

Table S6: Result of GO analysis. Significant clusters in the category 'biological processes' are listed according to ascending p-values.

No.	Cluster name	Gene symbols	p-value	FDR
1	Metabolic process	<i>Ugt1a10, Cbs, Gstm1, Atp8b1, Dcxr, Mthfd1, Acy1, Aldh1a3, Aldh1l1, Eya4, Acaa2, Gcdh</i>	1.0×10^{-4}	0.028
2	ER-associated protein catabolic process	<i>Nploc4, Fbxo2, Fbxo6</i>	2.0×10^{-4}	0.043
3	Chromatin modification	<i>Chd3, Myst2, Eya4, Ash1l, Aebp2, Chd9</i>	4.0×10^{-4}	0.049
4	Glycoprotein catabolic process	<i>Fbxo2, Fbxo6</i>	7.0×10^{-4}	0.061
5	Bile acid and bile salt transport	<i>Atp8b1, Slco1c1</i>	7.0×10^{-4}	0.061
6	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	<i>Fbxo2, Fbxo6</i>	1.1×10^{-3}	0.069
7	Protein catabolic process	<i>Acy1, Fbxo2, Fbxo6</i>	1.4×10^{-3}	0.069
8	Leukotriene metabolic process	<i>Alox5ap, Cyp4f16</i>	2.5×10^{-3}	0.069
9	Adult behavior	<i>Slc1a2, Gabrg2</i>	3.1×10^{-3}	0.069
10	Cellular response to extracellular stimulus	<i>Slc1a2, Adora2b</i>	3.6×10^{-3}	0.069
11	Immortalization of host cell by virus	<i>Tyms</i>	3.7×10^{-3}	0.069
12	Nucleus accumbens development	<i>Aldh1a3</i>	3.7×10^{-3}	0.069
13	Stem cell development	<i>Msi2</i>	3.7×10^{-3}	0.069
14	Establishment of endothelial blood-brain barrier	<i>Abcb1b</i>	3.7×10^{-3}	0.069
15	Skeletal muscle fiber adaptation	<i>Acta1</i>	3.7×10^{-3}	0.069
16	Homocysteine catabolic process	<i>Cbs</i>	3.7×10^{-3}	0.069
17	Cysteine biosynthetic process via cystathionine	<i>Cbs</i>	3.7×10^{-3}	0.069
18	Cysteine biosynthetic process from serine	<i>Cbs</i>	3.7×10^{-3}	0.069
19	dTMP biosynthetic process	<i>Tyms</i>	3.7×10^{-3}	0.069
20	Xylulose metabolic process	<i>Dcxr</i>	3.7×10^{-3}	0.069
21	Positive regulation of chronic inflammatory response to non-antigenic stimulus	<i>Adora2b</i>	3.7×10^{-3}	0.069
22	3'-Phosphoadenosine 5'-phosphosulfate transport	<i>Slc35b2</i>	3.7×10^{-3}	0.069
23	tRNA processing	<i>Adat1, Elac2, Aars Itgae, Cd97, Chl1, Adam22, Emb, Pvrl3, Col20a1, Chst10</i>	4.0×10^{-3}	0.071
24	Cell adhesion	<i>Sap130, Myst2</i>	4.3×10^{-3}	0.072
25	Histone H3 acetylation	<i>Abcb1b, Ugt1a10, Timp4,</i>	5.7×10^{-3}	0.072
26	Response to drug		6.5×10^{-3}	0.072

		<i>Slc1a2, Tyms, Aldh1a3</i>		
27	Inner ear development	<i>Sparc, Eya4</i>	6.8×10^{-3}	0.072
28	Olfactory pit development	<i>Aldh1a3</i>	7.5×10^{-3}	0.072
29	Intestinal epithelial cell maturation	<i>Tyms</i>	7.5×10^{-3}	0.072
30	Optic cup morphogenesis involved in camera-type eye development	<i>Aldh1a3</i>	7.5×10^{-3}	0.072
31	Meiotic chromosome movement towards spindle pole	<i>Fmn2</i>	7.5×10^{-3}	0.072
32	Regulation of type I interferon-mediated signaling pathway	<i>Hsp90ab1</i>	7.5×10^{-3}	0.072
33	Protein import into peroxisome matrix, translocation	<i>Pex6</i>	7.5×10^{-3}	0.072
34	Retinoic acid biosynthetic process	<i>Aldh1a3</i>	7.5×10^{-3}	0.072
35	Hydrogen sulfide biosynthetic process	<i>Cbs</i>	7.5×10^{-3}	0.072
36	Transsulfuration	<i>Cbs</i>	7.5×10^{-3}	0.072
37	Histidine biosynthetic process	<i>Mthfd1</i>	7.5×10^{-3}	0.072
38	Deoxyribonucleoside monophosphate biosynthetic process	<i>Tyms</i>	7.5×10^{-3}	0.072
39	Fatty-acyl-CoA biosynthetic process	<i>Gcdh</i>	7.5×10^{-3}	0.072
40	Cellular response to unfolded protein	<i>Aars</i>	7.5×10^{-3}	0.072
41	Regulation of endosome size	<i>Als2</i>	7.5×10^{-3}	0.072
42	Cellular membrane fusion	<i>Nploc4, Vti1a</i>	8.1×10^{-3}	0.072
43	Cellular amino acid biosynthetic process	<i>Cbs, Mthfd1</i>	8.1×10^{-3}	0.072
44	Endosome transport	<i>Hgs, Als2</i>	9.4×10^{-3}	0.072
45	Response to amino acid stimulus	<i>Sls1a2, Aars</i>	9.9×10^{-3}	0.072
46	Skin development	<i>Krt9, Aars</i>	1.0×10^{-2}	0.072
47	Xenobiotic metabolic process	<i>Ugt1a10, Gstm1</i>	1.0×10^{-2}	0.072
48	One-carbon metabolic process	<i>Mthfd1, Aldh1l1</i>	1.0×10^{-2}	0.072
49	Negative regulation of cell adhesion	<i>Adam22, Myo1f</i>	1.1×10^{-2}	0.072
50	Transcription	<i>Sap130, Ascc2, 2610305D13Rik, Hey2, Sox5, Cdc5l, Chd3, Myst2, Eya4, Tmf1, Ash1l, Cebpg, Polr1c, Aebp2, Chd9, Zfp472</i>	1.1×10^{-2}	0.072
51	Cytokinesis, completion of separation	<i>Spast</i>	1.1×10^{-2}	0.072
52	Establishment of meiotic spindle localization	<i>Fmn2</i>	1.1×10^{-2}	0.072

53	Polar body extrusion after meiotic divisions	<i>Fmn2</i>	1.1 x 10 ⁻²	0.072
54	Regulation of translational fidelity	<i>Aars</i>	1.1 x 10 ⁻²	0.072
55	Positive regulation of guanylate cyclase activity	<i>Adora2b</i>	1.1 x 10 ⁻²	0.072
56	L-cysteine catabolic process	<i>Cbs</i>	1.1 x 10 ⁻²	0.072
57	10-Formyltetrahydrofolate catabolic process	<i>Aldh1l1</i>	1.1 x 10 ⁻²	0.072
58	dUMP metabolic process	<i>Tyms</i>	1.1 x 10 ⁻²	0.072
59	L-Serine catabolic process	<i>Cbs</i>	1.1 x 10 ⁻²	0.072
60	Alanyl-tRNA aminoacylation	<i>Aars</i>	1.1 x 10 ⁻²	0.072
61	Protein hexamerization	<i>Spast</i>	1.1 x 10 ⁻²	0.072
62	D-Aspartate import	<i>Slc1a2</i>	1.1 x 10 ⁻²	0.072
63	Glucose-6-phosphate transport	<i>G6pc3</i>	1.1 x 10 ⁻²	0.072
64	Positive regulation of I-kappaB kinase-NF-kappaB cascade	<i>Golt1b, Lgals9, Slc35b2</i>	1.2 x 10 ⁻²	0.075
65	Response to steroid hormone stimulus	<i>Abcb1b, Acta1</i>	1.4 x 10 ⁻²	0.075
66	Response to glucocorticoid stimulus	<i>Ugt1a10, Sparc, Tyms</i>	1.4 x 10 ⁻²	0.075
67	Adult locomotory behavior	<i>Chl1, Adam22</i>	1.4 x 10 ⁻²	0.075
68	Central nervous system development	<i>Timp4, Sh3gl2, Adam22</i>	1.4 x 10 ⁻²	0.075
69	Regulation of timing of neuron differentiation	<i>Sox5</i>	1.5 x 10 ⁻²	0.075
70	Leukotriene production involved in inflammatory response	<i>Alox5ap</i>	1.5 x 10 ⁻²	0.075
71	Microtubule severing	<i>Spast</i>	1.5 x 10 ⁻²	0.075
72	Meiotic metaphase I	<i>Fmn2</i>	1.5 x 10 ⁻²	0.075
73	Spindle assembly checkpoint	<i>Bub3</i>	1.5 x 10 ⁻²	0.075
74	Regulation of JUN kinase activity	<i>Cbs</i>	1.5 x 10 ⁻²	0.075
75	Regulation of interferon-gamma-mediated signaling pathway	<i>Hsp90ab1</i>	1.5 x 10 ⁻²	0.075
76	Positive regulation of retinoic acid receptor signaling pathway	<i>Aldh1a3</i>	1.5 x 10 ⁻²	0.075
77	Positive regulation of norepinephrine secretion	<i>Adora2b</i>	1.5 x 10 ⁻²	0.075
78	Cysteine biosynthetic process	<i>Cbs</i>	1.5 x 10 ⁻²	0.075
79	Proline catabolic process	<i>Prodh</i>	1.5 x 10 ⁻²	0.075
80	D-Xylose metabolic process	<i>Dcxr</i>	1.5 x 10 ⁻²	0.075
81	Lipoxygenase pathway	<i>Alox5ap</i>	1.5 x 10 ⁻²	0.075
82	Visual behavior	<i>Slc1a2</i>	1.9 x 10 ⁻²	0.082
83	Negative regulation of collagen biosynthetic	<i>Adora2b</i>	1.9 x 10 ⁻²	0.082

	process			
84	Relaxation of vascular smooth muscle	<i>Adora2b</i>	1.9×10^{-2}	0.082
85	Positive regulation of Rac protein signal transduction	<i>Als2</i>	1.9×10^{-2}	0.082
86	Proline metabolic process	<i>Prodh</i>	1.9×10^{-2}	0.082
87	Sulfate assimilation	<i>Papss2</i>	1.9×10^{-2}	0.082
88	Glucose 6-phosphate metabolic process	<i>G6pc3</i>	1.9×10^{-2}	0.082
89	Tyrosine catabolic process	<i>Gstz1</i>	1.9×10^{-2}	0.082
90	Kynurenine metabolic process	<i>Ccbl2</i>	1.9×10^{-2}	0.082
91	Skeletal muscle thin filament assembly	<i>Acta1</i>	1.9×10^{-2}	0.082
92	Cellular response to calcium ion	<i>Alox5ap</i>	1.9×10^{-2}	0.082
93	ER to Golgi vesicle-mediated transport	<i>Spast, Sec22c</i>	1.9×10^{-2}	0.082
94	Chromatin assembly or disassembly	<i>Chd3, Chd9</i>	2.0×10^{-2}	0.082
95	Response to unfolded protein	<i>Hsp90ab1, Fbxo6</i>	2.2×10^{-2}	0.082
96	Receptor recycling	<i>Als2</i>	2.2×10^{-2}	0.082
97	Face development	<i>Aldh1a3</i>	2.2×10^{-2}	0.082
98	Embryonic camera-type eye development	<i>Aldh1a3</i>	2.2×10^{-2}	0.082
99	Enucleate erythrocyte differentiation	<i>Cebpg</i>	2.2×10^{-2}	0.082
100	Positive regulation of catecholamine secretion	<i>Adora2b</i>	2.2×10^{-2}	0.082
101	Negative regulation of Notch signaling pathway	<i>Hey2</i>	2.2×10^{-2}	0.082
102	Positive regulation of Rac GTPase activity	<i>Als2</i>	2.2×10^{-2}	0.082
103	Neutrophil degranulation	<i>Myo1f</i>	2.2×10^{-2}	0.082
104	Glutamate biosynthetic process	<i>Prodh</i>	2.2×10^{-2}	0.082
105	L-Phenylalanine catabolic process	<i>Gstz1</i>	2.2×10^{-2}	0.082
106	Histone H4-K8 acetylation	<i>Myst2</i>	2.2×10^{-2}	0.082
107	Histone H4-K5 acetylation	<i>Myst2</i>	2.2×10^{-2}	0.082
108	Response to organophosphorus	<i>Tyms</i>	2.2×10^{-2}	0.082
109	Positive regulation of steroid biosynthetic process	<i>Adora2b</i>	2.2×10^{-2}	0.082
110	L-Glutamate import	<i>Slc1a2</i>	2.2×10^{-2}	0.082
111	Cartilage development	<i>Tyms, Sox5</i>	2.4×10^{-2}	0.087
112	Regulation of Rab GTPase activity	<i>Tbc1d9b, Als2</i>	2.6×10^{-2}	0.087
113	Cerebellar Purkinje cell layer development	<i>Aars</i>	2.6×10^{-2}	0.087
114	Retina morphogenesis in camera-type eye	<i>Pvrl3</i>	2.6×10^{-2}	0.087
115	Schwann cell differentiation	<i>Adam22</i>	2.6×10^{-2}	0.087
116	Regulation of chromosome	<i>Bub3</i>	2.6×10^{-2}	0.087

	segregation			
117	Negative regulation of JAK-STAT cascade	<i>Hgs</i>	2.6×10^{-2}	0.087
118	Negative regulation of proteasomal ubiquitin-dependent protein catabolic process	<i>Hsp90ab1</i>	2.6×10^{-2}	0.087
119	Homocysteine metabolic process	<i>Cbs</i>	2.6×10^{-2}	0.087
120	Histone H4-K12 acetylation	<i>Myst2</i>	2.6×10^{-2}	0.087
121	Myelination in the peripheral nervous system	<i>Adam22</i>	2.6×10^{-2}	0.087
122	Transmembrane transport	<i>Slc43a3, Abcc10, Slc25a34, Abcb1b, Slc35b2, Slc37a1</i>	2.8×10^{-2}	0.089
123	Regulation of transcription	<i>Sap130, Ascc2, Hey2, Sox5, Cdc5l, Chd3, Myst2, Eya4, Tmf1, Ash1l, Cebpg, Aebp2, Chd9</i>	2.9×10^{-2}	0.089
124	Ribosome biogenesis	<i>Krr1, Mrpl10</i>	2.9×10^{-2}	0.089
125	Myofibril assembly	<i>Acta1</i>	3.0×10^{-2}	0.089
126	Embryonic eye morphogenesis	<i>Aldh1a3</i>	3.0×10^{-2}	0.089
127	Positive regulation of cGMP biosynthetic process	<i>Adora2b</i>	3.0×10^{-2}	0.089
128	Induction of apoptosis by oxidative stress	<i>Prodh</i>	3.0×10^{-2}	0.089
129	Folic acid and derivative metabolic process	<i>Folh1</i>	3.0×10^{-2}	0.089
130	Bilirubin conjugation	<i>Ugt1a10</i>	3.0×10^{-2}	0.089
131	Transcription from RNA polymerase I promoter	<i>Polr1c</i>	3.0×10^{-2}	0.089
132	Coenzyme A biosynthetic process	<i>Pank3</i>	3.0×10^{-2}	0.089
133	Histone H4-K16 acetylation	<i>Myst2</i>	3.0×10^{-2}	0.089
134	Response to extracellular stimulus	<i>Acta1</i>	3.0×10^{-2}	0.089
135	Lysosomal transport	<i>Als2</i>	3.0×10^{-2}	0.089
136	Cellular amino acid metabolic process	<i>Acy1, Ccbl2</i>	3.0×10^{-2}	0.090
137	Response to lipopolysaccharide	<i>Ugt1a10, Timp4, Sparc</i>	3.1×10^{-2}	0.091
138	Biosynthetic process	<i>Aldh1l1, Ccbl2</i>	3.2×10^{-2}	0.091
139	Proteolysis	<i>Folh1, Acy1, Adam22, Masp2, Fbxo2, Fbxo6</i>	3.3×10^{-2}	0.091
140	Regulation of small GTPase mediated signal transduction	<i>4930474N05Rik, Rgl1</i>	3.3×10^{-2}	0.091
141	Lens morphogenesis in camera-type eye	<i>Pvrl3</i>	3.3×10^{-2}	0.091
142	Regulation of exit from mitosis	<i>Mad2l1bp</i>	3.3×10^{-2}	0.091
143	Attachment of spindle microtubules to kinetochore	<i>Bub3</i>	3.3×10^{-2}	0.091
144	Positive regulation of Notch signaling pathway	<i>Hey2</i>	3.3×10^{-2}	0.091

145	Retinal metabolic process	<i>Aldh1a3</i>	3.3×10^{-2}	0.091
146	Neutrophil mediated immunity	<i>Myo1f</i>	3.3×10^{-2}	0.091
147	Response to L-ascorbic acid	<i>Sparc</i>	3.3×10^{-2}	0.091
148	Protein homotrimerization	<i>Alox5ap</i>	3.3×10^{-2}	0.091
149	Transport	<i>Golt1b, Abcc10, Slc25a34, Abcb1b, Slc1a2, Stx8, Hgs, Slco1c1, Gabrg2, Vti1a, Slc35b2, Sec22c</i>	3.5×10^{-2}	0.096
150	Oxidation reduction	<i>Dcxr, Mthfd1, Aldh1a3, Prodh, Aldh1l1, Gcdh, Cyp4f16</i>	3.6×10^{-2}	0.096
151	Positive regulation of cardiac muscle cell proliferation	<i>Hey2</i>	3.7×10^{-2}	0.096
152	Bone development	<i>Papss2</i>	3.7×10^{-2}	0.096
153	Positive regulation of mast cell degranulation	<i>Adora2b</i>	3.7×10^{-2}	0.096
154	L-Serine metabolic process	<i>Cbs</i>	3.7×10^{-2}	0.096
155	Nucleosome disassembly	<i>Cebpg</i>	3.7×10^{-2}	0.096
156	Regulation of innate immune response	<i>Myo1f</i>	3.7×10^{-2}	0.096
157	DNA packaging	<i>Ash1l</i>	4.1×10^{-2}	0.101
158	Multicellular organismal aging	<i>Slc1a2</i>	4.1×10^{-2}	0.101
159	Regulation of protein ubiquitination	<i>Fbxo2</i>	4.1×10^{-2}	0.101
160	Natural killer cell mediated cytotoxicity	<i>Cebpg</i>	4.1×10^{-2}	0.101
161	Tetrahydrofolate metabolic process	<i>Mthfd1</i>	4.1×10^{-2}	0.101
162	Biphenyl metabolic process	<i>Ugt1a10</i>	4.1×10^{-2}	0.101
163	Protein targeting to peroxisome	<i>Pex6</i>	4.1×10^{-2}	0.101
164	Protein folding	<i>Ppil3, Hsp90ab1, Aars</i>	4.2×10^{-2}	0.103
165	Synaptic vesicle transport	<i>Sh3gl2</i>	4.4×10^{-2}	0.104
166	Methionine biosynthetic process	<i>Mthfd1</i>	4.4×10^{-2}	0.104
167	Folic acid and derivative biosynthetic process	<i>Mthfd1</i>	4.4×10^{-2}	0.104
168	tRNA aminoacylation	<i>Aars</i>	4.4×10^{-2}	0.104
169	Acetyl-CoA metabolic process	<i>Acaa2</i>	4.4×10^{-2}	0.104
170	Intermediate filament organization	<i>Krt9</i>	4.4×10^{-2}	0.104
171	Complement activation, lectin pathway	<i>Masp2</i>	4.4×10^{-2}	0.104
172	Response to folic acid	<i>Cbs</i>	4.4×10^{-2}	0.104
173	NADP metabolic process	<i>Dcxr</i>	4.8×10^{-2}	0.111
174	Dicarboxylic acid transport	<i>Slc1a2</i>	4.8×10^{-2}	0.111