

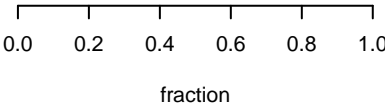
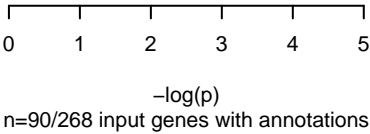
GO:BP
Ncol_Nvec_vc1.1_XM_001633398.3

fraction genes in fg and expected value

establishment or maintenance of apical/b...	GO:0035088
positive regulation of epithelial cell p...	GO:0050679
3'-UTR-mediated mRNA destabilization	GO:0061158
cellular response to salt	GO:1902075
histone H3-K4 methylation	GO:0051568
intra-Golgi vesicle-mediated transport	GO:0006891
inner ear receptor cell development	GO:0060119
negative regulation of cellular protein ...	GO:1903363
regulation of miRNA metabolic process	GO:2000628
regulation of retinoic acid receptor sig...	GO:0048385
protein localization to cell surface	GO:0034394
xenobiotic metabolic process	GO:0006805
embryonic organ development	GO:0048568
positive regulation of histone methylati...	GO:0031062
cellular response to retinoic acid	GO:0071300
ether metabolic process	GO:0018904
histone H3-K4 trimethylation	GO:0080182
negative regulation of ubiquitin-depende...	GO:2000059
negative regulation of mRNA metabolic pr...	GO:1903312
liver development	GO:0001889
regulation of cellular response to growt...	GO:0090287
hepaticobiliary system development	GO:0061008
heart development	GO:0007507
regulation of transforming growth factor...	GO:0071634
transforming growth factor beta producti...	GO:0071604
cellular response to vitamin D	GO:0071305
negative regulation of cardiac muscle ti...	GO:0055026
secondary palate development	GO:0062009
growth	GO:0040007
heart morphogenesis	GO:0003007

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p=1.4E-02	n=6
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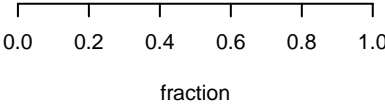
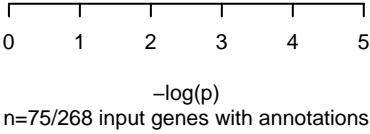
GO:MF
Ncol_Nvec_vc1.1_XM_001633398.3

fraction genes in fg and expected value

mRNA 3'-UTR binding	GO:0003730
structural constituent of muscle	GO:0008307
channel activity	GO:0015267
intramolecular transferase activity, pho...	GO:0016868
protein homodimerization activity	GO:0042803
voltage-gated channel activity	GO:0022832
voltage-gated ion channel activity	GO:0005244
organic cation transmembrane transporter...	GO:0015101
ion channel activity	GO:0005216
spectrin binding	GO:0030507
ammonium transmembrane transporter activ...	GO:0008519
ion gated channel activity	GO:0022839
voltage-gated cation channel activity	GO:0022843
exoribonuclease activity, producing 5'-p...	GO:0016896
3'-5'-exoribonuclease activity	GO:0000175
monosaccharide binding	GO:0048029
glycine N-choloyltransferase activity	GO:0047963
vascular endothelial growth factor recep...	GO:0043184
medium-chain acyl-CoA hydrolase activity	GO:0052815
long-chain acyl-CoA hydrolase activity	GO:0052816
very long chain acyl-CoA hydrolase activ...	GO:0052817
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159
histone pre-mRNA stem-loop binding	GO:0071207
neurotrophin binding	GO:0043121
transketolase activity	GO:0004802
CCR5 chemokine receptor binding	GO:0031730
aconitate hydratase activity	GO:0003994
DNA clamp loader activity	GO:0003689
cis-stilbene-oxide hydrolase activity	GO:0033961
open rectifier potassium channel activit...	GO:0005252

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GO:CC
Ncol_Nvec_vc1.1_XM_001633398.3

fraction genes in fg and expected value

dystrophin-associated glycoprotein compl...	GO:0016010
muscle cell projection membrane	GO:0036195
COPI vesicle coat	GO:0030126
Set1C/COMPASS complex	GO:0048188
Sin3-type complex	GO:0070822
euchromatin	GO:0000791
dendrite terminus	GO:0044292
cytosolic ribosome	GO:0022626
COPI-coated vesicle membrane	GO:0030663
BRCA1-A complex	GO:0070531
Shu complex	GO:0097196
axonemal heterotrimeric kinesin-II compl...	GO:0030993
histone pre-mRNA 3'end processing comple...	GO:0071204
kinesin II complex	GO:0016939
proteasome storage granule	GO:0034515
dendritic growth cone	GO:0044294
syntrophin complex	GO:0016013
BRCA1-BARD1 complex	GO:0031436
histone methyltransferase complex	GO:0035097
stress fiber	GO:0001725
contractile actin filament bundle	GO:0097517
striated muscle dense body	GO:0055120
tertiary granule lumen	GO:1904724
ciliary tip	GO:0097542
actin filament bundle	GO:0032432
ribosomal subunit	GO:0044391
coated vesicle membrane	GO:0030662
ribonucleoprotein complex	GO:1990904
cytoplasmic stress granule	GO:0010494
proteasome regulatory particle	GO:0005838

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