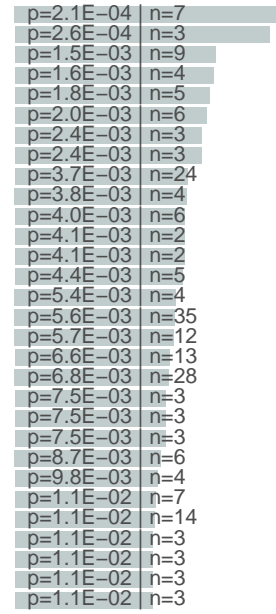


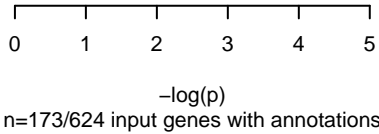
GO:BP
Elav_Nvec_vc1.1_XM_032366627.2

fraction genes in fg and expected value

negative regulation of epithelial cell p...	GO:0050680
epithelial cell proliferation involved i...	GO:2001013
regulation of epithelial cell migration	GO:0010632
endochondral ossification	GO:0001958
myoblast fusion	GO:0007520
blood vessel endothelial cell migration	GO:0043534
nephron tubule epithelial cell different...	GO:0072160
stabilization of membrane potential	GO:0030322
positive regulation of transport	GO:0051050
glutamate secretion	GO:0014047
negative regulation of intracellular tra...	GO:0032387
positive regulation of cytolysis	GO:0045919
canonical Wnt signaling pathway involved...	GO:0061290
cochlea development	GO:0090102
regulation of membrane invagination	GO:1905153
tube development	GO:0035295
positive regulation of developmental gro...	GO:0048639
muscle organ development	GO:0007517
embryo development ending in birth or eg...	GO:0009792
negative regulation of neurotransmitter ...	GO:0046929
germarium-derived oocyte fate determinat...	GO:0007294
zymogen activation	GO:0031638
chromosome organization involved in meio...	GO:0070192
regulation of hematopoietic stem cell di...	GO:1902036
positive regulation of transmembrane tra...	GO:0034764
regulation of hormone levels	GO:0010817
definitive hemopoiesis	GO:0060216
regulation of extracellular matrix organ...	GO:1903053
regulation of Rac protein signal transdu...	GO:0035020
cytoplasmic transport, nurse cell to ooc...	GO:0007303



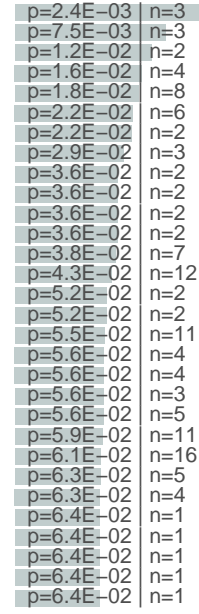
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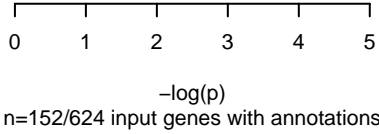
GO:MF
Elav_Nvec_vc1.1_XM_032366627.2

fraction genes in fg and expected value

potassium ion leak channel activity	GO:0022841
HMG box domain binding	GO:0071837
toxin transmembrane transporter activity	GO:0019534
SMAD binding	GO:0046332
actin binding	GO:0003779
secondary active transmembrane transport...	GO:0015291
calcium-dependent cysteine-type endopept...	GO:0004198
solute:sodium symporter activity	GO:0015370
actin monomer binding	GO:0003785
AP-2 adaptor complex binding	GO:0035612
phosphatidylinositol-5-phosphate binding	GO:0010314
phosphatidylinositol-4,5-bisphosphate ph...	GO:0106019
active ion transmembrane transporter act...	GO:0022853
ATP hydrolysis activity	GO:0016887
dynactin binding	GO:0034452
glutamate binding	GO:0016595
signaling receptor activity	GO:0038023
cytokine receptor binding	GO:0005126
sodium ion transmembrane transporter act...	GO:0015081
cysteine-type endopeptidase activity	GO:0004197
PDZ domain binding	GO:0030165
molecular transducer activity	GO:0060089
nucleoside-triphosphatase activity	GO:0017111
ion channel regulator activity	GO:0099106
lipase activity	GO:0016298
sodium:dicarboxylate symporter activity	GO:0017153
CCR5 chemokine receptor binding	GO:0031730
ribonuclease III activity	GO:0004525
histone kinase activity (H3-T11 specific...	GO:0035402
CCR chemokine receptor binding	GO:0048020



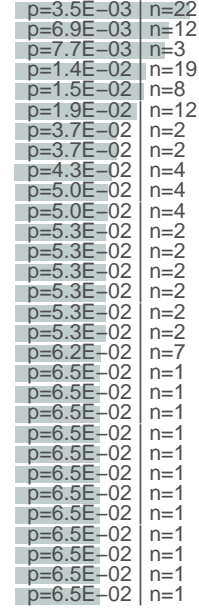
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GO:CC
Elav_Nvec_vc1.1_XM_032366627.2

fraction genes in fg and expected value

intrinsic component of plasma membrane	GO:0031226
nuclear speck	GO:0016607
presynaptic active zone membrane	GO:0048787
integral component of plasma membrane	GO:0005887
actin-based cell projection	GO:0098858
cell leading edge	GO:0031252
phagocytic cup	GO:0001891
intrinsic component of the cytoplasmic s...	GO:0031235
microvillus	GO:0005902
filopodium	GO:0030175
dendritic shaft	GO:0043198
endonuclease complex	GO:1905348
filopodium membrane	GO:0031527
astrocyte projection	GO:0097449
aster	GO:0005818
glial cell projection	GO:0097386
endoribonuclease complex	GO:1902555
endocytic vesicle	GO:0030139
protein farnesyltransferase complex	GO:0005965
ciliary cap	GO:0061822
nuclear pore cytoplasmic filaments	GO:0044614
cytoplasmic periphery of the nuclear por...	GO:1990723
trRNA-intron endonuclease complex	GO:0000214
microvesicle	GO:1990742
pinosome	GO:0044352
macropinosome	GO:0044354
tubular endosome	GO:0097422
ribonuclease III complex	GO:1903095
sperm individualization complex	GO:0070864
investment cone	GO:0070865



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