

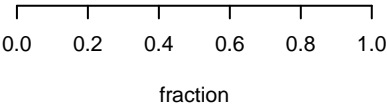
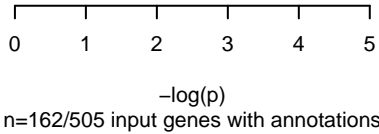
GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_001631543.3

fraction genes in fg and expected value

|   |            |
|---|------------|
| vesicle budding from membrane               | GO:0006900 |
| response to water deprivation               | GO:0009414 |
| central nervous system development          | GO:0007417 |
| locomotory behavior                         | GO:0007626 |
| spleen development                          | GO:0048536 |
| response to starvation                      | GO:0042594 |
| embryonic ectodermal digestive tract mor... | GO:0048613 |
| vesicle transport along actin filament      | GO:0030050 |
| regulation of store-operated calcium ent... | GO:2001256 |
| positive regulation of transforming grow... | GO:0032915 |
| positive regulation of gastrulation         | GO:2000543 |
| positive regulation of prostaglandin bio... | GO:0031394 |
| thrombopoietin-mediated signaling pathwa... | GO:0038163 |
| endoplasmic reticulum to Golgi vesicle-m... | GO:0006888 |
| regulation of cellular catabolic process    | GO:0031329 |
| protein localization to cell surface        | GO:0034394 |
| histone H3-K9 methylation                   | GO:0051567 |
| heparan sulfate proteoglycan biosynthesi... | GO:0015012 |
| positive regulation of organic acid tran... | GO:0032892 |
| positive regulation of transcription of ... | GO:0007221 |
| mitochondrial DNA metabolic process         | GO:0032042 |
| endoplasmic reticulum organization          | GO:0007029 |
| carbohydrate derivative biosynthetic pro... | GO:1901137 |
| glomerulus development                      | GO:0032835 |
| regulation of cell maturation               | GO:1903429 |
| negative regulation of inclusion body as... | GO:0090084 |
| actin nucleation                            | GO:0045010 |
| negative regulation of protein localizat... | GO:2000009 |
| fatty-acyl-CoA biosynthetic process         | GO:0046949 |
| histone H3-K9 trimethylation                | GO:0036124 |

|           |      |
|-----------|------|
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| p=8.1E-04 | n=3  |
| p=1.7E-03 | n=27 |
| p=1.9E-03 | n=16 |
| p=2.0E-03 | n=4  |
| p=2.2E-03 | n=12 |
| p=3.6E-03 | n=2  |
| p=3.6E-03 | n=2  |
| p=3.6E-03 | n=2  |
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| p=3.6E-03 | n=2  |
| p=3.6E-03 | n=2  |
| p=3.6E-03 | n=2  |
| p=3.9E-03 | n=8  |
| p=4.3E-03 | n=24 |
| p=5.8E-03 | n=4  |
| p=6.2E-03 | n=3  |
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| p=6.9E-03 | n=20 |
| p=7.8E-03 | n=4  |
| p=8.4E-03 | n=5  |
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| p=1.0E-02 | n=2  |
| p=1.0E-02 | n=2  |

|         |         |
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| fg=0.02 | bg=0.00 |
| fg=0.17 | bg=0.09 |
| fg=0.10 | bg=0.04 |
| fg=0.02 | bg=0.00 |
| fg=0.07 | bg=0.03 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
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| 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=0.03 | bg=0.01 |
| fg=0.12 | bg=0.06 |
| fg=0.02 | bg=0.01 |
| fg=0.03 | bg=0.01 |
| fg=0.02 | 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 |



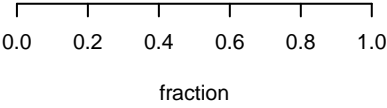
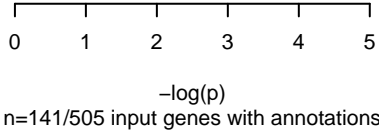
GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_001631543.3

fraction genes in fg and expected value

|   |            |
|---|------------|
| ribosome binding                            | GO:0043022 |
| proteasome binding                          | GO:0070628 |
| catalytic activity, acting on a glycopro... | GO:0140103 |
| transporter activity                        | GO:0005215 |
| beta-1,3-galactosyltransferase activity     | GO:0048531 |
| peptidase activator activity involved in... | GO:0016505 |
| cysteine-type endopeptidase activator ac... | GO:0008656 |
| triglyceride lipase activity                | GO:0004806 |
| transmembrane transporter activity          | GO:0022857 |
| low-density lipoprotein particle recepto... | GO:0050750 |
| lipoprotein particle receptor binding       | GO:0070325 |
| transcription coregulator binding           | GO:0001221 |
| inorganic molecular entity transmembrane... | GO:0015318 |
| UDP-glycosyltransferase activity            | GO:0008194 |
| small GTPase binding                        | GO:0031267 |
| ion transmembrane transporter activity      | GO:0015075 |
| single-stranded DNA binding                 | GO:0003697 |
| active ion transmembrane transporter act... | GO:0022853 |
| protein heterodimerization activity         | GO:0046982 |
| transcription coactivator binding           | GO:0001223 |
| glucuronosyltransferase activity            | GO:0015020 |
| dynactin binding                            | GO:0034452 |
| cysteine-type endopeptidase regulator ac... | GO:0043028 |
| active transmembrane transporter activit... | GO:0022804 |
| peptidase regulator activity                | GO:0061134 |
| secondary active transmembrane transport... | GO:0015291 |
| acid-sensing ion channel activity           | GO:0044736 |
| nerve growth factor binding                 | GO:0048406 |
| L-proline transmembrane transporter acti... | GO:0015193 |
| L-tryptophan transmembrane transporter a... | GO:0015196 |

|           |      |
|-----------|------|
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| p=1.2E-03 | n=4  |
| p=3.6E-03 | n=3  |
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| p=9.3E-03 | n=3  |
| p=1.0E-02 | n=2  |
| p=1.0E-02 | n=2  |
| p=1.0E-02 | n=2  |
| p=1.1E-02 | n=20 |
| p=1.3E-02 | n=3  |
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| p=2.1E-02 | n=12 |
| p=2.3E-02 | n=16 |
| p=2.6E-02 | n=5  |
| p=2.6E-02 | n=7  |
| p=2.8E-02 | n=14 |
| p=3.1E-02 | n=2  |
| p=4.5E-02 | n=2  |
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| p=4.5E-02 | n=9  |
| p=4.6E-02 | n=3  |
| p=5.3E-02 | n=5  |
| p=5.9E-02 | n=1  |
| p=5.9E-02 | n=1  |
| p=5.9E-02 | n=1  |

|         |         |
|---------|---------|
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| fg=0.03 | bg=0.00 |
| fg=0.02 | bg=0.00 |
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| fg=0.02 | bg=0.00 |
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| fg=0.02 | bg=0.00 |
| fg=0.11 | bg=0.06 |
| fg=0.04 | bg=0.01 |
| fg=0.09 | bg=0.04 |
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| fg=0.04 | bg=0.01 |
| fg=0.05 | bg=0.02 |
| fg=0.10 | bg=0.06 |
| 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=0.06 | bg=0.03 |
| fg=0.02 | bg=0.01 |
| fg=0.04 | bg=0.01 |
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| fg=0.01 | bg=0.00 |



GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_001631543.3

fraction genes in fg and expected value

|   |            |
|---|------------|
| cell body fiber                             | GO:0070852 |
| basal dendrite                              | GO:0097441 |
| Golgi membrane                              | GO:0000139 |
| post-mRNA release spliceosomal complex      | GO:0071014 |
| transport vesicle membrane                  | GO:0030658 |
| apical dendrite                             | GO:0097440 |
| Golgi apparatus subcompartment              | GO:0098791 |
| oligosaccharyltransferase complex           | GO:0008250 |
| actin cap                                   | GO:0030478 |
| FAR/SIN/STRIPAK complex                     | GO:0090443 |
| endoplasmic reticulum membrane              | GO:0005789 |
| integral component of endoplasmic reticu... | GO:0030176 |
| nuclear outer membrane-endoplasmic retic... | GO:0042175 |
| endoplasmic reticulum subcompartment        | GO:0098827 |
| intrinsic component of endoplasmic retic... | GO:0031227 |
| Golgi stack                                 | GO:0005795 |
| alpha DNA polymerase:primase complex        | GO:0005658 |
| Golgi-associated vesicle membrane           | GO:0030660 |
| integral component of organelle membrane    | GO:0031301 |
| actin-based cell projection                 | GO:0098858 |
| integral component of membrane              | GO:0016021 |
| XY body                                     | GO:0001741 |
| microvillus                                 | GO:0005902 |
| intrinsic component of membrane             | GO:0031224 |
| intrinsic component of organelle membran... | GO:0031300 |
| Golgi cisterna                              | GO:0031985 |
| filopodium tip                              | GO:0032433 |
| exocytic vesicle membrane                   | GO:0099501 |
| organelle subcompartment                    | GO:0031984 |
| transcription elongation factor complex     | GO:0008023 |

|           |      |
|-----------|------|
| p=7.8E-04 | n=3  |
| p=7.8E-04 | n=3  |
| p=9.2E-04 | n=18 |
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| p=5.1E-03 | n=7  |
| p=6.0E-03 | n=3  |
| p=7.1E-03 | n=19 |
| p=1.0E-02 | n=2  |
| p=1.0E-02 | n=2  |
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| p=1.3E-02 | n=8  |
| p=1.3E-02 | n=20 |
| p=1.4E-02 | n=20 |
| p=1.8E-02 | n=8  |
| p=1.9E-02 | n=7  |
| p=1.9E-02 | n=2  |
| p=2.3E-02 | n=4  |
| p=2.8E-02 | n=11 |
| p=2.9E-02 | n=7  |
| p=2.9E-02 | n=32 |
| p=3.1E-02 | n=2  |
| p=3.2E-02 | n=4  |
| p=3.5E-02 | n=33 |
| p=3.6E-02 | n=11 |
| p=4.2E-02 | n=5  |
| p=4.5E-02 | n=2  |
| p=5.0E-02 | n=4  |
| p=5.4E-02 | n=33 |
| p=5.5E-02 | n=3  |

|         |         |
|---------|---------|
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| fg=0.02 | bg=0.00 |
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| fg=0.01 | bg=0.00 |
| fg=0.04 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.12 | bg=0.07 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.12 | bg=0.07 |
| fg=0.05 | bg=0.02 |
| fg=0.12 | bg=0.07 |
| fg=0.12 | bg=0.07 |
| fg=0.05 | bg=0.02 |
| fg=0.04 | bg=0.02 |
| fg=0.01 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.07 | bg=0.04 |
| fg=0.04 | bg=0.02 |
| fg=0.20 | bg=0.14 |
| fg=0.01 | bg=0.00 |
| fg=0.03 | bg=0.01 |
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| fg=0.01 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.21 | bg=0.12 |
| fg=0.02 | bg=0.01 |

