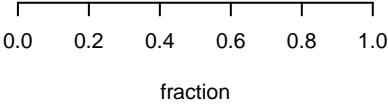
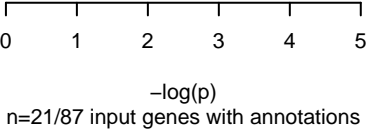


GO:BP
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

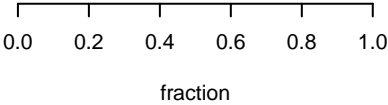
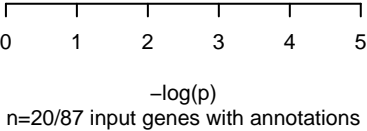
| | | | | | |
|---|------------|-----------|-----|---------|---------|
| positive regulation of osteoclast differ... | GO:0045672 | p=7.4E-03 | n=2 | fg=0.10 | bg=0.01 |
| foam cell differentiation | GO:0090077 | p=1.4E-02 | n=2 | fg=0.10 | bg=0.01 |
| negative regulation of intrinsic apoptot... | GO:2001243 | p=1.4E-02 | n=2 | fg=0.10 | bg=0.01 |
| positive regulation of intrinsic apoptot... | GO:2001244 | p=1.4E-02 | n=2 | fg=0.10 | bg=0.01 |
| central nervous system segmentation | GO:0035283 | p=1.4E-02 | n=2 | fg=0.10 | bg=0.01 |
| brain segmentation | GO:0035284 | p=1.4E-02 | n=2 | fg=0.10 | bg=0.01 |
| cytokine-mediated signaling pathway | GO:0019221 | p=1.9E-02 | n=3 | fg=0.14 | bg=0.03 |
| regulation of intrinsic apoptotic signal... | GO:2001242 | p=3.3E-02 | n=2 | fg=0.10 | bg=0.01 |
| regulation of response to DNA damage sti... | GO:2001020 | p=3.3E-02 | n=2 | fg=0.10 | bg=0.01 |
| potassium ion transmembrane transport | GO:0071805 | p=3.6E-02 | n=3 | fg=0.14 | bg=0.04 |
| positive regulation of apoptotic signal... | GO:2001235 | p=4.5E-02 | n=2 | fg=0.10 | bg=0.02 |
| positive regulation of intracellular pro... | GO:0090316 | p=4.5E-02 | n=2 | fg=0.10 | bg=0.02 |
| histone H2A K63-linked ubiquitination | GO:0070535 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| determination of ventral identity | GO:0048264 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| regulation of B cell apoptotic process | GO:0002902 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| negative regulation of B cell apoptotic ... | GO:0002903 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| nucleoside biosynthetic process | GO:0009163 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| positive regulation of intrinsic apoptot... | GO:1902255 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| negative regulation of macrophage derive... | GO:0010745 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| protein-containing complex remodeling | GO:0034367 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| protein-lipid complex remodeling | GO:0034368 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| plasma lipoprotein particle remodeling | GO:0034369 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| queuosine metabolic process | GO:0046116 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| low-density lipoprotein particle remodel... | GO:0034374 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| high-density lipoprotein particle remode... | GO:0034375 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| neurotrophin signaling pathway | GO:0038179 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| neuron intrinsic apoptotic signaling pat... | GO:0036480 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| negative regulation of extrinsic apoptot... | GO:2001240 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| regulation of cholesterol storage | GO:0010885 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |
| negative regulation of cholesterol stora... | GO:0010887 | p=5.1E-02 | n=1 | fg=0.05 | bg=0.00 |



GO:MF
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

| | | | | | |
|---|------------|-----------|-----|---------|---------|
| voltage-gated potassium channel activity | GO:0005249 | p=9.7E-03 | n=3 | fg=0.15 | bg=0.02 |
| antigen binding | GO:0003823 | p=1.6E-02 | n=2 | fg=0.10 | bg=0.01 |
| identical protein binding | GO:0042802 | p=1.9E-02 | n=8 | fg=0.40 | bg=0.19 |
| protein homodimerization activity | GO:0042803 | p=2.3E-02 | n=6 | fg=0.30 | bg=0.12 |
| DNA-binding transcription factor activit... | GO:0000981 | p=3.5E-02 | n=6 | fg=0.30 | bg=0.13 |
| carboxylic acid binding | GO:0031406 | p=3.8E-02 | n=2 | fg=0.10 | bg=0.02 |
| core promoter sequence-specific DNA bind... | GO:0001046 | p=3.8E-02 | n=2 | fg=0.10 | bg=0.02 |
| organic acid binding | GO:0043177 | p=3.8E-02 | n=2 | fg=0.10 | bg=0.02 |
| protein dimerization activity | GO:0046983 | p=4.3E-02 | n=7 | fg=0.35 | bg=0.18 |
| outward rectifier potassium channel acti... | GO:0015271 | p=5.1E-02 | n=2 | fg=0.10 | bg=0.02 |
| DNA-binding transcription activator acti... | GO:0001228 | p=5.1E-02 | n=4 | fg=0.20 | bg=0.07 |
| DNA-binding transcription activator acti... | GO:0001216 | p=5.1E-02 | n=4 | fg=0.20 | bg=0.07 |
| ion gated channel activity | GO:0022839 | p=5.1E-02 | n=4 | fg=0.20 | bg=0.07 |
| R-SMAD binding | GO:0070412 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| protein phosphatase activator activity | GO:0072542 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| oxidoreductase activity, acting on perox... | GO:0016684 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| monocarboxylic acid binding | GO:0033293 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| fatty acid binding | GO:0005504 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| macromolecule transmembrane transporter ... | GO:0022884 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| phosphatase activator activity | GO:0019211 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| protein transporter activity | GO:0140318 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| BH3 domain binding | GO:0051434 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| death domain binding | GO:0070513 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| peroxidase activity | GO:0004601 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| peptide transmembrane transporter activi... | GO:1904680 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| protein phosphatase regulator activity | GO:0019888 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| protein transmembrane transporter activi... | GO:0008320 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| ABC-type sterol transporter activity | GO:0034041 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| phosphatase regulator activity | GO:0019208 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| glucuronosyltransferase activity | GO:0015020 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |



GO:CC
Ncol_Nvec_vc1.1_XM_032370011.2

fraction genes in fg and expected value

| | | | | | |
|---|------------|-----------|-----|---------|---------|
| voltage-gated potassium channel complex | GO:0008076 | p=6.7E-03 | n=3 | fg=0.14 | bg=0.02 |
| midbody | GO:0030496 | p=3.8E-02 | n=2 | fg=0.09 | bg=0.02 |
| exocytic vesicle | GO:0070382 | p=5.0E-02 | n=3 | fg=0.14 | bg=0.04 |
| chromosome, telomeric region | GO:0000781 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| Bcl-2 family protein complex | GO:0097136 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| autophagosome membrane | GO:0000421 | p=5.5E-02 | n=1 | fg=0.05 | bg=0.00 |
| exocytic vesicle membrane | GO:0099501 | p=8.2E-02 | n=2 | fg=0.09 | bg=0.02 |
| transport vesicle | GO:0030133 | p=8.8E-02 | n=3 | fg=0.14 | bg=0.05 |
| transport vesicle membrane | GO:0030658 | p=9.9E-02 | n=2 | fg=0.09 | bg=0.03 |
| site of double-strand break | GO:0035861 | p=1.1E-01 | n=1 | fg=0.05 | bg=0.01 |
| site of DNA damage | GO:0090734 | p=1.1E-01 | n=1 | fg=0.05 | bg=0.01 |
| protein-DNA complex | GO:0032993 | p=1.1E-01 | n=1 | fg=0.05 | bg=0.01 |
| Golgi lumen | GO:0005796 | p=1.1E-01 | n=1 | fg=0.05 | bg=0.01 |
| transcription factor AP-1 complex | GO:0035976 | p=1.1E-01 | n=1 | fg=0.05 | bg=0.01 |
| apical plasma membrane | GO:0016324 | p=1.4E-01 | n=3 | fg=0.14 | bg=0.06 |
| cis-Golgi network | GO:0005801 | p=1.6E-01 | n=1 | fg=0.05 | bg=0.01 |
| apical part of cell | GO:0045177 | p=1.8E-01 | n=3 | fg=0.14 | bg=0.07 |
| organelle envelope | GO:0031967 | p=1.9E-01 | n=3 | fg=0.14 | bg=0.07 |
| envelope | GO:0031975 | p=1.9E-01 | n=3 | fg=0.14 | bg=0.07 |
| synaptic vesicle | GO:0008021 | p=2.0E-01 | n=2 | fg=0.09 | bg=0.04 |
| autophagosome | GO:0005776 | p=2.0E-01 | n=1 | fg=0.05 | bg=0.01 |
| brush border membrane | GO:0031526 | p=2.0E-01 | n=1 | fg=0.05 | bg=0.01 |
| external side of plasma membrane | GO:0009897 | p=2.0E-01 | n=1 | fg=0.05 | bg=0.01 |
| mitochondrial envelope | GO:0005740 | p=2.2E-01 | n=2 | fg=0.09 | bg=0.04 |
| nucleoplasm | GO:0005654 | p=2.3E-01 | n=7 | fg=0.32 | bg=0.23 |
| mitochondrion | GO:0005739 | p=2.4E-01 | n=3 | fg=0.14 | bg=0.08 |
| bounding membrane of organelle | GO:0098588 | p=2.4E-01 | n=5 | fg=0.23 | bg=0.15 |
| intracellular canalculus | GO:0046691 | p=2.5E-01 | n=1 | fg=0.05 | bg=0.01 |
| juxtaparanode region of axon | GO:0044224 | p=2.5E-01 | n=1 | fg=0.05 | bg=0.01 |
| cell surface | GO:0009986 | p=2.8E-01 | n=2 | fg=0.09 | bg=0.05 |

