GO:BP
gc026

fraction genes in fg and expected valu...

G protein−coupled receptor signaling pat... GO:0007186	p=1.7E−07	n=19	fg=0.53	bg=0.08
limb bud formation GO:0060174	p=3.8E−07	n=3	fg=0.08	bg=0.00
adenylate cyclase−inhibiting G protein−c... GO:0007193	p=1.3E−05	n=5	fg=0.14	bg=0.01
Spemann organizer formation at the anter... GO:0060064	p=2.1E−05	n=2	fg=0.06	bg=0.00
positive regulation of collateral sprout... GO:0048697	p=2.1E−05	n=2	fg=0.06	bg=0.00
canonical Wnt signaling pathway involved... GO:0044338	p=2.1E−05	n=2	fg=0.06	bg=0.00
canonical Wnt signaling pathway involved... GO:0044339	p=2.1E−05	n=2	fg=0.06	bg=0.00
canonical Wnt signaling pathway involved... GO:1904954	p=2.1E−05	n=2	fg=0.06	bg=0.00
canonical Wnt signaling pathway involved... GO:1905474	p=2.1E−05	n=2	fg=0.06	bg=0.00
anterior/posterior axis specification GO:0009948	p=2.6E−05	n=3	fg=0.08	bg=0.00
positive regulation of adiponectin secre... GO:0070165	p=4.1E−05	n=3	fg=0.08	bg=0.00
head morphogenesis GO:0060323	p=8.7E−05	n=3	fg=0.08	bg=0.00
negative regulation of lipid catabolic p... GO:0050995	p=1.0E−04	n=3	fg=0.08	bg=0.00
mesoderm formation GO:0001707	p=1.6E−04	n=3	fg=0.08	bg=0.00
neuropeptide signaling pathway GO:0007218	p=1.6E−04	n=3	fg=0.08	bg=0.00
activation of phospholipase C activity GO:0007202	p=1.6E−04	n=3	fg=0.08	bg=0.00
dorsal/ventral axis specification GO:0009950	p=2.1E−04	n=2	fg=0.06	bg=0.00
response to blue light GO:0009637	p=3.2E−04	n=2	fg=0.06	bg=0.00
positive regulation of branching involve... GO:0090190	p=3.2E−04	n=2	fg=0.06	bg=0.00
cellular response to UV−A GO:0071492	p=4.4E−04	n=2	fg=0.06	bg=0.00
positive regulation of melanin biosynthe... GO:0048023	p=4.4E−04	n=2	fg=0.06	bg=0.00
aortic valve morphogenesis GO:0003180	p=5.9E−04	n=2	fg=0.06	bg=0.00
negative regulation of melanin biosynthe... GO:0048022	p=5.9E−04	n=2	fg=0.06	bg=0.00
negative regulation of axon extension in... GO:0048843	p=5.9E−04	n=2	fg=0.06	bg=0.00
negative regulation of ossification GO:0030279	p=7.5E−04	n=2	fg=0.06	bg=0.00
negative regulation of pri−miRNA transcr... GO:1902894	p=7.5E−04	n=2	fg=0.06	bg=0.00
negative regulation of myoblast differen... GO:0045662	p=7.5E−04	n=2	fg=0.06	bg=0.00
cellular response to 1−oleoyl−sn−glycero... GO:1904566	p=9.4E−04	n=2	fg=0.06	bg=0.00
negative regulation of biomineral tissue... GO:0070168	p=9.4E−04	n=2	fg=0.06	bg=0.00
positive regulation of smooth muscle cel... GO:0071673	p=9.4E−04	n=2	fg=0.06	bg=0.00

−log(p)   0 1 2 3 4 5
fraction   0.0 0.2 0.4 0.6 0.8 1.0

n=36/107 input genes with annotations

GO:MF
gc026

fraction genes in fg and expected valu...

cytokine activity GO:0005125	p=1.9E−05	n=3	fg=0.09	bg=0.00
nicotinic acid receptor activity GO:0070553	p=3.9E−05	n=3	fg=0.09	bg=0.00
purinergic nucleotide receptor activity GO:0001614	p=4.7E−05	n=3	fg=0.09	bg=0.00
GTP binding GO:0005525	p=3.0E−04	n=6	fg=0.17	bg=0.03
all−trans retinal binding GO:0005503	p=4.2E−04	n=2	fg=0.06	bg=0.00
frizzled binding GO:0005109	p=5.6E−04	n=2	fg=0.06	bg=0.00
lysophosphatidic acid receptor activity GO:0070915	p=1.1E−03	n=2	fg=0.06	bg=0.00
antigen binding GO:0003823	p=1.3E−03	n=2	fg=0.06	bg=0.00
lysophosphatidic acid binding GO:0035727	p=1.5E−03	n=2	fg=0.06	bg=0.00
peptide hormone binding GO:0017046	p=2.8E−03	n=3	fg=0.09	bg=0.01
cyclase activity GO:0009975	p=3.0E−03	n=2	fg=0.06	bg=0.00
11−cis retinal binding GO:0005502	p=4.1E−03	n=2	fg=0.06	bg=0.00
phosphorus−oxygen lyase activity GO:0016849	p=4.4E−03	n=2	fg=0.06	bg=0.00
extracellular matrix protein binding GO:1990430	p=4.4E−03	n=2	fg=0.06	bg=0.00
G protein−coupled neurotransmitter recep... GO:0099579	p=4.4E−03	n=2	fg=0.06	bg=0.00
G protein−coupled neurotransmitter recep... GO:0150047	p=4.4E−03	n=2	fg=0.06	bg=0.00
orexin receptor activity GO:0016499	p=4.6E−03	n=1	fg=0.03	bg=0.00
type III transforming growth factor beta... GO:0034714	p=4.6E−03	n=1	fg=0.03	bg=0.00
type II transforming growth factor beta ... GO:0005114	p=4.6E−03	n=1	fg=0.03	bg=0.00
neuropeptide receptor activity GO:0008188	p=5.5E−03	n=3	fg=0.09	bg=0.01
peptide receptor activity GO:0001653	p=5.6E−03	n=7	fg=0.20	bg=0.02
protein heterodimerization activity GO:0046982	p=5.6E−03	n=4	fg=0.11	bg=0.02
G protein−coupled GABA receptor activity GO:0004965	p=6.2E−03	n=2	fg=0.06	bg=0.00
G protein−coupled photoreceptor activity GO:0008020	p=6.7E−03	n=2	fg=0.06	bg=0.00
transmembrane signaling receptor activit... GO:0004888	p=7.2E−03	n=18	fg=0.51	bg=0.08
protein kinase A binding GO:0051018	p=9.3E−03	n=2	fg=0.06	bg=0.00
G−protein alpha−subunit binding GO:0001965	p=1.1E−02	n=2	fg=0.06	bg=0.00
mu−type opioid receptor binding GO:0031852	p=1.4E−02	n=1	fg=0.03	bg=0.00
bradykinin receptor activity GO:0004947	p=1.4E−02	n=1	fg=0.03	bg=0.00
protein antigen binding GO:1990405	p=1.4E−02	n=1	fg=0.03	bg=0.00

−log(p)   0 1 2 3 4 5
fraction   0.0 0.2 0.4 0.6 0.8 1.0

n=35/107 input genes with annotations

GO:CC
gc026

fraction genes in fg and expected valu...

GABA−ergic synapse GO:0098982	p=5.4E−05	n=5	fg=0.14	bg=0.01
extracellular space GO:0005615	p=7.1E−05	n=8	fg=0.22	bg=0.04
plasma membrane GO:0005886	p=9.1E−05	n=24	fg=0.67	bg=0.25
dendritic shaft GO:0043198	p=1.5E−04	n=4	fg=0.11	bg=0.01
neuron projection membrane GO:0032589	p=6.5E−04	n=3	fg=0.08	bg=0.00
postsynaptic membrane GO:0045211	p=8.5E−04	n=5	fg=0.14	bg=0.02
dendritic spine GO:0043197	p=1.4E−03	n=4	fg=0.11	bg=0.01
extracellular matrix GO:0031012	p=1.5E−03	n=5	fg=0.14	bg=0.01
glutamatergic synapse GO:0098978	p=3.4E−03	n=6	fg=0.17	bg=0.04
transforming growth factor beta ligand−r... GO:0070021	p=4.7E−03	n=1	fg=0.03	bg=0.00
transforming growth factor beta complex GO:0099126	p=4.7E−03	n=1	fg=0.03	bg=0.00
G protein−coupled GABA receptor complex GO:1902712	p=5.0E−03	n=2	fg=0.06	bg=0.00
G protein−coupled receptor heterodimeric... GO:0038039	p=6.4E−03	n=2	fg=0.06	bg=0.00
presynaptic membrane GO:0042734	p=7.4E−03	n=4	fg=0.11	bg=0.02
extrinsic component of external side of ... GO:0031232	p=9.3E−03	n=1	fg=0.03	bg=0.00
cerebellar Golgi cell to granule cell sy... GO:0099192	p=9.3E−03	n=1	fg=0.03	bg=0.00
axolemma GO:0030673	p=1.0E−02	n=2	fg=0.06	bg=0.00
Schaffer collateral − CA1 synapse GO:0098685	p=1.2E−02	n=3	fg=0.08	bg=0.01
photoreceptor outer segment GO:0001750	p=1.8E−02	n=2	fg=0.06	bg=0.01
dendrite membrane GO:0032590	p=1.9E−02	n=1	fg=0.03	bg=0.00
neuronal cell body GO:0043025	p=1.9E−02	n=5	fg=0.14	bg=0.04
main axon GO:0044304	p=2.0E−02	n=2	fg=0.06	bg=0.01
extrinsic component of postsynaptic memb... GO:0098890	p=2.8E−02	n=1	fg=0.03	bg=0.00
cell body GO:0044297	p=3.1E−02	n=5	fg=0.14	bg=0.05
photoreceptor cell cilium GO:0097733	p=3.2E−02	n=2	fg=0.06	bg=0.01
endoplasmic reticulum lumen GO:0005788	p=4.0E−02	n=2	fg=0.06	bg=0.01
9+0 non−motile cilium GO:0097731	p=4.0E−02	n=2	fg=0.06	bg=0.01
endosome GO:0005768	p=5.3E−02	n=5	fg=0.14	bg=0.06
cell surface GO:0009986	p=5.3E−02	n=5	fg=0.14	bg=0.04
extrinsic component of synaptic membrane GO:0099243	p=5.9E−02	n=1	fg=0.03	bg=0.00

−log(p)   0 1 2 3 4 5
fraction   0.0 0.2 0.4 0.6 0.8 1.0

n=36/107 input genes with annotations