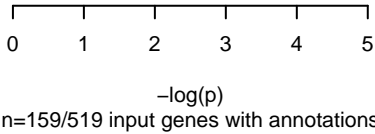


GO:BP
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

oocyte microtubule cytoskeleton organiza...	GO:0016325	p=1.2E-03	n=4
T cell differentiation involved in immun...	GO:0002292	p=1.8E-03	n=3
removal of superoxide radicals	GO:0019430	p=1.8E-03	n=3
cellular response to cadmium ion	GO:0071276	p=1.8E-03	n=4
protein maturation by copper ion transfe...	GO:0015680	p=3.4E-03	n=2
response to selenium ion	GO:0010269	p=3.4E-03	n=2
intrinsic apoptotic signaling pathway in...	GO:0008631	p=4.0E-03	n=4
positive regulation of osteoclast differ...	GO:0045672	p=5.9E-03	n=3
regulation of embryonic pattern specific...	GO:1902875	p=9.0E-03	n=3
regulation of vascular associated smooth...	GO:1904752	p=9.0E-03	n=3
response to manganese ion	GO:0010042	p=9.0E-03	n=3
regulation of pole plasm oskar mRNA loca...	GO:0007317	p=9.0E-03	n=3
regulation of cell development	GO:0060284	p=9.5E-03	n=26
negative regulation of miRNA-mediated ge...	GO:0060965	p=9.9E-03	n=2
antibiotic biosynthetic process	GO:0017000	p=9.9E-03	n=2
establishment or maintenance of polarity...	GO:0016332	p=9.9E-03	n=2
stress response to copper ion	GO:1990169	p=9.9E-03	n=2
transdifferentiation	GO:0060290	p=9.9E-03	n=2
sevenless signaling pathway	GO:0045500	p=9.9E-03	n=2
locomotory behavior	GO:0007626	p=1.0E-02	n=14
intracellular lipid transport	GO:0032365	p=1.3E-02	n=3
myotube cell development	GO:0014904	p=1.3E-02	n=3
skeletal muscle fiber development	GO:0048741	p=1.3E-02	n=3
Schwann cell differentiation	GO:0014037	p=1.3E-02	n=3
regulation of primary metabolic process	GO:0080090	p=1.4E-02	n=75
regulation of nitrogen compound metaboli...	GO:0051171	p=1.5E-02	n=73
regulation of autophagosome assembly	GO:2000785	p=1.5E-02	n=4
forebrain neuron development	GO:0021884	p=1.8E-02	n=3
oocyte dorsal/ventral axis specification	GO:0007310	p=1.8E-02	n=3
regulation of oxidative stress-induced i...	GO:1902175	p=1.8E-02	n=3

fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.16	bg=0.10
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.09	bg=0.04
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.47	bg=0.39
fg=0.46	bg=0.37
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00

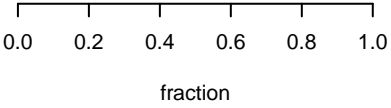
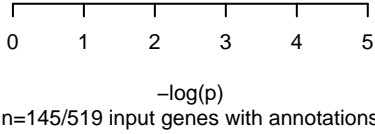


GO:MF
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

superoxide dismutase copper chaperone ac...	GO:0016532	p=3.7E-03	n=2
rRNA (guanine) methyltransferase activit...	GO:0016435	p=3.7E-03	n=2
copper ion binding	GO:0005507	p=6.2E-03	n=4
MAP kinase activity	GO:0004707	p=6.6E-03	n=3
transcription regulator activity	GO:0140110	p=9.5E-03	n=24
lysophospholipid acyltransferase activit...	GO:0071617	p=1.0E-02	n=3
lysophosphatidic acid acyltransferase ac...	GO:0042171	p=1.0E-02	n=3
calcium-dependent protein serine/threoni...	GO:0004723	p=1.1E-02	n=2
1-acylglycerophosphocholine O-acyltransf...	GO:0047184	p=1.1E-02	n=2
small GTPase binding	GO:0031267	p=1.1E-02	n=13
O-acyltransferase activity	GO:0008374	p=2.0E-02	n=3
DNA-binding transcription factor activit...	GO:0000981	p=2.0E-02	n=15
potassium channel activity	GO:0005267	p=2.1E-02	n=4
voltage-gated potassium channel activity	GO:0005249	p=2.6E-02	n=3
transcription coregulator activity	GO:0003712	p=2.7E-02	n=13
cis-regulatory region sequence-specific ...	GO:0000987	p=3.7E-02	n=9
RNA polymerase II cis-regulatory region ...	GO:0000978	p=3.7E-02	n=9
GTPase activator activity	GO:0005096	p=4.0E-02	n=7
DNA-(apurinic or apyrimidinic site) endo...	GO:0003906	p=4.7E-02	n=2
R-SMAD binding	GO:0070412	p=4.7E-02	n=2
1-acylglycerol-3-phosphate O-acyltransfe...	GO:0003841	p=4.7E-02	n=2
phosphotransferase activity, for other s...	GO:0016780	p=4.7E-02	n=2
potassium ion transmembrane transporter ...	GO:0015079	p=4.8E-02	n=4
GTPase binding	GO:0051020	p=4.8E-02	n=13
deoxyribonuclease activity	GO:0004536	p=5.0E-02	n=3
ADP binding	GO:0043531	p=5.9E-02	n=3
sphingolipid transfer activity	GO:0120016	p=6.1E-02	n=1
ceramide transfer activity	GO:0120017	p=6.1E-02	n=1
tropomyosin binding	GO:0005523	p=6.1E-02	n=1
thioether S-methyltransferase activity	GO:0004790	p=6.1E-02	n=1

fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.17	bg=0.10
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.09	bg=0.04
fg=0.02	bg=0.00
fg=0.10	bg=0.06
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.09	bg=0.05
fg=0.06	bg=0.03
fg=0.06	bg=0.03
fg=0.05	bg=0.02
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.09	bg=0.05
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

Golgi cis cisterna	GO:0000137	p=1.9E-03	n=3
tight junction	GO:0070160	p=1.3E-02	n=4
voltage-gated potassium channel complex	GO:0008076	p=1.8E-02	n=3
potassium channel complex	GO:0034705	p=1.8E-02	n=3
MLL1/2 complex	GO:0044665	p=2.4E-02	n=3
bicellular tight junction	GO:0005923	p=3.1E-02	n=3
MLL3/4 complex	GO:0044666	p=3.1E-02	n=2
Set1C/COMPASS complex	GO:0048188	p=3.1E-02	n=2
axon cytoplasm	GO:1904115	p=4.5E-02	n=2
autophagosome membrane	GO:0000421	p=4.5E-02	n=2
apical junction complex	GO:0043296	p=5.1E-02	n=4
polytene chromosome band	GO:0005704	p=6.0E-02	n=1
cytoplasmic periphery of the nuclear por...	GO:1990723	p=6.0E-02	n=1
nuclear pore cytoplasmic filaments	GO:0044614	p=6.0E-02	n=1
NLS-dependent protein nuclear import com...	GO:0042564	p=6.0E-02	n=1
TSC1-TSC2 complex	GO:0033596	p=6.0E-02	n=1
smooth septate junction	GO:0005920	p=6.0E-02	n=1
anterior cell cortex	GO:0061802	p=6.0E-02	n=1
Schmidt-Lanterman incisure	GO:0043220	p=6.0E-02	n=1
internode region of axon	GO:0033269	p=6.0E-02	n=1
kinesin I complex	GO:0016938	p=6.0E-02	n=1
compact myelin	GO:0043218	p=6.0E-02	n=1
proteasome core complex, beta-subunit co...	GO:0019774	p=6.0E-02	n=1
apicolateral plasma membrane	GO:0016327	p=6.1E-02	n=2
apical dendrite	GO:0097440	p=6.1E-02	n=2
endosome	GO:0005768	p=6.3E-02	n=17
magnesium-dependent protein serine/threo...	GO:0005963	p=7.8E-02	n=2
U5 snRNP	GO:0005682	p=7.8E-02	n=2
spliceosomal snRNP complex	GO:0097525	p=8.8E-02	n=3
Golgi-associated vesicle	GO:0005798	p=9.4E-02	n=5

fg=0.02	bg=0.00
fg=0.02	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.11	bg=0.07
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.01
fg=0.03	bg=0.02

