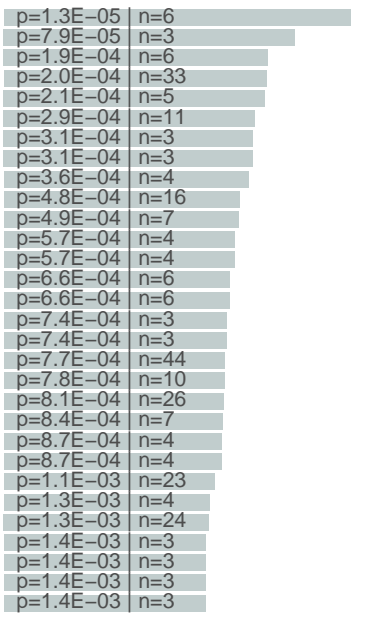


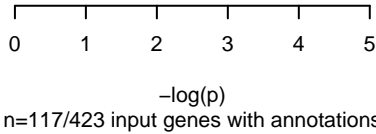
GO:BP  
Elav\_Nvec\_vc1.1\_XM\_032376608.2

fraction genes in fg and expected value

cellular response to retinoic acid	GO:0071300
stem cell fate specification	GO:0048866
somatic stem cell population maintenance	GO:0035019
positive regulation of gene expression	GO:0010628
epidermis morphogenesis	GO:0048730
imaginal disc-derived wing morphogenesis	GO:0007476
non-canonical Wnt signaling pathway via ...	GO:0038031
heart jogging	GO:0003146
developmental induction	GO:0031128
renal system development	GO:0072001
regulation of organ growth	GO:0046620
proximal/distal pattern formation	GO:0009954
segment polarity determination	GO:0007367
positive regulation of canonical Wnt sig...	GO:0090263
epithelial to mesenchymal transition	GO:0001837
beta-catenin-TCF complex assembly	GO:1904837
regulation of imaginal disc growth	GO:0045570
regulation of cellular macromolecule bio...	GO:2000112
dorsal/ventral pattern formation	GO:0009953
behavior	GO:0007610
transforming growth factor beta receptor...	GO:0007179
positive regulation of mesenchymal cell ...	GO:0002053
cellular response to glucose starvation	GO:0042149
embryo development ending in birth or eg...	GO:0009792
prostate gland development	GO:0030850
positive regulation of transcription by ...	GO:0045944
lens morphogenesis in camera-type eye	GO:0002089
morphogenesis of an epithelial bud	GO:0060572
response to cycloheximide	GO:0046898
Kupffer's vesicle development	GO:0070121



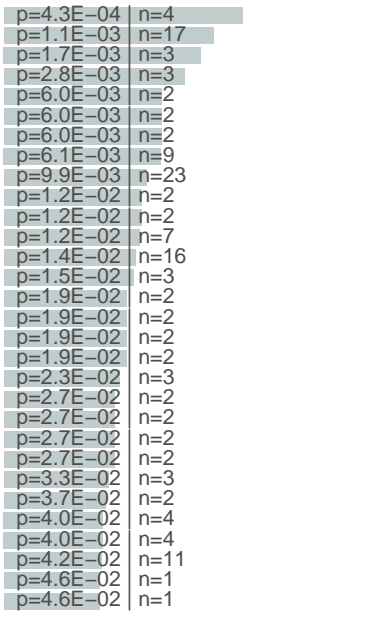
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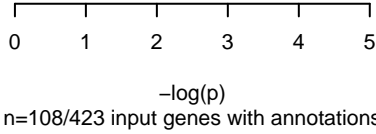
GO:MF  
Elav\_Nvec\_vc1.1\_XM\_032376608.2

fraction genes in fg and expected value

transcription coregulator binding	GO:0001221
DNA-binding transcription factor activit...	GO:0003700
Wnt-protein binding	GO:0017147
calcium-release channel activity	GO:0015278
oxidoreductase activity, acting on the C...	GO:0016899
inosine kinase activity	GO:0008906
phosphoenolpyruvate carboxykinase (GTP) ...	GO:0004613
RNA polymerase II cis-regulatory region ...	GO:0000978
protein dimerization activity	GO:0046983
lactate dehydrogenase activity	GO:0004457
DNA binding domain binding	GO:0050692
ion gated channel activity	GO:0022839
protein domain specific binding	GO:0019904
nucleobase-containing compound kinase ac...	GO:0019205
nucleoside diphosphate kinase activity	GO:0004550
epinephrine binding	GO:0051379
catecholamine binding	GO:1901338
transcription coactivator binding	GO:0001223
E-box binding	GO:0070888
cysteine-type endopeptidase regulator ac...	GO:0043028
mitogen-activated protein kinase kinase ...	GO:0031434
O-methyltransferase activity	GO:0008171
coreceptor activity	GO:0015026
SMAD binding	GO:0046332
adrenergic receptor binding	GO:0031690
voltage-gated channel activity	GO:0022832
voltage-gated ion channel activity	GO:0005244
protein heterodimerization activity	GO:0046982
receptor tyrosine kinase-like orphan rec...	GO:0005115
DNA topoisomerase type II (double strand...	GO:0072586



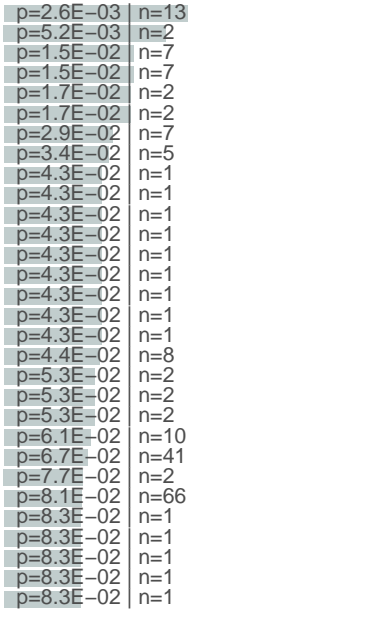
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GO:CC  
Elav\_Nvec\_vc1.1\_XM\_032376608.2

fraction genes in fg and expected value

chromatin	GO:0000785
beta-catenin-TCF complex	GO:1990907
basolateral plasma membrane	GO:0016323
basal plasma membrane	GO:0009925
sensory dendrite	GO:0071683
Golgi cis cisterna	GO:0000137
basal part of cell	GO:0045178
receptor complex	GO:0043235
Scrib-APC-beta-catenin complex	GO:0034750
catenin-TCF7L2 complex	GO:0071664
condensin complex	GO:0000796
apoptosome	GO:0043293
smooth septate junction	GO:0005920
fascia adherens	GO:0005916
polycystin complex	GO:0002133
axonemal basal plate	GO:0097541
beta-catenin-TCF7L2 complex	GO:0070369
cell cortex	GO:0005938
MLL1 complex	GO:0071339
Golgi lumen	GO:0005796
calcium channel complex	GO:0034704
cytoplasmic region	GO:0099568
nucleoplasm	GO:0005654
MLL1/2 complex	GO:0044665
nucleus	GO:0005634
Sin3 complex	GO:0016580
beta-catenin destruction complex	GO:0030877
Wnt signalosome	GO:1990909
COPII vesicle coat	GO:0030127
eukaryotic translation elongation factor...	GO:0005853



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