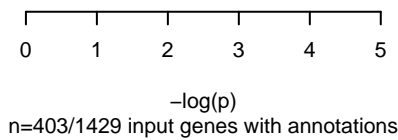


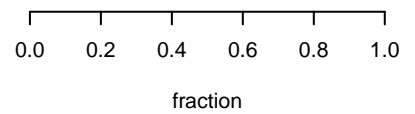
GO:BP
Elav_Nvec_vc1.1_XM_048732912.1

fraction genes in fg and expected value

lymphangiogenesis	GO:0001946	p=1.2E-03	n=5
ventricular septum development	GO:0003281	p=1.6E-03	n=8
germ-line cyst encapsulation	GO:0048138	p=2.2E-03	n=4
heart valve development	GO:0003170	p=2.5E-03	n=6
mitotic cell cycle checkpoint signaling	GO:0007093	p=2.7E-03	n=14
regulation of GTPase activity	GO:0043087	p=2.7E-03	n=22
multicellular organismal homeostasis	GO:0048871	p=2.7E-03	n=22
mitotic spindle organization	GO:0007052	p=3.0E-03	n=15
purine nucleobase transport	GO:0006863	p=3.3E-03	n=3
regulation of hemoglobin biosynthetic pr...	GO:0046984	p=3.3E-03	n=3
osteoclast development	GO:0036035	p=3.3E-03	n=3
protein targeting	GO:0006605	p=3.5E-03	n=27
regulation of establishment of protein l...	GO:1903747	p=4.4E-03	n=6
erythrocyte homeostasis	GO:0034101	p=5.2E-03	n=10
microtubule polymerization	GO:0046785	p=5.3E-03	n=7
mitotic centrosome separation	GO:0007100	p=5.4E-03	n=5
regulation of translation in response to...	GO:0043555	p=5.4E-03	n=5
establishment of chromosome localization	GO:0051303	p=5.5E-03	n=9
asymmetric cell division	GO:0008356	p=5.5E-03	n=12
regulation of microtubule cytoskeleton o...	GO:0070507	p=6.1E-03	n=17
somatic stem cell population maintenance	GO:0035019	p=7.8E-03	n=8
germarium-derived egg chamber formation	GO:0007293	p=7.8E-03	n=8
carbohydrate derivative transport	GO:1901264	p=7.9E-03	n=7
negative regulation of exocytosis	GO:0045920	p=9.5E-03	n=5
axonogenesis	GO:0007409	p=9.8E-03	n=35
positive regulation of GTPase activity	GO:0043547	p=1.0E-02	n=18
organelle localization	GO:0051640	p=1.0E-02	n=50
vulval development	GO:0040025	p=1.1E-02	n=12
negative regulation of microtubule polym...	GO:0031111	p=1.1E-02	n=6
regulation of erythrocyte differentiatio...	GO:0045646	p=1.1E-02	n=6



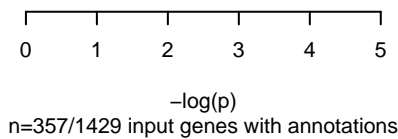
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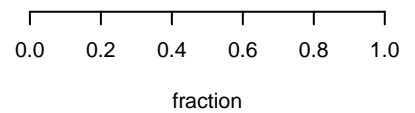
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Elav_Nvec_vc1.1_XM_048732912.1

fraction genes in fg and expected value

nuclear receptor binding	GO:0016922	p=7.4E-04	n=14
tubulin binding	GO:0015631	p=2.6E-03	n=22
hormone receptor binding	GO:0051427	p=2.9E-03	n=14
protein serine/threonine kinase activity	GO:0004674	p=4.1E-03	n=25
nucleoside-triphosphatase regulator acti...	GO:0060589	p=1.0E-02	n=26
ATP binding	GO:0005524	p=1.4E-02	n=24
ATPase regulator activity	GO:0060590	p=1.7E-02	n=6
magnesium ion binding	GO:0000287	p=2.1E-02	n=14
dynein complex binding	GO:0070840	p=2.1E-02	n=4
carbohydrate derivative transmembrane tr...	GO:1901505	p=2.1E-02	n=4
armadillo repeat domain binding	GO:0070016	p=2.3E-02	n=2
DNA binding, bending	GO:0008301	p=2.3E-02	n=2
nucleobase transmembrane transporter act...	GO:0015205	p=2.3E-02	n=2
calcium-induced calcium release activity	GO:0048763	p=2.3E-02	n=2
purine nucleobase transmembrane transpor...	GO:0005345	p=2.3E-02	n=2
nucleoside transmembrane transporter act...	GO:0005337	p=2.3E-02	n=2
L-malate dehydrogenase activity	GO:0030060	p=2.3E-02	n=2
lipid phosphatase activity	GO:0042577	p=2.3E-02	n=2
guanylyltransferase activity	GO:0070568	p=2.3E-02	n=2
general transcription initiation factor ...	GO:0140223	p=2.3E-02	n=2
nucleobase-containing compound transmemb...	GO:0015932	p=2.4E-02	n=5
nuclear receptor coactivator activity	GO:0030374	p=2.4E-02	n=5
ABC-type transporter activity	GO:0140359	p=2.7E-02	n=3
adenyl nucleotide binding	GO:0030554	p=3.0E-02	n=26
ATP hydrolysis activity	GO:0016887	p=3.0E-02	n=24
small molecule binding	GO:0036094	p=3.1E-02	n=48
alpha-tubulin binding	GO:0043014	p=3.4E-02	n=4
vitamin binding	GO:0019842	p=3.7E-02	n=7
molecular function regulator activity	GO:0098772	p=3.8E-02	n=49
adenyl ribonucleotide binding	GO:0032559	p=3.9E-02	n=25



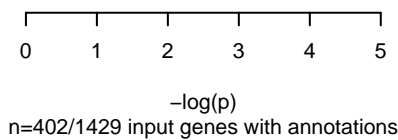
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GO:CC
Elav_Nvec_vc1.1_XM_048732912.1

fraction genes in fg and expected value

spindle pole	GO:0000922	p=3.8E-03	n=13
rough endoplasmic reticulum membrane	GO:0030867	p=5.7E-03	n=4
ISWI-type complex	GO:0031010	p=5.7E-03	n=4
spindle	GO:0005819	p=5.7E-03	n=28
neuronal cell body	GO:0043025	p=5.9E-03	n=36
integral component of Golgi membrane	GO:0030173	p=7.1E-03	n=6
midbody	GO:0030496	p=9.2E-03	n=13
mitotic spindle	GO:0072686	p=1.9E-02	n=11
cytoplasmic side of endoplasmic reticulum	GO:0098554	p=2.1E-02	n=4
cyclin-dependent protein kinase holoenzyme	GO:0000307	p=2.1E-02	n=4
spindle microtubule	GO:0005876	p=2.1E-02	n=7
actomyosin contractile ring	GO:0005826	p=2.2E-02	n=2
calneurin complex	GO:0005955	p=2.2E-02	n=2
GAIT complex	GO:0097452	p=2.2E-02	n=2
collagen and cuticulin-based cuticle extension	GO:0060102	p=2.2E-02	n=2
Parkin-FBXW7-Cul1 ubiquitin ligase complex	GO:1990452	p=2.2E-02	n=2
annulate lamellae	GO:0005642	p=2.2E-02	n=2
kinesin complex	GO:0005871	p=2.3E-02	n=5
kinetochore microtubule	GO:0005828	p=2.6E-02	n=3
ER to Golgi transport vesicle membrane	GO:0012507	p=3.3E-02	n=4
aster	GO:0005818	p=4.6E-02	n=3
spindle pole centrosome	GO:0031616	p=4.6E-02	n=3
cytosol	GO:0005829	p=4.7E-02	n=17
polysomal ribosome	GO:0042788	p=4.9E-02	n=4
microtubule	GO:0005874	p=5.1E-02	n=12
basal part of cell	GO:0045178	p=5.3E-02	n=16
lipid droplet	GO:0005811	p=5.4E-02	n=7
spindle midzone	GO:0051233	p=5.9E-02	n=5
COPII-coated ER to Golgi transport vesicle	GO:0030134	p=5.9E-02	n=5
ESC(E/Z) complex	GO:0035098	p=6.0E-02	n=2



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