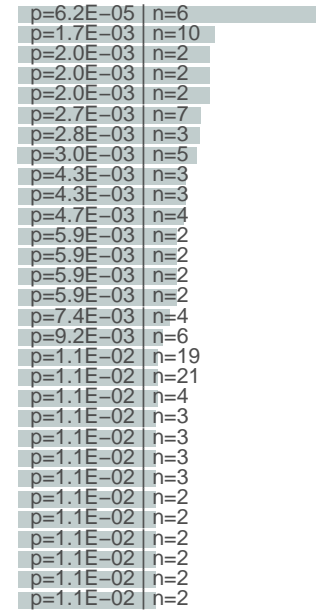


GO:BP
Elav_Nvec_vc1.1_XM_032373099.2

fraction genes in fg and expected value

| | |
|---|------------|
| negative regulation of smoothened signal... | GO:0045879 |
| cytokine-mediated signaling pathway | GO:0019221 |
| actin cortical patch localization | GO:0051666 |
| negative regulation of type 2 immune res... | GO:0002829 |
| lysine transport | GO:0015819 |
| cellular lipid catabolic process | GO:0044242 |
| cellular response to angiotensin | GO:1904385 |
| cellular response to interleukin-1 | GO:0071347 |
| encapsulation of foreign target | GO:0035010 |
| negative regulation of T cell differenti... | GO:0045581 |
| cellular iron ion homeostasis | GO:0006879 |
| haltere development | GO:0007482 |
| light-induced release of internally sequ... | GO:0008377 |
| S-adenosylmethionine cycle | GO:0033353 |
| chondroitin sulfate proteoglycan biosynt... | GO:0050650 |
| dauer larval development | GO:0040024 |
| insulin receptor signaling pathway | GO:0008286 |
| regulation of neurogenesis | GO:0050767 |
| regulation of cell development | GO:0060284 |
| neural tube patterning | GO:0021532 |
| positive regulation of cell maturation | GO:1903431 |
| negative regulation of vasculature devel... | GO:1901343 |
| aminoglycan biosynthetic process | GO:0006023 |
| glycosaminoglycan biosynthetic process | GO:0006024 |
| sperm capacitation | GO:0048240 |
| SCF complex assembly | GO:0010265 |
| S-adenosylhomocysteine metabolic process | GO:0046498 |
| positive regulation of neuron maturation | GO:0014042 |
| L-cysteine metabolic process | GO:0046439 |
| negative regulation of centrosome duplic... | GO:0010826 |



-log(p)
n=122/340 input genes with annotations

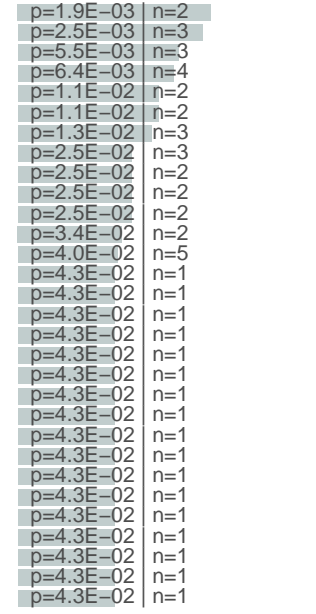
| | |
|---------|---------|
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| fg=0.08 | bg=0.03 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.06 | bg=0.02 |
| fg=0.02 | bg=0.00 |
| fg=0.04 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.05 | bg=0.02 |
| fg=0.16 | bg=0.09 |
| fg=0.17 | bg=0.10 |
| fg=0.03 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
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| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |

fraction

GO:MF
Elav_Nvec_vc1.1_XM_032373099.2

fraction genes in fg and expected value

| | |
|---|------------|
| phosphotransferase activity, carboxyl gr... | GO:0016774 |
| UDP-galactose:beta-N-acetylglucosamine b... | GO:0008499 |
| protein-disulfide reductase (NAD(P)) act... | GO:0047134 |
| phosphatase regulator activity | GO:0019208 |
| phosphatase activator activity | GO:0019211 |
| protein phosphatase activator activity | GO:0072542 |
| nucleobase-containing compound transmemb... | GO:0015932 |
| protein phosphatase regulator activity | GO:0019888 |
| peptide antigen binding | GO:0042605 |
| glucuronosyltransferase activity | GO:0015020 |
| L-cystine transmembrane transporter acti... | GO:0015184 |
| sulfur amino acid transmembrane transpor... | GO:0000099 |
| G protein-coupled receptor activity | GO:0004930 |
| CoA carboxylase activity | GO:0016421 |
| glutamate-5-semialdehyde dehydrogenase a... | GO:0004350 |
| phosphatidylinositol 3-kinase catalytic ... | GO:0036313 |
| purine-specific nucleoside:sodium sympor... | GO:0015390 |
| nucleobase:cation symporter activity | GO:0015391 |
| growth hormone-releasing hormone recepto... | GO:0016520 |
| myosin head/neck binding | GO:0032028 |
| pyrimidine nucleobase transmembrane tran... | GO:0005350 |
| intracellular sodium activated potassium... | GO:0005228 |
| N-acetylgalactosaminyl-proteoglycan 3-be... | GO:0050510 |
| RNA guanylyltransferase activity | GO:0008192 |
| tRNA guanylyltransferase activity | GO:0008193 |
| purine nucleoside transmembrane transpor... | GO:0015211 |
| P-type calcium transporter activity invo... | GO:0086039 |
| glutamate 5-kinase activity | GO:0004349 |
| pyrimidine- and adenine-specific:sodium ... | GO:0015389 |
| pseudophosphatase activity | GO:0001691 |



-log(p)
n=103/340 input genes with annotations

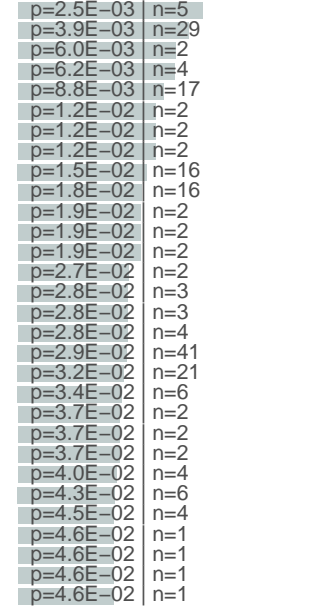
| | |
|---------|---------|
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| fg=0.03 | bg=0.00 |
| fg=0.03 | bg=0.00 |
| fg=0.04 | bg=0.01 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.03 | bg=0.01 |
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| fg=0.02 | bg=0.00 |
| fg=0.05 | bg=0.02 |
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| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
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| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |

fraction

GO:CC
Elav_Nvec_vc1.1_XM_032373099.2

fraction genes in fg and expected value

| | |
|---|------------|
| rough endoplasmic reticulum | GO:0005791 |
| integral component of membrane | GO:0016021 |
| mitochondria-associated endoplasmic reti... | GO:0044233 |
| ciliary membrane | GO:0060170 |
| endoplasmic reticulum subcompartment | GO:0098827 |
| inaD signaling complex | GO:0016027 |
| lumenal side of endoplasmic reticulum me... | GO:0098553 |
| integral component of lumenal side of en... | GO:0071556 |
| endoplasmic reticulum membrane | GO:0005789 |
| nuclear outer membrane-endoplasmic retic... | GO:0042175 |
| fungus-type vacuole | GO:0000324 |
| fungus-type vacuole membrane | GO:0000329 |
| lumenal side of membrane | GO:0098576 |
| cell tip | GO:0051286 |
| transcription elongation factor complex | GO:0008023 |
| Golgi medial cisterna | GO:0005797 |
| cation channel complex | GO:0034703 |
| organelle membrane | GO:0031090 |
| Golgi apparatus | GO:0005794 |
| integral component of endoplasmic reticu... | GO:0030176 |
| storage vacuole | GO:0000322 |
| cell pole | GO:0060187 |
| secondary lysosome | GO:0005767 |
| autophagosome | GO:0005776 |
| intrinsic component of endoplasmic retic... | GO:0031227 |
| ion channel complex | GO:0034702 |
| rhabdomere microvillus | GO:0035996 |
| rhabdomere microvillus membrane | GO:0035997 |
| Shu complex | GO:0097196 |
| apical cytoplasm | GO:0090651 |



-log(p)
n=123/340 input genes with annotations

| | |
|---------|---------|
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| fg=0.24 | bg=0.14 |
| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.14 | bg=0.07 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.13 | bg=0.07 |
| fg=0.13 | bg=0.07 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.01 |
| fg=0.02 | bg=0.01 |
| fg=0.03 | bg=0.01 |
| fg=0.33 | bg=0.24 |
| fg=0.17 | bg=0.11 |
| fg=0.05 | bg=0.02 |
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| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.05 | bg=0.02 |
| fg=0.03 | bg=0.01 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |

fraction