Term	−log(p)	n	fg	bg
cellular response to nerve growth factor... GO:1990090	p=8.6E−05	n=3	fg=0.16	bg=0.01
specification of segmental identity, abd... GO:0007385	p=2.1E−03	n=2	fg=0.11	bg=0.00
syncytial blastoderm mitotic cell cycle GO:0035186	p=2.1E−03	n=2	fg=0.11	bg=0.00
phosphate ion homeostasis GO:0055062	p=2.1E−03	n=2	fg=0.11	bg=0.00
regulation of stem cell population maint... GO:2000036	p=2.1E−03	n=2	fg=0.11	bg=0.00
morphogenesis of an epithelial fold GO:0060571	p=2.1E−03	n=2	fg=0.11	bg=0.00
branch elongation of an epithelium GO:0060602	p=2.1E−03	n=2	fg=0.11	bg=0.00
mammary gland duct morphogenesis GO:0060603	p=2.1E−03	n=2	fg=0.11	bg=0.00
negative regulation of response to gamma... GO:2001229	p=2.1E−03	n=2	fg=0.11	bg=0.00
epidermis morphogenesis GO:0048730	p=2.1E−03	n=2	fg=0.11	bg=0.00
divalent inorganic anion homeostasis GO:0072505	p=2.1E−03	n=2	fg=0.11	bg=0.00
anterior neuropore closure GO:0021506	p=2.1E−03	n=2	fg=0.11	bg=0.00
female pregnancy GO:0007565	p=2.7E−03	n=3	fg=0.16	bg=0.02
neuron development GO:0048666	p=3.6E−03	n=9	fg=0.47	bg=0.19
embryonic body morphogenesis GO:0010172	p=4.2E−03	n=3	fg=0.16	bg=0.02
somatic stem cell population maintenance GO:0035019	p=4.2E−03	n=3	fg=0.16	bg=0.02
basement membrane organization GO:0071711	p=6.0E−03	n=2	fg=0.11	bg=0.01
monovalent inorganic anion homeostasis GO:0055083	p=6.0E−03	n=2	fg=0.11	bg=0.01
blastocyst formation GO:0001825	p=6.0E−03	n=2	fg=0.11	bg=0.01
negative regulation of epidermal growth ... GO:0042059	p=6.0E−03	n=2	fg=0.11	bg=0.01
lens morphogenesis in camera−type eye GO:0002089	p=6.0E−03	n=2	fg=0.11	bg=0.01
developmental induction GO:0031128	p=6.0E−03	n=2	fg=0.11	bg=0.01
regulation of extracellular matrix disas... GO:0010715	p=6.0E−03	n=2	fg=0.11	bg=0.01
bile acid biosynthetic process GO:0006699	p=6.0E−03	n=2	fg=0.11	bg=0.01
DNA methylation GO:0006306	p=6.0E−03	n=2	fg=0.11	bg=0.01
positive regulation of animal organ morp... GO:0110110	p=6.0E−03	n=2	fg=0.11	bg=0.01
transcription, DNA−templated GO:0006351	p=6.6E−03	n=11	fg=0.58	bg=0.29
regulation of gene expression, epigeneti... GO:0040029	p=8.4E−03	n=3	fg=0.16	bg=0.02
positive regulation of locomotion GO:0040017	p=9.9E−03	n=5	fg=0.26	bg=0.08
positive regulation of apoptotic process GO:0043065	p=9.9E−03	n=5	fg=0.26	bg=0.08

−log(p)
n=19/66 input genes with annotations

fraction

Term	−log(p)	n	fg	bg
methylated histone binding GO:0035064	p=6.7E−03	n=2	fg=0.11	bg=0.01
single−stranded RNA binding GO:0003727	p=6.7E−03	n=2	fg=0.11	bg=0.01
protein tyrosine kinase binding GO:1990782	p=3.1E−02	n=2	fg=0.11	bg=0.02
protein C−terminus binding GO:0008022	p=3.1E−02	n=2	fg=0.11	bg=0.02
chromatin binding GO:0003682	p=3.2E−02	n=4	fg=0.22	bg=0.07
enzyme regulator activity GO:0030234	p=3.3E−02	n=5	fg=0.28	bg=0.11
guanyl−nucleotide exchange factor activi... GO:0005085	p=4.2E−02	n=2	fg=0.11	bg=0.02
phosphatidylinositol bisphosphate kinase... GO:0052813	p=5.0E−02	n=1	fg=0.06	bg=0.00
beta−1 adrenergic receptor binding GO:0031697	p=5.0E−02	n=1	fg=0.06	bg=0.00
dystroglycan binding GO:0002162	p=5.0E−02	n=1	fg=0.06	bg=0.00
poly−pyrimidine tract binding GO:0008187	p=5.0E−02	n=1	fg=0.06	bg=0.00
P−type sodium transporter activity GO:0008554	p=5.0E−02	n=1	fg=0.06	bg=0.00
ABC−type bile acid transporter activity GO:0015432	p=5.0E−02	n=1	fg=0.06	bg=0.00
mRNA 3'−UTR AU−rich region binding GO:0035925	p=5.0E−02	n=1	fg=0.06	bg=0.00
bile acid transmembrane transporter acti... GO:0015125	p=5.0E−02	n=1	fg=0.06	bg=0.00
canalicular bile acid transmembrane tran... GO:0015126	p=5.0E−02	n=1	fg=0.06	bg=0.00
poly(U) RNA binding GO:0008266	p=5.0E−02	n=1	fg=0.06	bg=0.00
phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934	p=5.0E−02	n=1	fg=0.06	bg=0.00
chromatin DNA binding GO:0031490	p=5.0E−02	n=1	fg=0.06	bg=0.00
rRNA primary transcript binding GO:0042134	p=5.0E−02	n=1	fg=0.06	bg=0.00
ATPase−coupled organic acid transmembran... GO:0033283	p=5.0E−02	n=1	fg=0.06	bg=0.00
ATPase−coupled carboxylic acid transmemb... GO:0033284	p=5.0E−02	n=1	fg=0.06	bg=0.00
GDP−dissociation inhibitor activity GO:0005092	p=5.0E−02	n=1	fg=0.06	bg=0.00
ATPase−coupled monocarboxylic acid trans... GO:0033285	p=5.0E−02	n=1	fg=0.06	bg=0.00
ubiquitin−protein transferase activator ... GO:0097027	p=5.0E−02	n=1	fg=0.06	bg=0.00
ubiquitin−protein transferase regulator ... GO:0055106	p=5.0E−02	n=1	fg=0.06	bg=0.00
nuclear receptor coactivator activity GO:0030374	p=5.0E−02	n=1	fg=0.06	bg=0.00
acylglycerol lipase activity GO:0047372	p=5.0E−02	n=1	fg=0.06	bg=0.00
1−phosphatidylinositol−3−kinase activity GO:0016303	p=5.0E−02	n=1	fg=0.06	bg=0.00
phosphatidylinositol kinase activity GO:0052742	p=5.0E−02	n=1	fg=0.06	bg=0.00

−log(p)
n=18/66 input genes with annotations

fraction

Term	−log(p)	n	fg	bg
intercalary heterochromatin GO:0005725	p=2.1E−03	n=2	fg=0.11	bg=0.00
cell cortex GO:0005938	p=5.8E−03	n=4	fg=0.21	bg=0.04
PRC1 complex GO:0035102	p=6.2E−03	n=2	fg=0.11	bg=0.01
cytoplasmic region GO:0099568	p=7.2E−03	n=4	fg=0.21	bg=0.04
nuclear lumen GO:0031981	p=1.2E−02	n=10	fg=0.53	bg=0.27
Golgi apparatus GO:0005794	p=1.4E−02	n=7	fg=0.37	bg=0.15
nucleoplasm GO:0005654	p=1.6E−02	n=9	fg=0.47	bg=0.23
growth cone GO:0030426	p=1.9E−02	n=3	fg=0.16	bg=0.03
site of polarized growth GO:0030427	p=2.4E−02	n=3	fg=0.16	bg=0.03
distal axon GO:0150034	p=2.7E−02	n=4	fg=0.21	bg=0.06
nuclear chromosome GO:0000228	p=4.0E−02	n=3	fg=0.16	bg=0.04
membrane−enclosed lumen GO:0031974	p=4.2E−02	n=10	fg=0.53	bg=0.32
intracellular organelle lumen GO:0070013	p=4.2E−02	n=10	fg=0.53	bg=0.32
organelle lumen GO:0043233	p=4.2E−02	n=10	fg=0.53	bg=0.32
Golgi apparatus subcompartment GO:0098791	p=4.4E−02	n=4	fg=0.21	bg=0.07
microtubule plus−end GO:0035371	p=4.7E−02	n=1	fg=0.05	bg=0.00
cortical microtubule plus−end GO:1903754	p=4.7E−02	n=1	fg=0.05	bg=0.00
Cajal body GO:0015030	p=4.7E−02	n=1	fg=0.05	bg=0.00
cytoplasmic microtubule plus−end GO:1904511	p=4.7E−02	n=1	fg=0.05	bg=0.00
NuRD complex GO:0016581	p=4.7E−02	n=1	fg=0.05	bg=0.00
polysomal ribosome GO:0042788	p=4.7E−02	n=1	fg=0.05	bg=0.00
centrosomal corona GO:0031592	p=4.7E−02	n=1	fg=0.05	bg=0.00
cortical microtubule GO:0055028	p=4.7E−02	n=1	fg=0.05	bg=0.00
RNA polymerase III transcription regulat... GO:0090576	p=4.7E−02	n=1	fg=0.05	bg=0.00
gut granule GO:0044840	p=4.7E−02	n=1	fg=0.05	bg=0.00
gut granule membrane GO:0044841	p=4.7E−02	n=1	fg=0.05	bg=0.00
hippocampal mossy fiber to CA3 synapse GO:0098686	p=4.7E−02	n=1	fg=0.05	bg=0.00
type I terminal bouton GO:0061174	p=4.7E−02	n=1	fg=0.05	bg=0.00
excitatory synapse GO:0060076	p=4.7E−02	n=1	fg=0.05	bg=0.00
PML body GO:0016605	p=4.7E−02	n=1	fg=0.05	bg=0.00

−log(p)
n=19/66 input genes with annotations

fraction