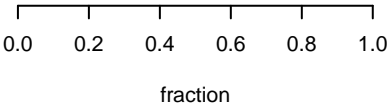
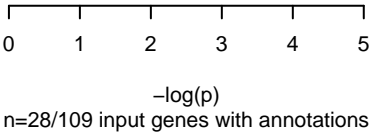


GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_032362607.2

fraction genes in fg and expected value

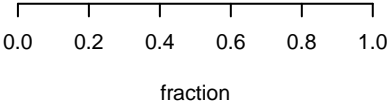
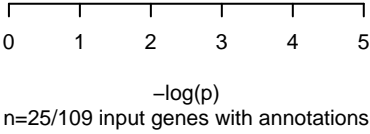
response to mercury ion	GO:0046689	p=1.4E-03	n=2	fg=0.07	bg=0.00
regulation of R7 cell differentiation	GO:0045676	p=4.6E-03	n=2	fg=0.07	bg=0.00
dormancy process	GO:0022611	p=6.1E-03	n=2	fg=0.07	bg=0.00
glycerolipid catabolic process	GO:0046503	p=7.7E-03	n=2	fg=0.07	bg=0.01
tissue remodeling	GO:0048771	p=9.2E-03	n=3	fg=0.11	bg=0.02
tricarboxylic acid metabolic process	GO:0072350	p=9.6E-03	n=2	fg=0.07	bg=0.01
blood vessel remodeling	GO:0001974	p=1.2E-02	n=2	fg=0.07	bg=0.01
SRP-dependent cotranslational protein ta...	GO:0006614	p=1.2E-02	n=2	fg=0.07	bg=0.01
cotranslational protein targeting to mem...	GO:0006613	p=1.4E-02	n=2	fg=0.07	bg=0.01
notum development	GO:0007477	p=1.5E-02	n=1	fg=0.04	bg=0.00
positive regulation of lysosomal protein...	GO:1905167	p=1.5E-02	n=1	fg=0.04	bg=0.00
aminoglycoside antibiotic metabolic proc...	GO:0030647	p=1.5E-02	n=1	fg=0.04	bg=0.00
positive regulation of protein depolymer...	GO:1901881	p=1.5E-02	n=1	fg=0.04	bg=0.00
positive regulation of protein catabolic...	GO:1904352	p=1.5E-02	n=1	fg=0.04	bg=0.00
regulation of spermidine biosynthetic pr...	GO:1901304	p=1.5E-02	n=1	fg=0.04	bg=0.00
positive regulation of spermidine biosyn...	GO:1901307	p=1.5E-02	n=1	fg=0.04	bg=0.00
response to vitamin A	GO:0033189	p=1.5E-02	n=1	fg=0.04	bg=0.00
regulation of endothelial cell activatio...	GO:1904987	p=1.5E-02	n=1	fg=0.04	bg=0.00
negative regulation of endothelial cell ...	GO:1904988	p=1.5E-02	n=1	fg=0.04	bg=0.00
bile acid secretion	GO:0032782	p=1.5E-02	n=1	fg=0.04	bg=0.00
regulation of polyamine biosynthetic pro...	GO:0010967	p=1.5E-02	n=1	fg=0.04	bg=0.00
positive regulation of CD4-positive, alp...	GO:2000516	p=1.5E-02	n=1	fg=0.04	bg=0.00
indole metabolic process	GO:0042431	p=1.5E-02	n=1	fg=0.04	bg=0.00
negative regulation of sevenless signal...	GO:0045873	p=1.5E-02	n=1	fg=0.04	bg=0.00
spermidine catabolic process	GO:0046203	p=1.5E-02	n=1	fg=0.04	bg=0.00
spermine catabolic process	GO:0046208	p=1.5E-02	n=1	fg=0.04	bg=0.00
negative regulation of determination of ...	GO:2000016	p=1.5E-02	n=1	fg=0.04	bg=0.00
regulation of phosphate transmembrane tr...	GO:2000185	p=1.5E-02	n=1	fg=0.04	bg=0.00
negative regulation of compound eye phot...	GO:0110118	p=1.5E-02	n=1	fg=0.04	bg=0.00
prepulse inhibition	GO:0060134	p=1.5E-02	n=1	fg=0.04	bg=0.00



GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_032362607.2

fraction genes in fg and expected value

glycerophosphodiester phosphodiesterase ...	GO:0008889	p=1.6E-02	n=1	fg=0.04	bg=0.00
phosphate ion binding	GO:0042301	p=1.6E-02	n=1	fg=0.04	bg=0.00
citrate (Si)-synthase activity	GO:0004108	p=1.6E-02	n=1	fg=0.04	bg=0.00
acyltransferase activity, acyl groups co...	GO:0046912	p=1.6E-02	n=1	fg=0.04	bg=0.00
glycerophosphoinositol glycerophosphodie...	GO:0047395	p=1.6E-02	n=1	fg=0.04	bg=0.00
signal recognition particle binding	GO:0005047	p=1.6E-02	n=1	fg=0.04	bg=0.00
citrate synthase activity	GO:0036440	p=1.6E-02	n=1	fg=0.04	bg=0.00
rRNA primary transcript binding	GO:0042134	p=1.6E-02	n=1	fg=0.04	bg=0.00
polyamine oxidase activity	GO:0046592	p=1.6E-02	n=1	fg=0.04	bg=0.00
oxidoreductase activity, acting on the C...	GO:0016647	p=1.6E-02	n=1	fg=0.04	bg=0.00
sodium:phosphate symporter activity	GO:0005436	p=1.6E-02	n=1	fg=0.04	bg=0.00
CoA carboxylase activity	GO:0016421	p=1.6E-02	n=1	fg=0.04	bg=0.00
L-tyrosine aminotransferase activity	GO:0070547	p=1.6E-02	n=1	fg=0.04	bg=0.00
phosphatidylinositol-4,5-bisphosphate 4-...	GO:0034597	p=1.6E-02	n=1	fg=0.04	bg=0.00
growth factor activity	GO:0008083	p=1.6E-02	n=1	fg=0.04	bg=0.00
L-tyrosine:2-oxoglutarate aminotransfera...	GO:0004838	p=1.6E-02	n=1	fg=0.04	bg=0.00
7S RNA binding	GO:0008312	p=1.6E-02	n=1	fg=0.04	bg=0.00
propionyl-CoA carboxylase activity	GO:0004658	p=1.6E-02	n=1	fg=0.04	bg=0.00
intracellular sodium activated potassium...	GO:0005228	p=1.6E-02	n=1	fg=0.04	bg=0.00
spermine:oxygen oxidoreductase (spermidi...	GO:0052901	p=1.6E-02	n=1	fg=0.04	bg=0.00
N1-acetylspermidine:oxygen oxidoreductas...	GO:0052904	p=1.6E-02	n=1	fg=0.04	bg=0.00
carboxylic ester hydrolase activity	GO:0052689	p=2.8E-02	n=2	fg=0.08	bg=0.01
anion binding	GO:0043168	p=2.9E-02	n=7	fg=0.28	bg=0.13
gamma-glutamylcyclotransferase activity	GO:0003839	p=3.1E-02	n=1	fg=0.04	bg=0.00
phosphate ion transmembrane transporter ...	GO:0015114	p=3.1E-02	n=1	fg=0.04	bg=0.00
ligase activity, forming carbon-carbon b...	GO:0016885	p=3.1E-02	n=1	fg=0.04	bg=0.00
TPR domain binding	GO:0030911	p=3.1E-02	n=1	fg=0.04	bg=0.00
acylglycerol lipase activity	GO:0047372	p=3.1E-02	n=1	fg=0.04	bg=0.00
armadillo repeat domain binding	GO:0070016	p=3.1E-02	n=1	fg=0.04	bg=0.00
lipase activity	GO:0016298	p=3.4E-02	n=2	fg=0.08	bg=0.01



GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_032362607.2

fraction genes in fg and expected value

signal recognition particle, endoplasmic...	GO:0005786	p=1.5E-02	n=1	fg=0.04	bg=0.00
signal recognition particle	GO:0048500	p=1.5E-02	n=1	fg=0.04	bg=0.00
katanin complex	GO:0008352	p=1.5E-02	n=1	fg=0.04	bg=0.00
histone methyltransferase complex	GO:0035097	p=2.3E-02	n=2	fg=0.07	bg=0.01
microvillus	GO:0005902	p=2.5E-02	n=2	fg=0.07	bg=0.01
cytosolic aryl hydrocarbon receptor comp...	GO:0034752	p=3.0E-02	n=1	fg=0.04	bg=0.00
methyltransferase complex	GO:0034708	p=3.1E-02	n=2	fg=0.07	bg=0.01
nuclear aryl hydrocarbon receptor comple...	GO:0034753	p=4.4E-02	n=1	fg=0.04	bg=0.00
cytosol	GO:0005829	p=5.7E-02	n=15	fg=0.56	bg=0.39
peroxisomal matrix	GO:0005782	p=5.8E-02	n=1	fg=0.04	bg=0.00
intercellular canaliculus	GO:0046581	p=5.8E-02	n=1	fg=0.04	bg=0.00
microvillus membrane	GO:0031528	p=5.8E-02	n=1	fg=0.04	bg=0.00
microbody lumen	GO:0031907	p=5.8E-02	n=1	fg=0.04	bg=0.00
aryl hydrocarbon receptor complex	GO:0034751	p=5.8E-02	n=1	fg=0.04	bg=0.00
Set1C/COMPASS complex	GO:0048188	p=5.8E-02	n=1	fg=0.04	bg=0.00
MLL1 complex	GO:0071339	p=7.3E-02	n=1	fg=0.04	bg=0.00
organelle membrane contact site	GO:0044232	p=8.6E-02	n=1	fg=0.04	bg=0.00
MLL1/2 complex	GO:0044665	p=1.0E-01	n=1	fg=0.04	bg=0.00
actin-based cell projection	GO:0098858	p=1.0E-01	n=2	fg=0.07	bg=0.02
transmembrane transporter complex	GO:1902495	p=1.1E-01	n=2	fg=0.07	bg=0.02
fusome	GO:0045169	p=1.1E-01	n=1	fg=0.04	bg=0.00
transporter complex	GO:1990351	p=1.2E-01	n=2	fg=0.07	bg=0.02
voltage-gated potassium channel complex	GO:0008076	p=1.3E-01	n=1	fg=0.04	bg=0.00
potassium channel complex	GO:0034705	p=1.3E-01	n=1	fg=0.04	bg=0.00
integral component of plasma membrane	GO:0005887	p=1.4E-01	n=4	fg=0.15	bg=0.08
respiratory chain complex I	GO:0045271	p=1.7E-01	n=1	fg=0.04	bg=0.01
mitochondrial respiratory chain complex ...	GO:0005747	p=1.7E-01	n=1	fg=0.04	bg=0.01
NADH dehydrogenase complex	GO:0030964	p=1.7E-01	n=1	fg=0.04	bg=0.01
intrinsic component of plasma membrane	GO:0031226	p=1.7E-01	n=4	fg=0.15	bg=0.08
brush border membrane	GO:0031526	p=1.8E-01	n=1	fg=0.04	bg=0.01

