modification	4	1,5E-02-1,63E-02	<i>Nckap1l, Vegfa, Hfe, Cdk1</i>
Carbohydrate Metabolism	3	5,04E-03-1,5E-02	<i>Aco1, Atp2b2, Vdac1</i>
DNA Replication, Recombination, and Repair	3	1E-02-2E-02	<i>Vegfa, Dnmt3a, Cdk1</i>
Drug Metabolism	2	2,87E-03-2,87E-03	<i>Vegfa, Igfbp7</i>
RNA Post-Transcriptional Modification	2	7,51E-03-7,51E-03	<i>Aco1, Cdk1</i>
Amino Acid Metabolism	2	2E-02-2,34E-02	<i>Dnmt3a, Mthfd1</i>

**B- Hypothalamus**

Category	# of genes	P value	Genes
Cellular Assembly and Organization	4	1,21E-03-4,14E-02	<i>Ston2, Fmod, Nf1, Cit</i>
Molecular Transport	4	1,21E-03-4,72E-02	<i>Nf1, Pdyn, Hla-C, Ero1l</i>
Cell Death	3	1,21E-03-3,09E-02	<i>Fmod, Nf1, Hla-C</i>
Cell-To-Cell Signaling and Interaction	3	1,21E-03-2,5E-02	<i>Nf1, Pdyn, Hla-C</i>
Cellular Growth and Proliferation	3	1,21E-03-4,72E-02	<i>Nf1, Hla-C, Cit</i>
Small Molecule Biochemistry	3	6,01E-03-2,03E-02	<i>Nf1, Pdyn, Ero1l</i>
Cellular Development	3	9,61E-03-4,94E-02	<i>Nf1, Cit, Ero1l</i>
Cellular Compromise	2	1,21E-03-2,15E-02	<i>Pdyn, Cit</i>
DNA Replication, Recombination, and Repair	2	1,08E-02-1,44E-02	<i>Kat6a, Cit</i>
Cellular Function and Maintenance	2	3,09E-02-3,56E-02	<i>Nf1, Cit</i>