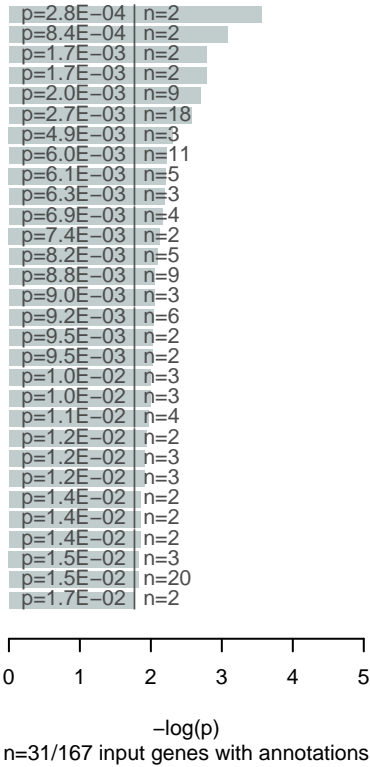


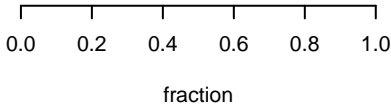
GO:BP
Fox_Nvec_vc1.1_XM_001627136.3

fraction genes in fg and expected value

regulation of cardioblast differentiatio...	GO:0051890
cardiac ventricle formation	GO:0003211
cardiac right ventricle morphogenesis	GO:0003215
atrial septum morphogenesis	GO:0060413
positive regulation of transcription by ...	GO:0045944
regulation of cellular macromolecule bio...	GO:2000112
neuroepithelial cell differentiation	GO:0060563
positive regulation of gene expression	GO:0010628
renal system development	GO:0072001
adenylate cyclase–modulating G protein–c...	GO:0007188
neural tube development	GO:0021915
convergent extension involved in gastrul...	GO:0060027
Wnt signaling pathway	GO:0016055
negative regulation of cellular macromol...	GO:2000113
regulation of cell cycle G1/S phase tran...	GO:1902806
muscle structure development	GO:0061061
regulation of cardiac conduction	GO:1903779
aorta development	GO:0035904
cellular response to antibiotic	GO:0071236
cAMP–mediated signaling	GO:0019933
canonical Wnt signaling pathway	GO:0060070
cellular response to glucocorticoid stim...	GO:0071385
neural tube formation	GO:0001841
sodium ion transport	GO:0006814
adenylate cyclase–activating G protein–c...	GO:0007189
cellular response to corticosteroid stim...	GO:0071384
ventricular septum morphogenesis	GO:0060412
cyclic–nucleotide–mediated signaling	GO:0019935
cellular nitrogen compound biosynthetic ...	GO:0044271
establishment or maintenance of cytoskel...	GO:0030952



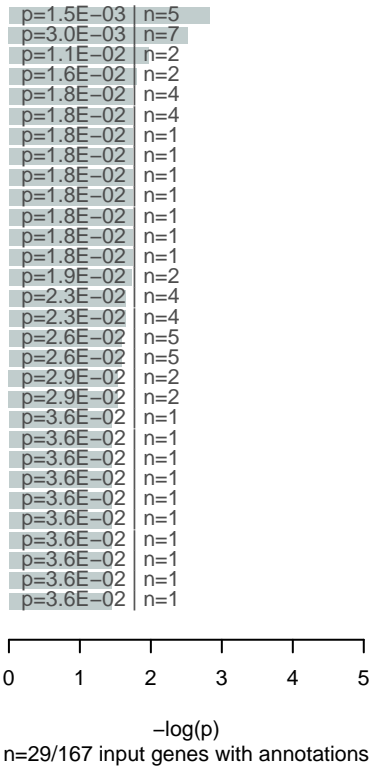
fg=0.06	bg=0.00
fg=0.06	bg=0.00
fg=0.06	bg=0.00
fg=0.06	bg=0.00
fg=0.29	bg=0.10
fg=0.58	bg=0.25
fg=0.10	bg=0.01
fg=0.35	bg=0.16
fg=0.16	bg=0.04
fg=0.10	bg=0.01
fg=0.13	bg=0.03
fg=0.06	bg=0.00
fg=0.16	bg=0.04
fg=0.29	bg=0.12
fg=0.10	bg=0.01
fg=0.19	bg=0.06
fg=0.06	bg=0.00
fg=0.06	bg=0.00
fg=0.10	bg=0.01
fg=0.10	bg=0.01
fg=0.13	bg=0.03
fg=0.06	bg=0.01
fg=0.10	bg=0.02
fg=0.10	bg=0.02
fg=0.06	bg=0.01
fg=0.06	bg=0.01
fg=0.06	bg=0.01
fg=0.06	bg=0.01
fg=0.10	bg=0.02
fg=0.65	bg=0.34
fg=0.06	bg=0.01



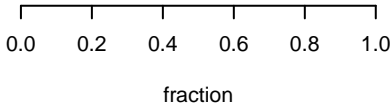
GO:MF
Fox_Nvec_vc1.1_XM_001627136.3

fraction genes in fg and expected value

mRNA binding	GO:0003729
sequence–specific DNA binding	GO:0043565
E–box binding	GO:0070888
ubiquitin conjugating enzyme activity	GO:0061631
cis–regulatory region sequence–specific ...	GO:0000987
RNA polymerase II cis–regulatory region ...	GO:0000978
mevalonate kinase activity	GO:0004496
D5 dopamine receptor binding	GO:0031752
serum response element binding	GO:0010736
malate dehydrogenase (decarboxylating) (...)	GO:0004471
malate dehydrogenase (decarboxylating) (...)	GO:0004473
sphingomyelin phosphodiesterase D activi...	GO:0050290
siRNA binding	GO:0035197
ubiquitin–like protein conjugating enzym...	GO:0061650
DNA–binding transcription activator acti...	GO:0001228
DNA–binding transcription activator acti...	GO:0001216
transcription coregulator activity	GO:0003712
sequence–specific double–stranded DNA bi...	GO:1990837
oxidoreductase activity, acting on CH–OH...	GO:0016614
manganese ion binding	GO:0030145
nitric–oxide synthase regulator activity	GO:0030235
sodium:bicarbonate symporter activity	GO:0008510
malate dehydrogenase activity	GO:0016615
nitric–oxide synthase inhibitor activity	GO:0036487
ISG15 transferase activity	GO:0042296
calcium–dependent ATPase activity	GO:0030899
malic enzyme activity	GO:0004470
sphingomyelin phosphodiesterase activity	GO:0004767
ATPase inhibitor activity	GO:0042030
methyl–CpG binding	GO:0008327



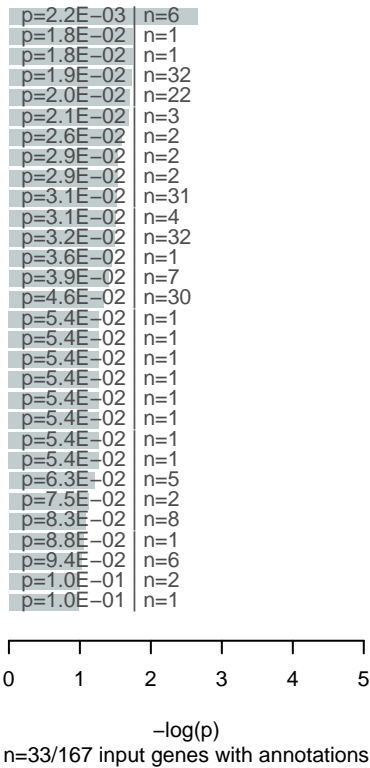
fg=0.17	bg=0.03
fg=0.24	bg=0.07
fg=0.07	bg=0.01
fg=0.07	bg=0.01
fg=0.14	bg=0.04
fg=0.14	bg=0.04
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.07	bg=0.01
fg=0.14	bg=0.04
fg=0.14	bg=0.04
fg=0.17	bg=0.06
fg=0.17	bg=0.06
fg=0.07	bg=0.01
fg=0.07	bg=0.01
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00



GO:CC
Fox_Nvec_vc1.1_XM_001627136.3

fraction genes in fg and expected value

transcription regulator complex	GO:0005667
synaptic cleft	GO:0043083
TSC1–TSC2 complex	GO:0033596
intracellular organelle	GO:0043229
nucleus	GO:0005634
RNA polymerase II transcription regulato...	GO:0090575
neuronal cell body membrane	GO:0032809
cell body membrane	GO:0044298
neuron projection membrane	GO:0032589
membrane–bounded organelle	GO:0043227
cell projection membrane	GO:0031253
organelle	GO:0043226
inner dynein arm	GO:0036156
microtubule cytoskeleton	GO:0015630
intracellular membrane–bounded organelle	GO:0043231
exon–exon junction complex	GO:0035145
axonemal dynein complex	GO:0005858
postsynaptic specialization membrane	GO:0099634
dendritic spine membrane	GO:0032591
CHD–type complex	GO:0090545
postsynaptic density membrane	GO:0098839
NuRD complex	GO:0016581
chaperone complex	GO:0101031
microtubule organizing center	GO:0005815
leading edge membrane	GO:0031256
cytoskeleton	GO:0005856
sperm principal piece	GO:0097228
plasma membrane region	GO:0098590
postsynaptic membrane	GO:0045211
GTPase complex	GO:1905360



fg=0.18	bg=0.04
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.97	bg=0.84
fg=0.67	bg=0.48
fg=0.09	bg=0.02
fg=0.06	bg=0.01
fg=0.06	bg=0.01
fg=0.06	bg=0.01
fg=0.94	bg=0.81
fg=0.12	bg=0.04
fg=0.97	bg=0.85
fg=0.03	bg=0.00
fg=0.21	bg=0.10
fg=0.91	bg=0.78
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.03	bg=0.00
fg=0.15	bg=0.07
fg=0.06	bg=0.01
fg=0.24	bg=0.14
fg=0.03	bg=0.00
fg=0.18	bg=0.10
fg=0.06	bg=0.02
fg=0.03	bg=0.00

