## GO:BP
## Fox_Nvec_vc1.1_XM_032374310.2

**fraction genes in fg and expected valu**

| Term | p | n | fg | bg |
|---|---|---|---|---|
| neuroepithelial cell differentiation GO:0060563 | p=1.2E−04 | n=7 | fg=0.06 | bg=0.01 |
| somatic stem cell population maintenance GO:0035019 | p=2.1E−04 | n=6 | fg=0.05 | bg=0.01 |
| regulation of bone remodeling GO:0046850 | p=2.3E−04 | n=4 | fg=0.03 | bg=0.00 |
| regulation of hematopoietic stem cell di... GO:1902036 | p=2.3E−04 | n=5 | fg=0.04 | bg=0.01 |
| limb bud formation GO:0060174 | p=3.3E−04 | n=3 | fg=0.03 | bg=0.00 |
| epicardial cell to mesenchymal cell tran... GO:0003347 | p=3.3E−04 | n=3 | fg=0.03 | bg=0.00 |
| cardioblast differentiation GO:0010002 | p=8.0E−04 | n=3 | fg=0.03 | bg=0.00 |
| glial cell growth GO:0042065 | p=8.0E−04 | n=3 | fg=0.03 | bg=0.00 |
| bone trabecula morphogenesis GO:0061430 | p=8.0E−04 | n=3 | fg=0.03 | bg=0.00 |
| bone mineralization GO:0030282 | p=9.3E−04 | n=6 | fg=0.05 | bg=0.01 |
| coronary vasculature development GO:0060976 | p=9.6E−04 | n=4 | fg=0.03 | bg=0.00 |
| cholesterol homeostasis GO:0042632 | p=1.1E−03 | n=5 | fg=0.04 | bg=0.01 |
| somatic muscle development GO:0007525 | p=1.4E−03 | n=5 | fg=0.04 | bg=0.01 |
| lateral sprouting from an epithelium GO:0060601 | p=1.5E−03 | n=3 | fg=0.03 | bg=0.00 |
| membranous septum morphogenesis GO:0003149 | p=1.5E−03 | n=3 | fg=0.03 | bg=0.00 |
| cell migration in hindbrain GO:0021535 | p=1.5E−03 | n=3 | fg=0.03 | bg=0.00 |
| negative regulation of astrocyte differe... GO:0048712 | p=1.5E−03 | n=3 | fg=0.03 | bg=0.00 |
| hair follicle development GO:0001942 | p=1.8E−03 | n=5 | fg=0.04 | bg=0.01 |
| positive regulation of microglial cell a... GO:1903980 | p=2.0E−03 | n=2 | fg=0.02 | bg=0.00 |
| negative regulation of endoribonuclease ... GO:0060702 | p=2.0E−03 | n=2 | fg=0.02 | bg=0.00 |
| positive regulation of astrocyte activat... GO:0061890 | p=2.0E−03 | n=2 | fg=0.02 | bg=0.00 |
| positive regulation of neuron differenti... GO:0045666 | p=2.2E−03 | n=12 | fg=0.10 | bg=0.04 |
| morphogenesis of embryonic epithelium GO:0016331 | p=2.4E−03 | n=12 | fg=0.10 | bg=0.03 |
| innervation GO:0060384 | p=2.6E−03 | n=3 | fg=0.03 | bg=0.00 |
| positive regulation of osteoclast differ... GO:0045672 | p=2.6E−03 | n=3 | fg=0.03 | bg=0.00 |
| regulation of mesoderm formation GO:1905902 | p=2.6E−03 | n=3 | fg=0.03 | bg=0.00 |
| ventricular cardiac muscle tissue morpho... GO:0055010 | p=2.6E−03 | n=3 | fg=0.03 | bg=0.00 |
| inner ear receptor cell development GO:0060119 | p=2.8E−03 | n=5 | fg=0.04 | bg=0.01 |
| regulation of canonical Wnt signaling pa... GO:0060828 | p=2.9E−03 | n=8 | fg=0.07 | bg=0.02 |
| positive regulation of developmental gro... GO:0048639 | p=3.2E−03 | n=10 | fg=0.08 | bg=0.03 |

−log(p)
n=120/422 input genes with annotations

fraction

## GO:MF
## Fox_Nvec_vc1.1_XM_032374310.2

**fraction genes in fg and expected valu**

| Term | p | n | fg | bg |
|---|---|---|---|---|
| small GTPase binding GO:0031267 | p=8.7E−04 | n=13 | fg=0.12 | bg=0.04 |
| eukaryotic initiation factor 4E binding GO:0008190 | p=2.1E−03 | n=2 | fg=0.02 | bg=0.00 |
| endoribonuclease inhibitor activity GO:0060698 | p=2.1E−03 | n=2 | fg=0.02 | bg=0.00 |
| thioredoxin−disulfide reductase activity GO:0004791 | p=2.1E−03 | n=2 | fg=0.02 | bg=0.00 |
| PTB domain binding GO:0051425 | p=6.1E−03 | n=2 | fg=0.02 | bg=0.00 |
| RNA polymerase II cis−regulatory region ... GO:0000978 | p=6.5E−03 | n=9 | fg=0.08 | bg=0.03 |
| DNA−binding transcription factor activit... GO:0000981 | p=9.8E−03 | n=13 | fg=0.12 | bg=0.06 |
| single−stranded telomeric DNA binding GO:0043047 | p=1.2E−02 | n=2 | fg=0.02 | bg=0.00 |
| receptor−receptor interaction GO:0090722 | p=1.2E−02 | n=2 | fg=0.02 | bg=0.00 |
| fibroblast growth factor−activated recep... GO:0005007 | p=1.2E−02 | n=2 | fg=0.02 | bg=0.00 |
| glycosaminoglycan binding GO:0005539 | p=1.2E−02 | n=3 | fg=0.03 | bg=0.00 |
| binding GO:0005488 | p=1.4E−02 | n=96 | fg=0.88 | bg=0.76 |
| DNA−binding transcription activator acti... GO:0001228 | p=1.9E−02 | n=8 | fg=0.07 | bg=0.03 |
| DNA−binding transcription activator acti... GO:0001216 | p=1.9E−02 | n=8 | fg=0.07 | bg=0.03 |
| JUN kinase binding GO:0008432 | p=1.9E−02 | n=2 | fg=0.02 | bg=0.00 |
| sphingolipid binding GO:0046625 | p=1.9E−02 | n=2 | fg=0.02 | bg=0.00 |
| sequence−specific single stranded DNA bi... GO:0098847 | p=1.9E−02 | n=2 | fg=0.02 | bg=0.00 |
| phosphatidylinositol−4,5−bisphosphate 3−... GO:0046934 | p=2.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| proteoglycan binding GO:0043394 | p=2.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| phosphatidylinositol bisphosphate kinase... GO:0052813 | p=2.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| phosphotransferase activity, for other s... GO:0016780 | p=2.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| protein binding GO:0005515 | p=3.3E−02 | n=78 | fg=0.72 | bg=0.59 |
| phosphatidylinositol kinase activity GO:0052742 | p=3.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| peptidase activator activity GO:0016504 | p=3.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| phosphatidylinositol 3−kinase activity GO:0035004 | p=3.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| 1−phosphatidylinositol−3−kinase activity GO:0016303 | p=3.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| MAP kinase kinase kinase activity GO:0004709 | p=3.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| single−stranded DNA binding GO:0003697 | p=4.1E−02 | n=4 | fg=0.04 | bg=0.01 |
| lipid binding GO:0008289 | p=4.4E−02 | n=10 | fg=0.09 | bg=0.05 |
| selenium binding GO:0008430 | p=4.6E−02 | n=1 | fg=0.01 | bg=0.00 |

−log(p)
n=109/422 input genes with annotations

fraction

## GO:CC
## Fox_Nvec_vc1.1_XM_032374310.2

**fraction genes in fg and expected valu**

| Term | p | n | fg | bg |
|---|---|---|---|---|
| cytoplasmic side of plasma membrane GO:0009898 | p=2.1E−03 | n=8 | fg=0.07 | bg=0.02 |
| filamentous actin GO:0031941 | p=1.1E−02 | n=2 | fg=0.02 | bg=0.00 |
| Cul4A−RING E3 ubiquitin ligase complex GO:0031464 | p=1.1E−02 | n=2 | fg=0.02 | bg=0.00 |
| intrinsic component of the cytoplasmic s... GO:0031235 | p=1.8E−02 | n=2 | fg=0.02 | bg=0.00 |
| COPII−coated ER to Golgi transport vesic... GO:0030134 | p=2.6E−02 | n=3 | fg=0.03 | bg=0.01 |
| nuclear body GO:0016604 | p=2.6E−02 | n=13 | fg=0.11 | bg=0.06 |
| excitatory synapse GO:0060076 | p=3.5E−02 | n=2 | fg=0.02 | bg=0.00 |
| ciliary transition zone GO:0035869 | p=3.6E−02 | n=4 | fg=0.03 | bg=0.01 |
| sperm connecting piece GO:0097224 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| endosome to plasma membrane transport ve... GO:0070381 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| lipoprotein particle GO:1990777 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| tRNA−intron endonuclease complex GO:0000214 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| amyloid−beta complex GO:0106003 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| core−binding factor complex GO:0016513 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| MutSbeta complex GO:0032302 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| growth cone leading edge GO:0061850 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| apoptosome GO:0043293 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| centralspindlin complex GO:0097149 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| intermediate−density lipoprotein particl... GO:0034363 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| high−density lipoprotein particle GO:0034364 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| plasma lipoprotein particle GO:0034358 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| triglyceride−rich plasma lipoprotein par... GO:0034385 | p=4.4E−02 | n=1 | fg=0.01 | bg=0.00 |
| nuclear envelope lumen GO:0005641 | p=4.5E−02 | n=2 | fg=0.02 | bg=0.00 |
| protein−containing complex GO:0032991 | p=4.5E−02 | n=60 | fg=0.50 | bg=0.42 |
| nucleoplasm GO:0005654 | p=5.0E−02 | n=43 | fg=0.36 | bg=0.29 |
| MKS complex GO:0036038 | p=5.7E−02 | n=2 | fg=0.02 | bg=0.00 |
| Cul3−RING ubiquitin ligase complex GO:0031463 | p=5.7E−02 | n=2 | fg=0.02 | bg=0.00 |
| clathrin−coated pit GO:0005905 | p=5.7E−02 | n=2 | fg=0.02 | bg=0.00 |
| actin cytoskeleton GO:0015629 | p=6.3E−02 | n=7 | fg=0.06 | bg=0.03 |
| membrane−enclosed lumen GO:0031974 | p=6.8E−02 | n=58 | fg=0.49 | bg=0.42 |

−log(p)
n=119/422 input genes with annotations

fraction