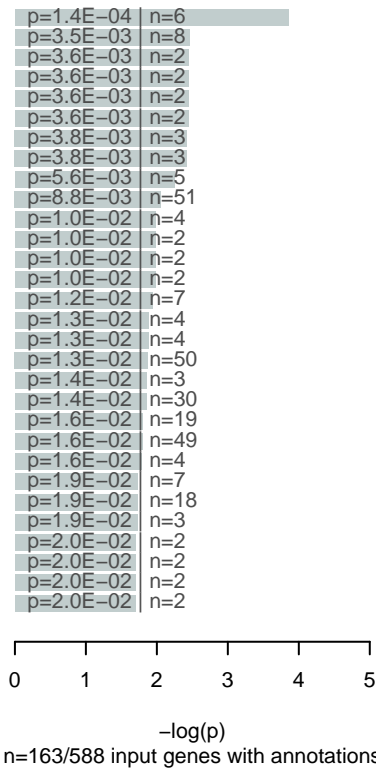


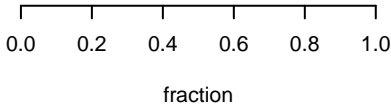
GO:BP
Elav_Nvec_vc1.1_XM_001624716.3

fraction genes in fg and expected value

regulation of mRNA 3'-end processing	GO:0031440
peptidyl-lysine acetylation	GO:0018394
positive regulation of nuclear-transcrib...	GO:1900153
regulation of protein autoubiquitination	GO:1902498
positive regulation of nuclear-transcrib...	GO:0060213
regulation of transcription from RNA pol...	GO:0010767
syncytial blastoderm mitotic cell cycle	GO:0035186
cell-cell junction maintenance	GO:0045217
mRNA polyadenylation	GO:0006378
RNA biosynthetic process	GO:0032774
histone deacetylation	GO:0016575
positive regulation of protein localizat...	GO:1904781
protein O-linked mannosylation	GO:0035269
positive regulation of protein deacetyla...	GO:0090312
internal peptidyl-lysine acetylation	GO:0018393
regulation of protein acetylation	GO:1901983
protein deacetylation	GO:0006476
nucleic acid-templated transcription	GO:0097659
endothelial cell apoptotic process	GO:0072577
negative regulation of macromolecule bio...	GO:0010558
regulation of mitotic cell cycle	GO:0007346
transcription, DNA-templated	GO:0006351
protein O-linked glycosylation	GO:0006493
internal protein amino acid acetylation	GO:0006475
negative regulation of transcription by ...	GO:0000122
termination of RNA polymerase II transcr...	GO:0006369
atrioventricular valve morphogenesis	GO:0003181
mitral valve morphogenesis	GO:0003183
mitral valve development	GO:0003174
rhombomere morphogenesis	GO:0021593



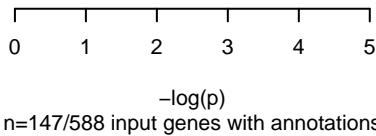
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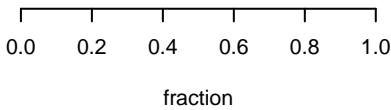
GO:MF
Elav_Nvec_vc1.1_XM_001624716.3

fraction genes in fg and expected value

manganese ion binding	GO:0030145
microtubule binding	GO:0008017
polynucleotide adenyllyltransferase activ...	GO:0004652
isomerase activity	GO:0016853
DNA-binding transcription factor activit...	GO:0000981
DNA-directed 5'-3' RNA polymerase activi...	GO:0003899
MHC protein binding	GO:0042287
transcription regulator activity	GO:0140110
nucleotidyltransferase activity	GO:0016779
transcription coregulator activity	GO:0003712
5'-3' RNA polymerase activity	GO:0034062
RNA polymerase activity	GO:0097747
transcription factor binding	GO:0008134
RNA polymerase II transcription regulato...	GO:0000977
intramolecular transferase activity	GO:0016866
acetylglucosaminyltransferase activity	GO:0008375
histone deacetylase activity	GO:0004407
tau protein binding	GO:0048156
macrolide binding	GO:0005527
FK506 binding	GO:0005528
xylosyltransferase activity	GO:0042285
UDP-xylosyltransferase activity	GO:0035252
minor groove of adenine-thymine-rich DNA...	GO:0003680
core promoter sequence-specific DNA bind...	GO:0001046
DNA-binding transcription factor binding	GO:0140297
DNA-binding transcription repressor acti...	GO:0001227
DNA-binding transcription repressor acti...	GO:0001217
DNA-binding transcription factor activit...	GO:0003700
protein lysine deacetylase activity	GO:0033558
intramolecular transferase activity, pho...	GO:0016868



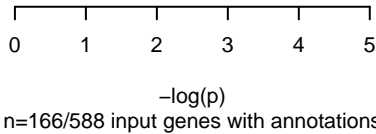
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GO:CC
Elav_Nvec_vc1.1_XM_001624716.3

fraction genes in fg and expected value

P-body	GO:0000932
nucleus	GO:0005634
oligosaccharyltransferase complex	GO:0008250
lamellar body	GO:0042599
intercalary heterochromatin	GO:0005725
cytolytic granule	GO:0044194
platelet alpha granule	GO:0031091
costamere	GO:0043034
spot adherens junction	GO:0005914
mitotic spindle pole	GO:0097431
microtubule	GO:0005874
zymogen granule	GO:0042588
nuclear lumen	GO:0031981
cytoplasmic microtubule	GO:0005881
histone deacetylase complex	GO:0000118
kinetochore	GO:0000776
ficolin-1-rich granule	GO:0101002
centrosome	GO:0005813
chromatin	GO:0000785
secretory granule	GO:0030141
axon cytoplasm	GO:1904115
microtubule cytoskeleton	GO:0015630
caveola	GO:0005901
transferase complex, transferring phosph...	GO:0061695
ficolin-1-rich granule lumen	GO:1904813
Golgi medial cisterna	GO:0005797
host cell nucleus	GO:0042025
cytoplasmic periphery of the nuclear por...	GO:1990723
host intracellular region	GO:0043656
host cell	GO:0043657



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