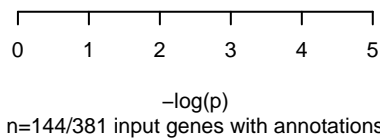


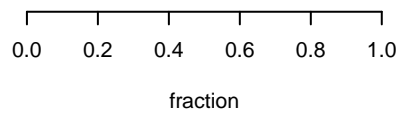
GO:BP
Fox_Nvec_vc1.1_XM_032363418.2

fraction genes in fg and expected value

| | | | |
|---|------------|-----------|------|
| autophagosome maturation | GO:0097352 | p=1.1E-03 | n=5 |
| GTP metabolic process | GO:0046039 | p=1.3E-03 | n=4 |
| cristae formation | GO:0042407 | p=2.6E-03 | n=3 |
| regulation of oskar mRNA translation | GO:0046011 | p=2.8E-03 | n=2 |
| regulation of deacetylase activity | GO:0150065 | p=2.8E-03 | n=2 |
| negative regulation of molecular function | GO:0044362 | p=2.8E-03 | n=2 |
| determination of digestive tract left/right | GO:0071907 | p=2.8E-03 | n=2 |
| intracellular estrogen receptor signaling | GO:0030520 | p=3.8E-03 | n=4 |
| guanosine-containing compound metabolic process | GO:1901068 | p=3.8E-03 | n=4 |
| cellular response to estradiol stimulus | GO:0071392 | p=4.4E-03 | n=3 |
| membrane organization | GO:0061024 | p=6.5E-03 | n=22 |
| protein heterotetramerization | GO:0051290 | p=6.8E-03 | n=3 |
| molybdopterin cofactor biosynthetic process | GO:0032324 | p=8.2E-03 | n=2 |
| cellular response to nitric oxide | GO:0071732 | p=8.2E-03 | n=2 |
| maintenance of presynaptic active zone structure | GO:0048790 | p=8.2E-03 | n=2 |
| vestibulocochlear nerve development | GO:0021562 | p=8.2E-03 | n=2 |
| regulation of neural retina development | GO:0061074 | p=8.2E-03 | n=2 |
| regulation of retina development in camera-type eye | GO:1902866 | p=8.2E-03 | n=2 |
| response to bronchodilator | GO:0097366 | p=9.8E-03 | n=3 |
| regulation of localization | GO:0032879 | p=1.1E-02 | n=41 |
| protein import into nucleus | GO:0006606 | p=1.1E-02 | n=7 |
| asymmetric cell division | GO:0008356 | p=1.2E-02 | n=6 |
| positive regulation of organelle assembly | GO:1902117 | p=1.3E-02 | n=5 |
| localization | GO:0051179 | p=1.3E-02 | n=82 |
| intracellular transport | GO:0046907 | p=1.3E-02 | n=38 |
| cytoskeleton-dependent intracellular transport | GO:0030705 | p=1.4E-02 | n=7 |
| regulation of histone deacetylation | GO:0031063 | p=1.6E-02 | n=2 |
| proximal/distal axis specification | GO:0009946 | p=1.6E-02 | n=2 |
| detection of chemical stimulus involved in sensory perception | GO:0050911 | p=1.6E-02 | n=2 |
| regulation of lipid transport | GO:0032368 | p=1.6E-02 | n=4 |



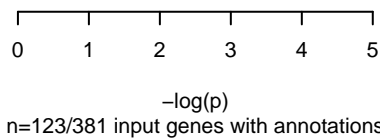
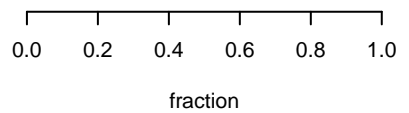
| | |
|---------|---------|
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| fg=0.02 | bg=0.00 |
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| fg=0.03 | bg=0.00 |
| fg=0.03 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.15 | bg=0.08 |
| fg=0.02 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.28 | bg=0.20 |
| fg=0.05 | bg=0.02 |
| fg=0.04 | bg=0.01 |
| fg=0.03 | bg=0.01 |
| fg=0.57 | bg=0.43 |
| fg=0.26 | bg=0.19 |
| fg=0.05 | bg=0.02 |
| fg=0.01 | bg=0.00 |
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| fg=0.01 | bg=0.00 |
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GO:MF
Fox_Nvec_vc1.1_XM_032363418.2

fraction genes in fg and expected value

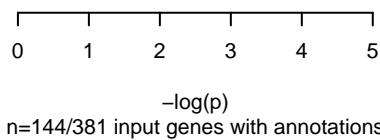
| | | | |
|--|------------|-----------|------|
| sulfurtransferase activity | GO:0016783 | p=1.3E-03 | n=3 |
| mitogen-activated protein kinase binding | GO:0051019 | p=2.5E-03 | n=4 |
| nuclear estrogen receptor binding | GO:0030331 | p=3.4E-03 | n=4 |
| GTPase binding | GO:0051020 | p=5.8E-03 | n=14 |
| cation channel activity | GO:0005261 | p=7.5E-03 | n=9 |
| protein phosphatase 1 binding | GO:0008157 | p=1.3E-02 | n=3 |
| small GTPase binding | GO:0031267 | p=1.9E-02 | n=11 |
| hormone receptor binding | GO:0051427 | p=2.2E-02 | n=6 |
| metal ion transmembrane transporter acti... | GO:0046873 | p=2.8E-02 | n=9 |
| potassium ion transmembrane transporter ... | GO:0015079 | p=2.8E-02 | n=4 |
| intramolecular oxidoreductase activity, ... | GO:0016864 | p=3.5E-02 | n=2 |
| MAP kinase kinase activity | GO:0004708 | p=3.5E-02 | n=2 |
| protein disulfide isomerase activity | GO:0003756 | p=3.5E-02 | n=2 |
| transcription coactivator activity | GO:0003713 | p=4.3E-02 | n=8 |
| mRNA 3'-UTR binding | GO:0003730 | p=4.7E-02 | n=3 |
| MAP kinase activity | GO:0004707 | p=4.7E-02 | n=2 |
| inositol phosphate phosphatase activity | GO:0052745 | p=4.7E-02 | n=2 |
| biotin-protein ligase activity | GO:0018271 | p=5.2E-02 | n=1 |
| polyamine binding | GO:0019808 | p=5.2E-02 | n=1 |
| transmembrane receptor protein phosphata... | GO:0019198 | p=5.2E-02 | n=1 |
| oxidoreductase activity, acting on NAD(P)... | GO:0050664 | p=5.2E-02 | n=1 |
| U6 snRNA (adenine-(43)-N(6))-methyltrans... | GO:0120048 | p=5.2E-02 | n=1 |
| rRNA (adenine-N6)-methyltransferase act... | GO:0008988 | p=5.2E-02 | n=1 |
| importin- α family protein binding | GO:0061676 | p=5.2E-02 | n=1 |
| myosin II binding | GO:0045159 | p=5.2E-02 | n=1 |
| oxidative DNA demethylase activity | GO:0035516 | p=5.2E-02 | n=1 |
| URM1 activating enzyme activity | GO:0042292 | p=5.2E-02 | n=1 |
| pre-mRNA 5'-splice site binding | GO:0030627 | p=5.2E-02 | n=1 |
| aminophospholipid flippase activity | GO:0015247 | p=5.2E-02 | n=1 |
| U6 snRNA 3'-end binding | GO:0030629 | p=5.2E-02 | n=1 |

[illegible]

GO:CC
Fox_Nvec_vc1.1_XM_032363418.2

fraction genes in fg and expected value

| | | | |
|---|------------|-----------|------|
| midbody | GO:0030496 | p=1.9E-03 | n=8 |
| apicolateral plasma membrane | GO:0016327 | p=4.4E-03 | n=3 |
| endolysosome membrane | GO:0036020 | p=8.2E-03 | n=2 |
| fusome | GO:0045169 | p=9.8E-03 | n=3 |
| late endosome | GO:0005770 | p=1.1E-02 | n=8 |
| nuclear envelope | GO:0005635 | p=1.2E-02 | n=13 |
| M band | GO:0031430 | p=2.3E-02 | n=3 |
| mediator complex | GO:0016592 | p=2.3E-02 | n=3 |
| proximal dendrite | GO:1990635 | p=2.5E-02 | n=2 |
| presynaptic active zone | GO:0048786 | p=3.1E-02 | n=4 |
| organelle envelope | GO:0031967 | p=4.4E-02 | n=22 |
| envelope | GO:0031975 | p=4.4E-02 | n=22 |
| presynaptic active zone membrane | GO:0048787 | p=5.0E-02 | n=2 |
| microvillus membrane | GO:0031528 | p=5.0E-02 | n=2 |
| aminoacyl-tRNA synthetase multienzyme co... | GO:0017101 | p=5.0E-02 | n=2 |
| secretory granule membrane | GO:0030667 | p=5.1E-02 | n=6 |
| desmosome | GO:0030057 | p=5.3E-02 | n=1 |
| rhabdomere microvillus | GO:0035996 | p=5.3E-02 | n=1 |
| rhabdomere microvillus membrane | GO:0035997 | p=5.3E-02 | n=1 |
| Shu complex | GO:0097196 | p=5.3E-02 | n=1 |
| SAM complex | GO:0001401 | p=5.3E-02 | n=1 |
| spectrin | GO:0008091 | p=5.3E-02 | n=1 |
| spectrosome | GO:0045170 | p=5.3E-02 | n=1 |
| microvesicle | GO:1990742 | p=5.3E-02 | n=1 |
| postsynaptic actin cytoskeleton | GO:0098871 | p=5.3E-02 | n=1 |
| dense core granule membrane | GO:0032127 | p=5.3E-02 | n=1 |
| cytoskeleton of presynaptic active zone | GO:0048788 | p=5.3E-02 | n=1 |
| integral component of lysosomal membrane | GO:1905103 | p=5.3E-02 | n=1 |
| presynaptic active zone cytoplasmic comp... | GO:0098831 | p=5.3E-02 | n=1 |
| RNA nuclear export complex | GO:0042565 | p=5.3E-02 | n=1 |

[illegible]