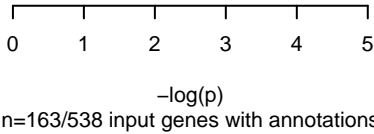


GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_001628945.3

fraction genes in fg and expected value

cellular response to stress	GO:0033554	p=3.8E-04	n=51
lymphoid progenitor cell differentiation	GO:0002320	p=8.3E-04	n=3
Rab protein signal transduction	GO:0032482	p=1.3E-03	n=4
positive regulation of transcription by ...	GO:0045944	p=1.9E-03	n=25
adherens junction maintenance	GO:0034334	p=2.0E-03	n=3
histone H2B ubiquitination	GO:0033523	p=2.0E-03	n=3
myeloid leukocyte differentiation	GO:0002573	p=2.6E-03	n=8
DNA catabolic process, endonucleolytic	GO:0000737	p=3.0E-03	n=4
mesodermal cell fate specification	GO:0007501	p=3.0E-03	n=4
ISG15-protein conjugation	GO:0032020	p=3.6E-03	n=2
positive regulation of megakaryocyte dif...	GO:0045654	p=3.6E-03	n=2
otic placode formation	GO:0043049	p=3.6E-03	n=2
determination of ventral identity	GO:0048264	p=3.6E-03	n=2
regulation of primitive erythrocyte diff...	GO:0010725	p=3.6E-03	n=2
positive regulation of oviposition	GO:1901046	p=3.8E-03	n=3
morphogenesis of embryonic epithelium	GO:0016331	p=3.9E-03	n=12
neuron fate commitment	GO:0048663	p=4.1E-03	n=7
histone H3-K9 modification	GO:0061647	p=4.3E-03	n=4
positive regulation of hemopoiesis	GO:1903708	p=4.5E-03	n=6
proteolysis	GO:0006508	p=5.2E-03	n=31
histone H3-K4 methylation	GO:0051568	p=5.6E-03	n=5
regeneration	GO:0031099	p=6.0E-03	n=10
larval somatic muscle development	GO:0007526	p=6.3E-03	n=3
regulation of G1/S transition of mitotic...	GO:2000045	p=6.6E-03	n=7
positive regulation of gene expression	GO:0010628	p=6.7E-03	n=37
somatic stem cell population maintenance	GO:0035019	p=7.0E-03	n=5
germarium-derived egg chamber formation	GO:0007293	p=7.0E-03	n=5
T cell receptor signaling pathway	GO:0050852	p=7.0E-03	n=5
cell-cell signaling by wnt	GO:0198738	p=8.0E-03	n=13
protein monoubiquitination	GO:0006513	p=8.6E-03	n=5

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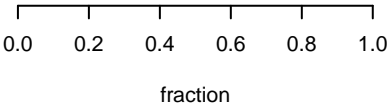
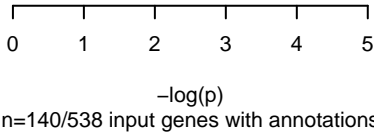


GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_001628945.3

fraction genes in fg and expected value

core promoter sequence-specific DNA bind...	GO:0001046	p=3.1E-03	n=5
ISG15 transferase activity	GO:0042296	p=3.5E-03	n=2
transcription coactivator activity	GO:0003713	p=4.7E-03	n=11
DNA-binding transcription activator acti...	GO:0001228	p=1.0E-02	n=10
DNA-binding transcription activator acti...	GO:0001216	p=1.0E-02	n=10
poly(U) RNA binding	GO:0008266	p=1.3E-02	n=3
DNA-binding transcription factor activit...	GO:0003700	p=1.7E-02	n=17
receptor ligand activity	GO:0048018	p=1.8E-02	n=3
poly-pyrimidine tract binding	GO:0008187	p=1.8E-02	n=3
protein binding	GO:0005515	p=2.0E-02	n=94
signaling receptor activator activity	GO:0030546	p=2.4E-02	n=3
chromatin binding	GO:0003682	p=2.8E-02	n=13
signaling receptor regulator activity	GO:0030545	p=3.0E-02	n=3
demethylase activity	GO:0032451	p=3.0E-02	n=3
cis-regulatory region sequence-specific ...	GO:0000987	p=3.0E-02	n=9
RNA polymerase II cis-regulatory region ...	GO:0000978	p=3.0E-02	n=9
sphingolipid binding	GO:0046625	p=3.1E-02	n=2
misfolded protein binding	GO:0051787	p=3.1E-02	n=2
RNA polymerase II complex binding	GO:0000993	p=3.1E-02	n=2
histone H3-methyl-lysine-4 demethylase a...	GO:0032453	p=3.1E-02	n=2
alcohol binding	GO:0043178	p=3.7E-02	n=3
ubiquitin conjugating enzyme activity	GO:0061631	p=3.7E-02	n=3
histone acetyltransferase binding	GO:0035035	p=3.7E-02	n=3
lipid transfer activity	GO:0120013	p=4.4E-02	n=2
sodium channel activity	GO:0005272	p=4.4E-02	n=2
ubiquitin-like protein conjugating enzym...	GO:0061650	p=4.5E-02	n=3
small molecule binding	GO:0036094	p=5.3E-02	n=21
nucleotide binding	GO:0000166	p=5.8E-02	n=17
nucleoside phosphate binding	GO:1901265	p=5.8E-02	n=17
cadmium ion binding	GO:0046870	p=5.9E-02	n=1

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GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_001628945.3

fraction genes in fg and expected value

extrinsic component of cytoplasmic side ...	GO:0031234	p=7.9E-03	n=5
nucleoplasm	GO:0005654	p=8.5E-03	n=63
polysome	GO:0005844	p=1.4E-02	n=5
non-membrane-bounded organelle	GO:0043228	p=1.8E-02	n=69
intracellular non-membrane-bounded organ...	GO:0043232	p=1.8E-02	n=69
transcription regulator complex	GO:0005667	p=1.9E-02	n=12
nucleolus	GO:0005730	p=2.8E-02	n=23
presynaptic periaxial zone	GO:0036062	p=3.4E-02	n=2
anchored component of plasma membrane	GO:0046658	p=3.4E-02	n=2
ciliary basal body	GO:0036064	p=4.3E-02	n=6
heterotrimeric G-protein complex	GO:0005834	p=4.9E-02	n=2
GTPase complex	GO:1905360	p=4.9E-02	n=2
histone acetyltransferase complex	GO:0000123	p=5.1E-02	n=4
endocytic vesicle	GO:0030139	p=5.2E-02	n=7
cleavage furrow	GO:0032154	p=5.2E-02	n=3
ciliary base	GO:0097546	p=5.2E-02	n=3
midbody	GO:0030496	p=5.2E-02	n=6
bleb	GO:0032059	p=6.2E-02	n=1
EKC/KEOPS complex	GO:0000408	p=6.2E-02	n=1
interleukin-5 receptor complex	GO:0005895	p=6.2E-02	n=1
core-binding factor complex	GO:0016513	p=6.2E-02	n=1
DNA polymerase III, core complex	GO:0044776	p=6.2E-02	n=1
apoptosome	GO:0043293	p=6.2E-02	n=1
centralspindlin complex	GO:0097149	p=6.2E-02	n=1
cyclin E1-CDK2 complex	GO:0097134	p=6.2E-02	n=1
cyclin E2-CDK2 complex	GO:0097135	p=6.2E-02	n=1
insulin-responsive compartment	GO:0032593	p=6.2E-02	n=1
Grb2-Sos complex	GO:0070618	p=6.2E-02	n=1
CHOP-C/EBP complex	GO:0036488	p=6.2E-02	n=1
TRAPPII protein complex	GO:1990071	p=6.2E-02	n=1

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