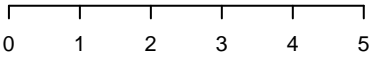


GO:BP
Fox_Nvec_vc1.1_XM_032361849.2

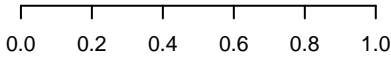
fraction genes in fg and expected value

regulation of cardioblast differentiatio...	GO:0051890	p=1.2E-03	n=2
negative regulation of alpha-beta T cell...	GO:0046642	p=1.2E-03	n=2
positive regulation of T cell anergy	GO:0002669	p=1.2E-03	n=2
biological process involved in interacti...	GO:0051701	p=1.8E-03	n=4
dorsal/ventral axis specification, ovari...	GO:0008069	p=3.5E-03	n=2
negative regulation of glutamate secreti...	GO:0014050	p=3.5E-03	n=2
regulation of peptidyl-tyrosine phosphor...	GO:0050730	p=4.2E-03	n=5
vasculogenesis	GO:0001570	p=5.4E-03	n=3
hematopoietic progenitor cell differenti...	GO:0002244	p=6.0E-03	n=4
neuron differentiation	GO:0030182	p=6.5E-03	n=20
response to insecticide	GO:0017085	p=6.8E-03	n=2
thyroid gland development	GO:0030878	p=6.8E-03	n=2
regulation of protein deubiquitination	GO:0090085	p=6.8E-03	n=2
regulation of synaptic plasticity	GO:0048167	p=8.9E-03	n=5
cognition	GO:0050890	p=9.4E-03	n=9
inositol lipid-mediated signaling	GO:0048017	p=9.7E-03	n=4
detection of stimulus involved in sensor...	GO:0062149	p=1.1E-02	n=3
regulation of lipid storage	GO:0010883	p=1.1E-02	n=3
carbohydrate derivative transport	GO:1901264	p=1.1E-02	n=3
neurotrophin signaling pathway	GO:0038179	p=1.1E-02	n=2
response to epidermal growth factor	GO:0070849	p=1.1E-02	n=2
tongue development	GO:0043586	p=1.1E-02	n=2
regulation of adenylate cyclase activity	GO:0045761	p=1.1E-02	n=2
cellular response to epidermal growth fa...	GO:0071364	p=1.1E-02	n=2
neurotrophin TRK receptor signaling path...	GO:0048011	p=1.1E-02	n=2
receptor recycling	GO:0001881	p=1.1E-02	n=2
negative regulation of lipid storage	GO:0010888	p=1.1E-02	n=2
Golgi to endosome transport	GO:0006895	p=1.1E-02	n=2
negative regulation of extrinsic apoptot...	GO:1902042	p=1.1E-02	n=2
positive regulation of protein metabolic...	GO:0051247	p=1.2E-02	n=15



-log(p)
n=63/238 input genes with annotations

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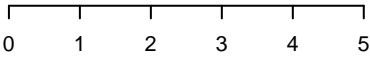


fraction

GO:MF
Fox_Nvec_vc1.1_XM_032361849.2

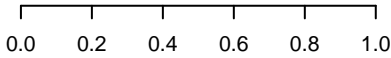
fraction genes in fg and expected value

cyclase regulator activity	GO:0010851	p=4.1E-03	n=2
alcohol binding	GO:0043178	p=5.1E-03	n=3
enzyme activator activity	GO:0008047	p=7.4E-03	n=8
ribonucleoprotein complex binding	GO:0043021	p=1.3E-02	n=4
protein tyrosine kinase binding	GO:1990782	p=1.4E-02	n=3
cholesterol binding	GO:0015485	p=1.9E-02	n=2
potassium channel inhibitor activity	GO:0019870	p=1.9E-02	n=2
outward rectifier potassium channel acti...	GO:0015271	p=2.6E-02	n=2
sterol binding	GO:0032934	p=2.6E-02	n=2
voltage-gated cation channel activity	GO:0022843	p=2.8E-02	n=3
protein serine/threonine kinase activity	GO:0004674	p=3.3E-02	n=6
phosphotyrosine residue binding	GO:0001784	p=3.4E-02	n=2
steroid binding	GO:0005496	p=3.4E-02	n=2
protein-macromolecule adaptor activity	GO:0030674	p=3.4E-02	n=5
molecular adaptor activity	GO:0060090	p=3.4E-02	n=5
alpha-sialidase activity	GO:0016997	p=3.8E-02	n=1
glycerol-3-phosphate dehydrogenase [NAD(...	GO:0047952	p=3.8E-02	n=1
histone pre-mRNA stem-loop binding	GO:0071207	p=3.8E-02	n=1
CXCR chemokine receptor binding	GO:0045236	p=3.8E-02	n=1
ribokinase activity	GO:0004747	p=3.8E-02	n=1
A2A adenosine receptor binding	GO:0031687	p=3.8E-02	n=1
cyclase inhibitor activity	GO:0010852	p=3.8E-02	n=1
G protein-coupled glutamate receptor act...	GO:0098988	p=3.8E-02	n=1
adenylate cyclase regulator activity	GO:0010854	p=3.8E-02	n=1
adenylate cyclase inhibitor activity	GO:0010855	p=3.8E-02	n=1
adenylate cyclase activator activity	GO:0010856	p=3.8E-02	n=1
inositol 1,3,4,5 tetrakisphosphate bindi...	GO:0043533	p=3.8E-02	n=1
neurotransmitter receptor activity invol...	GO:0099583	p=3.8E-02	n=1
exo-alpha-sialidase activity	GO:0004308	p=3.8E-02	n=1
mRNA 5'-UTR binding	GO:0048027	p=3.8E-02	n=1



-log(p)
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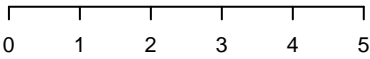


fraction

GO:CC
Fox_Nvec_vc1.1_XM_032361849.2

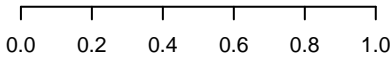
fraction genes in fg and expected value

axon	GO:0030424	p=2.6E-03	n=12
cell tip	GO:0051286	p=6.8E-03	n=2
polysome	GO:0005844	p=7.1E-03	n=3
protein phosphatase type 2A complex	GO:0000159	p=1.1E-02	n=2
intrinsic component of postsynaptic memb...	GO:0098936	p=2.2E-02	n=2
intrinsic component of synaptic membrane	GO:0099240	p=2.2E-02	n=2
integral component of synaptic membrane	GO:0099699	p=2.2E-02	n=2
intrinsic component of presynaptic membr...	GO:0098889	p=2.2E-02	n=2
integral component of postsynaptic membr...	GO:0099055	p=2.2E-02	n=2
integral component of presynaptic membra...	GO:0099056	p=2.2E-02	n=2
magnesium-dependent protein serine/threo...	GO:0005963	p=2.2E-02	n=2
distal axon	GO:0150034	p=2.3E-02	n=7
exocytic vesicle membrane	GO:0099501	p=3.0E-02	n=3
early endosome	GO:0005769	p=3.0E-02	n=6
Golgi-associated vesicle lumen	GO:0070931	p=3.5E-02	n=1
growing cell tip	GO:0035838	p=3.5E-02	n=1
Scc2-Scc4 cohesin loading complex	GO:0090694	p=3.5E-02	n=1
SMC loading complex	GO:0032116	p=3.5E-02	n=1
dihydrolipoyl dehydrogenase complex	GO:0045240	p=3.5E-02	n=1
mitochondrial alpha-ketoglutarate dehydr...	GO:0005947	p=3.5E-02	n=1
G protein-coupled receptor complex	GO:0097648	p=3.5E-02	n=1
neuronal ribonucleoprotein granule	GO:0071598	p=3.5E-02	n=1
histone pre-mRNA 3'end processing comple...	GO:0071204	p=3.5E-02	n=1
PAN complex	GO:0031251	p=3.5E-02	n=1
ESCRT-0 complex	GO:0033565	p=3.5E-02	n=1
glycerol-3-phosphate dehydrogenase compl...	GO:0009331	p=3.5E-02	n=1
cell cortex of cell tip	GO:0051285	p=3.5E-02	n=1
new growing cell tip	GO:0035841	p=3.5E-02	n=1
G protein-coupled receptor dimeric compl...	GO:0038037	p=3.5E-02	n=1
G protein-coupled receptor homodimeric c...	GO:0038038	p=3.5E-02	n=1



-log(p)
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fraction