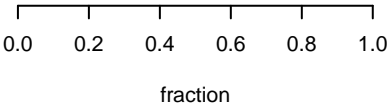
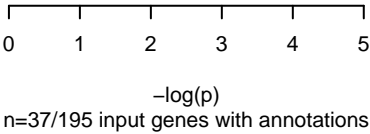


GO:BP
Ncol_Nvec_vc1.1_XM_032364814.2

fraction genes in fg and expected value

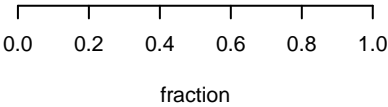
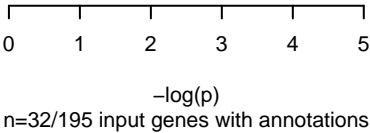
regulation of neurotransmitter secretion	GO:0046928	p=1.7E-03	n=4	fg=0.11	bg=0.02
action potential	GO:0001508	p=2.2E-03	n=6	fg=0.16	bg=0.04
sensory processing	GO:0050893	p=6.1E-03	n=3	fg=0.08	bg=0.01
regulation of mRNA stability	GO:0043488	p=6.1E-03	n=3	fg=0.08	bg=0.01
positive regulation of axon extension	GO:0045773	p=6.1E-03	n=3	fg=0.08	bg=0.01
inorganic ion transmembrane transport	GO:0098660	p=9.5E-03	n=10	fg=0.27	bg=0.12
regulation of axon guidance	GO:1902667	p=1.1E-02	n=3	fg=0.08	bg=0.01
memory	GO:0007613	p=1.7E-02	n=5	fg=0.14	bg=0.04
adult locomotory behavior	GO:0008344	p=1.7E-02	n=4	fg=0.11	bg=0.03
cellular biogenic amine metabolic proces...	GO:0006576	p=1.9E-02	n=3	fg=0.08	bg=0.02
neuron projection regeneration	GO:0031102	p=1.9E-02	n=3	fg=0.08	bg=0.02
axon regeneration	GO:0031103	p=1.9E-02	n=3	fg=0.08	bg=0.02
negative regulation of cellular amide me...	GO:0034249	p=1.9E-02	n=3	fg=0.08	bg=0.02
cellular response to cytokine stimulus	GO:0071345	p=2.2E-02	n=6	fg=0.16	bg=0.06
locomotory behavior	GO:0007626	p=2.2E-02	n=8	fg=0.22	bg=0.10
positive regulation of neuron projection...	GO:0010976	p=2.3E-02	n=4	fg=0.11	bg=0.03
positive regulation of neurotransmitter ...	GO:0001956	p=2.3E-02	n=2	fg=0.05	bg=0.01
nervous system process involved in regul...	GO:0001976	p=2.3E-02	n=2	fg=0.05	bg=0.01
regulation of response to oxidative stre...	GO:1902882	p=2.3E-02	n=2	fg=0.05	bg=0.01
positive regulation of axon regeneration	GO:0048680	p=2.3E-02	n=2	fg=0.05	bg=0.01
B cell homeostasis	GO:0001782	p=2.3E-02	n=2	fg=0.05	bg=0.01
nuclear-transcribed mRNA catabolic proce...	GO:0000288	p=2.3E-02	n=2	fg=0.05	bg=0.01
protein transmembrane transport	GO:0071806	p=2.3E-02	n=2	fg=0.05	bg=0.01
response to estradiol	GO:0032355	p=2.3E-02	n=2	fg=0.05	bg=0.01
mRNA destabilization	GO:0061157	p=2.3E-02	n=2	fg=0.05	bg=0.01
positive regulation of neuron projection...	GO:0070572	p=2.3E-02	n=2	fg=0.05	bg=0.01
positive regulation of neurotransmitter ...	GO:0051590	p=2.3E-02	n=2	fg=0.05	bg=0.01
positive regulation of mRNA catabolic pr...	GO:0061014	p=2.3E-02	n=2	fg=0.05	bg=0.01
RNA destabilization	GO:0050779	p=2.3E-02	n=2	fg=0.05	bg=0.01
heart contraction	GO:0060047	p=2.6E-02	n=6	fg=0.16	bg=0.07



GO:MF
Ncol_Nvec_vc1.1_XM_032364814.2

fraction genes in fg and expected value

ion gated channel activity	GO:0022839	p=1.6E-04	n=9	fg=0.28	bg=0.07
excitatory extracellular ligand-gated io...	GO:0005231	p=5.5E-03	n=3	fg=0.09	bg=0.01
high voltage-gated calcium channel activ...	GO:0008331	p=7.5E-03	n=2	fg=0.06	bg=0.01
ligand-gated anion channel activity	GO:0099095	p=1.7E-02	n=3	fg=0.09	bg=0.02
voltage-gated potassium channel activity	GO:0005249	p=3.6E-02	n=3	fg=0.09	bg=0.02
extracellularly glutamate-gated chloride...	GO:0008068	p=4.0E-02	n=2	fg=0.06	bg=0.01
transmitter-gated ion channel activity	GO:0022824	p=4.0E-02	n=2	fg=0.06	bg=0.01
extracellularly glutamate-gated ion chan...	GO:0005234	p=4.0E-02	n=2	fg=0.06	bg=0.01
transmitter-gated channel activity	GO:0022835	p=4.0E-02	n=2	fg=0.06	bg=0.01
glutamate binding	GO:0016595	p=4.0E-02	n=2	fg=0.06	bg=0.01
anion channel activity	GO:0005253	p=4.8E-02	n=3	fg=0.09	bg=0.03
chloride channel activity	GO:0005254	p=4.8E-02	n=3	fg=0.09	bg=0.03
chloride transmembrane transporter activ...	GO:0015108	p=4.8E-02	n=3	fg=0.09	bg=0.03
identical protein binding	GO:0042802	p=5.3E-02	n=10	fg=0.31	bg=0.19
inorganic anion transmembrane transporte...	GO:0015103	p=6.3E-02	n=3	fg=0.09	bg=0.03
amino acid binding	GO:0016597	p=6.3E-02	n=2	fg=0.06	bg=0.01
voltage-gated cation channel activity	GO:0022843	p=6.8E-02	n=5	fg=0.16	bg=0.04
potassium channel activity	GO:0005267	p=7.9E-02	n=3	fg=0.09	bg=0.03
potassium ion transmembrane transporter ...	GO:0015079	p=7.9E-02	n=3	fg=0.09	bg=0.03
voltage-gated ion channel activity	GO:0005244	p=8.3E-02	n=5	fg=0.16	bg=0.04
voltage-gated channel activity	GO:0022832	p=8.3E-02	n=5	fg=0.16	bg=0.04
phosphotransferase activity, carboxyl gr...	GO:0016774	p=8.8E-02	n=1	fg=0.03	bg=0.00
BH3 domain binding	GO:0051434	p=8.8E-02	n=1	fg=0.03	bg=0.00
exonuclease activity	GO:0004527	p=8.8E-02	n=1	fg=0.03	bg=0.00
1-alkenylglycerophosphocholine O-acyltra...	GO:0047159	p=8.8E-02	n=1	fg=0.03	bg=0.00
1-acylglycerophosphocholine O-acyltransf...	GO:0047184	p=8.8E-02	n=1	fg=0.03	bg=0.00
neurotransmitter receptor activity invol...	GO:0099529	p=8.8E-02	n=1	fg=0.03	bg=0.00
phosphatidylinositol-4-phosphate binding	GO:0070273	p=8.8E-02	n=1	fg=0.03	bg=0.00
nuclease activity	GO:0004518	p=8.8E-02	n=1	fg=0.03	bg=0.00
open rectifier potassium channel activit...	GO:0005252	p=8.8E-02	n=1	fg=0.03	bg=0.00



GO:CC
Ncol_Nvec_vc1.1_XM_032364814.2

fraction genes in fg and expected value

cation channel complex	GO:0034703	p=6.0E-03	n=5	fg=0.14	bg=0.04
plasma membrane protein complex	GO:0098797	p=7.6E-03	n=6	fg=0.17	bg=0.05
integral component of plasma membrane	GO:0005887	p=2.0E-02	n=10	fg=0.29	bg=0.15
voltage-gated potassium channel complex	GO:0008076	p=2.5E-02	n=3	fg=0.09	bg=0.02
potassium channel complex	GO:0034705	p=2.5E-02	n=3	fg=0.09	bg=0.02
intrinsic component of plasma membrane	GO:0031226	p=3.5E-02	n=10	fg=0.29	bg=0.16
neuron projection membrane	GO:0032589	p=4.8E-02	n=3	fg=0.09	bg=0.02
presynapse	GO:0098793	p=6.2E-02	n=6	fg=0.17	bg=0.08
voltage-gated calcium channel complex	GO:0005891	p=6.2E-02	n=2	fg=0.06	bg=0.01
transporter complex	GO:1990351	p=7.7E-02	n=6	fg=0.17	bg=0.04
transmembrane transporter complex	GO:1902495	p=7.7E-02	n=6	fg=0.17	bg=0.04
ion channel complex	GO:0034702	p=7.7E-02	n=6	fg=0.17	bg=0.04
integral component of mitochondrial memb...	GO:0032592	p=8.7E-02	n=1	fg=0.03	bg=0.00
intrinsic component of mitochondrial mem...	GO:0098573	p=8.7E-02	n=1	fg=0.03	bg=0.00
acetylcholine-gated channel complex	GO:0005892	p=8.7E-02	n=1	fg=0.03	bg=0.00
muscle cell projection	GO:0036194	p=8.7E-02	n=1	fg=0.03	bg=0.00
muscle cell projection membrane	GO:0036195	p=8.7E-02	n=1	fg=0.03	bg=0.00
intrinsic component of mitochondrial out...	GO:0031306	p=8.7E-02	n=1	fg=0.03	bg=0.00
integral component of mitochondrial oute...	GO:0031307	p=8.7E-02	n=1	fg=0.03	bg=0.00
Bcl-2 family protein complex	GO:0097136	p=8.7E-02	n=1	fg=0.03	bg=0.00
L-type voltage-gated calcium channel com...	GO:1990454	p=8.7E-02	n=1	fg=0.03	bg=0.00
9+2 non-motile cilium	GO:0097732	p=8.7E-02	n=1	fg=0.03	bg=0.00
smooth muscle contractile fiber	GO:0030485	p=8.7E-02	n=1	fg=0.03	bg=0.00
kinocilium	GO:0060091	p=8.7E-02	n=1	fg=0.03	bg=0.00
outer membrane	GO:0019867	p=8.8E-02	n=2	fg=0.06	bg=0.01
mitochondrial outer membrane	GO:0005741	p=8.8E-02	n=2	fg=0.06	bg=0.01
organelle outer membrane	GO:0031968	p=8.8E-02	n=2	fg=0.06	bg=0.01
integral component of membrane	GO:0016021	p=9.4E-02	n=15	fg=0.43	bg=0.25
leading edge membrane	GO:0031256	p=1.1E-01	n=3	fg=0.09	bg=0.03
mitochondrial membrane	GO:0031966	p=1.1E-01	n=3	fg=0.09	bg=0.03

