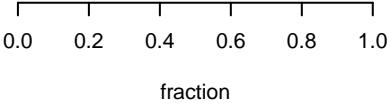
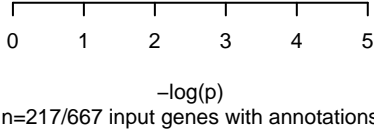


GO:BP
Elav_Nvec_vc1.1_XM_001625588.3

fraction genes in fg and expected value

NAD biosynthetic process	GO:0009435	p=9.9E-04	n=5
positive regulation of stem cell prolif...	GO:2000648	p=1.0E-03	n=6
nose development	GO:0043584	p=1.9E-03	n=3
regulation of fibroblast apoptotic proce...	GO:2000269	p=1.9E-03	n=3
epithelial cell migration, open tracheal...	GO:0007427	p=1.9E-03	n=3
glomerulus morphogenesis	GO:0072102	p=1.9E-03	n=3
establishment of mitotic spindle localiz...	GO:0040001	p=6.3E-03	n=6
circumferential growth involved in left ...	GO:0003243	p=6.4E-03	n=2
somatic motor neuron differentiation	GO:0021523	p=6.4E-03	n=2
tRNA catabolic process	GO:0016078	p=6.4E-03	n=2
third ventricle development	GO:0021678	p=6.4E-03	n=2
plasminogen activation	GO:0031639	p=6.4E-03	n=2
negative regulation of sprouting angioge...	GO:1903671	p=6.4E-03	n=2
negative regulation of cell migration in...	GO:0090051	p=6.4E-03	n=2
maintenance of epithelial integrity, ope...	GO:0035160	p=6.4E-03	n=2
cellular response to 3-methylcholanthren...	GO:1904682	p=6.4E-03	n=2
peptidyl-arginine omega-N-methylation	GO:0035247	p=6.4E-03	n=2
positive regulation of transcription fac...	GO:1901485	p=6.4E-03	n=2
histone H4-R3 methylation	GO:0043985	p=6.4E-03	n=2
platelet activating factor biosynthetic ...	GO:0006663	p=6.4E-03	n=2
spindle assembly	GO:0051225	p=7.0E-03	n=9
positive regulation of neuroblast prolif...	GO:0002052	p=8.5E-03	n=4
rostrocaudal neural tube patterning	GO:0021903	p=8.5E-03	n=3
protein localization to ciliary transiti...	GO:1904491	p=8.5E-03	n=3
cellular response to corticosteroid stim...	GO:0071384	p=8.9E-03	n=5
actin filament organization	GO:0007015	p=9.2E-03	n=14
negative regulation of cell cycle G1/S p...	GO:1902807	p=1.2E-02	n=5
negative regulation of G1/S transition o...	GO:2000134	p=1.2E-02	n=5
establishment of mitotic spindle orienta...	GO:0000132	p=1.2E-02	n=5
NAD metabolic process	GO:0019674	p=1.5E-02	n=5

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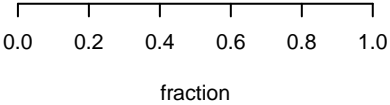
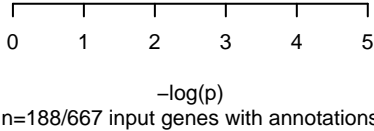


GO:MF
Elav_Nvec_vc1.1_XM_001625588.3

fraction genes in fg and expected value

methyl-CpG binding	GO:0008327	p=1.9E-03	n=3
TFIID-class transcription factor complex...	GO:0001094	p=4.4E-03	n=3
1-alkylglycerophosphocholine O-acetyltra...	GO:0047192	p=6.3E-03	n=2
carbon-nitrogen ligase activity, with gl...	GO:0016884	p=6.3E-03	n=2
protein-arginine omega-N monomethyltrans...	GO:0035241	p=6.3E-03	n=2
histone methyltransferase activity (H4-R...	GO:0044020	p=6.3E-03	n=2
ligand-activated transcription factor ac...	GO:0098531	p=1.4E-02	n=3
nuclear receptor activity	GO:0004879	p=1.4E-02	n=3
integrin binding	GO:0005178	p=1.7E-02	n=5
1-acylglycerophosphocholine O-acyltransf...	GO:0047184	p=1.8E-02	n=2
2-acylglycerol-3-phosphate O-acyltransfe...	GO:0047144	p=1.8E-02	n=2
double-stranded DNA binding	GO:0003690	p=2.4E-02	n=18
sequence-specific double-stranded DNA bi...	GO:1990837	p=2.7E-02	n=16
transcription cis-regulatory region bind...	GO:0000976	p=2.8E-02	n=15
transcription coregulator binding	GO:0001221	p=2.9E-02	n=3
cis-regulatory region sequence-specific ...	GO:0000987	p=3.2E-02	n=11
RNA polymerase II cis-regulatory region ...	GO:0000978	p=3.2E-02	n=11
oxidoreductase activity, acting on singl...	GO:0016701	p=3.4E-02	n=2
dynein light intermediate chain binding	GO:0051959	p=3.4E-02	n=2
FAD binding	GO:0071949	p=3.4E-02	n=2
beta-catenin binding	GO:0008013	p=3.9E-02	n=3
RNA polymerase II transcription regulato...	GO:0000977	p=4.6E-02	n=13
transcription regulatory region nucleic ...	GO:0001067	p=4.8E-02	n=16
actin monomer binding	GO:0003785	p=5.3E-02	n=2
cyclic nucleotide binding	GO:0030551	p=5.3E-02	n=2
sphingolipid binding	GO:0046625	p=5.3E-02	n=2
histone H3-methyl-lysine-4 demethylase a...	GO:0032453	p=5.3E-02	n=2
transcription coactivator binding	GO:0001223	p=5.3E-02	n=2
protein kinase C binding	GO:0005080	p=6.4E-02	n=3
mitogen-activated protein kinase binding	GO:0051019	p=6.4E-02	n=3

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GO:CC
Elav_Nvec_vc1.1_XM_001625588.3

fraction genes in fg and expected value

ESCRT I complex	GO:0000813	p=6.0E-03	n=2
cytosolic aryl hydrocarbon receptor comp...	GO:0034752	p=6.0E-03	n=2
neuron projection cytoplasm	GO:0120111	p=7.5E-03	n=4
ruffle membrane	GO:0032587	p=1.1E-02	n=4
AP-type membrane coat adaptor complex	GO:0030119	p=1.3E-02	n=3
nuclear aryl hydrocarbon receptor comple...	GO:0034753	p=1.7E-02	n=2
nuclear matrix	GO:0016363	p=2.1E-02	n=6
transcription elongation factor complex	GO:0008023	p=2.4E-02	n=4
cytoskeleton	GO:0005856	p=2.6E-02	n=41
nuclear protein-containing complex	GO:0140513	p=2.8E-02	n=34
centriole	GO:0005814	p=2.9E-02	n=6
methyltransferase complex	GO:0034708	p=3.3E-02	n=6
lipid droplet	GO:0005811	p=3.3E-02	n=5
cytosolic small ribosomal subunit	GO:0022627	p=3.7E-02	n=4
protein-DNA complex	GO:0032993	p=4.3E-02	n=6
transcription repressor complex	GO:0017053	p=4.5E-02	n=4
dendrite cytoplasm	GO:0032839	p=5.1E-02	n=2
methylosome	GO:0034709	p=5.1E-02	n=2
intercellular canaliculus	GO:0046581	p=5.1E-02	n=2
intrinsic component of the cytoplasmic s...	GO:0031235	p=5.1E-02	n=2
DNA packaging complex	GO:0044815	p=5.3E-02	n=5
cell division site	GO:0032153	p=5.4E-02	n=4
ruffle	GO:0001726	p=6.8E-02	n=5
filopodium membrane	GO:0031527	p=7.3E-02	n=2
meiotic spindle	GO:0072687	p=7.3E-02	n=2
axon cytoplasm	GO:1904115	p=7.3E-02	n=2
Ino80 complex	GO:0031011	p=7.3E-02	n=2
PcG protein complex	GO:0031519	p=7.3E-02	n=3
histone deacetylase complex	GO:0000118	p=7.3E-02	n=3
membrane coat	GO:0030117	p=7.4E-02	n=4

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