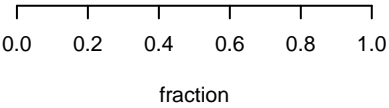
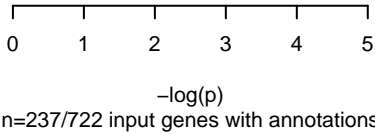


GO:BP
Ncol_Nvec_vc1.1_XM_032381562.2

fraction genes in fg and expected value

adrenal gland development	GO:0030325	p=5.8E-05	n=4
positive regulation of neuron apoptotic ...	GO:0043525	p=7.3E-05	n=9
male courtship behavior, veined wing gen...	GO:0045433	p=2.5E-03	n=3
regulation of extrinsic apoptotic signal...	GO:2001239	p=3.6E-03	n=5
potassium ion transmembrane transport	GO:0071805	p=4.2E-03	n=8
vasculature development	GO:0001944	p=4.6E-03	n=18
head involution	GO:0008258	p=5.1E-03	n=4
negative regulation of purine nucleotide...	GO:1900543	p=5.1E-03	n=4
skeletal muscle fiber development	GO:0048741	p=5.1E-03	n=4
positive regulation of behavior	GO:0048520	p=5.6E-03	n=7
copper ion transport	GO:0006825	p=5.8E-03	n=3
regulation of sodium ion transmembrane t...	GO:2000649	p=5.8E-03	n=3
ciliary basal body-plasma membrane docki...	GO:0097711	p=6.3E-03	n=8
regulation of G2/M transition of mitotic...	GO:0010389	p=7.4E-03	n=10
protein deacylation	GO:0035601	p=7.5E-03	n=6
osteoblast differentiation	GO:0001649	p=7.6E-03	n=8
protein maturation by copper ion transfe...	GO:0015680	p=7.7E-03	n=2
negative regulation of dauer larval deve...	GO:0061067	p=7.7E-03	n=2
disruption of cells of another organism	GO:0044364	p=7.7E-03	n=2
regulation of iron ion transmembrane tra...	GO:0034759	p=7.7E-03	n=2
response to odorant	GO:1990834	p=7.7E-03	n=2
Sertoli cell proliferation	GO:0060011	p=7.7E-03	n=2
negative regulation of transforming grow...	GO:0071635	p=7.7E-03	n=2
killing of cells of another organism	GO:0031640	p=7.7E-03	n=2
negative regulation of oxidative phospho...	GO:0090324	p=7.7E-03	n=2
negative regulation of pancreatic juice ...	GO:0090188	p=7.7E-03	n=2
regulation of cilium beat frequency invo...	GO:0060296	p=7.7E-03	n=2
male germ-line sex determination	GO:0019100	p=7.7E-03	n=2
positive regulation of lamellipodium ass...	GO:0010592	p=7.9E-03	n=4
limb morphogenesis	GO:0035108	p=9.1E-03	n=8

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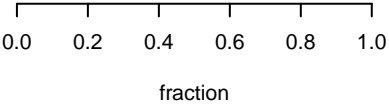
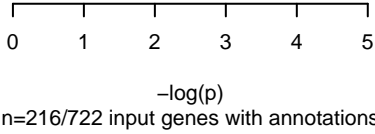


GO:MF
Ncol_Nvec_vc1.1_XM_032381562.2

fraction genes in fg and expected value

translation factor activity, RNA binding	GO:0008135	p=5.5E-04	n=9
voltage-gated cation channel activity	GO:0022843	p=2.5E-03	n=7
ribosome binding	GO:0043022	p=6.1E-03	n=5
calcium-activated potassium channel acti...	GO:0015269	p=6.5E-03	n=3
BH3 domain binding	GO:0051434	p=8.3E-03	n=2
actinin binding	GO:0048185	p=8.3E-03	n=2
superoxide dismutase copper chaperone ac...	GO:0016532	p=8.3E-03	n=2
histone deacetylase activity	GO:0004407	p=9.1E-03	n=4
hormone binding	GO:0042562	p=1.3E-02	n=4
voltage-gated potassium channel activity	GO:0005249	p=1.3E-02	n=4
signaling adaptor activity	GO:0035591	p=1.9E-02	n=5
carbohydrate kinase activity	GO:0019200	p=2.0E-02	n=3
activin-activated receptor activity	GO:0017002	p=2.3E-02	n=2
transforming growth factor beta-activate...	GO:0005024	p=2.3E-02	n=2
transmembrane receptor protein serine/th...	GO:0004675	p=2.3E-02	n=2
microtubule motor activity	GO:0003777	p=2.5E-02	n=4
kinase activity	GO:0016301	p=2.9E-02	n=22
quaternary ammonium group binding	GO:0050997	p=4.2E-02	n=3
carbohydrate derivative binding	GO:0097367	p=4.4E-02	n=24
phosphotransferase activity, alcohol gro...	GO:0016773	p=4.4E-02	n=20
dynein light intermediate chain binding	GO:0051959	p=4.4E-02	n=2
palmitoyl-(protein) hydrolase activity	GO:0008474	p=4.4E-02	n=2
phosphatidylethanolamine binding	GO:0008429	p=4.4E-02	n=2
palmitoyl hydrolase activity	GO:0098599	p=4.4E-02	n=2
magnesium ion binding	GO:0000287	p=4.7E-02	n=9
transferase activity, transferring phosp...	GO:0016772	p=4.9E-02	n=26
translation initiation factor activity	GO:0003743	p=5.1E-02	n=4
transferase activity	GO:0016740	p=5.3E-02	n=54
protein kinase activity	GO:0004672	p=5.4E-02	n=17
heparin binding	GO:0008201	p=5.5E-02	n=3

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GO:CC
Ncol_Nvec_vc1.1_XM_032381562.2

fraction genes in fg and expected value

activin receptor complex	GO:0048179	p=8.3E-03	n=2
voltage-gated potassium channel complex	GO:0008076	p=9.1E-03	n=4
centriole	GO:0005814	p=1.9E-02	n=7
EARP complex	GO:1990745	p=2.3E-02	n=2
eukaryotic translation initiation factor...	GO:0005850	p=2.3E-02	n=2
GARP complex	GO:0000938	p=2.3E-02	n=2
Bcl-2 family protein complex	GO:0097136	p=2.3E-02	n=2
histone deacetylase complex	GO:0000118	p=2.5E-02	n=4
actin filament	GO:0005884	p=3.2E-02	n=4
chromosome, centromeric region	GO:0000775	p=5.9E-02	n=8
perikaryon	GO:0043204	p=6.1E-02	n=5
eukaryotic translation initiation factor...	GO:0005851	p=6.9E-02	n=2
RNA polymerase II, core complex	GO:0005665	p=6.9E-02	n=2
sperm fibrous sheath	GO:0035686	p=6.9E-02	n=2
intermediate filament cytoskeleton	GO:0045111	p=7.1E-02	n=3
neuron projection cytoplasm	GO:0120111	p=7.1E-02	n=3
A band	GO:0031672	p=7.4E-02	n=4
phagocytic vesicle	GO:0045335	p=8.1E-02	n=5
M band	GO:0031430	p=8.9E-02	n=3
protein farnesyltransferase complex	GO:0005965	p=9.1E-02	n=1
protein kinase CK2 complex	GO:0005956	p=9.1E-02	n=1
ciliary cap	GO:0061822	p=9.1E-02	n=1
FACT complex	GO:0035101	p=9.1E-02	n=1
translation initiation ternary complex	GO:0044207	p=9.1E-02	n=1
eukaryotic 48S preinitiation complex	GO:0033290	p=9.1E-02	n=1
astrocyte end-foot	GO:0097450	p=9.1E-02	n=1
clathrin-sculpted gamma-aminobutyric aci...	GO:0061200	p=9.1E-02	n=1
glial limiting end-foot	GO:0097451	p=9.1E-02	n=1
clathrin-sculpted gamma-aminobutyric aci...	GO:0061202	p=9.1E-02	n=1
pinosome	GO:0044352	p=9.1E-02	n=1

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