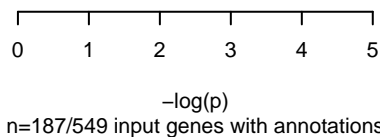


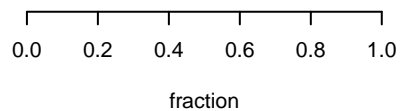
GO:BP
Fox_Nvec_vc1.1_XM_001638761.3

fraction genes in fg and expected value

establishment of mitotic spindle orienta...	GO:0000132	p=9.4E-04	n=6
renal system development	GO:0072001	p=1.0E-03	n=15
GTP metabolic process	GO:0046039	p=3.4E-03	n=4
cell fate determination	GO:0001709	p=4.3E-03	n=8
protein maturation by copper ion transfe...	GO:0015680	p=4.8E-03	n=2
nodal signaling pathway	GO:0038092	p=4.8E-03	n=2
male germ cell proliferation	GO:0002176	p=4.8E-03	n=2
regulation of iron ion transmembrane tra...	GO:0034759	p=4.8E-03	n=2
regulation of single stranded viral RNA ...	GO:0045091	p=4.8E-03	n=2
cellular response to copper ion	GO:0071280	p=4.8E-03	n=2
negative regulation of viral transcripti...	GO:0032897	p=4.8E-03	n=2
ovarian follicle cell-cell adhesion	GO:0007299	p=4.8E-03	n=2
carnitine biosynthetic process	GO:0045329	p=4.8E-03	n=2
apoptotic nuclear changes	GO:0030262	p=5.0E-03	n=4
myelination in peripheral nervous system	GO:0022011	p=5.6E-03	n=3
cellular response to interleukin-4	GO:0071353	p=5.6E-03	n=3
hemidesmosome assembly	GO:0031581	p=5.6E-03	n=3
positive regulation of vascular associat...	GO:1904754	p=5.6E-03	n=3
regulation of protein targeting to membr...	GO:0090313	p=5.6E-03	n=3
lymph gland development	GO:0048542	p=7.9E-03	n=5
neuroepithelial cell differentiation	GO:0060563	p=8.8E-03	n=6
negative regulation of cell projection o...	GO:0031345	p=9.3E-03	n=8
regulation of cell migration involved in...	GO:0090049	p=9.3E-03	n=3
guanosine-containing compound metabolic ...	GO:1901068	p=9.7E-03	n=4
somatic muscle development	GO:0007525	p=1.0E-02	n=5
negative regulation of epithelial cell p...	GO:0050680	p=1.2E-02	n=5
defense response to fungus	GO:0050832	p=1.3E-02	n=4
regulation of execution phase of apoptos...	GO:1900117	p=1.3E-02	n=4
regulation of hematopoietic stem cell di...	GO:1902036	p=1.3E-02	n=4
epidermis morphogenesis	GO:0048730	p=1.3E-02	n=4



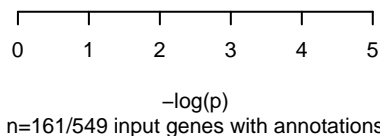
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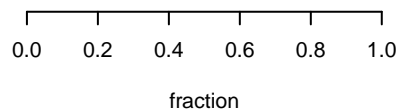
GO:MF
Fox_Nvec_vc1.1_XM_001638761.3

fraction genes in fg and expected value

E-box binding	GO:0070888	p=1.7E-03	n=5
inositol bisphosphate phosphatase activi...	GO:0016312	p=4.6E-03	n=2
gamma-butyrobetaine dioxygenase activity	GO:0008336	p=4.6E-03	n=2
superoxide dismutase copper chaperone ac...	GO:0016532	p=4.6E-03	n=2
dynein intermediate chain binding	GO:0045505	p=5.3E-03	n=3
enzyme binding	GO:0019899	p=7.2E-03	n=49
HMG box domain binding	GO:0071837	p=8.8E-03	n=3
ribosome binding	GO:0043022	p=1.2E-02	n=4
RNA polymerase II intronic transcription...	GO:0001162	p=1.3E-02	n=2
U2 snRNA binding	GO:0030620	p=1.3E-02	n=2
small GTPase binding	GO:0031267	p=2.5E-02	n=13
glycolipid binding	GO:0051861	p=2.5E-02	n=2
xylosyltransferase activity	GO:0042285	p=2.5E-02	n=2
FAD binding	GO:0071949	p=2.5E-02	n=2
UDP-xylosyltransferase activity	GO:0035252	p=2.5E-02	n=2
GTPase binding	GO:0051020	p=2.6E-02	n=15
heparin binding	GO:0008201	p=2.6E-02	n=3
ubiquitin binding	GO:0043130	p=3.0E-02	n=4
phosphatidylinositol phosphate phosphata...	GO:0052866	p=3.4E-02	n=3
glycosaminoglycan binding	GO:0005539	p=3.4E-02	n=3
growth factor binding	GO:0019838	p=3.6E-02	n=4
actin monomer binding	GO:0003785	p=4.0E-02	n=2
dynein light chain binding	GO:0045503	p=4.0E-02	n=2
satellite DNA binding	GO:0003696	p=4.0E-02	n=2
intronic transcription regulatory region...	GO:0001161	p=4.0E-02	n=2
calcium-activated potassium channel acti...	GO:0015269	p=4.0E-02	n=2
pentosyltransferase activity	GO:0016763	p=4.3E-02	n=3
copper ion binding	GO:0005507	p=5.3E-02	n=3
bicarbonate transmembrane transporter ac...	GO:0015106	p=5.7E-02	n=2
MAP kinase kinase activity	GO:0004708	p=5.7E-02	n=2



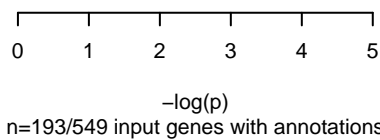
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GO:CC
Fox_Nvec_vc1.1_XM_001638761.3

fraction genes in fg and expected value

intraciliary transport particle A	GO:0030991	p=1.5E-02	n=2
ruffle	GO:0001726	p=1.5E-02	n=6
apical junction complex	GO:0043296	p=2.5E-02	n=5
zonula adherens	GO:0005915	p=4.4E-02	n=2
intraciliary transport particle	GO:0030990	p=4.4E-02	n=2
sperm fibrous sheath	GO:0035686	p=4.4E-02	n=2
ruffle membrane	GO:0032587	p=4.9E-02	n=3
M band	GO:0031430	p=4.9E-02	n=3
protein kinase CK2 complex	GO:0005956	p=7.1E-02	n=1
smooth septate junction	GO:0005920	p=7.1E-02	n=1
clathrin-sculpted gamma-aminobutyric aci...	GO:0061200	p=7.1E-02	n=1
clathrin-sculpted gamma-aminobutyric aci...	GO:0061202	p=7.1E-02	n=1
anterior cell cortex	GO:0061802	p=7.1E-02	n=1
omegasome membrane	GO:1903349	p=7.1E-02	n=1
nuclear RNA export factor complex	GO:0042272	p=7.1E-02	n=
CatSper complex	GO:0036128	p=7.1E-02	n=1
BAT3 complex	GO:0071818	p=7.1E-02	n=1
internode region of axon	GO:0033269	p=7.1E-02	n=1
eukaryotic 43S preinitiation complex	GO:0016282	p=7.1E-02	n=1
bub1-bub3 complex	GO:1990298	p=7.1E-02	n=1
methionyl glutamyl tRNA synthetase compl...	GO:0017102	p=7.1E-02	n=1
omegasome	GO:1990462	p=7.1E-02	n=1
Ric1-Rgp1 guanyl-nucleotide exchange fac...	GO:0034066	p=7.1E-02	n=1
U7 snRNP	GO:0005683	p=7.1E-02	n=1
intrinsic component of omegasome membran...	GO:0097630	p=7.1E-02	n=1
integral component of omegasome membrane	GO:0097631	p=7.1E-02	n=1
clathrin-sculpted vesicle	GO:0060198	p=7.1E-02	n=1
Schmidt-Lanterman incisure	GO:0043220	p=7.1E-02	n=1
compact myelin	GO:0043218	p=7.1E-02	n=1
DNA topoisomerase type II (double strand...	GO:0009330	p=7.1E-02	n=1

[illegible]