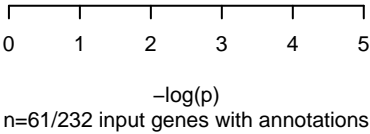


GO:BP
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

positive regulation of osteoclast differ...	GO:0045672	p=6.7E-04	n=3
skeletal muscle fiber development	GO:0048741	p=6.7E-04	n=3
sevenless signaling pathway	GO:0045500	p=3.3E-03	n=2
positive regulation of cellular response...	GO:1900409	p=3.3E-03	n=2
foam cell differentiation	GO:0090077	p=6.4E-03	n=2
regulation of photoreceptor cell differe...	GO:0046532	p=6.4E-03	n=3
potassium ion transmembrane transport	GO:0071805	p=7.4E-03	n=4
cholesterol homeostasis	GO:0042632	p=8.1E-03	n=3
cellular response to lipoprotein particl...	GO:0071402	p=1.0E-02	n=2
positive regulation of tissue remodeling	GO:0034105	p=1.0E-02	n=2
central nervous system segmentation	GO:0035283	p=1.0E-02	n=2
brain segmentation	GO:0035284	p=1.0E-02	n=2
oocyte microtubule cytoskeleton polariza...	GO:0008103	p=1.0E-02	n=2
regulation of early endosome to late end...	GO:2000641	p=1.0E-02	n=2
response to toxic substance	GO:0009636	p=1.1E-02	n=8
dephosphorylation	GO:0016311	p=1.5E-02	n=7
positive regulation of wound healing	GO:0090303	p=1.5E-02	n=2
positive regulation of alpha-beta T cell...	GO:0046638	p=1.5E-02	n=2
lymph vessel morphogenesis	GO:0036303	p=1.5E-02	n=2
cardiac muscle hypertrophy in response t...	GO:0014898	p=1.5E-02	n=2
cardiac muscle adaptation	GO:0014887	p=1.5E-02	n=2
regulation of pole plasm oskar mRNA loca...	GO:0007317	p=1.5E-02	n=2
muscle hypertrophy in response to stress	GO:0003299	p=1.5E-02	n=2
lymphangiogenesis	GO:0001946	p=1.5E-02	n=2
regulation of intracellular mRNA localiz...	GO:1904580	p=1.5E-02	n=2
regulation of embryonic pattern specific...	GO:1902875	p=1.5E-02	n=2
cellular response to extracellular stimu...	GO:0031668	p=1.7E-02	n=6
regulation of cell development	GO:0060284	p=1.8E-02	n=13
cellular response to starvation	GO:0009267	p=1.9E-02	n=5
T cell differentiation	GO:0030217	p=2.1E-02	n=4

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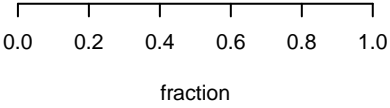
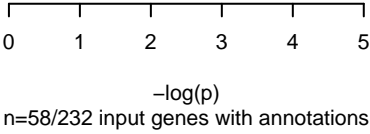


GO:MF
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

calcium-dependent protein serine/threoni...	GO:0004723	p=1.3E-03	n=2
voltage-gated potassium channel activity	GO:0005249	p=4.6E-03	n=3
lysophospholipid acyltransferase activit...	GO:0071617	p=1.2E-02	n=2
MAP kinase activity	GO:0004707	p=1.2E-02	n=2
lysophosphatidic acid acyltransferase ac...	GO:0042171	p=1.2E-02	n=2
protein heterodimerization activity	GO:0046982	p=1.6E-02	n=8
cholesterol binding	GO:0015485	p=1.8E-02	n=2
outward rectifier potassium channel acti...	GO:0015271	p=2.4E-02	n=2
sterol binding	GO:0032934	p=2.4E-02	n=2
ADP binding	GO:0043531	p=3.2E-02	n=2
steroid binding	GO:0005496	p=3.2E-02	n=2
tRNA (guanine-N1-)-methyltransferase act...	GO:0009019	p=3.6E-02	n=1
ABC-type sterol transporter activity	GO:0034041	p=3.6E-02	n=1
N-acetylglucosamine-1-phosphodiester alp...	GO:0003944	p=3.6E-02	n=1
tropomyosin binding	GO:0005523	p=3.6E-02	n=1
myosin tail binding	GO:0032029	p=3.6E-02	n=1
malate dehydrogenase (decarboxylating) (...)	GO:0004471	p=3.6E-02	n=1
malate dehydrogenase (decarboxylating) (...)	GO:0004473	p=3.6E-02	n=1
glutamate-ammonia ligase activity	GO:0004356	p=3.6E-02	n=1
ammonia ligase activity	GO:0016211	p=3.6E-02	n=1
N-acylsphingosine amidohydrolase activit...	GO:0017040	p=3.6E-02	n=1
N-acylneuraminate-9-phosphatase activity	GO:0050124	p=3.6E-02	n=1
intracellular sodium activated potassium...	GO:0005228	p=3.6E-02	n=1
calmodulin-dependent protein phosphatase...	GO:0033192	p=3.6E-02	n=1
DNA-binding transcription factor activit...	GO:0000981	p=3.6E-02	n=8
antigen binding	GO:0003823	p=4.0E-02	n=2
protein-disulfide reductase activity	GO:0015035	p=4.0E-02	n=2
alcohol binding	GO:0043178	p=4.9E-02	n=2
disulfide oxidoreductase activity	GO:0015036	p=5.8E-02	n=2
protein dimerization activity	GO:0046983	p=6.2E-02	n=12

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GO:CC
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

voltage-gated potassium channel complex	GO:0008076	p=2.9E-03	n=3
autophagosome membrane	GO:0000421	p=1.1E-02	n=2
transport vesicle membrane	GO:0030658	p=2.1E-02	n=4
magnesium-dependent protein serine/threo...	GO:0005963	p=2.2E-02	n=2
exocytic vesicle membrane	GO:0099501	p=3.0E-02	n=3
cuticular plate	GO:0032437	p=3.5E-02	n=1
calcineurin complex	GO:0005955	p=3.5E-02	n=1
kinesin I complex	GO:0016938	p=3.5E-02	n=1
brush border	GO:0005903	p=4.8E-02	n=3
transport vesicle	GO:0030133	p=5.9E-02	n=6
ciliary rootlet	GO:0035253	p=6.9E-02	n=1
COPII vesicle coat	GO:0030127	p=6.9E-02	n=1
transcription factor AP-1 complex	GO:0035976	p=6.9E-02	n=1
filamentous actin	GO:0031941	p=6.9E-02	n=1
cluster of actin-based cell projections	GO:0098862	p=7.1E-02	n=3
cortical actin cytoskeleton	GO:0030864	p=7.3E-02	n=2
mitochondrion	GO:0005739	p=7.4E-02	n=13
coated vesicle	GO:0030135	p=9.3E-02	n=4
cortical cytoskeleton	GO:0030863	p=9.4E-02	n=2
protein serine/threonine phosphatase com...	GO:0008287	p=9.4E-02	n=2
clathrin-coated vesicle	GO:0030136	p=9.8E-02	n=3
microtubule plus-end	GO:0035371	p=1.0E-01	n=1
Bcl-2 family protein complex	GO:0097136	p=1.0E-01	n=1
axon cytoplasm	GO:1904115	p=1.0E-01	n=1
actin cap	GO:0030478	p=1.0E-01	n=1
early endosome membrane	GO:0031901	p=1.0E-01	n=2
protein-DNA complex	GO:0032993	p=1.0E-01	n=2
phosphatase complex	GO:1903293	p=1.2E-01	n=2
exocytic vesicle	GO:0070382	p=1.2E-01	n=4
lysosomal lumen	GO:0043202	p=1.3E-01	n=2

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