GO:BP
Ncol_Nvec_vc1.1_XM_032386356.2

fraction genes in fg and expected value

Term	p-value	n	fg	bg
neuron fate specification GO:0048665	p=7.5E−04	n=4	fg=0.06	bg=0.01
negative regulation of activated T cell ... GO:0046007	p=1.4E−03	n=2	fg=0.03	bg=0.00
negative regulation of B cell proliferat... GO:0030889	p=1.4E−03	n=2	fg=0.03	bg=0.00
regulation of retinal ganglion cell axon... GO:0090259	p=1.4E−03	n=2	fg=0.03	bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151	p=1.4E−03	n=2	fg=0.03	bg=0.00
platelet activating factor biosynthetic ... GO:0006663	p=1.4E−03	n=2	fg=0.03	bg=0.00
motor neuron axon guidance GO:0008045	p=2.5E−03	n=4	fg=0.06	bg=0.01
dorsal root ganglion development GO:1990791	p=4.2E−03	n=2	fg=0.03	bg=0.00
vestibulocochlear nerve development GO:0021562	p=4.2E−03	n=2	fg=0.03	bg=0.00
trigeminal nerve development GO:0021559	p=4.2E−03	n=2	fg=0.03	bg=0.00
lipid modification GO:0030258	p=4.7E−03	n=5	fg=0.07	bg=0.02
negative regulation of MAPK cascade GO:0043409	p=5.4E−03	n=5	fg=0.07	bg=0.02
insulin receptor signaling pathway GO:0008286	p=8.1E−03	n=5	fg=0.07	bg=0.02
cell migration in hindbrain GO:0021535	p=8.1E−03	n=2	fg=0.03	bg=0.00
positive regulation of axon extension in... GO:0048842	p=8.1E−03	n=2	fg=0.03	bg=0.00
positive regulation of steroid biosynthe... GO:0010893	p=8.1E−03	n=2	fg=0.03	bg=0.00
dendrite arborization GO:0140059	p=8.1E−03	n=2	fg=0.03	bg=0.00
ruffle assembly GO:0097178	p=8.1E−03	n=2	fg=0.03	bg=0.00
foam cell differentiation GO:0090077	p=8.1E−03	n=2	fg=0.03	bg=0.00
alcohol metabolic process GO:0006066	p=9.3E−03	n=6	fg=0.09	bg=0.03
suckling behavior GO:0001967	p=1.3E−02	n=2	fg=0.03	bg=0.00
response to epidermal growth factor GO:0070849	p=1.3E−02	n=2	fg=0.03	bg=0.00
sequestering of triglyceride GO:0030730	p=1.3E−02	n=2	fg=0.03	bg=0.00
cellular response to epidermal growth fa... GO:0071364	p=1.3E−02	n=2	fg=0.03	bg=0.00
cellular response to lipoprotein particl... GO:0071402	p=1.3E−02	n=2	fg=0.03	bg=0.00
negative regulation of lipid storage GO:0010888	p=1.3E−02	n=2	fg=0.03	bg=0.00
negative regulation of neuron projection... GO:0010977	p=1.3E−02	n=4	fg=0.06	bg=0.01
negative regulation of protein serine/th... GO:0071901	p=1.5E−02	n=4	fg=0.06	bg=0.01
sensory perception GO:0007600	p=1.9E−02	n=9	fg=0.13	bg=0.06
positive regulation of hormone biosynthe... GO:0046886	p=1.9E−02	n=2	fg=0.03	bg=0.00

x-axis left: 0 1 2 3 4 5 −log(p)
n=69/227 input genes with annotations

x-axis right: 0.0 0.2 0.4 0.6 0.8 1.0 fraction

GO:MF
Ncol_Nvec_vc1.1_XM_032386356.2

fraction genes in fg and expected value

Term	p-value	n	fg	bg
1−acylglycerophosphocholine O−acyltransf... GO:0047184	p=1.3E−03	n=2	fg=0.03	bg=0.00
2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144	p=1.3E−03	n=2	fg=0.03	bg=0.00
phosphatidylinositol−3,4,5−trisphosphate... GO:0034485	p=1.3E−03	n=2	fg=0.03	bg=0.00
1−alkylglycerophosphocholine O−acetyltra... GO:0047192	p=1.3E−03	n=2	fg=0.03	bg=0.00
inositol−polyphosphate 5−phosphatase act... GO:0004445	p=1.3E−03	n=2	fg=0.03	bg=0.00
inositol−1,3,4,5−tetrakisphosphate 5−pho... GO:0052659	p=3.8E−03	n=2	fg=0.03	bg=0.00
1−acylglycerol−3−phosphate O−acyltransf... GO:0003841	p=3.8E−03	n=2	fg=0.03	bg=0.00
potassium channel regulator activity GO:0015459	p=6.2E−03	n=3	fg=0.05	bg=0.01
transmitter−gated ion channel activity GO:0022824	p=1.2E−02	n=2	fg=0.03	bg=0.00
transmitter−gated channel activity GO:0022835	p=1.2E−02	n=2	fg=0.03	bg=0.00
ubiquitin−like protein ligase activity GO:0061659	p=1.5E−02	n=6	fg=0.10	bg=0.04
ubiquitin protein ligase activity GO:0061630	p=1.5E−02	n=6	fg=0.10	bg=0.04
ubiquitin−protein transferase activity GO:0004842	p=1.6E−02	n=8	fg=0.14	bg=0.06
cholesterol binding GO:0015485	p=1.8E−02	n=2	fg=0.03	bg=0.00
potassium channel inhibitor activity GO:0019870	p=1.8E−02	n=2	fg=0.03	bg=0.00
ubiquitin−like protein transferase activ... GO:0019787	p=1.9E−02	n=8	fg=0.14	bg=0.06
sterol binding GO:0032934	p=2.4E−02	n=2	fg=0.03	bg=0.00
steroid binding GO:0005496	p=3.2E−02	n=2	fg=0.03	bg=0.00
NEDD8 conjugating enzyme activity GO:0061654	p=3.6E−02	n=1	fg=0.02	bg=0.00
1−alkenylglycerophosphocholine O−acyltra... GO:0047159	p=3.6E−02	n=1	fg=0.02	bg=0.00
semaphorin receptor activity GO:0017154	p=3.6E−02	n=1	fg=0.02	bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946	p=3.6E−02	n=1	fg=0.02	bg=0.00
phorbol ester receptor activity GO:0001565	p=3.6E−02	n=1	fg=0.02	bg=0.00
dolichyl−phosphate beta−glucosyltransfer... GO:0004581	p=3.6E−02	n=1	fg=0.02	bg=0.00
platelet−derived growth factor receptor ... GO:0005161	p=3.6E−02	n=1	fg=0.02	bg=0.00
oxidoreductase activity, acting on the C... GO:0052890	p=3.6E−02	n=1	fg=0.02	bg=0.00
vascular endothelial growth factor bindi... GO:0038085	p=3.6E−02	n=1	fg=0.02	bg=0.00
butyryl−CoA dehydrogenase activity GO:0004085	p=3.6E−02	n=1	fg=0.02	bg=0.00
MDM2/MDM4 family protein binding GO:0097371	p=3.6E−02	n=1	fg=0.02	bg=0.00
ABC−type sterol transporter activity GO:0034041	p=3.6E−02	n=1	fg=0.02	bg=0.00

x-axis left: 0 1 2 3 4 5 −log(p)
n=58/227 input genes with annotations

x-axis right: 0.0 0.2 0.4 0.6 0.8 1.0 fraction

GO:CC
Ncol_Nvec_vc1.1_XM_032386356.2

fraction genes in fg and expected value

Term	p-value	n	fg	bg
voltage−gated potassium channel complex GO:0008076	p=3.6E−03	n=3	fg=0.04	bg=0.01
endoplasmic reticulum membrane GO:0005789	p=4.5E−03	n=12	fg=0.18	bg=0.08
lipid droplet GO:0005811	p=4.6E−03	n=4	fg=0.06	bg=0.01
exocytic vesicle GO:0070382	p=1.5E−02	n=6	fg=0.09	bg=0.03
plasma membrane proton−transporting V−ty... GO:0033181	p=1.9E−02	n=2	fg=0.03	bg=0.00
mitochondrial nucleoid GO:0042645	p=1.9E−02	n=2	fg=0.03	bg=0.00
nucleoid GO:0009295	p=1.9E−02	n=2	fg=0.03	bg=0.00
postsynaptic membrane GO:0045211	p=2.4E−02	n=4	fg=0.06	bg=0.02
cytoplasm GO:0005737	p=2.4E−02	n=62	fg=0.91	bg=0.80
vacuolar proton−transporting V−type ATPa... GO:0016471	p=2.6E−02	n=2	fg=0.03	bg=0.00
transport vesicle membrane GO:0030658	p=2.7E−02	n=4	fg=0.06	bg=0.02
dendritic shaft GO:0043198	p=2.8E−02	n=3	fg=0.04	bg=0.01
presynapse GO:0098793	p=2.9E−02	n=8	fg=0.12	bg=0.05
synaptic vesicle GO:0008021	p=3.2E−02	n=5	fg=0.07	bg=0.03
cell leading edge GO:0031252	p=3.3E−02	n=6	fg=0.09	bg=0.04
proton−transporting V−type ATPase comple... GO:0033176	p=3.4E−02	n=2	fg=0.03	bg=0.00
cytoplasmic microtubule GO:0005881	p=3.4E−02	n=2	fg=0.03	bg=0.00
proton−transporting two−sector ATPase co... GO:0016469	p=3.4E−02	n=2	fg=0.03	bg=0.00
exocytic vesicle membrane GO:0099501	p=3.7E−02	n=3	fg=0.04	bg=0.01
cell surface GO:0009986	p=3.7E−02	n=6	fg=0.09	bg=0.04
isocitrate dehydrogenase complex (NAD+) GO:0045242	p=3.8E−02	n=1	fg=0.01	bg=0.00
death−inducing signaling complex GO:0031264	p=3.8E−02	n=1	fg=0.01	bg=0.00
9+2 non−motile cilium GO:0097732	p=3.8E−02	n=1	fg=0.01	bg=0.00
axonemal microtubule GO:0005879	p=3.8E−02	n=1	fg=0.01	bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245	p=3.8E−02	n=1	fg=0.01	bg=0.00
kinocilium GO:0060091	p=3.8E−02	n=1	fg=0.01	bg=0.00
semaphorin receptor complex GO:0002116	p=3.8E−02	n=1	fg=0.01	bg=0.00
mitochondrial isocitrate dehydrogenase c... GO:0098798	p=3.8E−02	n=1	fg=0.01	bg=0.00
mitochondrial protein−containing complex GO:0098798	p=4.7E−02	n=4	fg=0.06	bg=0.02
leading edge membrane GO:0031256	p=6.5E−02	n=3	fg=0.04	bg=0.01

x-axis left: 0 1 2 3 4 5 −log(p)
n=68/227 input genes with annotations

x-axis right: 0.0 0.2 0.4 0.6 0.8 1.0 fraction