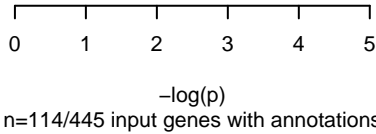


GO:BP  
Fox\_Nvec\_vc1.1\_XM\_032374843.2

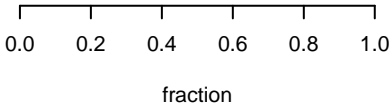
cardiac right ventricle morphogenesis	GO:0003215
intermembrane lipid transfer	GO:0120009
nephric duct formation	GO:0072179
regulation of cardioblast differentiatio...	GO:0051890
ventral spinal cord development	GO:0021517
positive regulation of RNA metabolic pro...	GO:0051254
neuroepithelial cell differentiation	GO:0060563
cardiac ventricle formation	GO:0003211
positive regulation of cysteine-type end...	GO:2001269
response to UV-C	GO:0010225
regulation of nephron tubule epithelial ...	GO:0072182
somite specification	GO:0001757
regulation of calcium ion transport	GO:0051924
regulation of cellular macromolecule bio...	GO:2000112
leukocyte migration	GO:0050900
regulation of transcription by RNA polym...	GO:0006357
cell differentiation in spinal cord	GO:0021515
cell differentiation in hindbrain	GO:0021533
polyol catabolic process	GO:0046174
positive regulation of macromolecule bio...	GO:0010557
pronephros development	GO:0048793
positive regulation of cell population p...	GO:0008284
calcium ion export	GO:1901660
proton motive force-driven mitochondrial...	GO:0042776
uterus development	GO:0060065
somite rostral/caudal axis specification	GO:0032525
lymphoid progenitor cell differentiation	GO:0002320
positive regulation of mesonephros devel...	GO:0061213
regulation of mesonephros development	GO:0061217
positive regulation of transcription, DN...	GO:0045893

p=2.8E-04	n=3
p=1.8E-03	n=2
p=1.8E-03	n=2
p=1.8E-03	n=2
p=3.5E-03	n=3
p=3.8E-03	n=25
p=4.7E-03	n=5
p=5.2E-03	n=2
p=5.2E-03	n=2
p=5.2E-03	n=2
p=5.2E-03	n=2
p=5.2E-03	n=2
p=5.5E-03	n=7
p=5.7E-03	n=40
p=5.9E-03	n=6
p=7.0E-03	n=27
p=7.1E-03	n=3
p=7.1E-03	n=3
p=7.1E-03	n=3
p=8.0E-03	n=25
p=9.4E-03	n=3
p=9.8E-03	n=13
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.1E-02	n=21



fraction genes in fg and expected value

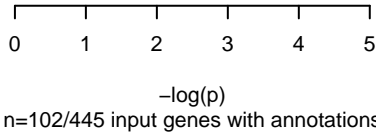
fg=0.03	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.00
fg=0.22	bg=0.13
fg=0.04	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.06	bg=0.02
fg=0.35	bg=0.24
fg=0.05	bg=0.01
fg=0.24	bg=0.15
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.22	bg=0.14
fg=0.03	bg=0.00
fg=0.11	bg=0.06
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=0.02	bg=0.00
fg=0.18	bg=0.11



GO:MF  
Fox\_Nvec\_vc1.1\_XM\_032374843.2

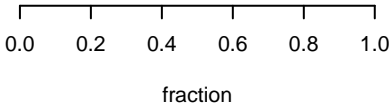
mRNA binding	GO:0003729
inositol bisphosphate phosphatase activi...	GO:0016312
transcription coregulator activity	GO:0003712
Arp2/3 complex binding	GO:0071933
C2H2 zinc finger domain binding	GO:0070742
methyl-CpG binding	GO:0008327
nuclear receptor coactivator activity	GO:0030374
RNA polymerase II complex binding	GO:0000993
NF-kappaB binding	GO:0051059
protein kinase A regulatory subunit bind...	GO:0034237
E-box binding	GO:0070888
lipid transfer activity	GO:0120013
protein tyrosine/serine/threonine phosph...	GO:0008138
HMG box domain binding	GO:0071837
sphingolipid transfer activity	GO:0120016
ceramide transfer activity	GO:0120017
3'-flap-structured DNA binding	GO:0070337
phosphatidylserine decarboxylase activit...	GO:0004609
interleukin-2 receptor binding	GO:0005134
oxidative DNA demethylase activity	GO:0035516
sphingolipid transporter activity	GO:0046624
telomeric G-quadruplex DNA binding	GO:0061849
BIR domain binding	GO:1990525
FAD transmembrane transporter activity	GO:0015230
D5 dopamine receptor binding	GO:0031752
serum response element binding	GO:0010736
polynucleotide phosphatase activity	GO:0098518
8-hydroxy-2'-deoxyguanosine DNA binding	GO:1905773
nucleotidase activity	GO:0008252
5'-nucleotidase activity	GO:0008253

p=1.1E-03	n=10
p=1.8E-03	n=2
p=4.2E-03	n=12
p=5.4E-03	n=2
p=1.0E-02	n=2
p=1.0E-02	n=2
p=1.3E-02	n=3
p=1.7E-02	n=2
p=1.7E-02	n=2
p=1.7E-02	n=2
p=2.0E-02	n=3
p=2.5E-02	n=2
p=3.4E-02	n=2
p=3.4E-02	n=2
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1



fraction genes in fg and expected value

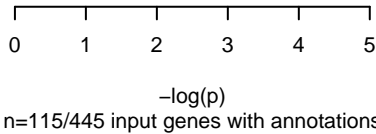
fg=0.10	bg=0.03
fg=0.02	bg=0.00
fg=0.12	bg=0.05
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	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=0.01	bg=0.00
fg=0.01	bg=0.00



GO:CC  
Fox\_Nvec\_vc1.1\_XM\_032374843.2

nuclear speck	GO:0016607
exon-exon junction complex	GO:0035145
transcription regulator complex	GO:0005667
chaperone complex	GO:0101031
myelin sheath	GO:0043209
mitochondrial proton-transporting ATP sy...	GO:0000276
SAM complex	GO:0001401
DSIF complex	GO:0032044
integrin alpha4-beta7 complex	GO:0034669
TSC1-TSC2 complex	GO:0033596
proton-transporting ATP synthase complex...	GO:0045263
proton-transporting ATP synthase, centra...	GO:0045269
serine-type peptidase complex	GO:1905286
mitochondrial proton-transporting ATP sy...	GO:0005756
signal recognition particle, endoplasmic...	GO:0005786
serine-type endopeptidase complex	GO:1905370
methionyl glutamyl tRNA synthetase compl...	GO:0017102
signal recognition particle	GO:0048500
synaptic cleft	GO:0043083
replication fork	GO:0005657
nucleus	GO:0005634
leading edge membrane	GO:0031256
striated muscle dense body	GO:0055120
caveola	GO:0005901
pronucleus	GO:0045120
recycling endosome membrane	GO:0055038
postsynaptic membrane	GO:0045211
mitochondrial proton-transporting ATP sy...	GO:0000275
outer mitochondrial membrane protein com...	GO:0098799
integrin alpha9-beta1 complex	GO:0034679

p=8.4E-03	n=9
p=1.0E-02	n=2
p=2.5E-02	n=9
p=3.3E-02	n=2
p=3.7E-02	n=5
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.3E-02	n=1
p=4.4E-02	n=3
p=4.8E-02	n=69
p=5.4E-02	n=4
p=6.5E-02	n=2
p=7.2E-02	n=3
p=7.7E-02	n=2
p=7.7E-02	n=2
p=8.2E-02	n=4
p=8.3E-02	n=1
p=8.3E-02	n=1
p=8.3E-02	n=1



fraction genes in fg and expected value

fg=0.08	bg=0.03
fg=0.02	bg=0.00
fg=0.08	bg=0.04
fg=0.02	bg=0.00
fg=0.04	bg=0.02
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=0.01	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=0.01	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=0.03	bg=0.01
fg=0.60	bg=0.50
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00

