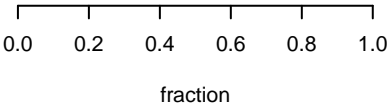
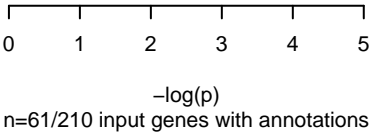


GO:BP
Ncol_Nvec_vc1.1_XM_032384420.2

fraction genes in fg and expected value

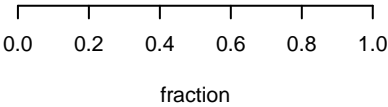
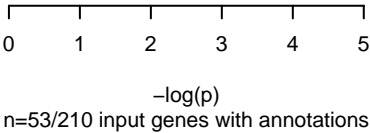
negative regulation of sequestering of t...	GO:0010891	p=1.1E-03	n=2	fg=0.03	bg=0.00
proximal/distal pattern formation, imagi...	GO:0007449	p=1.1E-03	n=2	fg=0.03	bg=0.00
motor neuron axon guidance	GO:0008045	p=1.6E-03	n=4	fg=0.07	bg=0.01
monocarboxylic acid catabolic process	GO:0072329	p=3.1E-03	n=4	fg=0.07	bg=0.01
somatic sex determination	GO:0018993	p=6.4E-03	n=2	fg=0.03	bg=0.00
semicircular canal development	GO:0060872	p=6.4E-03	n=2	fg=0.03	bg=0.00
negative regulation of alpha-beta T cell...	GO:0046639	p=6.4E-03	n=2	fg=0.03	bg=0.00
triglyceride catabolic process	GO:0019433	p=6.4E-03	n=2	fg=0.03	bg=0.00
branching involved in salivary gland mor...	GO:0060445	p=6.4E-03	n=2	fg=0.03	bg=0.00
branching involved in ureteric bud morph...	GO:0001658	p=6.4E-03	n=3	fg=0.05	bg=0.01
positive regulation of cell population p...	GO:0008284	p=6.7E-03	n=9	fg=0.15	bg=0.06
hippocampus development	GO:0021766	p=7.4E-03	n=4	fg=0.07	bg=0.01
cranial nerve morphogenesis	GO:0021602	p=1.0E-02	n=3	fg=0.05	bg=0.01
forebrain regionalization	GO:0021871	p=1.0E-02	n=2	fg=0.03	bg=0.00
positive regulation of cell migration in...	GO:0090050	p=1.0E-02	n=2	fg=0.03	bg=0.00
artery development	GO:0060840	p=1.2E-02	n=3	fg=0.05	bg=0.01
forebrain generation of neurons	GO:0021872	p=1.5E-02	n=3	fg=0.05	bg=0.01
positive regulation of mitotic cell cycl...	GO:1901992	p=1.5E-02	n=3	fg=0.05	bg=0.01
outflow tract morphogenesis	GO:0003151	p=1.5E-02	n=3	fg=0.05	bg=0.01
metanephros development	GO:0001656	p=1.5E-02	n=3	fg=0.05	bg=0.01
fatty acid catabolic process	GO:0009062	p=1.5E-02	n=3	fg=0.05	bg=0.01
negative regulation of receptor-mediated...	GO:0048261	p=1.5E-02	n=2	fg=0.03	bg=0.00
pole cell migration	GO:0007280	p=1.5E-02	n=2	fg=0.03	bg=0.00
optic nerve development	GO:0021554	p=1.5E-02	n=2	fg=0.03	bg=0.00
spinal cord motor neuron differentiation	GO:0021522	p=1.5E-02	n=2	fg=0.03	bg=0.00
positive regulation of alpha-beta T cell...	GO:0046638	p=1.5E-02	n=2	fg=0.03	bg=0.00
optic nerve morphogenesis	GO:0021631	p=1.5E-02	n=2	fg=0.03	bg=0.00
cranial nerve structural organization	GO:0021604	p=1.5E-02	n=2	fg=0.03	bg=0.00
cell migration involved in sprouting ang...	GO:0002042	p=1.5E-02	n=2	fg=0.03	bg=0.00
positive regulation of sprouting angioge...	GO:1903672	p=1.5E-02	n=2	fg=0.03	bg=0.00



GO:MF
Ncol_Nvec_vc1.1_XM_032384420.2

fraction genes in fg and expected value

triglyceride lipase activity	GO:0004806	p=3.2E-03	n=2	fg=0.04	bg=0.00
phospholipase A2 activity	GO:0004623	p=6.3E-03	n=2	fg=0.04	bg=0.00
transferase activity, transferring alkyl...	GO:0016765	p=1.5E-02	n=2	fg=0.04	bg=0.00
oxidoreductase activity, acting on NAD(P...	GO:0016651	p=2.7E-02	n=3	fg=0.06	bg=0.01
primary active transmembrane transporter...	GO:0015399	p=2.9E-02	n=4	fg=0.08	bg=0.02
acyltransferase activity, transferring g...	GO:0016747	p=3.0E-02	n=3	fg=0.06	bg=0.01
GDP-dissociation inhibitor binding	GO:0051021	p=3.3E-02	n=1	fg=0.02	bg=0.00
1-phosphatidylinositol-3-phosphate 4-kin...	GO:0052811	p=3.3E-02	n=1	fg=0.02	bg=0.00
lysophosphatidic acid binding	GO:0035727	p=3.3E-02	n=1	fg=0.02	bg=0.00
farnesyltransterase activity	GO:0004311	p=3.3E-02	n=1	fg=0.02	bg=0.00
protein farnesyltransferase activity	GO:0004660	p=3.3E-02	n=1	fg=0.02	bg=0.00
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597	p=3.3E-02	n=1	fg=0.02	bg=0.00
phosphatidylinositol phosphate kinase ac...	GO:0016307	p=3.3E-02	n=1	fg=0.02	bg=0.00
1-phosphatidylinositol-4-phosphate 5-kin...	GO:0016308	p=3.3E-02	n=1	fg=0.02	bg=0.00
1-phosphatidylinositol-5-phosphate 4-kin...	GO:0016309	p=3.3E-02	n=1	fg=0.02	bg=0.00
CCR5 chemokine receptor binding	GO:0031730	p=3.3E-02	n=1	fg=0.02	bg=0.00
semaphorin receptor activity	GO:0017154	p=3.3E-02	n=1	fg=0.02	bg=0.00
S100 protein binding	GO:0044548	p=3.3E-02	n=1	fg=0.02	bg=0.00
propionyl-CoA carboxylase activity	GO:0004658	p=3.3E-02	n=1	fg=0.02	bg=0.00
endoribonuclease activity, producing 3'-...	GO:0016892	p=3.3E-02	n=1	fg=0.02	bg=0.00
endonuclease activity, active with eithe...	GO:0016894	p=3.3E-02	n=1	fg=0.02	bg=0.00
rRNA primary transcript binding	GO:0042134	p=3.3E-02	n=1	fg=0.02	bg=0.00
tRNA-intron endonuclease activity	GO:0000213	p=3.3E-02	n=1	fg=0.02	bg=0.00
mono-olein transacylation activity	GO:0051264	p=3.3E-02	n=1	fg=0.02	bg=0.00
diolien transacylation activity	GO:0051265	p=3.3E-02	n=1	fg=0.02	bg=0.00
open rectifier potassium channel activit...	GO:0005252	p=3.3E-02	n=1	fg=0.02	bg=0.00
very-low-density lipoprotein particle re...	GO:0070326	p=3.3E-02	n=1	fg=0.02	bg=0.00
CCR chemokine receptor binding	GO:0048020	p=3.3E-02	n=1	fg=0.02	bg=0.00
protein tyrosine phosphatase activity, m...	GO:0030946	p=3.3E-02	n=1	fg=0.02	bg=0.00
signaling receptor inhibitor activity	GO:0030547	p=3.3E-02	n=1	fg=0.02	bg=0.00



GO:CC
Ncol_Nvec_vc1.1_XM_032384420.2

fraction genes in fg and expected value

ficolin-1-rich granule membrane	GO:0101003	p=1.4E-02	n=2	fg=0.03	bg=0.00
cell periphery	GO:0071944	p=1.4E-02	n=25	fg=0.43	bg=0.29
vacuolar proton-transporting V-type ATPa...	GO:0016471	p=1.9E-02	n=2	fg=0.03	bg=0.00
endoplasmic reticulum tubular network	GO:0071782	p=1.9E-02	n=2	fg=0.03	bg=0.00
proton-transporting V-type ATPase comple...	GO:0033176	p=2.5E-02	n=2	fg=0.03	bg=0.00
proton-transporting two-sector ATPase co...	GO:0016469	p=2.5E-02	n=2	fg=0.03	bg=0.00
cytosol	GO:0005829	p=2.9E-02	n=30	fg=0.52	bg=0.39
collagen and cuticulin-based cuticle ext...	GO:0060102	p=3.2E-02	n=1	fg=0.02	bg=0.00
katanin complex	GO:0008352	p=3.2E-02	n=1	fg=0.02	bg=0.00
insulin-responsive compartment	GO:0032593	p=3.2E-02	n=1	fg=0.02	bg=0.00
apical cytoplasm	GO:0090651	p=3.2E-02	n=1	fg=0.02	bg=0.00
core-binding factor complex	GO:0016513	p=3.2E-02	n=1	fg=0.02	bg=0.00
rough endoplasmic reticulum lumen	GO:0048237	p=3.2E-02	n=1	fg=0.02	bg=0.00
CCR4-NOT complex	GO:0030014	p=3.2E-02	n=1	fg=0.02	bg=0.00
CCR4-NOT core complex	GO:0030015	p=3.2E-02	n=1	fg=0.02	bg=0.00
semaphorin receptor complex	GO:0002116	p=3.2E-02	n=1	fg=0.02	bg=0.00
protein farnesyltransferase complex	GO:0005965	p=3.2E-02	n=1	fg=0.02	bg=0.00
tRNA-intron endonuclease complex	GO:0000214	p=3.2E-02	n=1	fg=0.02	bg=0.00
membrane	GO:0016020	p=3.8E-02	n=34	fg=0.59	bg=0.46
ficolin-1-rich granule	GO:0101002	p=5.3E-02	n=3	fg=0.05	bg=0.01
NADH dehydrogenase complex	GO:0030964	p=5.4E-02	n=2	fg=0.03	bg=0.01
mitochondrial respiratory chain complex ...	GO:0005747	p=5.4E-02	n=2	fg=0.03	bg=0.01
respiratory chain complex I	GO:0045271	p=5.4E-02	n=2	fg=0.03	bg=0.01
endosome	GO:0005768	p=6.2E-02	n=9	fg=0.16	bg=0.09
transcription repressor complex	GO:0017053	p=6.3E-02	n=2	fg=0.03	bg=0.01
cell body fiber	GO:0070852	p=6.3E-02	n=1	fg=0.02	bg=0.00
dystroglycan complex	GO:0016011	p=6.3E-02	n=1	fg=0.02	bg=0.00
sarcoglycan complex	GO:0016012	p=6.3E-02	n=1	fg=0.02	bg=0.00
neurofilament	GO:0005883	p=6.3E-02	n=1	fg=0.02	bg=0.00
Hedgehog signaling complex	GO:0035301	p=6.3E-02	n=1	fg=0.02	bg=0.00

