

Gene Ontology : biological process. Level: 3	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
neurological process	7.17	12.1	1.73E-03	1
tissue remodeling	0.56	2.38	2.30E-03	1
primary metabolic process	54.74	48.16	1.65E-02	1
macromolecule metabolic process	47.57	41.25	2.19E-02	1
response to abiotic stimulus	0.64	1.94	2.45E-02	1
cell communication	32.83	38.66	2.56E-02	1
behavior	3.27	5.4	4.75E-02	1
cellular metabolic process	55.86	50.76	6.35E-02	1
digestion	0.32	1.08	6.52E-02	1
circulation	1.04	2.16	9.48E-02	1
detection of stimulus	0.4	1.08	1.45E-01	1
developmental growth	0.48	0	2.00E-01	1
molting cycle	0.56	0	2.00E-01	1
endocrine process	0	0.22	2.69E-01	1
sleep	0	0.22	2.69E-01	1
multicellular organismal homeostasis	0.16	0.43	2.95E-01	1
organismal movement	0.16	0.43	2.95E-01	1
death	6.22	4.97	3.57E-01	1
catabolic process	4.3	5.4	3.63E-01	1
regulation of a molecular function	3.19	4.1	3.71E-01	1
coagulation	0.96	0.43	3.76E-01	1
aging	0.32	0.65	3.95E-01	1
response to stress	7.81	6.48	4.08E-01	1
regulation of biological quality	2.07	1.3	4.20E-01	1
localization of cell	5.18	4.1	4.49E-01	1
thermoregulation	0.08	0.22	4.66E-01	1
organ growth	0.08	0.22	4.66E-01	1
cellular developmental process	16.57	15.12	5.07E-01	1
autophagy	0.24	0	5.68E-01	1
homeostasis of number of cells	0.24	0	5.68E-01	1
body growth	0.24	0	5.68E-01	1
interspecies interaction between organisms	0.24	0	5.68E-01	1
cell organization and biogenesis	18.41	17.06	5.72E-01	1
defense response	4.38	3.67	5.88E-01	1
cell proliferation	6.85	7.56	5.97E-01	1

response to external stimulus	5.26	4.54	6.20E-01	1
muscle contraction	1.35	1.73	6.50E-01	1
response to chemical stimulus	3.27	3.67	6.54E-01	1
regulation of biological process	35.86	34.77	0.6912833	1
response to endogenous stimulus	2.31	1.94	0.7156244	1
cell activation	2.39	1.94	0.7157399	1
response to biotic stimulus	2.31	2.59	0.7234653	1
synapse organization and biogenesis	0.56	0.65	0.7345141	1
multicellular organismal development	22.47	21.6	0.7438192	1
establishment of localization	20.96	20.3	0.7890163	1
developmental maturation	1.12	0.86	0.7934371	1
cell homeostasis	1.99	1.73	0.8442724	1
chemical homeostasis	2.07	2.16	0.8518755	1
protein localization	6.29	6.05	0.9107316	1
cell adhesion	7.65	7.78	0.918937	1
anatomical structure development	21.35	21.6	0.9471706	1
RNA localization	0.32	0.22	1	1
maintenance of localization	0.16	0	1	1
behavioral interaction between organisms	0.4	0.22	1	1
cell division	1.67	1.51	1	1
reproductive process	1.67	1.51	1	1
biosynthetic process	9	8.86	1	1
regulation of body fluids	1.04	0.86	1	1
cell recognition	0.48	0.43	1	1
nitrogen compound metabolic process	2.79	2.59	1	1
secondary metabolic process	0.24	0.22	1	1
respiratory gaseous exchange	0.32	0.22	1	1
cytokine production	1.12	1.08	1	1
pigmentation during development	0.16	0.22	1	1
cell cycle	7.09	6.91	1	1
membrane docking	0.4	0.22	1	1
sexual reproduction	1.99	1.94	1	1
chromosome segregation	0.4	0.43	1	1
extracellular matrix organization and biogenesis	0.64	0.43	1	1
circadian rhythm	0.24	0.22	1	1
excretion	0.32	0.22	1	1

immune system process

7.17

7.13

1

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Gene Ontology : biological process. Level: 4	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
protein metabolic process	27.54	20.88	0.005665717	1
sensory perception	3.85	6.81	0.01311375	1
cellular macromolecule metabolic process	26.15	20.44	0.01545811	1
bone remodeling	0.57	1.98	0.01897887	1
biopolymer metabolic process	38.36	32.53	0.03037133	1
adult behavior	0.25	1.1	0.03826845	1
phosphorus metabolic process	9.43	6.15	0.03852618	1
detection of external stimulus	0.16	0.88	0.04988037	1
positive regulation of biological process	11.31	8.13	0.05967504	1
detection of abiotic stimulus	0.08	0.66	0.06361406	1
glucose homeostasis	0.08	0.66	0.06361406	1
rhythmic behavior	0	0.44	0.07367107	1
regulation of binding	0	0.44	0.07367107	1
response to radiation	0.41	1.32	0.07998575	1
regulation of locomotion	0.49	1.32	0.09926941	1
learning and/or memory	0.82	1.76	0.111236	1
response to organic substance	0.16	0.66	0.1273231	1
cell aging	0.16	0.66	0.1273231	1
signal transduction	30.25	34.07	0.1388143	1
regulation of growth	1.64	0.66	0.1583784	1
response to wounding	3.93	2.42	0.1787818	1
regulation of blood vessel size	0.08	0.44	0.1811172	1
smooth muscle contraction	0.08	0.44	0.1811172	1
drug metabolic process	0.08	0.44	0.1811172	1
hair cycle	0.57	0	0.2000642	1
molting cycle process	0.57	0	0.2000642	1
regulation of multicellular organismal process	2.87	4.18	0.2123753	1
embryonic development	3.69	2.42	0.2238763	1
cell-cell signaling	7.05	8.79	0.2517451	1
cellular catabolic process	3.77	5.05	0.2683857	1
response to gravity	0	0.22	0.2716418	1
homeiothermy	0	0.22	0.2716418	1
response to mechanical stimulus	0	0.22	0.2716418	1
chemosensory behavior	0	0.22	0.2716418	1
striated muscle contraction	0.16	0.44	0.2986204	1

glycerol ether metabolic process	0.16	0.44	0.2986204	1
cytokinesis	0.16	0.44	0.2986204	1
tissue homeostasis	0.16	0.44	0.2986204	1
antigen processing and presentation	0.41	0	0.3318527	1
interleukin-6 production	0.41	0	0.3318527	1
response to drug	0.25	0.66	0.3535703	1
alkene metabolic process	0.25	0.66	0.3535703	1
locomotory behavior	2.13	2.86	0.367473	1
cell motility	5.33	4.18	0.3797009	1
organelle organization and biogenesis	9.34	7.91	0.3878559	1
macromolecule catabolic process	2.7	3.52	0.4150318	1
response to other organism	1.72	2.42	0.4213928	1
nucleobase, nucleoside, nucleotide and nucleic acid met	25.25	23.3	0.4448913	1
response to protein stimulus	0.66	0.22	0.4584797	1
cell differentiation	17.05	15.38	0.4604103	1
alcohol metabolic process	2.54	1.76	0.4659934	1
interferon-gamma production	0.08	0.22	0.4696125	1
detection of chemical stimulus	0.08	0.22	0.4696125	1
response to temperature stimulus	0.08	0.22	0.4696125	1
response to pain	0.08	0.22	0.4696125	1
musculoskeletal movement	0.08	0.22	0.4696125	1
sulfur metabolic process	0.49	0.88	0.4741691	1
anatomical structure morphogenesis	11.48	10.11	0.4843789	1
oxygen and reactive oxygen species metabolic process	0.57	0.88	0.5027782	1
reproductive developmental process	0.57	0.88	0.5027782	1
cofactor metabolic process	1.64	1.1	0.5031182	1
immune response	4.51	5.27	0.5180336	1
appendage development	0.82	0.44	0.5305785	1
pattern specification process	1.89	1.32	0.5307622	1
negative regulation of biological process	11.89	10.77	0.5491735	1
regulation of cellular process	31.97	30.33	0.5544919	1
regulation of coagulation	0.25	0	0.5672571	1
response to hormone stimulus	0.25	0	0.5672571	1
symbiosis, encompassing mutualism through parasitism	0.25	0	0.5672571	1
aldehyde metabolic process	0.25	0	0.5672571	1
leukocyte homeostasis	0.25	0	0.5672571	1

regulation of metabolic process	18.77	20	0.5765539	1
response to extracellular stimulus	0.33	0	0.5796803	1
regulation of response to stimulus	0.33	0	0.5796803	1
epithelial cell proliferation	0.25	0.44	0.6173481	1
interleukin-2 production	0.25	0.44	0.6173481	1
fear response	0.25	0.44	0.6173481	1
aromatic compound metabolic process	1.56	1.1	0.6450092	1
regulation of catalytic activity	3.28	3.74	0.6506001	1
response to xenobiotic stimulus	0.33	0.44	0.6656493	1
organic acid metabolic process	3.69	4.18	0.6677004	1
gametogenesis	1.97	1.54	0.6855553	1
response to DNA damage stimulus	2.13	1.76	0.7016256	1
leukocyte activation	2.38	1.98	0.7149152	1
heterocycle metabolic process	0.74	0.44	0.7371745	1
vitamin metabolic process	0.74	0.44	0.7371745	1
cell cycle process	6.31	6.81	0.7373835	1
hormone metabolic process	0.66	0.88	0.744756	1
one-carbon compound metabolic process	0.66	0.88	0.744756	1
regulation of developmental process	3.28	2.86	0.7547742	1
hemostasis	0.98	0.66	0.771524	1
lipid metabolic process	5.25	5.49	0.8078098	1
cellular localization	5.41	5.71	0.8099349	1
tube development	1.39	1.1	0.8106824	1
ion homeostasis	1.89	1.54	0.8360171	1
transport	20.82	20.22	0.8387658	1
amino acid and derivative metabolic process	2.21	1.98	0.8518027	1
membrane organization and biogenesis	2.54	2.64	0.8638721	1
cell-cell adhesion	2.95	3.08	0.8726646	1
carbohydrate metabolic process	3.61	3.3	0.8817467	1
macromolecule complex assembly	3.77	3.96	0.8862178	1
system development	19.1	18.68	0.8886906	1
mitotic cell cycle	1.89	1.76	1	1
response to toxin	0.08	0	1	1
response to inorganic substance	0.08	0	1	1
maintenance of protein localization	0.08	0	1	1
cellular biosynthetic process	8.28	8.35	1	1

feeding behavior	0.41	0.44	1	1
stem cell division	0.08	0	1	1
interleukin-8 production	0.08	0	1	1
interleukin-13 production	0.08	0	1	1
generation of precursor metabolites and energy	3.61	3.52	1	1
cellular structure disassembly	0.25	0.22	1	1
fertilization	0.16	0.22	1	1
cell-cell recognition	0.08	0	1	1
interleukin-1 production	0.08	0	1	1
viral reproductive process	0.41	0.22	1	1
reproductive process in a multicellular organism	0.57	0.44	1	1
chemokine production	0.08	0	1	1
pigment metabolic process	0.16	0	1	1
nitric oxide metabolic process	0.16	0.22	1	1
smooth muscle cell proliferation	0.08	0	1	1
response to tumor cell	0.08	0	1	1
cytoplasm organization and biogenesis	0.16	0.22	1	1
amine metabolic process	2.7	2.64	1	1
urea cycle intermediate metabolic process	0.08	0	1	1
secretion	2.95	2.86	1	1
establishment of protein localization	6.07	5.93	1	1
collagen fibril organization	0.16	0.22	1	1
cholesterol homeostasis	0.08	0	1	1
response to osmotic stress	0.16	0	1	1
blood pressure regulation	0.25	0.22	1	1
endothelial cell proliferation	0.16	0.22	1	1
keratinocyte proliferation	0.08	0	1	1
response to hypoxia	0.08	0	1	1
reproductive behavior	0.33	0.22	1	1
interleukin-12 production	0.16	0.22	1	1
cellular defense response	0.33	0.22	1	1
cell redox homeostasis	0.08	0	1	1
neuromuscular process	0.16	0.22	1	1
regulation of cytokine production	0.08	0	1	1
peptide metabolic process	0.16	0.22	1	1
sequestering of metal ion	0.08	0	1	1

macroautophagy	0.08	0	1	1
social behavior	0.08	0	1	1
meiotic cell cycle	0.57	0.44	1	1
establishment of RNA localization	0.33	0.22	1	1
detection of biotic stimulus	0.16	0.22	1	1
ribonucleoprotein complex biogenesis and assembly	0.82	0.88	1	1
interleukin-4 production	0.08	0	1	1
osmoregulation	0.08	0	1	1
fibroblast proliferation	0.16	0.22	1	1
detection of endogenous stimulus	0.08	0	1	1
neuron recognition	0.25	0.22	1	1
granulocyte macrophage colony-stimulating factor produ	0.16	0	1	1
cell-substrate adhesion	0.41	0.44	1	1
regulation of gene expression, epigenetic	0.33	0.22	1	1
asymmetric cell division	0.16	0	1	1
tumor necrosis factor-beta production	0.16	0	1	1
metabolic compound salvage	0.16	0	1	1
entrainment of circadian clock	0.08	0	1	1
interleukin-3 production	0.08	0	1	1
grooming behavior	0.08	0	1	1
external encapsulating structure organization and bioger	0.16	0	1	1
behavioral defense response	0.16	0.22	1	1



Gene Ontology : biological process. Level: 5	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
biopolymer modification	17.88	11.14	0.000946105	1
sensory perception of chemical stimulus	0.94	3.02	0.004519434	1
cell surface receptor linked signal transduction	13.34	18.79	0.008701017	1
cellular protein metabolic process	26.95	20.88	0.01376415	1
regulation of bone remodeling	0	0.7	0.01944723	1
phosphate metabolic process	9.84	6.5	0.03816538	1
sensory perception of light stimulus	1.54	3.02	0.06615464	1
response to amphetamine	0	0.46	0.07243981	1
vasoconstriction	0	0.46	0.07243981	1
positive regulation of cellular process	9.32	6.5	0.08640517	1
polysaccharide metabolic process	0.26	0.93	0.08936988	1
transmission of nerve impulse	4.11	6.03	0.1083607	1
regulation of cell adhesion	0.68	0	0.1176141	1
nitrogen compound biosynthetic process	0.6	1.39	0.1246316	1
female gamete generation	0.17	0.7	0.1246602	1
sulfur compound biosynthetic process	0.17	0.7	0.1246602	1
regulation of transferase activity	1.97	3.25	0.1359861	1
urogenital system development	0.68	1.62	0.1379155	1
response to light stimulus	0.43	1.16	0.1450318	1
negative regulation of multicellular organismal process	0.09	0.46	0.178425	1
detection of stimulus during sensory perception	0.09	0.46	0.178425	1
regulation of cell motility	0.51	1.16	0.1786355	1
response to bacterium	0.51	1.16	0.1786355	1
cell fate commitment	0.86	1.62	0.1802032	1
embryonic development (sensu Metazoa)	1.37	0.46	0.1812811	1
biopolymer catabolic process	2.05	3.25	0.1938639	1
hair cycle process	0.6	0	0.1999694	1
water-soluble vitamin metabolic process	0.6	0	0.1999694	1
nucleoside metabolic process	0.51	0	0.2000239	1
nuclear organization and biogenesis	0.51	0	0.2000239	1
intracellular signaling cascade	15.4	12.76	0.2030225	1
inflammatory response	2.82	1.62	0.2079993	1
cellular macromolecule catabolic process	2.48	3.71	0.2314653	1
positive regulation of metabolic process	4.11	2.78	0.2386537	1
ion transport	7.44	9.28	0.2512664	1

cofactor biosynthetic process	1.2	0.46	0.2619532	1
fluid secretion	0	0.23	0.269375	1
cocaine metabolic process	0	0.23	0.269375	1
mechanosensory behavior	0	0.23	0.269375	1
response to alkaloid	0	0.23	0.269375	1
response to carbohydrate stimulus	0	0.23	0.269375	1
endothelial cell differentiation	0	0.23	0.269375	1
fast regulation of arterial pressure	0	0.23	0.269375	1
sequestering of lipid	0	0.23	0.269375	1
antibiotic metabolic process	0	0.23	0.269375	1
retinal homeostasis	0	0.23	0.269375	1
urothelial cell proliferation	0	0.23	0.269375	1
detection of gravity	0	0.23	0.269375	1
microtubule organizing center organization and biogenesis	0	0.23	0.269375	1
response to ethanol	0	0.23	0.269375	1
dosage compensation	0	0.23	0.269375	1
organic acid catabolic process	0	0.23	0.269375	1
regulation of posture	0	0.23	0.269375	1
exocrine system development	0	0.23	0.269375	1
eating behavior	0	0.23	0.269375	1
parturition	0	0.23	0.269375	1
circadian behavior	0	0.23	0.269375	1
regulation of DNA binding	0	0.23	0.269375	1
nervous system development	10.01	8.12	0.290489	1
cellular lipid metabolic process	4.45	5.8	0.291837	1
response to fungus	0.17	0.46	0.2946967	1
fat-soluble vitamin metabolic process	0.17	0.46	0.2946967	1
mesenchymal cell differentiation	0.17	0.46	0.2946967	1
photoreceptor cell differentiation	0.17	0.46	0.2946967	1
hormone biosynthetic process	0.17	0.46	0.2946967	1
calcium-dependent cell-cell adhesion	0.17	0.46	0.2946967	1
regulation of catabolic process	0.17	0.46	0.2946967	1
alcohol catabolic process	0.77	0.23	0.3044141	1
cytoskeleton organization and biogenesis	5.73	4.41	0.3204322	1
regulation of heart contraction	0.6	1.16	0.3239519	1
regulation of cyclase activity	0.43	0	0.3323761	1

negative regulation of growth	0.43	0	0.3323761	1
regulation of lyase activity	0.43	0	0.3323761	1
protein secretion	0.43	0	0.3323761	1
DNA damage response, signal transduction	0.43	0	0.3323761	1
mitochondrion organization and biogenesis	0.43	0	0.3323761	1
regulation of signal transduction	4.96	3.71	0.3479831	1
response to oxidative stress	0.26	0.7	0.3524705	1
adult locomotory behavior	0.26	0.7	0.3524705	1
lipid catabolic process	0.68	1.16	0.3534935	1
regulation of immune system process	1.03	0.46	0.3755928	1
reproductive structure development	0.34	0.7	0.3951182	1
cell morphogenesis	6.07	4.87	0.3984851	1
membrane invagination	2.14	1.39	0.4167417	1
organ development	13.94	15.55	0.4224799	1
regionalization	1.28	0.7	0.4287577	1
sensory perception of mechanical stimulus	1.28	0.7	0.4287577	1
cell development	12.4	10.9	0.4363132	1
heterophilic cell adhesion	0.43	0.7	0.4508248	1
amine transport	0.68	0.23	0.4585975	1
regulation of secretion	0.68	0.23	0.4585975	1
response to unfolded protein	0.68	0.23	0.4585975	1
endosome organization and biogenesis	0.09	0.23	0.4663102	1
Golgi organization and biogenesis	0.09	0.23	0.4663102	1
vesicle organization and biogenesis	0.09	0.23	0.4663102	1
superoxide metabolic process	0.09	0.23	0.4663102	1
aromatic compound biosynthetic process	0.09	0.23	0.4663102	1
bone resorption	0.09	0.23	0.4663102	1
digestive process	0.09	0.23	0.4663102	1
regulation of balance	0.09	0.23	0.4663102	1
detection of calcium ion	0.09	0.23	0.4663102	1
cell activation during immune response	0.09	0.23	0.4663102	1
negative regulation of locomotion	0.09	0.23	0.4663102	1
calcium-independent cell-cell adhesion	0.09	0.23	0.4663102	1
response to cold	0.09	0.23	0.4663102	1
regulation of oxidoreductase activity	0.09	0.23	0.4663102	1
glycerol ether biosynthetic process	0.09	0.23	0.4663102	1

acid secretion	0.09	0.23	0.4663102	1
regulation of carbohydrate metabolic process	0.09	0.23	0.4663102	1
fertilization (sensu Metazoa)	0.09	0.23	0.4663102	1
pteridine and derivative metabolic process	0.09	0.23	0.4663102	1
sex determination	0.09	0.23	0.4663102	1
terpene metabolic process	0.09	0.23	0.4663102	1
sensory perception of temperature stimulus	0.09	0.23	0.4663102	1
localization within membrane	0.09	0.23	0.4663102	1
coenzyme metabolic process	1.54	0.93	0.4705845	1
sex differentiation	0.6	0.93	0.5001345	1
protein-DNA complex assembly	0.6	0.93	0.5001345	1
morphogenesis of a branching structure	0.6	0.93	0.5001345	1
learning	0.6	0.93	0.5001345	1
regulation of anatomical structure morphogenesis	0.6	0.93	0.5001345	1
lipid transport	0.86	0.46	0.5316294	1
appendage morphogenesis	0.86	0.46	0.5316294	1
embryonic pattern specification	0.86	0.46	0.5316294	1
nucleotide metabolic process	2.05	1.39	0.5331728	1
lymphocyte activation	2.22	1.62	0.5545998	1
negative regulation of developmental process	0.86	1.16	0.5650768	1
immune effector process	0.86	1.16	0.5650768	1
regulation of transport	0.86	1.16	0.5650768	1
regulation of cell activation	0.86	1.16	0.5650768	1
regulation of cellular metabolic process	18.91	20.19	0.5679732	1
regulation of body size	0.26	0	0.5681721	1
negative regulation of coagulation	0.26	0	0.5681721	1
nucleobase metabolic process	0.26	0	0.5681721	1
axis specification	0.26	0	0.5681721	1
alcohol biosynthetic process	0.26	0	0.5681721	1
regulation of defense response	0.26	0	0.5681721	1
gene silencing	0.26	0	0.5681721	1
interaction with host	0.26	0	0.5681721	1
lactation	0.26	0	0.5681721	1
negative regulation of metabolic process	4.19	3.48	0.5682617	1
cell migration	4.28	3.48	0.5684334	1
RNA metabolic process	19.76	18.33	0.5685241	1

response to nutrient levels	0.34	0	0.5792585	1
vitamin biosynthetic process	0.34	0	0.5792585	1
oligosaccharide metabolic process	0.34	0	0.5792585	1
cell wall catabolic process	0.34	0	0.5792585	1
immune response-regulating signal transduction	0.34	0	0.5792585	1
secretory pathway	2.31	2.78	0.5856398	1
negative regulation of cellular process	11.46	10.44	0.5928768	1
chromosome organization and biogenesis	2.74	2.09	0.5930421	1
peptide transport	0.26	0.46	0.6157702	1
regulation of muscle contraction	0.26	0.46	0.6157702	1
vacuole organization and biogenesis	0.26	0.46	0.6157702	1
wound healing	1.37	0.93	0.6163635	1
regulation of cell proliferation	5.22	5.8	0.6196558	1
regulation of cell cycle	5.39	6.03	0.6236839	1
plasma membrane organization and biogenesis	0.34	0.46	0.6632268	1
xenobiotic metabolic process	0.34	0.46	0.6632268	1
nitrogen compound catabolic process	0.34	0.46	0.6632268	1
myeloid leukocyte activation	0.34	0.46	0.6632268	1
carboxylic acid metabolic process	3.85	4.41	0.6661591	1
embryonic morphogenesis	1.8	1.39	0.667289	1
cell ion homeostasis	1.8	1.39	0.667289	1
fat cell differentiation	0.51	0.23	0.6820303	1
determination of symmetry	0.51	0.23	0.6820303	1
carbohydrate transport	0.51	0.23	0.6820303	1
cell cycle phase	2.4	1.86	0.7038767	1
organic acid biosynthetic process	0.51	0.7	0.7090337	1
response to virus	0.6	0.7	0.7343629	1
regulation of neurological process	0.6	0.7	0.7343629	1
regulation of cell organization and biogenesis	0.77	0.46	0.7372031	1
innate immune response	0.77	0.93	0.7568814	1
negative regulation of enzyme activity	0.94	0.7	0.7705156	1
regulation of hydrolase activity	0.94	1.16	0.7772335	1
tube morphogenesis	1.03	1.16	0.7872186	1
macromolecule biosynthetic process	5.39	4.87	0.800563	1
anatomical structure formation	1.71	1.39	0.8244722	1
homophilic cell adhesion	1.63	1.39	0.8244781	1

regulation of cell differentiation	2.14	1.86	0.8441696	1
electron transport	2.14	1.86	0.8441696	1
regulation of protein metabolic process	2.22	2.32	0.8517048	1
cellular carbohydrate metabolic process	3.08	3.25	0.8717725	1
establishment of cellular localization	5.56	5.8	0.9026782	1
protein transport	5.9	6.03	0.9055007	1
peroxisome organization and biogenesis	0.17	0.23	1	1
pregnancy	0.34	0.23	1	1
sulfur utilization	0.09	0	1	1
intercellular junction assembly and maintenance	0.17	0.23	1	1
humoral immune response	1.2	1.16	1	1
energy derivation by oxidation of organic compounds	1.37	1.16	1	1
muscle cell differentiation	0.68	0.7	1	1
DNA metabolic process	4.96	4.87	1	1
regulation of helicase activity	0.09	0	1	1
neurotransmitter transport	0.68	0.46	1	1
regulation of lipid metabolic process	0.09	0	1	1
transcription	18.48	18.33	1	1
pigment biosynthetic process	0.09	0	1	1
two-component signal transduction system (phosphorela	0.17	0.23	1	1
porphyrin metabolic process	0.17	0.23	1	1
detection of hormone stimulus	0.09	0	1	1
keratinocyte differentiation	0.51	0.46	1	1
behavioral fear response	0.17	0.23	1	1
polyol transport	0.09	0	1	1
maternal behavior	0.17	0.23	1	1
antigen processing and presentation via MHC class Ib	0.09	0	1	1
alkene biosynthetic process	0.17	0.23	1	1
mating behavior	0.17	0	1	1
mechanoreceptor differentiation	0.26	0.23	1	1
protein complex assembly	2.74	2.55	1	1
response to metal ion	0.09	0	1	1
imprinting	0.09	0	1	1
autophagic vacuole formation	0.09	0	1	1
male gamete generation	1.28	1.16	1	1
regulation of growth rate	0.09	0	1	1

menstrual cycle	0.17	0.23	1	1
vesicle-mediated transport	4.7	4.64	1	1
membrane fusion	0.26	0.23	1	1
carbohydrate catabolic process	0.77	0.7	1	1
positive regulation of developmental process	0.86	0.93	1	1
protein-RNA complex assembly	0.68	0.7	1	1
behavioral response to pain	0.09	0	1	1
lymphocyte homeostasis	0.17	0	1	1
indole and derivative metabolic process	0.09	0	1	1
startle response	0.09	0	1	1
polyol metabolic process	0.17	0.23	1	1
regulation of pH	0.26	0.23	1	1
sperm motility	0.17	0.23	1	1
nucleobase, nucleoside, nucleotide and nucleic acid tran	0.43	0.23	1	1
sulfation	0.17	0	1	1
taxis	1.28	1.16	1	1
sensory perception of pain	0.26	0.23	1	1
endocrine system development	0.09	0	1	1
water homeostasis	0.09	0	1	1
viral infectious cycle	0.43	0.23	1	1
morphogenesis of an epithelium	1.2	1.16	1	1
antigen processing and presentation of exogenous antig	0.09	0	1	1
regulation of response to biotic stimulus	0.09	0	1	1
positive regulation of response to stimulus	0.09	0	1	1
positive regulation of gene expression, epigenetic	0.09	0	1	1
fluid transport	0.09	0	1	1
detection of tumor cell	0.09	0	1	1
immune response to tumor cell	0.09	0	1	1
nutrient import	0.09	0	1	1
hydrogen transport	0.43	0.23	1	1
positive regulation of multicellular organismal process	1.11	0.93	1	1
positive regulation of cytokine production	0.09	0	1	1
regulation of embryonic development	0.17	0	1	1
nucleoside salvage	0.17	0	1	1
vasodilation	0.09	0	1	1
regulation of cell redox homeostasis	0.09	0	1	1

maintenance of cellular localization	0.09	0	1	1
gas transport	0.09	0	1	1
response to axon injury	0.09	0	1	1
methylation	0.34	0.23	1	1
regeneration	0.09	0	1	1
antigen processing and presentation of peptide or polysaccharide	0.09	0	1	1
generation of a signal involved in cell-cell signaling	1.11	1.16	1	1
pigment cell differentiation	0.17	0	1	1
cofactor catabolic process	0.26	0.23	1	1
phenol metabolic process	0.51	0.46	1	1
myeloid cell homeostasis	0.09	0	1	1
organic acid transport	0.51	0.46	1	1
organelle localization	0.26	0.23	1	1
movement in environment of other organism during symbiosis	0.17	0	1	1
regulation of organ size	0.09	0	1	1
ethanol metabolic process	0.09	0	1	1
vitamin transport	0.17	0	1	1
regulation of biosynthetic process	1.37	1.39	1	1
aromatic compound catabolic process	0.17	0.23	1	1
purine salvage	0.17	0	1	1
hormone catabolic process	0.09	0	1	1
negative regulation of gene expression, epigenetic	0.09	0	1	1
positive regulation of locomotion	0.17	0.23	1	1
quinone cofactor metabolic process	0.09	0	1	1
suckling behavior	0.17	0	1	1
cofactor transport	0.09	0	1	1
ciliary or flagellar motility	0.17	0	1	1
ribosome biogenesis and assembly	0.17	0.23	1	1
cell-matrix adhesion	0.43	0.46	1	1
amino acid derivative metabolic process	0.77	0.7	1	1
cell envelope organization and biogenesis	0.17	0	1	1
nucleotide-sugar metabolic process	0.09	0	1	1
memory	0.17	0.23	1	1
protein complex disassembly	0.09	0	1	1
adaptive immune response	0.68	0.7	1	1
modification of morphology or physiology of other organisms	0.09	0	1	1



positive regulation of enzyme activity	2.14	2.09	1	1
nitric oxide biosynthetic process	0.17	0.23	1	1
response to X-ray	0.09	0	1	1
cell glucose homeostasis	0.09	0	1	1

Gene Ontology : biological process. Level: 6	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
protein modification	18.93	11.87	0.001320007	1
sensory perception of smell	1.02	3.03	0.00867637	1
G-protein coupled receptor protein signaling pathway	6.93	10.86	0.01683893	1
adult walking behavior	0	0.76	0.01908822	1
phosphorylation	8.86	5.3	0.02899869	1
embryonic development (sensu Vertebrata)	1.11	0	0.04382327	1
visual behavior	0.09	0.76	0.06110558	1
visual perception	1.66	3.28	0.06460708	1
anterior/posterior pattern formation	0.92	0	0.0709744	1
DNA strand elongation	0	0.51	0.0715566	1
negative regulation of bone remodeling	0	0.51	0.0715566	1
regulation of phospholipase A2 activity	0	0.51	0.0715566	1
cellular lipid catabolic process	0.28	1.01	0.08760815	1
cellular polysaccharide metabolic process	0.28	1.01	0.08760815	1
amine biosynthetic process	0.65	1.52	0.122405	1
smoothened signaling pathway	0.18	0.76	0.12275	1
energy reserve metabolic process	0.18	0.76	0.12275	1
regulation of kinase activity	2.12	3.54	0.1336111	1
protein oligomerization	0.46	1.26	0.1436778	1
defense response to bacterium	0.46	1.26	0.1436778	1
sensory organ development	0.83	1.77	0.1531851	1
DNA recombination	0.83	1.77	0.1531851	1
regulation of cell size	1.94	0.76	0.1609293	1
protein catabolic process	1.94	3.28	0.1678934	1
modification-dependent macromolecule catabolic proces	1.39	2.53	0.1689792	1
detection of light stimulus	0.09	0.51	0.1764934	1
defense response to fungus	0.09	0.51	0.1764934	1
neuron adhesion	0.09	0.51	0.1764934	1
vitamin A metabolic process	0.09	0.51	0.1764934	1
synaptic vesicle transport	0.28	0.76	0.1980979	1
positive regulation of immune system process	1.02	0.25	0.1995551	1
exocytosis	1.11	2.02	0.2034832	1
synaptic transmission	4.16	5.81	0.2062397	1
kidney development	0.74	1.52	0.2214429	1
Wnt receptor signaling pathway	1.39	2.27	0.2470893	1

positive regulation of cell differentiation	0.46	1.01	0.2598048	1
Notch signaling pathway	0.46	1.01	0.2598048	1
cyclic nucleotide metabolic process	0.46	1.01	0.2598048	1
regulation of cell migration	0.46	1.01	0.2598048	1
glutamate signaling pathway	0.46	1.01	0.2598048	1
biopolymer glycosylation	1.94	1.01	0.261897	1
mRNA metabolic process	2.03	1.01	0.2631478	1
carbohydrate mediated signaling	0	0.25	0.2677485	1
locomotor rhythm	0	0.25	0.2677485	1
positive regulation of bone remodeling	0	0.25	0.2677485	1
S-adenosylmethionine metabolic process	0	0.25	0.2677485	1
protein insertion into membrane	0	0.25	0.2677485	1
baroreceptor feedback regulation of blood pressure	0	0.25	0.2677485	1
circadian sleep/wake cycle	0	0.25	0.2677485	1
negative regulation of carbohydrate metabolic process	0	0.25	0.2677485	1
regulation of nitric oxide biosynthetic process	0	0.25	0.2677485	1
peptide modification	0	0.25	0.2677485	1
positive regulation of catabolic process	0	0.25	0.2677485	1
polysaccharide catabolic process	0	0.25	0.2677485	1
response to cocaine	0	0.25	0.2677485	1
carboxylic acid catabolic process	0	0.25	0.2677485	1
regulation of blood pressure by hormones	0	0.25	0.2677485	1
superoxide release	0	0.25	0.2677485	1
behavioral response to ethanol	0	0.25	0.2677485	1
amino acid derivative catabolic process	0	0.25	0.2677485	1
sensory perception of taste	0	0.25	0.2677485	1
regulation of cellular catabolic process	0	0.25	0.2677485	1
phospholipid scrambling	0	0.25	0.2677485	1
response to reactive oxygen species	0	0.25	0.2677485	1
response to morphine	0	0.25	0.2677485	1
muscle cell development	0	0.25	0.2677485	1
centrosome organization and biogenesis	0	0.25	0.2677485	1
antibiotic biosynthetic process	0	0.25	0.2677485	1
detection of bacterium	0	0.25	0.2677485	1
negative regulation of catabolic process	0	0.25	0.2677485	1
DNA geometric change	0	0.25	0.2677485	1

glutathione metabolic process	0	0.25	0.2677485	1
DNA ligation	0	0.25	0.2677485	1
regulation of vasoconstriction	0	0.25	0.2677485	1
nitric oxide mediated signal transduction	0	0.25	0.2677485	1
RNA processing	2.95	1.77	0.2713158	1
substrate-bound cell migration	0.18	0.51	0.2918811	1
cell fate determination	0.18	0.51	0.2918811	1
cell-cell signaling during cell fate commitment	0.18	0.51	0.2918811	1
glycerolipid metabolic process	0.18	0.51	0.2918811	1
mesenchymal cell development	0.18	0.51	0.2918811	1
biopolymer biosynthetic process	0.18	0.51	0.2918811	1
peptidoglycan metabolic process	0.18	0.51	0.2918811	1
neutral lipid metabolic process	0.18	0.51	0.2918811	1
female sex differentiation	0.18	0.51	0.2918811	1
monosaccharide metabolic process	1.57	0.76	0.3124353	1
skeletal development	2.95	4.04	0.3202762	1
central nervous system development	3.05	4.04	0.3297796	1
oxidoreduction coenzyme metabolic process	0.55	0	0.351682	1
membrane lipid metabolic process	1.39	2.02	0.3538307	1
anion transport	1.39	2.02	0.3538307	1
positive regulation of cellular metabolic process	4.25	3.03	0.3638177	1
regulation of immune response	1.11	0.51	0.3761687	1
blood coagulation	1.11	0.51	0.3761687	1
main pathways of carbohydrate metabolic process	1.2	0.51	0.379194	1
coenzyme biosynthetic process	1.2	0.51	0.379194	1
negative regulation of signal transduction	1.2	0.51	0.379194	1
aminoglycan metabolic process	0.37	0.76	0.3932599	1
cell death	7.2	5.81	0.4150825	1
glycoprotein metabolic process	2.31	1.52	0.4168532	1
endocytosis	2.31	1.52	0.4168532	1
tissue development	3.14	4.04	0.4171678	1
sensory perception of sound	1.39	0.76	0.4290147	1
monocarboxylic acid metabolic process	2.12	2.78	0.438683	1
negative regulation of transferase activity	0.46	0.76	0.4480905	1
regulation of transmission of nerve impulse	0.46	0.76	0.4480905	1
establishment and/or maintenance of cell polarity	0.46	0.76	0.4480905	1

negative regulation of cellular metabolic process	4.25	3.28	0.4556657	1
intracellular receptor-mediated signaling pathway	0.74	0.25	0.4586838	1
regulation of ion transport	0.09	0.25	0.4639404	1
thermoception	0.09	0.25	0.4639404	1
pteridine and derivative biosynthetic process	0.09	0.25	0.4639404	1
peptide secretion	0.09	0.25	0.4639404	1
negative regulation of cell motility	0.09	0.25	0.4639404	1
regulation of smooth muscle contraction	0.09	0.25	0.4639404	1
positive regulation of heart contraction	0.09	0.25	0.4639404	1
molybdopterin cofactor metabolic process	0.09	0.25	0.4639404	1
positive regulation of carbohydrate metabolic process	0.09	0.25	0.4639404	1
ovulation	0.09	0.25	0.4639404	1
regulation of nitric-oxide synthase activity	0.09	0.25	0.4639404	1
natural killer cell activation	0.09	0.25	0.4639404	1
porphyrin catabolic process	0.09	0.25	0.4639404	1
leukocyte activation during immune response	0.09	0.25	0.4639404	1
arachidonic acid secretion	0.09	0.25	0.4639404	1
plasma membrane repair	0.09	0.25	0.4639404	1
oligopeptide transport	0.09	0.25	0.4639404	1
intestinal absorption	0.09	0.25	0.4639404	1
morphogenesis of an epithelial sheet	0.09	0.25	0.4639404	1
lipoprotein metabolic process	0.55	1.01	0.4718883	1
acute inflammatory response	0.55	1.01	0.4718883	1
positive regulation of transferase activity	1.48	2.02	0.4873266	1
branching morphogenesis of a tube	0.65	1.01	0.4982371	1
positive regulation of biosynthetic process	0.65	1.01	0.4982371	1
regulation of cell morphogenesis	0.65	1.01	0.4982371	1
neurogenesis	5.26	4.29	0.5025364	1
actin filament-based process	3.42	2.53	0.5030137	1
cell projection morphogenesis	3.42	2.53	0.5030137	1
limb morphogenesis	0.92	0.51	0.5323865	1
embryonic appendage morphogenesis	0.92	0.51	0.5323865	1
microtubule-based process	2.22	1.52	0.5325448	1
cytokine metabolic process	0.92	1.26	0.56311	1
regulation of fat cell differentiation	0.28	0	0.5688295	1
response to UV	0.28	0	0.5688295	1

receptor metabolic process	0.28	0	0.5688295	1
cardiac inotropy	0.28	0	0.5688295	1
response to nutrient	0.28	0	0.5688295	1
cytokine secretion	0.28	0	0.5688295	1
cortical cytoskeleton organization and biogenesis	0.28	0	0.5688295	1
acetyl-CoA metabolic process	0.28	0	0.5688295	1
leukocyte adhesion	0.28	0	0.5688295	1
RNA modification	0.28	0	0.5688295	1
positive regulation of cell organization and biogenesis	0.28	0	0.5688295	1
nucleobase biosynthetic process	0.28	0	0.5688295	1
nucleoside monophosphate metabolic process	0.28	0	0.5688295	1
regulation of inflammatory response	0.28	0	0.5688295	1
germ cell migration	0.28	0	0.5688295	1
negative regulation of cyclase activity	0.37	0	0.5789563	1
negative regulation of lyase activity	0.37	0	0.5789563	1
immune response-regulating cell surface receptor signal	0.37	0	0.5789563	1
regulation of protein secretion	0.37	0	0.5789563	1
positive regulation of secretion	0.37	0	0.5789563	1
water-soluble vitamin biosynthetic process	0.37	0	0.5789563	1
cellular respiration	0.37	0	0.5789563	1
protein import	1.11	1.52	0.5923102	1
vasculature development	2.86	2.27	0.592668	1
heart development	1.2	1.52	0.6082916	1
cellular morphogenesis during differentiation	3.23	2.53	0.6083547	1
amino acid derivative biosynthetic process	0.28	0.51	0.614638	1
proteoglycan metabolic process	0.28	0.51	0.614638	1
negative regulation of cell organization and biogenesis	0.28	0.51	0.614638	1
regulation of epithelial cell proliferation	0.28	0.51	0.614638	1
lysosome organization and biogenesis	0.28	0.51	0.614638	1
protein depolymerization	0.28	0.51	0.614638	1
cytokine and chemokine mediated signaling pathway	0.28	0.51	0.614638	1
protein folding	1.48	1.01	0.6165122	1
DNA replication	1.48	1.77	0.6420987	1
small GTPase mediated signal transduction	4.25	3.54	0.6554219	1
regulation of nucleobase, nucleoside, nucleotide and nu	19.3	20.45	0.6572536	1
regulation of action potential	0.37	0.51	0.661488	1

amine catabolic process	0.37	0.51	0.661488	1
gastrulation	0.37	0.51	0.661488	1
protein kinase cascade	4.52	3.79	0.6650541	1
M phase	1.94	1.52	0.6676904	1
lipid biosynthetic process	1.85	2.27	0.6717916	1
segmentation	0.55	0.25	0.6822859	1
determination of bilateral symmetry	0.55	0.25	0.6822859	1
positive regulation of transport	0.55	0.25	0.6822859	1
DNA packaging	2.22	1.77	0.6859411	1
germ cell development	0.65	0.25	0.6897683	1
group transfer coenzyme metabolic process	0.65	0.25	0.6897683	1
epithelial cell differentiation	0.65	0.25	0.6897683	1
cation transport	5.54	6.06	0.7042588	1
carboxylic acid biosynthetic process	0.55	0.76	0.7079658	1
cellular protein complex assembly	0.55	0.76	0.7079658	1
development of primary sexual characteristics	0.55	0.76	0.7079658	1
regulation of progression through cell cycle	5.72	6.31	0.7081859	1
intracellular transport	5.82	6.31	0.7107259	1
muscle development	2.49	2.78	0.7144068	1
positive regulation of cell proliferation	2.49	2.78	0.7144068	1
chromosome organization and biogenesis (sensu Eukaryota)	2.77	2.27	0.7152497	1
positive regulation of hydrolase activity	0.65	0.76	0.7327987	1
negative regulation of protein metabolic process	0.65	0.76	0.7327987	1
ribonucleotide metabolic process	0.83	0.51	0.7372247	1
biogenic amine metabolic process	0.83	0.51	0.7372247	1
leukocyte mediated immunity	0.74	1.01	0.7434302	1
cell maturation	0.83	1.01	0.7558127	1
antimicrobial humoral response	0.83	1.01	0.7558127	1
regulation of lymphocyte activation	0.83	1.01	0.7558127	1
negative regulation of cell differentiation	0.83	1.01	0.7558127	1
carbohydrate biosynthetic process	1.02	1.26	0.7765899	1
regulated secretory pathway	1.02	1.26	0.7765899	1
steroid metabolic process	1.29	1.01	0.7935596	1
T cell activation	1.57	1.26	0.8107554	1
dephosphorylation	1.75	2.02	0.8263799	1
amino acid metabolic process	1.85	2.02	0.8305251	1

organ morphogenesis	4.34	4.55	0.8862671	1
RNA biosynthetic process	18.47	18.69	0.9397939	1
synaptogenesis	0.28	0.25	1	1
B cell activation	1.11	1.01	1	1
mast cell activation	0.18	0.25	1	1
positive regulation of cyclase activity	0.09	0	1	1
benzene and derivative metabolic process	0.09	0	1	1
regulation of pigment cell differentiation	0.09	0	1	1
hemoglobin metabolic process	0.18	0	1	1
negative regulation of helicase activity	0.09	0	1	1
deoxyribonucleoside metabolic process	0.09	0	1	1
uroporphyrinogen III metabolic process	0.09	0	1	1
ameboidal cell migration	0.18	0	1	1
modification of host morphology or physiology	0.09	0	1	1
immune system development	2.77	2.78	1	1
positive regulation of protein metabolic process	1.02	1.01	1	1
oogenesis	0.18	0.25	1	1
amino sugar metabolic process	0.18	0	1	1
regulation of smooth muscle cell proliferation	0.09	0	1	1
negative regulation of heart contraction	0.09	0	1	1
morphogenesis of a polarized epithelium	0.09	0	1	1
spermatogenesis	1.39	1.26	1	1
stress-activated protein kinase signaling pathway	0.55	0.51	1	1
vitamin D metabolic process	0.09	0	1	1
purine nucleoside metabolic process	0.18	0	1	1
negative regulation of neurological process	0.09	0	1	1
DNA catabolic process	0.18	0	1	1
regulation of muscle cell differentiation	0.09	0	1	1
embryonic axis specification	0.09	0	1	1
DNA damage response, signal transduction by p53 class	0.18	0	1	1
vesicle fusion	0.18	0.25	1	1
cellular carbohydrate catabolic process	0.83	0.76	1	1
formation of immunological synapse	0.09	0	1	1
cell fate specification	0.18	0	1	1
DNA repair	1.94	1.77	1	1
pyrimidine base metabolic process	0.18	0	1	1



pyrimidine nucleoside metabolic process	0.09	0	1	1
translation	2.49	2.53	1	1
movement in host environment	0.18	0	1	1
melanocyte differentiation	0.18	0	1	1
positive regulation of lipid metabolic process	0.09	0	1	1
nucleotide-sugar biosynthetic process	0.09	0	1	1
nucleic acid transport	0.37	0.25	1	1
negative regulation of secretion	0.18	0	1	1
lipid raft organization and biogenesis	0.18	0	1	1
dorsal/ventral pattern formation	0.28	0.25	1	1
mitochondrial membrane organization and biogenesis	0.09	0	1	1
phosphoenolpyruvate-dependent sugar phosphotransfer	0.09	0	1	1
MHC class II biosynthetic process	0.18	0	1	1
proximal/distal pattern formation	0.09	0	1	1
positive regulation of lyase activity	0.09	0	1	1
negative regulation of defense response	0.18	0	1	1
nucleotide-sugar transport	0.09	0	1	1
regulation of cellular biosynthetic process	1.39	1.26	1	1
viral genome replication	0.28	0.25	1	1
positive regulation of cell motility	0.18	0.25	1	1
adaptive immune response (sensu Gnathostomata)	0.74	0.76	1	1
disruption of cells of other organism during symbiotic interaction	0.09	0	1	1
detection of fungus	0.09	0	1	1
response to mercury ion	0.09	0	1	1
catecholamine transport	0.09	0	1	1
long-term memory	0.09	0	1	1
nucleus localization	0.09	0	1	1
ER-nuclear signaling pathway	0.28	0.25	1	1
glycerol metabolic process	0.18	0.25	1	1
rRNA metabolic process	0.28	0.25	1	1
mitochondrial genome maintenance	0.09	0	1	1
endodermal cell fate commitment	0.09	0	1	1
morphogenesis of embryonic epithelium	0.55	0.51	1	1
nucleoside catabolic process	0.09	0	1	1
fatty acid transport	0.09	0	1	1
dicarboxylic acid metabolic process	0.18	0	1	1

respiratory tube development	0.55	0.51	1	1
hormone secretion	0.28	0.25	1	1
male pronucleus formation	0.09	0	1	1
production of molecular mediator of immune response	0.18	0.25	1	1
lipid modification	0.28	0.25	1	1
nucleoside triphosphate metabolic process	0.46	0.51	1	1
neutrophil homeostasis	0.09	0	1	1
T cell homeostasis	0.18	0	1	1
defense response to virus	0.18	0	1	1
biopolymer methylation	0.18	0	1	1
purine base metabolic process	0.09	0	1	1
second-messenger-mediated signaling	2.95	2.78	1	1
posttranscriptional gene silencing	0.09	0	1	1
dopamine transport	0.09	0	1	1
establishment of organelle localization	0.28	0.25	1	1
maintenance of DNA repeat elements	0.09	0	1	1
cytoskeletal anchoring	0.09	0	1	1
ribonucleoside metabolic process	0.18	0	1	1
endothelial cell migration	0.09	0	1	1
thiamin and derivative metabolic process	0.09	0	1	1
RNA catabolic process	0.18	0	1	1
entry into other organism during symbiotic interaction	0.18	0	1	1
nucleobase catabolic process	0.09	0	1	1
protein polymerization	0.55	0.51	1	1
negative regulation of biosynthetic process	0.46	0.25	1	1
water transport	0.09	0	1	1
regulation of fibroblast proliferation	0.18	0.25	1	1
regulation of vasodilation	0.09	0	1	1
peripheral nervous system development	0.28	0.25	1	1
anion homeostasis	0.09	0	1	1
embryonic organ development	0.28	0.25	1	1
choline transport	0.09	0	1	1
lymphocyte proliferation	0.83	0.76	1	1
regulation of GTPase activity	0.46	0.51	1	1
regulation of response to tumor cell	0.09	0	1	1
negative regulation of transport	0.28	0.25	1	1

chemotaxis	1.39	1.26	1	1
tRNA metabolic process	0.46	0.25	1	1
regulation of sensory perception	0.09	0	1	1
regulation of antiviral response	0.09	0	1	1
neural crest cell differentiation	0.18	0	1	1
hormone-mediated signaling	0.09	0	1	1
associative learning	0.18	0.25	1	1
isoprenoid metabolic process	0.18	0.25	1	1
neural tube development	0.37	0.25	1	1
regulation of protein stability	0.18	0	1	1
nuclear body organization and biogenesis	0.09	0	1	1
positive regulation of defense response	0.09	0	1	1
regulation of phosphorus metabolic process	0.65	0.51	1	1
protein maturation	0.09	0	1	1
initiation of viral infection	0.18	0	1	1
intercellular junction assembly	0.18	0.25	1	1
positive regulation of signal transduction	1.39	1.26	1	1
monoamine transport	0.09	0	1	1
chromosome condensation	0.18	0.25	1	1
pH reduction	0.09	0	1	1
gland development	0.28	0.25	1	1
male sex differentiation	0.28	0.25	1	1
indole derivative metabolic process	0.09	0	1	1
oxygen transport	0.09	0	1	1
sterol transport	0.18	0	1	1
pancreas development	0.09	0	1	1
negative regulation of cell proliferation	2.86	2.78	1	1
enzyme linked receptor protein signaling pathway	3.69	3.79	1	1
carboxylic acid transport	0.55	0.51	1	1
nucleoside diphosphate metabolic process	0.09	0	1	1
brown fat cell differentiation	0.09	0	1	1
heme metabolic process	0.09	0	1	1
modification of structure of other organism during symbic	0.09	0	1	1
smooth muscle cell differentiation	0.18	0	1	1
vitamin B6 metabolic process	0.09	0	1	1
cation homeostasis	1.75	1.52	1	1

cobalamin transport	0.09	0	1	1
purine nucleotide metabolic process	0.65	0.51	1	1
macrophage activation	0.28	0.25	1	1
intermediate filament-based process	0.09	0	1	1
gut development	0.28	0.25	1	1
cellular protein complex disassembly	0.09	0	1	1
nucleotide catabolic process	0.09	0	1	1
negative regulation of organ size	0.09	0	1	1
sulfate assimilation	0.09	0	1	1
negative regulation of cell adhesion	0.18	0	1	1
lipid raft localization	0.09	0	1	1
aminophospholipid transport	0.18	0	1	1
leukocyte migration	0.65	0.51	1	1
embryo implantation	0.09	0	1	1
regulation of protein complex assembly	0.09	0	1	1
proteolysis	6.37	6.31	1	1
integrin-mediated signaling pathway	0.55	0.51	1	1
nucleotide biosynthetic process	1.48	1.26	1	1
nucleobase transport	0.09	0	1	1
porphyrin biosynthetic process	0.09	0	1	1
response to starvation	0.09	0	1	1
regulation of endothelial cell proliferation	0.18	0.25	1	1
regulation of immune effector process	0.09	0	1	1
regulation of protein transport	0.18	0	1	1
interphase	0.74	0.51	1	1
pyrimidine nucleotide metabolic process	0.28	0.25	1	1
vesicle localization	0.18	0.25	1	1
coenzyme catabolic process	0.18	0	1	1
vesicle docking	0.46	0.25	1	1
B cell homeostasis	0.09	0	1	1
menstrual cycle process	0.18	0.25	1	1
genitalia development	0.18	0.25	1	1
antigen processing and presentation of lipid antigen via I	0.09	0	1	1
focal adhesion formation	0.18	0	1	1
positive regulation of response to biotic stimulus	0.09	0	1	1
positive regulation of cell adhesion	0.09	0	1	1

maintenance of cellular protein localization	0.09	0	1	1
ethanol oxidation	0.09	0	1	1
RNA-mediated gene silencing	0.09	0	1	1
monosaccharide transport	0.28	0.25	1	1

Gene Ontology : biological process. Level: 7	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
protein homooligomerization	0.11	1.55	0.005359601	1
biomineral formation	0.76	2.8	0.009100373	1
double-strand break repair	0.11	1.24	0.01759404	1
visual learning	0.11	0.93	0.05560903	1
cellular protein catabolic process	1.95	4.04	0.05866208	1
heparan sulfate proteoglycan metabolic process	0	0.62	0.06684507	1
adult heart development	0	0.62	0.06684507	1
epithelial to mesenchymal transition	0	0.62	0.06684507	1
calcium ion-dependent exocytosis	0	0.62	0.06684507	1
recombinational repair	0	0.62	0.06684507	1
positive regulation of phospholipase A2 activity	0	0.62	0.06684507	1
protein amino acid phosphorylation	9.87	6.52	0.07142957	1
regulation of protein kinase activity	2.28	4.35	0.07548919	1
intracellular protein transport	3.69	6.21	0.07890425	1
membrane lipid catabolic process	0.22	0.93	0.1126315	1
cyclic nucleotide biosynthetic process	0.22	0.93	0.1126315	1
acute-phase response	0.22	0.93	0.1126315	1
inorganic anion transport	1.19	2.48	0.1153819	1
DNA-dependent DNA replication	0.65	1.55	0.1648446	1
muscle fiber development	0.65	1.55	0.1648446	1
positive regulation of epithelial cell proliferation	0.11	0.62	0.1660901	1
polysaccharide biosynthetic process	0.11	0.62	0.1660901	1
detection of visible light	0.11	0.62	0.1660901	1
detection of light stimulus during sensory perception	0.11	0.62	0.1660901	1
endoderm development	0.11	0.62	0.1660901	1
fatty acid metabolic process	1.74	3.11	0.1721741	1
positive regulation of nucleobase, nucleoside, nucleotide	4.34	2.48	0.17787	1
cGMP metabolic process	0.33	0.93	0.1832001	1
glycolipid metabolic process	0.33	0.93	0.1832001	1
embryonic development (sensu Mammalia)	0.76	0	0.2005548	1
amino acid biosynthetic process	0.43	1.24	0.2160468	1
ear development	0.43	1.24	0.2160468	1
cell growth	2.17	0.93	0.22816	1
mRNA processing	2.17	0.93	0.22816	1
peptidoglycan catabolic process	0	0.31	0.2588424	1

apical junction assembly	0	0.31	0.2588424	1
germinal center formation	0	0.31	0.2588424	1
aspartate family amino acid metabolic process	0	0.31	0.2588424	1
negative regulation of ion transport	0	0.31	0.2588424	1
photoreceptor cell maintenance	0	0.31	0.2588424	1
behavioral response to cocaine	0	0.31	0.2588424	1
lipid phosphorylation	0	0.31	0.2588424	1
baroreceptor response to lowering of blood pressure	0	0.31	0.2588424	1
bile acid metabolic process	0	0.31	0.2588424	1
peroxisomal transport	0	0.31	0.2588424	1
negative regulation of cellular catabolic process	0	0.31	0.2588424	1
biogenic amine catabolic process	0	0.31	0.2588424	1
cellular extravasation	0	0.31	0.2588424	1
actin filament severing	0	0.31	0.2588424	1
positive regulation of vasoconstriction	0	0.31	0.2588424	1
positive regulation of cellular catabolic process	0	0.31	0.2588424	1
defense response to Gram-positive bacterium	0	0.31	0.2588424	1
receptor guanylyl cyclase signaling pathway	0	0.31	0.2588424	1
prostate gland development	0	0.31	0.2588424	1
cellular polysaccharide catabolic process	0	0.31	0.2588424	1
regulation of Notch signaling pathway	0	0.31	0.2588424	1
peptide amidation	0	0.31	0.2588424	1
salivary gland development	0	0.31	0.2588424	1
centrosome cycle	0	0.31	0.2588424	1
antibacterial humoral response	0	0.31	0.2588424	1
leading edge cell differentiation	0	0.31	0.2588424	1
metabotropic glutamate receptor signaling pathway	0	0.31	0.2588424	1
DNA duplex unwinding	0	0.31	0.2588424	1
antifungal humoral response	0	0.31	0.2588424	1
mitotic recombination	0	0.31	0.2588424	1
bilirubin conjugation	0	0.31	0.2588424	1
non-recombinational repair	0	0.31	0.2588424	1
positive regulation of nitric oxide biosynthetic process	0	0.31	0.2588424	1
response to hydrogen peroxide	0	0.31	0.2588424	1
norepinephrine-epinephrine regulation of blood pressure	0	0.31	0.2588424	1
ER overload response	0	0.31	0.2588424	1

extracellular polysaccharide metabolic process	0	0.31	0.2588424	1
regulation of urothelial cell proliferation	0	0.31	0.2588424	1
regulation of vesicle fusion	0	0.31	0.2588424	1
glycoprotein biosynthetic process	2.39	1.24	0.2636428	1
dicarboxylic acid transport	0.22	0.62	0.2765711	1
transmembrane receptor protein tyrosine phosphatase s	0.22	0.62	0.2765711	1
glucan metabolic process	0.22	0.62	0.2765711	1
development of primary female sexual characteristics	0.22	0.62	0.2765711	1
induction	0.22	0.62	0.2765711	1
glycoprotein catabolic process	0.22	0.62	0.2765711	1
acylglycerol metabolic process	0.22	0.62	0.2765711	1
frizzled signaling pathway	0.22	0.62	0.2765711	1
photoreceptor cell development	0.22	0.62	0.2765711	1
glutamine family amino acid metabolic process	0.22	0.62	0.2765711	1
proteoglycan biosynthetic process	0.22	0.62	0.2765711	1
aminoglycan biosynthetic process	0.22	0.62	0.2765711	1
negative regulation of progression through cell cycle	3.04	4.35	0.2825478	1
brain development	2.06	3.11	0.2871908	1
ectoderm development	1.84	0.93	0.315395	1
hexose metabolic process	1.84	0.93	0.315395	1
microtubule cytoskeleton organization and biogenesis	1.19	0.31	0.3167569	1
positive regulation of immune response	1.19	0.31	0.3167569	1
metal ion transport	5.31	6.83	0.3291208	1
ubiquitin cycle	4.45	3.11	0.3317314	1
dopamine receptor signaling pathway	0.54	0	0.3356444	1
pyridine nucleotide metabolic process	0.54	0	0.3356444	1
programmed cell death	8.35	6.52	0.3371278	1
phospholipid metabolic process	0.87	1.55	0.3393898	1
glycosaminoglycan metabolic process	0.43	0.93	0.383902	1
gonad development	0.43	0.93	0.383902	1
gliogenesis	0.43	0.93	0.383902	1
di-, tri-valent inorganic cation transport	2.17	3.11	0.3977976	1
negative regulation of nucleobase, nucleoside, nucleotid	4.56	3.42	0.4273414	1
eye development	0.54	0.93	0.4337513	1
calcium-mediated signaling	0.54	0.93	0.4337513	1
regulation of synaptic transmission	0.54	0.93	0.4337513	1



lipoprotein biosynthetic process	0.54	0.93	0.4337513	1
regulation of protein catabolic process	0.11	0.31	0.4508398	1
T-helper 1 type immune response	0.11	0.31	0.4508398	1
steroid catabolic process	0.11	0.31	0.4508398	1
S phase	0.11	0.31	0.4508398	1
regulation of smoothened signaling pathway	0.11	0.31	0.4508398	1
cytolysis	0.11	0.31	0.4508398	1
polyisoprenoid metabolic process	0.11	0.31	0.4508398	1
lymphocyte activation during immune response	0.11	0.31	0.4508398	1
myeloid leukocyte mediated immunity	0.11	0.31	0.4508398	1
regulation of macrophage activation	0.11	0.31	0.4508398	1
glycerolipid biosynthetic process	0.11	0.31	0.4508398	1
neutral lipid biosynthetic process	0.11	0.31	0.4508398	1
Mo-molybdopterin cofactor metabolic process	0.11	0.31	0.4508398	1
blastoderm segmentation	0.11	0.31	0.4508398	1
leukocyte degranulation	0.11	0.31	0.4508398	1
formation of primary germ layer	0.11	0.31	0.4508398	1
positive regulation of fibroblast proliferation	0.11	0.31	0.4508398	1
cardiac cell differentiation	0.11	0.31	0.4508398	1
sulfur amino acid metabolic process	0.11	0.31	0.4508398	1
molybdopterin cofactor biosynthetic process	0.11	0.31	0.4508398	1
neuromuscular synaptic transmission	0.11	0.31	0.4508398	1
positive regulation of cell migration	0.11	0.31	0.4508398	1
regulation of RNA metabolic process	0.11	0.31	0.4508398	1
lipoprotein catabolic process	0.11	0.31	0.4508398	1
retinoid metabolic process	0.11	0.31	0.4508398	1
retinoic acid metabolic process	0.11	0.31	0.4508398	1
lipopolysaccharide metabolic process	0.11	0.31	0.4508398	1
peptide hormone secretion	0.11	0.31	0.4508398	1
nuclear transport	1.52	2.17	0.4528719	1
steroid hormone receptor signaling pathway	0.87	0.31	0.4605045	1
monosaccharide catabolic process	0.98	0.31	0.4680323	1
nucleocytoplasmic transport	1.63	2.17	0.4732204	1
generation of neurons	5.97	4.66	0.482285	1
regulation of transcription	22.23	24.22	0.4872453	1
regulation of cell shape	0.76	1.24	0.4890871	1

regulation of T cell activation	0.76	1.24	0.4890871	1
metanephros development	0.76	1.24	0.4890871	1
phosphoinositide-mediated signaling	1.08	1.55	0.5539047	1
Ras protein signal transduction	2.93	2.17	0.5560774	1
regulation of epithelial cell differentiation	0.33	0	0.5728754	1
aerobic respiration	0.33	0	0.5728754	1
positive regulation of protein secretion	0.33	0	0.5728754	1
regulation of chemotaxis	0.33	0	0.5728754	1
positive chemotaxis	0.33	0	0.5728754	1
organic anion transport	0.33	0	0.5728754	1
pinocytosis	0.33	0	0.5728754	1
positive regulation of progression through cell cycle	0.33	0	0.5728754	1
serine family amino acid metabolic process	0.33	0	0.5728754	1
pyruvate metabolic process	0.33	0	0.5728754	1
unfolded protein response	0.33	0	0.5728754	1
folic acid and derivative metabolic process	0.33	0	0.5728754	1
monovalent inorganic cation homeostasis	0.33	0	0.5728754	1
somitogenesis	0.33	0	0.5728754	1
monosaccharide biosynthetic process	0.33	0	0.5728754	1
peptide cross-linking	0.33	0	0.5728754	1
regulation of cytokine secretion	0.33	0	0.5728754	1
oligosaccharide biosynthetic process	0.33	0	0.5728754	1
amino acid activation	0.33	0	0.5728754	1
gastrulation (sensu Deuterostomia)	0.33	0	0.5728754	1
oxidative phosphorylation	0.33	0	0.5728754	1
protein tetramerization	0.33	0	0.5728754	1
ribonucleoside monophosphate metabolic process	0.33	0	0.5728754	1
nucleoside monophosphate biosynthetic process	0.33	0	0.5728754	1
mitochondrial transport	0.43	0	0.5778086	1
regulation of Wnt receptor signaling pathway	0.43	0	0.5778086	1
negative regulation of cell size	0.43	0	0.5778086	1
base-excision repair	0.43	0	0.5778086	1
protein amino acid ADP-ribosylation	0.43	0	0.5778086	1
nucleotide-excision repair	0.43	0	0.5778086	1
biogenic amine biosynthetic process	0.33	0.62	0.6088771	1
ensheathment of neurons	0.33	0.62	0.6088771	1

negative regulation of lymphocyte activation	0.33	0.62	0.6088771	1
regulation of endocytosis	0.33	0.62	0.6088771	1
gamma-aminobutyric acid signaling pathway	0.33	0.62	0.6088771	1
cell projection organization and biogenesis	4.01	3.11	0.610386	1
RNA splicing	1.95	1.24	0.6229159	1
protein amino acid dephosphorylation	1.95	2.48	0.6505829	1
translational initiation	0.43	0.62	0.6522511	1
amino acid catabolic process	0.43	0.62	0.6522511	1
mesoderm development	0.43	0.62	0.6522511	1
steroid biosynthetic process	0.43	0.62	0.6522511	1
cell cycle checkpoint	0.65	0.31	0.6844136	1
determination of left/right symmetry	0.65	0.31	0.6844136	1
cartilage development	0.65	0.31	0.6844136	1
regulation of DNA metabolic process	0.65	0.31	0.6844136	1
leukocyte chemotaxis	0.76	0.31	0.6880704	1
hemopoietic or lymphoid organ development	3.04	3.42	0.7128128	1
blood vessel development	3.36	2.8	0.7159592	1
membrane lipid biosynthetic process	0.76	0.93	0.7247405	1
positive regulation of cellular biosynthetic process	0.76	0.93	0.7247405	1
actin cytoskeleton organization and biogenesis	3.8	3.11	0.7288196	1
ribonucleotide biosynthetic process	0.98	0.62	0.738273	1
transmembrane receptor protein serine/threonine kinase	1.08	0.62	0.7413155	1
embryonic limb morphogenesis	1.08	0.62	0.7413155	1
antimicrobial humoral response (sensu Vertebrata)	0.98	1.24	0.7507852	1
transcription, DNA-dependent	21.69	22.67	0.7544534	1
cytokine biosynthetic process	1.08	1.24	0.7650119	1
neuropeptide signaling pathway	1.3	1.55	0.7811147	1
striated muscle development	1.63	1.86	0.8024785	1
di-, tri-valent inorganic cation homeostasis	1.74	1.86	0.8106393	1
cyclic-nucleotide-mediated signaling	1.95	1.55	0.8116982	1
establishment and/or maintenance of chromatin architec	2.6	2.17	0.8360549	1
transmembrane receptor protein tyrosine kinase signalin	2.93	3.11	0.85016	1
tRNA processing	0.33	0.31	1	1
synaptic vesicle endocytosis	0.11	0	1	1
JAK-STAT cascade	0.43	0.31	1	1
pyrimidine ribonucleotide metabolic process	0.22	0.31	1	1

tissue regeneration	0.11	0	1	1
negative regulation of endothelial cell proliferation	0.22	0.31	1	1
long-chain fatty acid transport	0.11	0	1	1
ribonucleoside triphosphate metabolic process	0.54	0.62	1	1
regulation of melanocyte differentiation	0.11	0	1	1
mRNA catabolic process	0.11	0	1	1
monovalent inorganic cation transport	3.69	3.73	1	1
posttranslational protein folding	0.22	0	1	1
pyridoxine metabolic process	0.11	0	1	1
mRNA modification	0.11	0	1	1
lipid raft distribution	0.11	0	1	1
mesonephros development	0.11	0	1	1
pyrimidine base biosynthetic process	0.22	0	1	1
MAPKKK cascade	1.84	1.86	1	1
heme oxidation	0.11	0	1	1
mammary gland development	0.22	0	1	1
hexose transport	0.33	0.31	1	1
pyrimidine nucleotide biosynthetic process	0.33	0.31	1	1
chemokine metabolic process	0.11	0	1	1
thiamin metabolic process	0.11	0	1	1
regulation of G-protein coupled receptor protein signaling	0.54	0.31	1	1
regulation of translation	1.52	1.55	1	1
positive regulation of smooth muscle cell proliferation	0.11	0	1	1
Golgi vesicle transport	0.87	0.62	1	1
negative regulation of cellular biosynthetic process	0.43	0.31	1	1
ubiquinone metabolic process	0.11	0	1	1
odontogenesis	0.33	0.31	1	1
M phase of meiotic cell cycle	0.76	0.62	1	1
negative regulation of fibroblast proliferation	0.11	0	1	1
interphase of mitotic cell cycle	0.87	0.62	1	1
glycerol-3-phosphate metabolic process	0.11	0	1	1
G2 phase	0.22	0	1	1
entry into host	0.22	0	1	1
negative regulation of epithelial cell proliferation	0.22	0	1	1
regulation of sensory perception of pain	0.11	0	1	1
I-kappaB kinase/NF-kappaB cascade	1.84	1.86	1	1

cytoskeleton-dependent intracellular transport	1.41	1.24	1	1
androgen metabolic process	0.22	0.31	1	1
regulation of progression through mitotic cell cycle	0.22	0.31	1	1
pyrimidine nucleoside triphosphate metabolic process	0.22	0.31	1	1
embryonic epithelial tube formation	0.43	0.31	1	1
muscle maintenance	0.22	0	1	1
embryonic skeletal development	0.11	0	1	1
single strand break repair	0.22	0	1	1
regulation of antiviral response by host	0.11	0	1	1
protein amino acid alkylation	0.22	0	1	1
protein processing	1.08	0.93	1	1
regulation of neurotransmitter levels	1.74	1.55	1	1
protein amino acid deacetylation	0.33	0.31	1	1
pyrimidine transport	0.11	0	1	1
positive regulation of protein complex assembly	0.11	0	1	1
nucleoside triphosphate biosynthetic process	0.54	0.62	1	1
thyroid hormone metabolic process	0.11	0	1	1
regulation of innate immune response	0.11	0	1	1
regulation of protein modification	0.11	0	1	1
ribonucleoside diphosphate metabolic process	0.11	0	1	1
pyrimidine nucleoside catabolic process	0.11	0	1	1
cell killing	0.33	0.31	1	1
mitochondrial DNA metabolic process	0.11	0	1	1
ethanolamine and derivative metabolic process	0.22	0	1	1
C21-steroid hormone metabolic process	0.11	0	1	1
alpha-beta T cell activation	0.43	0.31	1	1
negative regulation of fat cell differentiation	0.11	0	1	1
entry into cell of other organism during symbiotic interacti	0.22	0	1	1
leg morphogenesis	0.11	0	1	1
hemoglobin biosynthetic process	0.22	0	1	1
RNA-mediated posttranscriptional gene silencing	0.11	0	1	1
activation of plasma proteins during acute inflammatory	0.43	0.31	1	1
metal ion homeostasis	1.84	1.86	1	1
B cell proliferation	0.33	0.31	1	1
anterior/posterior axis specification	0.11	0	1	1
neurotransmitter receptor metabolic process	0.11	0	1	1

neural tube patterning	0.11	0	1	1
regulation of leukocyte mediated immunity	0.11	0	1	1
regulation of amino acid metabolic process	0.54	0.62	1	1
vesicle docking during exocytosis	0.43	0.31	1	1
adrenal gland development	0.11	0	1	1
hindlimb morphogenesis	0.22	0	1	1
regulation of exocytosis	0.33	0.31	1	1
positive regulation of fat cell differentiation	0.11	0	1	1
serotonin receptor signaling pathway	0.11	0	1	1
purine nucleoside diphosphate metabolic process	0.11	0	1	1
receptor-mediated endocytosis	0.87	0.62	1	1
positive regulation of immune effector process	0.11	0	1	1
pentose metabolic process	0.11	0	1	1
protein amino acid acylation	0.22	0	1	1
regulation of nucleotide metabolic process	0.22	0.31	1	1
skeletal morphogenesis	0.11	0	1	1
antigen processing and presentation, exogenous lipid ar	0.11	0	1	1
T-helper 2 type immune response	0.11	0	1	1
embryonic gut development	0.22	0.31	1	1
glucosamine metabolic process	0.22	0	1	1
ectodermal gut development	0.22	0	1	1
digestive tract morphogenesis	0.22	0.31	1	1
rRNA processing	0.22	0.31	1	1
menstrual cycle phase	0.22	0.31	1	1
estrogen metabolic process	0.22	0.31	1	1
oocyte differentiation	0.22	0	1	1
negative regulation of protein transport	0.22	0	1	1
somatic cell DNA recombination	0.22	0	1	1
sphingolipid metabolic process	0.76	0.62	1	1
indole derivative biosynthetic process	0.11	0	1	1
establishment of nucleus localization	0.11	0	1	1
forelimb morphogenesis	0.22	0	1	1
phospholipid dephosphorylation	0.22	0	1	1
tubulin folding	0.22	0	1	1
lipid glycosylation	0.11	0	1	1
acetyl-CoA catabolic process	0.22	0	1	1

synaptic transmission, cholinergic	0.11	0	1	1
vacuolar transport	0.33	0.31	1	1
embryonic organ morphogenesis	0.33	0.31	1	1
ATP-dependent proteolysis	0.11	0	1	1
sterol metabolic process	0.54	0.62	1	1
positive regulation of protein transport	0.11	0	1	1
cholesterol transport	0.22	0	1	1
establishment of vesicle localization	0.22	0.31	1	1
germ-line stem cell division	0.11	0	1	1
endosome transport	0.54	0.31	1	1
glycolate metabolic process	0.11	0	1	1
telomere organization and biogenesis	0.11	0	1	1
dorsal/ventral axis specification	0.11	0	1	1
amino acid transport	0.33	0.31	1	1
regulation of lipid kinase activity	0.22	0	1	1
gonadotropin secretion	0.11	0	1	1
purine nucleotide biosynthetic process	0.76	0.62	1	1
anaphase	0.11	0	1	1
rRNA modification	0.11	0	1	1
regulation of synapse structure and activity	0.22	0	1	1
negative regulation of protein secretion	0.11	0	1	1
purine base biosynthetic process	0.11	0	1	1
peptidyl-amino acid modification	1.52	1.55	1	1
positive regulation of inflammatory response	0.11	0	1	1
coenzyme A metabolic process	0.11	0	1	1
oogenesis (sensu Mammalia)	0.11	0	1	1
interleukin-1 secretion	0.22	0	1	1
protein kinase B signaling cascade	0.11	0	1	1
nucleoside phosphate metabolic process	0.33	0.31	1	1
frizzled-2 signaling pathway	0.11	0	1	1
protein maturation via proteolysis	0.11	0	1	1
nucleoside diphosphate biosynthetic process	0.11	0	1	1
sister chromatid segregation	0.22	0.31	1	1
disruption by symbiont of host cells	0.11	0	1	1
gamma-delta T cell activation	0.11	0	1	1
catecholamine metabolic process	0.54	0.62	1	1

RNA 3'-end processing	0.22	0	1	1
regulation of small GTPase mediated signal transduction	2.17	2.17	1	1
uracil metabolic process	0.11	0	1	1
translational elongation	0.11	0	1	1
negative regulation of inflammatory response	0.22	0	1	1
acetylcholine receptor signaling, muscarinic pathway	0.11	0	1	1
cAMP metabolic process	0.22	0.31	1	1
isoprenoid biosynthetic process	0.11	0	1	1
regulation of cytokine and chemokine mediated signaling	0.11	0	1	1
indolalkylamine metabolic process	0.11	0	1	1
positive regulation of GTPase activity	0.11	0	1	1
positive regulation of response to tumor cell	0.11	0	1	1
polarized epithelial cell differentiation	0.11	0	1	1
di-, tri-valent inorganic anion homeostasis	0.11	0	1	1
M phase of mitotic cell cycle	1.63	1.55	1	1
spermatid differentiation	0.11	0	1	1
protein modification by small protein conjugation	0.65	0.62	1	1
re-entry into mitotic cell cycle	0.22	0	1	1
regulation of lymphocyte proliferation	0.65	0.62	1	1
thiamin diphosphate metabolic process	0.11	0	1	1
thiamin and derivative biosynthetic process	0.11	0	1	1
RNA transport	0.43	0.31	1	1
deoxyribonucleoside catabolic process	0.11	0	1	1
development of primary male sexual characteristics	0.33	0.31	1	1
somatic diversification of immune receptors	0.22	0.31	1	1
neural plate morphogenesis	0.33	0.31	1	1
tricarboxylic acid cycle intermediate metabolic process	0.43	0.31	1	1
purine transport	0.11	0	1	1
chondroitin sulfate proteoglycan metabolic process	0.11	0	1	1
metaphase	0.11	0	1	1
organic cation transport	0.22	0	1	1
neural crest cell development	0.22	0	1	1
regulation of blood coagulation	0.22	0	1	1
regulation of smooth muscle cell differentiation	0.11	0	1	1
oogenesis stage	0.11	0	1	1
purine ribonucleotide metabolic process	0.65	0.62	1	1



butyrate metabolic process	0.11	0	1	1
lymphocyte mediated immunity	0.76	0.62	1	1
PML body organization and biogenesis	0.11	0	1	1
positive regulation of lymphocyte activation	0.65	0.62	1	1
regulation of hormone secretion	0.11	0	1	1
positive regulation of vasodilation	0.11	0	1	1
protein amino acid sulfation	0.22	0	1	1
uroporphyrinogen III biosynthetic process	0.11	0	1	1
protein stabilization	0.22	0	1	1
platelet activation	0.11	0	1	1
negative regulation of muscle cell differentiation	0.11	0	1	1
regulation of B cell activation	0.54	0.31	1	1
tissue morphogenesis	0.76	0.62	1	1
positive regulation of ion transport	0.11	0	1	1
lung development	0.54	0.62	1	1
histidine family amino acid metabolic process	0.22	0.31	1	1
protein heterooligomerization	0.11	0	1	1
establishment of cell polarity	0.22	0	1	1
midgut development	0.11	0	1	1
pyrimidine nucleotide-sugar transport	0.11	0	1	1
membrane protein ectodomain proteolysis	0.11	0	1	1
modification of cellular component in other organism dur	0.11	0	1	1
pyrimidine base catabolic process	0.11	0	1	1
sister chromatid cohesion	0.22	0	1	1
aromatic amino acid family metabolic process	0.22	0.31	1	1
RNA editing	0.22	0	1	1
benzoate metabolic process	0.11	0	1	1
phagocytosis	0.33	0.31	1	1
specification of organ identity	0.22	0.31	1	1
T cell proliferation	0.98	0.93	1	1
modification by symbiont of host structure	0.11	0	1	1
vitamin B6 biosynthetic process	0.11	0	1	1
formate metabolic process	0.11	0	1	1
tricarboxylic acid transport	0.11	0	1	1
branched chain family amino acid metabolic process	0.22	0	1	1
conditioned taste aversion	0.11	0	1	1

beta-amyloid metabolic process	0.11	0	1	1
cyclic nucleotide catabolic process	0.11	0	1	1
regulation of carbohydrate biosynthetic process	0.11	0	1	1
nerve-nerve synaptic transmission	0.33	0.31	1	1
immunoglobulin production	0.22	0.31	1	1
purine ribonucleoside metabolic process	0.22	0	1	1
pyrimidine deoxyribonucleoside metabolic process	0.11	0	1	1
segment specification	0.22	0	1	1
regulation of phosphate metabolic process	0.76	0.62	1	1
monocarboxylic acid transport	0.11	0	1	1
establishment and/or maintenance of apical/basal cell pc	0.11	0	1	1
quinone cofactor biosynthetic process	0.11	0	1	1
regulation of immune response to tumor cell	0.11	0	1	1
purine nucleoside triphosphate metabolic process	0.54	0.62	1	1

Gene Ontology : biological process. Level: 8	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
ossification	0.97	3.45	0.01768197	1
proteolysis involved in cellular protein catabolic process	2.36	4.98	0.0559508	1
activation of phospholipase A2	0	0.77	0.07058603	1
double-strand break repair via homologous recombination	0	0.77	0.07058603	1
heparan sulfate proteoglycan biosynthetic process	0	0.77	0.07058603	1
DNA strand elongation during DNA replication	0	0.77	0.07058603	1
protein targeting	2.92	5.36	0.07934332	1
positive regulation of transcription	5.42	2.68	0.08691233	1
skeletal muscle development	0.83	2.3	0.09400779	1
regulation of programmed cell death	7.78	4.98	0.1574026	1
cell cycle arrest	1.39	2.68	0.1738405	1
BMP signaling pathway	0.14	0.77	0.1744102	1
detection of light stimulus during visual perception	0.14	0.77	0.1744102	1
activated T cell proliferation	0.14	0.77	0.1744102	1
catecholamine biosynthetic process	0.14	0.77	0.1744102	1
diacylglycerol metabolic process	0.14	0.77	0.1744102	1
glycolipid catabolic process	0.14	0.77	0.1744102	1
positive regulation of small GTPase mediated signal transduction	0.14	0.77	0.1744102	1
cGMP biosynthetic process	0.14	0.77	0.1744102	1
epidermis development	2.22	0.77	0.1800566	1
regulation of cyclin-dependent protein kinase activity	0.42	1.15	0.195049	1
regulation of synaptic plasticity	0.42	1.15	0.195049	1
glial cell differentiation	0.42	1.15	0.195049	1
intracellular protein transport across a membrane	0.42	1.15	0.195049	1
sodium ion transport	1.53	0.38	0.1993123	1
inner ear development	0.56	1.53	0.219653	1
apoptosis	10.56	7.66	0.2235061	1
neuron differentiation	6.81	4.6	0.2334345	1
phosphate transport	1.25	2.3	0.2451004	1
protein amino acid glycosylation	2.92	1.53	0.2607733	1
regulation of cell growth	2.08	0.77	0.2657904	1
positive regulation of Notch signaling pathway	0	0.38	0.266055	1
asparagine metabolic process	0	0.38	0.266055	1
regulation of DNA ligation	0	0.38	0.266055	1
phagocytosis, recognition	0	0.38	0.266055	1

vasoconstriction of artery during baroreceptor response	0	0.38	0.266055	1
inositol phosphate-mediated signaling	0	0.38	0.266055	1
low-density lipoprotein catabolic process	0	0.38	0.266055	1
bile acid biosynthetic process	0	0.38	0.266055	1
mesoderm morphogenesis	0	0.38	0.266055	1
fatty acid desaturation	0	0.38	0.266055	1
actomyosin structure organization and biogenesis	0	0.38	0.266055	1
bile acid catabolic process	0	0.38	0.266055	1
transcription from RNA polymerase I promoter	0	0.38	0.266055	1
regulation of rhodopsin gene activity	0	0.38	0.266055	1
catecholamine catabolic process	0	0.38	0.266055	1
platelet activating factor metabolic process	0	0.38	0.266055	1
DNA replication initiation	0	0.38	0.266055	1
aspartate family amino acid biosynthetic process	0	0.38	0.266055	1
phospholipid catabolic process	0	0.38	0.266055	1
phospholipid transfer to membrane	0	0.38	0.266055	1
antibacterial humoral response (sensu Vertebrata)	0	0.38	0.266055	1
centrosome separation	0	0.38	0.266055	1
protein deglycosylation	0	0.38	0.266055	1
glucan catabolic process	0	0.38	0.266055	1
ventricular system development	0	0.38	0.266055	1
increased strength of heart contraction by epinephrine-n	0	0.38	0.266055	1
inductive cell-cell signaling	0	0.38	0.266055	1
double-strand break repair via nonhomologous end joini	0	0.38	0.266055	1
DNA unwinding during replication	0	0.38	0.266055	1
positive regulation of vesicle fusion	0	0.38	0.266055	1
periodic partitioning	0	0.38	0.266055	1
positive regulation of urothelial cell proliferation	0	0.38	0.266055	1
transcription from mitochondrial promoter	0	0.38	0.266055	1
antifungal humoral response (sensu Vertebrata)	0	0.38	0.266055	1
positive regulation of heart contraction rate by epinephriri	0	0.38	0.266055	1
DNA damage induced protein phosphorylation	0	0.38	0.266055	1
striated muscle cell differentiation	0	0.38	0.266055	1
protein deubiquitination	0	0.38	0.266055	1
galactolipid metabolic process	0	0.38	0.266055	1
sterol catabolic process	0	0.38	0.266055	1

extracellular polysaccharide biosynthetic process	0	0.38	0.266055	1
lipopolysaccharide biosynthetic process	0	0.38	0.266055	1
negative regulation of macrophage activation	0	0.38	0.266055	1
transcription from RNA polymerase II promoter	10.28	7.66	0.2689963	1
sphingolipid catabolic process	0.28	0.77	0.2889035	1
glycosaminoglycan biosynthetic process	0.28	0.77	0.2889035	1
negative regulation of T cell activation	0.28	0.77	0.2889035	1
chloride transport	0.28	0.77	0.2889035	1
regulation of transcription factor activity	0.28	0.77	0.2889035	1
glycerophospholipid metabolic process	0.28	0.77	0.2889035	1
nuclear export	0.28	0.77	0.2889035	1
glutamine metabolic process	0.28	0.77	0.2889035	1
glycogen metabolic process	0.28	0.77	0.2889035	1
female gonad development	0.28	0.77	0.2889035	1
post-Golgi vesicle-mediated transport	0.28	0.77	0.2889035	1
eye development (sensu Vertebrata)	0.28	0.77	0.2889035	1
hexose catabolic process	1.25	0.38	0.3055197	1
chromatin assembly or disassembly	0.97	1.92	0.3204053	1
G-protein signaling, coupled to IP3 second messenger (i	0.97	1.92	0.3204053	1
interleukin-6 biosynthetic process	0.69	0	0.3328018	1
transforming growth factor beta receptor signaling pathw	0.69	0	0.3328018	1
transcription initiation	0.69	0	0.3328018	1
positive regulation of protein kinase activity	2.08	3.07	0.3491708	1
actin filament organization	0.83	0	0.3504891	1
calcium ion transport	2.22	3.45	0.3576195	1
protein autoprocessing	0.56	1.15	0.3909792	1
icosanoid metabolic process	0.56	1.15	0.3909792	1
ear morphogenesis	0.56	1.15	0.3909792	1
negative regulation of protein kinase activity	0.69	1.15	0.4449706	1
protein amino acid lipidation	0.69	1.15	0.4449706	1
activation of immune response	1.11	0.38	0.4582135	1
glutamine family amino acid biosynthetic process	0.14	0.38	0.4615241	1
male gonad development	0.14	0.38	0.4615241	1
S phase of mitotic cell cycle	0.14	0.38	0.4615241	1
negative regulation of progression through mitotic cell cy	0.14	0.38	0.4615241	1
mast cell mediated immunity	0.14	0.38	0.4615241	1

regulation of receptor mediated endocytosis	0.14	0.38	0.4615241	1
interferon-gamma biosynthetic process	0.14	0.38	0.4615241	1
regulation of gliogenesis	0.14	0.38	0.4615241	1
terpenoid metabolic process	0.14	0.38	0.4615241	1
insulin secretion	0.14	0.38	0.4615241	1
cAMP biosynthetic process	0.14	0.38	0.4615241	1
ARF protein signal transduction	0.14	0.38	0.4615241	1
intra-Golgi vesicle-mediated transport	0.14	0.38	0.4615241	1
insulin-like growth factor receptor signaling pathway	0.14	0.38	0.4615241	1
androgen biosynthetic process	0.14	0.38	0.4615241	1
Mo-molybdopterin cofactor biosynthetic process	0.14	0.38	0.4615241	1
regulation of JAK-STAT cascade	0.14	0.38	0.4615241	1
sulfur amino acid biosynthetic process	0.14	0.38	0.4615241	1
synaptic transmission, dopaminergic	0.14	0.38	0.4615241	1
T cell activation during immune response	0.14	0.38	0.4615241	1
Rac protein signal transduction	0.14	0.38	0.4615241	1
regulation of RNA stability	0.14	0.38	0.4615241	1
natural killer cell mediated immunity	0.14	0.38	0.4615241	1
aromatic amino acid family catabolic process	0.14	0.38	0.4615241	1
RNA splicing, via endonucleolytic cleavage and ligation	0.14	0.38	0.4615241	1
transcription from RNA polymerase III promoter	0.14	0.38	0.4615241	1
acidic amino acid transport	0.14	0.38	0.4615241	1
triacylglycerol metabolic process	0.14	0.38	0.4615241	1
L-phenylalanine metabolic process	0.14	0.38	0.4615241	1
acylglycerol biosynthetic process	0.14	0.38	0.4615241	1
G-protein signaling, coupled to cyclic nucleotide second	2.5	1.53	0.4691396	1
chromatin modification	2.5	1.53	0.4691396	1
ureteric bud development	0.83	1.53	0.4703257	1
negative regulation of transcription	5.56	4.21	0.515103	1
peptidyl-tyrosine modification	1.11	1.53	0.5303746	1
potassium ion transport	3.06	3.83	0.544697	1
tRNA aminoacylation	0.42	0	0.5693293	1
serine family amino acid biosynthetic process	0.42	0	0.5693293	1
ribonucleoside monophosphate biosynthetic process	0.42	0	0.5693293	1
gastrulation (sensu Vertebrata)	0.42	0	0.5693293	1
neurotransmitter uptake	0.42	0	0.5693293	1

cortical actin cytoskeleton organization and biogenesis	0.42	0	0.5693293	1
positive regulation of cytokine secretion	0.42	0	0.5693293	1
regulation of positive chemotaxis	0.42	0	0.5693293	1
negative regulation of B cell activation	0.42	0	0.5693293	1
hexose biosynthetic process	0.42	0	0.5693293	1
maintenance of fidelity during DNA-dependent DNA repl	0.42	0	0.5693293	1
folic acid and derivative biosynthetic process	0.42	0	0.5693293	1
embryonic digit morphogenesis	0.42	0	0.5693293	1
positive regulation of chemotaxis	0.42	0	0.5693293	1
actin filament-based movement	0.42	0	0.5693293	1
pyridine nucleotide biosynthetic process	0.42	0	0.5693293	1
ER to Golgi vesicle-mediated transport	0.56	0	0.57843	1
DNA integrity checkpoint	0.56	0	0.57843	1
fucose metabolic process	0.56	0	0.57843	1
transition metal ion homeostasis	0.56	0	0.57843	1
nicotinamide metabolic process	0.56	0	0.57843	1
regulation of striated muscle development	0.56	0	0.57843	1
spindle organization and biogenesis	0.56	0	0.57843	1
cAMP-mediated signaling	1.81	1.15	0.5801394	1
nuclear import	1.67	2.3	0.5901221	1
calcium ion homeostasis	1.81	2.3	0.6053717	1
sphingoid metabolic process	0.42	0.77	0.6132732	1
positive regulation of phosphate metabolic process	0.42	0.77	0.6132732	1
interleukin-2 biosynthetic process	0.42	0.77	0.6132732	1
axon ensheathment	0.42	0.77	0.6132732	1
insulin receptor signaling pathway	0.56	0.77	0.6595536	1
cell projection biogenesis	0.56	0.77	0.6595536	1
protein ubiquitination	0.56	0.77	0.6595536	1
positive regulation of lymphocyte proliferation	0.56	0.77	0.6595536	1
androgen receptor signaling pathway	0.83	0.38	0.68225	1
regulation of neurogenesis	0.83	0.38	0.68225	1
regulation of MAPK activity	0.83	1.15	0.7065722	1
hemopoiesis	3.75	4.21	0.7110969	1
positive regulation of protein biosynthetic process	0.97	1.15	0.7309491	1
regulation of cytokine biosynthetic process	1.25	1.53	0.7543467	1
glucose metabolic process	1.67	1.15	0.7705619	1

regulation of I-kappaB kinase/NF-kappaB cascade	1.67	1.15	0.7705619	1
microtubule-based movement	1.39	1.53	0.7706805	1
regulation of Ras protein signal transduction	2.36	1.92	0.8102265	1
Rho protein signal transduction	2.5	1.92	0.8115185	1
blood vessel morphogenesis	3.47	3.07	0.8435508	1
regulation of transcription, DNA-dependent	26.94	27.59	0.8709582	1
chondroitin sulfate metabolic process	0.14	0	1	1
eye development (sensu Endopterygota)	0.14	0	1	1
lymphocyte costimulation	0.14	0	1	1
positive regulation of B cell activation	0.28	0.38	1	1
interleukin-1 biosynthetic process	0.14	0	1	1
regulation of DNA recombination	0.14	0	1	1
acyl-CoA metabolic process	0.14	0	1	1
neurotransmitter metabolic process	0.69	0.77	1	1
negative regulation of smoothened signaling pathway	0.14	0	1	1
somatic diversification of immunoglobulins	0.28	0.38	1	1
neurite regeneration	0.14	0	1	1
lysosomal transport	0.28	0.38	1	1
ammonium transport	0.14	0	1	1
protein depalmitoylation	0.14	0	1	1
purine ribonucleoside diphosphate metabolic process	0.14	0	1	1
negative regulation of protein biosynthetic process	0.56	0.38	1	1
synaptic transmission, glutamatergic	0.28	0	1	1
cysteine metabolic process	0.14	0	1	1
'de novo' pyrimidine base biosynthetic process	0.28	0	1	1
cholesterol metabolic process	0.69	0.77	1	1
estrogen catabolic process	0.14	0	1	1
positive regulation of epithelial cell differentiation	0.14	0	1	1
purine nucleoside diphosphate biosynthetic process	0.14	0	1	1
regulation of leukocyte degranulation	0.14	0	1	1
positive regulation of T cell activation	0.69	0.77	1	1
regulation of DNA replication	0.28	0	1	1
receptor internalization	0.14	0	1	1
meiosis	0.97	0.77	1	1
mitosis	2.08	1.92	1	1
chondroitin sulfate proteoglycan biosynthetic process	0.14	0	1	1



sperm chromatin decondensation	0.14	0	1	1
RNA interference	0.14	0	1	1
interleukin-8 biosynthetic process	0.14	0	1	1
embryonic forelimb morphogenesis	0.14	0	1	1
peroxisomal long-chain fatty acid import	0.14	0	1	1
pyrimidine deoxyribonucleoside catabolic process	0.14	0	1	1
fatty acid biosynthetic process	0.83	0.77	1	1
regulation of lymphocyte mediated immunity	0.14	0	1	1
positive regulation of protein modification	0.14	0	1	1
male genitalia development	0.28	0.38	1	1
regulation of cyclic nucleotide metabolic process	0.28	0.38	1	1
glial cell migration	0.14	0	1	1
epidermal growth factor receptor signaling pathway	0.56	0.38	1	1
mRNA transcription	0.14	0	1	1
embryonic ectodermal gut development	0.28	0	1	1
estrogen biosynthetic process	0.14	0	1	1
sodium ion homeostasis	0.14	0	1	1
macrophage chemotaxis	0.28	0	1	1
protein amino acid methylation	0.28	0	1	1
induction of an organ	0.28	0.38	1	1
regulation of cell killing	0.28	0.38	1	1
UDP-N-acetylglucosamine transport	0.14	0	1	1
killing of cells of another organism	0.14	0	1	1
purine ribonucleotide biosynthetic process	0.83	0.77	1	1
patched ligand processing	0.14	0	1	1
regulation of fatty acid metabolic process	0.14	0	1	1
negative regulation of lymphocyte proliferation	0.28	0	1	1
neuroblast proliferation	0.14	0	1	1
midbrain development	0.28	0	1	1
arginine metabolic process	0.14	0	1	1
interleukin-13 biosynthetic process	0.14	0	1	1
neuron migration	1.67	1.53	1	1
fatty acid oxidation	0.28	0.38	1	1
modification by symbiont of host cellular component	0.14	0	1	1
establishment of apical/basal cell polarity	0.14	0	1	1
beta-tubulin folding	0.14	0	1	1

telomere maintenance	0.14	0	1	1
hydrogen ion homeostasis	0.28	0	1	1
positive regulation of endocytosis	0.28	0.38	1	1
chaperone cofactor-dependent protein folding	0.14	0	1	1
purine nucleoside triphosphate biosynthetic process	0.69	0.77	1	1
valine metabolic process	0.14	0	1	1
transcription-coupled nucleotide-excision repair	0.14	0	1	1
peptidyl-threonine modification	0.14	0	1	1
UDP-xylose transport	0.14	0	1	1
chondrocyte differentiation	0.14	0	1	1
succinyl-CoA metabolic process	0.28	0.38	1	1
amyloid precursor protein metabolic process	0.14	0	1	1
histidine family amino acid catabolic process	0.28	0.38	1	1
tripartite regional subdivision	0.14	0	1	1
oocyte development	0.28	0	1	1
regulation of gamma-delta T cell activation	0.14	0	1	1
pyrimidine ribonucleotide biosynthetic process	0.28	0.38	1	1
interleukin-12 biosynthetic process	0.28	0.38	1	1
N-acetylglucosamine metabolic process	0.28	0	1	1
ribonucleoside diphosphate biosynthetic process	0.14	0	1	1
phospholipid biosynthetic process	0.69	0.77	1	1
L-amino acid transport	0.14	0	1	1
negative regulation of smooth muscle cell differentiation	0.14	0	1	1
tricarboxylic acid cycle	0.28	0	1	1
negative regulation of nucleotide metabolic process	0.14	0	1	1
regulation of B cell proliferation	0.28	0.38	1	1
negative regulation of amino acid metabolic process	0.14	0	1	1
negative regulation of hormone secretion	0.14	0	1	1
neural crest cell migration	0.28	0	1	1
establishment of lymphocyte polarity	0.14	0	1	1
interleukin-1 beta secretion	0.28	0	1	1
ribonucleoside triphosphate biosynthetic process	0.69	0.77	1	1
regulation of translational initiation	0.28	0.38	1	1
mRNA transport	0.56	0.38	1	1
protein sumoylation	0.28	0	1	1
mitochondrial DNA replication	0.14	0	1	1

spindle checkpoint	0.14	0	1	1
hindbrain development	0.28	0	1	1
positive regulation of progression through mitotic cell cyc	0.14	0	1	1
choline metabolic process	0.14	0	1	1
embryonic digestive tract morphogenesis	0.28	0.38	1	1
purine ribonucleoside triphosphate metabolic process	0.69	0.77	1	1
long-chain fatty acid metabolic process	0.14	0	1	1
gut morphogenesis	0.28	0.38	1	1
uracil catabolic process	0.14	0	1	1
protein amino acid acetylation	0.14	0	1	1
chaperonin-mediated tubulin folding	0.14	0	1	1
positive regulation of DNA metabolic process	0.28	0.38	1	1
regulation of phosphorylation	0.97	0.77	1	1
bile acid transport	0.14	0	1	1
chemokine biosynthetic process	0.14	0	1	1
negative regulation of phosphate metabolic process	0.14	0	1	1
endoderm formation	0.14	0	1	1
vesicle targeting	0.28	0.38	1	1
negative regulation of small GTPase mediated signal tra	0.14	0	1	1
pyrimidine ribonucleoside triphosphate metabolic proces	0.28	0.38	1	1
peptidyl-asparagine modification	0.42	0.38	1	1
hyaluronan metabolic process	0.14	0	1	1
tyrosine metabolic process	0.14	0	1	1
neutral amino acid transport	0.14	0	1	1
microtubule bundle formation	0.28	0	1	1
signal peptide processing	0.28	0	1	1
somatic diversification of immune receptors via germline	0.28	0	1	1
nerve growth factor receptor signaling pathway	0.14	0	1	1
leukocyte mediated cytotoxicity	0.28	0.38	1	1
retrograde transport, endosome to Golgi	0.14	0	1	1
regulation of mitochondrial membrane permeability	0.14	0	1	1
odontogenesis (sensu Vertebrata)	0.42	0.38	1	1
transition metal ion transport	0.56	0.38	1	1
regulation of phosphoinositide 3-kinase activity	0.14	0	1	1
cartilage condensation	0.28	0	1	1
regulation of alpha-beta T cell activation	0.14	0	1	1

thymidine metabolic process	0.14	0	1	1
peptide hormone processing	0.14	0	1	1
blood vessel maturation	0.14	0	1	1
spermatid development	0.14	0	1	1
fibroblast growth factor receptor signaling pathway	0.28	0.38	1	1
phagocytosis, engulfment	0.14	0	1	1
signal complex formation	0.28	0	1	1
phosphate ion homeostasis	0.14	0	1	1
tumor necrosis factor-beta biosynthetic process	0.28	0	1	1
peptidyl-histidine modification	0.14	0	1	1
primary follicle stage, oogenesis (sensu Mammalia)	0.14	0	1	1
regulation of nucleotide biosynthetic process	0.14	0	1	1
regulation of MAPKKK cascade	0.28	0	1	1
neurotransmitter secretion	1.53	1.53	1	1
positive regulation of exocytosis	0.28	0	1	1
estrogen receptor signaling pathway	0.14	0	1	1
regulation of MHC class II biosynthetic process	0.28	0	1	1
RNA polyadenylation	0.28	0	1	1
positive regulation of immune response to tumor cell	0.14	0	1	1
regulation of pinocytosis	0.28	0	1	1
actin cytoskeleton reorganization	0.14	0	1	1
Notch receptor processing	0.14	0	1	1
ephrin receptor signaling pathway	0.14	0	1	1
mannose metabolic process	0.28	0	1	1
malate metabolic process	0.28	0	1	1
positive regulation of leukocyte mediated immunity	0.14	0	1	1
lymph node development	0.14	0	1	1
rostrocaudal neural tube patterning	0.14	0	1	1
negative regulation of blood coagulation	0.28	0	1	1
cGMP catabolic process	0.14	0	1	1
lymphocyte chemotaxis	0.28	0	1	1
L-serine metabolic process	0.28	0	1	1
succinate transport	0.14	0	1	1
regulation of gonadotropin secretion	0.14	0	1	1
actin polymerization and/or depolymerization	1.11	1.15	1	1
alpha-beta T cell proliferation	0.28	0	1	1

positive regulation of amino acid metabolic process	0.42	0.38	1	1
alveolus development	0.14	0	1	1
lipid raft polarization	0.14	0	1	1
branched chain family amino acid catabolic process	0.14	0	1	1
microtubule polymerization or depolymerization	0.14	0	1	1
base conversion or substitution editing	0.14	0	1	1
base-excision repair, gap-filling	0.14	0	1	1
G2 phase of mitotic cell cycle	0.28	0	1	1
eye morphogenesis	0.42	0.38	1	1
proton transport	0.69	0.38	1	1
regulation of T cell proliferation	0.83	0.77	1	1
posterior midgut development	0.14	0	1	1
glucose transport	0.42	0.38	1	1
B cell mediated immunity	0.69	0.38	1	1
intermediate mesoderm development	0.14	0	1	1
negative regulation of cytokine and chemokine mediated	0.14	0	1	1
thiamin diphosphate biosynthetic process	0.14	0	1	1
glucan biosynthetic process	0.14	0	1	1
citrate transport	0.14	0	1	1
RNA splicing, via transesterification reactions	0.69	0.77	1	1
regulation of catecholamine metabolic process	0.14	0	1	1
JNK cascade	0.83	0.77	1	1
regulation of calcium-mediated signaling	0.14	0	1	1
glycosphingolipid metabolic process	0.42	0.38	1	1
fructose metabolic process	0.14	0	1	1
follicle-stimulating hormone secretion	0.14	0	1	1
mRNA editing	0.14	0	1	1
histidine metabolic process	0.28	0.38	1	1
embryonic skeletal morphogenesis	0.14	0	1	1
G2/M transition of mitotic cell cycle	0.14	0	1	1
negative regulation of Wnt receptor signaling pathway	0.28	0	1	1
indolalkylamine biosynthetic process	0.14	0	1	1
establishment and/or maintenance of epithelial cell polar	0.14	0	1	1
interleukin-4 biosynthetic process	0.14	0	1	1
modification by organism of cell membrane in other orga	0.14	0	1	1
embryonic hindlimb morphogenesis	0.28	0	1	1

pyridoxine biosynthetic process	0.14	0	1	1
granulocyte macrophage colony-stimulating factor biosyn	0.28	0	1	1
forebrain development	1.11	1.15	1	1
purine ribonucleoside salvage	0.28	0	1	1
ubiquinone biosynthetic process	0.14	0	1	1
positive regulation of hormone secretion	0.14	0	1	1
T cell mediated immunity	0.14	0	1	1
vascular endothelial growth factor receptor signaling pat	0.14	0	1	1
regulation of actin filament length	0.69	0.77	1	1
negative regulation of DNA metabolic process	0.14	0	1	1
entry into host cell	0.28	0	1	1
opsonization	0.14	0	1	1
coenzyme A biosynthetic process	0.14	0	1	1
glycolipid biosynthetic process	0.28	0.38	1	1
protein heterotetramerization	0.14	0	1	1
sphingolipid biosynthetic process	0.28	0	1	1
arm morphogenesis	0.14	0	1	1
mRNA 3'-end processing	0.28	0	1	1
regulation of nucleocytoplasmic transport	0.28	0	1	1
G1/S transition of mitotic cell cycle	0.56	0.38	1	1
fused antrum stage, oogenesis (sensu Mammalia)	0.14	0	1	1
I-kappaB phosphorylation	0.28	0	1	1
neural tube formation	0.42	0.38	1	1
eosinophil chemotaxis	0.14	0	1	1
regulation of interleukin-1 secretion	0.28	0	1	1
male germ-line stem cell division	0.14	0	1	1
neutrophil chemotaxis	0.56	0.38	1	1
C21-steroid hormone biosynthetic process	0.14	0	1	1
tryptophan metabolic process	0.14	0	1	1
interleukin-3 biosynthetic process	0.14	0	1	1
cytoplasmic sequestering of protein	0.14	0	1	1
positive regulation of innate immune response	0.14	0	1	1

Gene Ontology : biological process. Level: 9	Percentage of genes with allele-specific expression	Percentage of genes without allele-specific expression	Unadjusted pvalue	Adjusted pvalueFDR
regulation of ossification	0	2	0.01934914	1
bone mineralization	0	2	0.01934914	1
positive regulation of transcription, DNA-dependent	8.87	3.33	0.02764696	1
positive regulation of programmed cell death	6.9	2.67	0.0648839	1
phototransduction	0	1.33	0.07242854	1
calcium-dependent phospholipase A2 activation	0	1.33	0.07242854	1
blood vessel remodeling	0	1.33	0.07242854	1
chromatin assembly	0.74	2.67	0.08893205	1
collagen catabolic process	0.49	2	0.1245022	1
regulation of apoptosis	13.55	8.67	0.1445579	1
regulation of transcription from RNA polymerase II prom	14.29	9.33	0.1541752	1
modification-dependent protein catabolic process	3.69	6.67	0.1647821	1
skeletal muscle fiber development	1.48	3.33	0.1770124	1
neuron fate commitment	0.25	1.33	0.1785873	1
regulation of neuronal synaptic plasticity	0.25	1.33	0.1785873	1
protein amino acid O-linked glycosylation	0.25	1.33	0.1785873	1
synaptic vesicle exocytosis	0.25	1.33	0.1785873	1
protein export from nucleus	0.25	1.33	0.1785873	1
phosphoinositide metabolic process	0.25	1.33	0.1785873	1
hair follicle development	1.72	0	0.1980866	1
regulation of mitosis	1.48	0	0.1981695	1
triacylglycerol biosynthetic process	0	0.67	0.2697842	1
striated muscle cell development	0	0.67	0.2697842	1
regulation of transcription from RNA polymerase I prom	0	0.67	0.2697842	1
S-adenosylmethionine biosynthetic process	0	0.67	0.2697842	1
neurotransmitter catabolic process	0	0.67	0.2697842	1
mesoderm formation	0	0.67	0.2697842	1
sphingoid catabolic process	0	0.67	0.2697842	1
Schwann cell differentiation	0	0.67	0.2697842	1
positive regulation of B cell proliferation	0	0.67	0.2697842	1
protein targeting to peroxisome	0	0.67	0.2697842	1
telencephalon development	0	0.67	0.2697842	1
positive regulation of DNA ligation	0	0.67	0.2697842	1
endochondral ossification	0	0.67	0.2697842	1
protein autoubiquitination	0	0.67	0.2697842	1

retrograde transport, vesicle recycling within Golgi	0	0.67	0.2697842	1
platelet activating factor biosynthetic process	0	0.67	0.2697842	1
positive regulation of gliogenesis	0	0.67	0.2697842	1
cholesterol catabolic process	0	0.67	0.2697842	1
ovulation (sensu Mammalia)	0	0.67	0.2697842	1
asparagine biosynthetic process	0	0.67	0.2697842	1
oxidized low-density lipoprotein catabolic process	0	0.67	0.2697842	1
segment polarity determination	0	0.67	0.2697842	1
mitotic centrosome separation	0	0.67	0.2697842	1
negative regulation of transcription factor activity	0	0.67	0.2697842	1
galactolipid catabolic process	0	0.67	0.2697842	1
glycogen catabolic process	0	0.67	0.2697842	1
fatty acid beta-oxidation	0	0.67	0.2697842	1
glutamine biosynthetic process	0	0.67	0.2697842	1
regulation of cGMP metabolic process	0	0.67	0.2697842	1
lagging strand elongation	0	0.67	0.2697842	1
Golgi to plasma membrane transport	0	0.67	0.2697842	1
leukotriene metabolic process	0.49	1.33	0.2952085	1
protein prenylation	0.49	1.33	0.2952085	1
eye development (sensu Mammalia)	0.49	1.33	0.2952085	1
ureteric bud branching	0.49	1.33	0.2952085	1
neurotransmitter biosynthetic process	0.49	1.33	0.2952085	1
actin filament depolymerization	0.49	1.33	0.2952085	1
positive regulation of neurogenesis	1.23	0	0.3307322	1
activation of protein kinase activity	1.97	3.33	0.3510684	1
G-protein signaling, coupled to cAMP nucleotide second messenger	3.2	1.33	0.3755438	1
inner ear morphogenesis	0.99	2	0.3940697	1
protein amino acid autophosphorylation	0.99	2	0.3940697	1
neuron development	9.36	6.67	0.3955965	1
negative regulation of programmed cell death	6.4	4	0.4111837	1
cytosolic calcium ion homeostasis	1.23	2	0.4503502	1
regulation of activated T cell proliferation	0.25	0.67	0.4671398	1
astrocyte differentiation	0.25	0.67	0.4671398	1
L-phenylalanine catabolic process	0.25	0.67	0.4671398	1
mast cell degranulation	0.25	0.67	0.4671398	1
norepinephrine metabolic process	0.25	0.67	0.4671398	1



regulation of S phase of mitotic cell cycle	0.25	0.67	0.4671398	1
protein targeting to lysosome	0.25	0.67	0.4671398	1
regulation of ARF protein signal transduction	0.25	0.67	0.4671398	1
phospholipase C activation	0.25	0.67	0.4671398	1
substrate-bound cell migration, cell extension	0.25	0.67	0.4671398	1
positive regulation of JAK-STAT cascade	0.25	0.67	0.4671398	1
glutamate transport	0.25	0.67	0.4671398	1
regulation of glial cell differentiation	0.25	0.67	0.4671398	1
apocarotenoid metabolic process	0.25	0.67	0.4671398	1
negative regulation of neurogenesis	0.25	0.67	0.4671398	1
positive regulation of receptor mediated endocytosis	0.25	0.67	0.4671398	1
negative regulation of cyclin-dependent protein kinase :	0.25	0.67	0.4671398	1
tRNA splicing	0.25	0.67	0.4671398	1
regulation of interferon-gamma biosynthetic process	0.25	0.67	0.4671398	1
regulation of BMP signaling pathway	0.25	0.67	0.4671398	1
regulation of calcium ion transport	0.25	0.67	0.4671398	1
regulation of mRNA stability	0.25	0.67	0.4671398	1
diacylglycerol biosynthetic process	0.25	0.67	0.4671398	1
glycosphingolipid catabolic process	0.25	0.67	0.4671398	1
axon cargo transport	0.25	0.67	0.4671398	1
angiogenesis	4.93	3.33	0.4971736	1
peptidyl-tyrosine phosphorylation	1.72	2.67	0.4983115	1
L-fucose metabolic process	0.74	0	0.5671713	1
positive regulation of positive chemotaxis	0.74	0	0.5671713	1
mismatch repair	0.74	0	0.5671713	1
tRNA aminoacylation for protein translation	0.74	0	0.5671713	1
energy coupled proton transport, down electrochemical	0.74	0	0.5671713	1
actin filament bundle formation	0.74	0	0.5671713	1
immune response-activating signal transduction	0.99	0	0.5783899	1
DNA damage checkpoint	0.99	0	0.5783899	1
transcription initiation from RNA polymerase II promote	0.99	0	0.5783899	1
negative regulation of cell growth	0.99	0	0.5783899	1
regulation of interleukin-6 biosynthetic process	0.99	0	0.5783899	1
chromatin remodeling	0.99	0	0.5783899	1
protein import into nucleus	2.96	4	0.5901606	1
meiosis I	0.74	1.33	0.6152426	1

regulation of interleukin-2 biosynthetic process	0.74	1.33	0.6152426	1
ceramide metabolic process	0.74	1.33	0.6152426	1
positive regulation of MAPK activity	0.74	1.33	0.6152426	1
positive regulation of phosphorylation	0.74	1.33	0.6152426	1
myelination	0.74	1.33	0.6152426	1
dopamine metabolic process	0.74	1.33	0.6152426	1
actin filament polymerization	0.99	1.33	0.6631452	1
positive regulation of T cell proliferation	0.99	1.33	0.6631452	1
regulation of actin polymerization and/or depolymerization	0.99	1.33	0.6631452	1
epidermis morphogenesis	1.72	0.67	0.6889394	1
protein amino acid N-linked glycosylation	1.72	0.67	0.6889394	1
glucose catabolic process	1.72	0.67	0.6889394	1
positive regulation of cytokine biosynthetic process	1.48	2	0.7080766	1
positive regulation of I-kappaB kinase/NF-kappaB cascade	2.71	2	0.7684468	1
regulation of Rho protein signal transduction	3.45	2.67	0.7910422	1
leukocyte differentiation	4.19	4.67	0.8155387	1
negative regulation of transcription, DNA-dependent	6.9	6	0.8485424	1
neutrophil apoptosis	0.25	0	1	1
regulation of granulocyte macrophage colony-stimulating factor production	0.49	0	1	1
regulation of microtubule polymerization or depolymerization	0.25	0	1	1
positive regulation of translational initiation	0.25	0	1	1
ectodermal gut morphogenesis	0.49	0	1	1
peptidyl-tyrosine sulfation	0.25	0	1	1
RNA export from nucleus	0.25	0	1	1
endoplasmic reticulum calcium ion homeostasis	0.25	0	1	1
primary neural tube formation	0.49	0.67	1	1
Cdc42 protein signal transduction	0.25	0	1	1
catecholamine uptake during transmission of nerve impulse	0.25	0	1	1
NADP metabolic process	0.49	0	1	1
amyloid precursor protein catabolic process	0.25	0	1	1
entry of virus into host cell	0.49	0	1	1
copper ion homeostasis	0.49	0	1	1
regulation of interleukin-13 biosynthetic process	0.25	0	1	1
glucose import	0.25	0	1	1
GTP metabolic process	0.49	0.67	1	1
thymidine catabolic process	0.25	0	1	1

transcription initiation from RNA polymerase III promote	0.25	0	1	1
zinc ion transport	0.25	0	1	1
energy coupled proton transport, against electrochemic	0.49	0	1	1
regulation of transforming growth factor beta receptor s	0.49	0	1	1
regulation of JNK activity	0.25	0	1	1
glutamate secretion	0.25	0	1	1
mitotic spindle organization and biogenesis	0.25	0	1	1
skin development	0.25	0	1	1
vasculogenesis	0.74	0.67	1	1
misfolded or incompletely synthesized protein catabolic	0.25	0	1	1
regulation of leukocyte mediated cytotoxicity	0.49	0.67	1	1
L-serine biosynthetic process	0.49	0	1	1
regulation of protein amino acid phosphorylation	1.23	1.33	1	1
gastrulation (sensu Mammalia)	0.49	0	1	1
microtubule polymerization	0.25	0	1	1
spermatid nuclear differentiation	0.25	0	1	1
cytolysis of cells of another organism	0.25	0	1	1
lamellipodium biogenesis	0.49	0	1	1
mitotic anaphase	0.25	0	1	1
positive regulation of lymphocyte mediated immunity	0.25	0	1	1
killing of cells in other organism during symbiotic interac	0.25	0	1	1
positive regulation of pinocytosis	0.49	0	1	1
microtubule depolymerization	0.25	0	1	1
fucose biosynthetic process	0.25	0	1	1
natural killer cell mediated immune response to tumor c	0.25	0	1	1
regulation of chromatin assembly or disassembly	0.25	0	1	1
regulation of cyclic nucleotide biosynthetic process	0.25	0	1	1
activated T cell apoptosis	0.25	0	1	1
regulation of Ras GTPase activity	0.25	0	1	1
chondroitin sulfate biosynthetic process	0.25	0	1	1
regulation of interleukin-3 biosynthetic process	0.25	0	1	1
phosphatidylcholine metabolic process	0.25	0	1	1
regulation of interleukin-1 beta secretion	0.49	0	1	1
positive regulation of alpha-beta T cell activation	0.25	0	1	1
negative regulation of striated muscle development	0.49	0	1	1
positive regulation of nucleocytoplasmic transport	0.25	0	1	1

regulation of neuron differentiation	1.72	1.33	1	1
positive regulation of gamma-delta T cell activation	0.25	0	1	1
covalent chromatin modification	1.23	0.67	1	1
positive regulation of MHC class II biosynthetic process	0.25	0	1	1
apoptotic program	1.97	1.33	1	1
negative regulation of cytokine biosynthetic process	0.49	0.67	1	1
protein targeting to vacuole	0.25	0	1	1
regulation of natural killer cell mediated immunity	0.25	0	1	1
prostanoid metabolic process	0.49	0	1	1
insulin processing	0.25	0	1	1
embryonic eye morphogenesis	0.25	0	1	1
fucose catabolic process	0.49	0	1	1
regulation of epidermal growth factor receptor activity	0.49	0	1	1
neuron apoptosis	0.49	0	1	1
negative regulation of gonadotropin secretion	0.25	0	1	1
glycerophospholipid biosynthetic process	0.49	0.67	1	1
T cell costimulation	0.25	0	1	1
regulation of synaptic transmission, glutamatergic	0.25	0	1	1
determination of anterior/posterior axis, embryo	0.25	0	1	1
positive regulation of interleukin-1 secretion	0.49	0	1	1
neuroblast proliferation (sensu Vertebrata)	0.25	0	1	1
GDP-mannose metabolic process	0.25	0	1	1
oocyte maturation	0.49	0	1	1
protein palmitoylation	0.25	0	1	1
regulation of interleukin-8 biosynthetic process	0.25	0	1	1
protein targeting to membrane	0.25	0	1	1
triacylglycerol mobilization	0.25	0	1	1
positive regulation of Ras protein signal transduction	0.25	0	1	1
serotonin secretion	0.25	0	1	1
spindle assembly	0.25	0	1	1
arginine biosynthetic process	0.25	0	1	1
chromatin disassembly	0.25	0	1	1
endosome to lysosome transport	0.25	0	1	1
regulation of chemokine biosynthetic process	0.25	0	1	1
positive regulation of gonadotropin secretion	0.25	0	1	1
iron ion homeostasis	0.49	0	1	1

negative regulation of cyclic nucleotide metabolic process	0.25	0	1	1
inflammatory cell apoptosis	0.49	0	1	1
gluconeogenesis	0.49	0	1	1
embryonic gut morphogenesis	0.49	0.67	1	1
catecholamine secretion	0.25	0	1	1
sequestering of calcium ion	0.25	0	1	1
somatic recombination of immunoglobulin gene segments	0.49	0	1	1
purine ribonucleoside triphosphate biosynthetic process	1.23	1.33	1	1
positive regulation of DNA replication	0.25	0	1	1
regulation of neurotransmitter secretion	0.74	0.67	1	1
tyrosine catabolic process	0.25	0	1	1
negative regulation of I-kappaB kinase/NF-kappaB cascade	0.25	0	1	1
cysteine biosynthetic process	0.25	0	1	1
regulation of cellular pH	0.25	0	1	1
regulation of follicle-stimulating hormone secretion	0.25	0	1	1
negative regulation of gliogenesis	0.25	0	1	1
modification by symbiont of host cell membrane	0.25	0	1	1
acetylcholine metabolic process	0.25	0	1	1
mRNA polyadenylation	0.49	0	1	1
succinyl-CoA pathway	0.25	0	1	1
immunoglobulin mediated immune response	1.23	0.67	1	1
icosanoid biosynthetic process	0.74	0.67	1	1
positive regulation of calcium-mediated signaling	0.25	0	1	1
negative regulation of MHC class II biosynthetic process	0.25	0	1	1
ovarian follicle development	0.49	0	1	1
regulation of JNK cascade	0.49	0	1	1
CTP metabolic process	0.49	0.67	1	1
negative regulation of B cell proliferation	0.49	0	1	1
protein targeting to mitochondrion	0.25	0	1	1
transmembrane receptor protein tyrosine kinase activation	0.25	0	1	1
NAD metabolic process	0.49	0	1	1
negative regulation of T cell proliferation	0.49	0	1	1
mitotic sister chromatid segregation	0.49	0.67	1	1
fibrinolysis	0.49	0	1	1
hemocyte differentiation (sensu Arthropoda)	0.25	0	1	1
negative regulation of DNA replication	0.25	0	1	1

regulation of odontogenesis (sensu Vertebrata)	0.25	0	1	1
negative regulation of nucleocytoplasmic transport	0.49	0	1	1
positive regulation of phosphoinositide 3-kinase activity	0.25	0	1	1
positive regulation of striated muscle development	0.25	0	1	1
negative regulation of phosphorylation	0.25	0	1	1
negative regulation of MAPK activity	0.74	0.67	1	1
positive regulation of transcription factor activity	0.49	0.67	1	1
glycosphingolipid biosynthetic process	0.49	0	1	1
regulation of cAMP metabolic process	0.49	0	1	1
regulation of fatty acid oxidation	0.25	0	1	1
peptidyl-threonine phosphorylation	0.25	0	1	1
iron ion transport	0.74	0.67	1	1
copper ion transport	0.25	0	1	1
myeloid cell differentiation	3.2	3.33	1	1
regulation of interleukin-12 biosynthetic process	0.49	0.67	1	1
eye morphogenesis (sensu Vertebrata)	0.25	0	1	1
embryonic arm morphogenesis	0.25	0	1	1
Golgi to endosome transport	0.25	0	1	1
positive regulation of leukocyte degranulation	0.25	0	1	1
negative regulation of nucleotide biosynthetic process	0.25	0	1	1
male meiosis	0.25	0	1	1
peptidyl-diphthamide metabolic process	0.25	0	1	1
ATP metabolic process	0.74	0.67	1	1
RNA splicing, via transesterification reactions with bulge	1.23	1.33	1	1
regulation of insulin receptor signaling pathway	0.25	0	1	1
establishment of T cell polarity	0.25	0	1	1
establishment of epithelial cell polarity	0.25	0	1	1
regulation of alpha-beta T cell proliferation	0.25	0	1	1
cilium biogenesis	0.25	0	1	1
regulation of tumor necrosis factor-beta biosynthetic process	0.25	0	1	1
complement activation	0.99	0.67	1	1
transformed cell apoptosis	0.49	0	1	1
regulation of interleukin-1 biosynthetic process	0.25	0	1	1
mitotic metaphase/anaphase transition	0.25	0	1	1
mitotic metaphase	0.25	0	1	1
histidine catabolic process	0.49	0.67	1	1

glycogen biosynthetic process	0.25	0	1	1
long-chain fatty acid biosynthetic process	0.25	0	1	1
midbrain-hindbrain boundary development	0.25	0	1	1
UTP metabolic process	0.49	0.67	1	1
pyrimidine ribonucleoside triphosphate biosynthetic pro	0.49	0.67	1	1
regulation of interleukin-4 biosynthetic process	0.25	0	1	1
female meiosis	0.49	0	1	1
positive regulation of fatty acid metabolic process	0.25	0	1	1
osteoblast differentiation	0.74	0.67	1	1
purine ribonucleoside diphosphate biosynthetic process	0.25	0	1	1
serotonin metabolic process	0.25	0	1	1
eye photoreceptor cell differentiation	0.49	0.67	1	1
regulation of fibroblast growth factor receptor signaling	0.25	0	1	1
negative regulation of Ras protein signal transduction	0.25	0	1	1