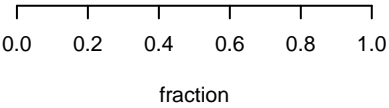
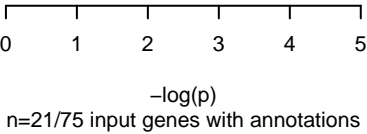


GO:BP
Elav_Nvec_vc1.1_XM_032364605.2

fraction genes in fg and expected value

| | | | |
|---------------------------------------------|------------|-----------|------|
| foam cell differentiation | GO:0090077 | p=7.6E-04 | n=2 |
| non-canonical Wnt signaling pathway via ... | GO:0038031 | p=7.6E-04 | n=2 |
| Wnt signaling pathway, calcium modulatin... | GO:0007223 | p=1.9E-03 | n=2 |
| heart morphogenesis | GO:0003007 | p=2.5E-03 | n=4 |
| salivary gland morphogenesis | GO:0007435 | p=2.9E-03 | n=3 |
| convergent extension involved in gastrul... | GO:0060027 | p=3.4E-03 | n=2 |
| chitin-based cuticle development | GO:0040003 | p=3.4E-03 | n=2 |
| sensory perception of taste | GO:0050909 | p=4.4E-03 | n=2 |
| negative regulation of cell-substrate ad... | GO:0010812 | p=4.4E-03 | n=2 |
| segment polarity determination | GO:0007367 | p=4.4E-03 | n=2 |
| border follicle cell migration | GO:0007298 | p=4.4E-03 | n=3 |
| actin filament organization | GO:0007015 | p=5.4E-03 | n=4 |
| ectoderm development | GO:0007398 | p=5.4E-03 | n=2 |
| hemocyte proliferation | GO:0035172 | p=7.9E-03 | n=2 |
| male genitalia development | GO:0030539 | p=7.9E-03 | n=2 |
| Wnt signaling pathway, planar cell polar... | GO:0060071 | p=9.2E-03 | n=2 |
| regulation of gastrulation | GO:0010470 | p=9.2E-03 | n=2 |
| regulation of localization | GO:0032879 | p=1.0E-02 | n=10 |
| convergent extension | GO:0060026 | p=1.1E-02 | n=3 |
| mitotic DNA damage checkpoint signaling | GO:0044773 | p=1.1E-02 | n=2 |
| Spemann organizer formation | GO:0060061 | p=1.2E-02 | n=1 |
| positive regulation of epithelial cell p... | GO:0060054 | p=1.2E-02 | n=1 |
| sensory organ precursor cell fate determ... | GO:0016360 | p=1.2E-02 | n=1 |
| cell adhesion involved in heart morphoge... | GO:0061343 | p=1.2E-02 | n=1 |
| canonical Wnt signaling pathway involved... | GO:0044338 | p=1.2E-02 | n=1 |
| canonical Wnt signaling pathway involved... | GO:0044339 | p=1.2E-02 | n=1 |
| regulation of ectoderm development | GO:2000383 | p=1.2E-02 | n=1 |
| negative regulation of ectoderm developm... | GO:2000384 | p=1.2E-02 | n=1 |
| cardiac muscle myoblast proliferation | GO:0110021 | p=1.2E-02 | n=1 |
| regulation of cardiac muscle myoblast pr... | GO:0110022 | p=1.2E-02 | n=1 |

| | |
|---------|---------|
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
| fg=0.19 | bg=0.03 |
| fg=0.14 | bg=0.01 |
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
| fg=0.10 | bg=0.00 |
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| fg=0.19 | bg=0.04 |
| fg=0.10 | bg=0.01 |
| fg=0.10 | bg=0.01 |
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| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
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| fg=0.05 | bg=0.00 |

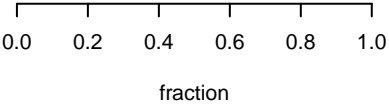
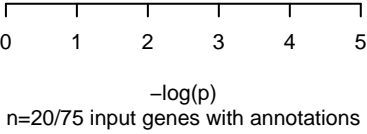


GO:MF
Elav_Nvec_vc1.1_XM_032364605.2

fraction genes in fg and expected value

| | | | |
|---------------------------------------------|------------|-----------|-----|
| GTPase activator activity | GO:0005096 | p=1.2E-02 | n=3 |
| BIR domain binding | GO:1990525 | p=1.3E-02 | n=1 |
| platelet-derived growth factor receptor ... | GO:0005161 | p=1.3E-02 | n=1 |
| alkylglycerophosphoethanolamine phosphod... | GO:0047391 | p=1.3E-02 | n=1 |
| ABC-type sterol transporter activity | GO:0034041 | p=1.3E-02 | n=1 |
| intracellular sodium activated potassium... | GO:0005228 | p=1.3E-02 | n=1 |
| telomerase RNA binding | GO:0070034 | p=2.5E-02 | n=1 |
| toxin transmembrane transporter activity | GO:0019534 | p=2.5E-02 | n=1 |
| cAMP response element binding protein bi... | GO:0008140 | p=2.5E-02 | n=1 |
| protein kinase B binding | GO:0043422 | p=2.5E-02 | n=1 |
| GDP-dissociation inhibitor activity | GO:0005092 | p=2.5E-02 | n=1 |
| cysteine-type endopeptidase activity inv... | GO:0097200 | p=2.5E-02 | n=1 |
| cysteine-type endopeptidase activity inv... | GO:0097153 | p=2.5E-02 | n=1 |
| ubiquitin-like protein ligase activity | GO:0061659 | p=3.2E-02 | n=3 |
| ubiquitin protein ligase activity | GO:0061630 | p=3.2E-02 | n=3 |
| ion channel regulator activity | GO:0099106 | p=3.5E-02 | n=2 |
| organic hydroxy compound transmembrane t... | GO:1901618 | p=3.7E-02 | n=1 |
| cAMP response element binding | GO:0035497 | p=3.7E-02 | n=1 |
| Wnt-activated receptor activity | GO:0042813 | p=3.7E-02 | n=1 |
| calcium-activated potassium channel acti... | GO:0015269 | p=3.7E-02 | n=1 |
| ATPase-coupled lipid transmembrane trans... | GO:0034040 | p=3.7E-02 | n=1 |
| histone acetyltransferase activity | GO:0004402 | p=3.7E-02 | n=1 |
| GTPase binding | GO:0051020 | p=3.9E-02 | n=4 |
| channel regulator activity | GO:0016247 | p=4.1E-02 | n=2 |
| PDZ domain binding | GO:0030165 | p=4.7E-02 | n=2 |
| peptide N-acetyltransferase activity | GO:0034212 | p=4.9E-02 | n=1 |
| syndecan binding | GO:0045545 | p=4.9E-02 | n=1 |
| peptide-lysine-N-acetyltransferase activ... | GO:0061733 | p=4.9E-02 | n=1 |
| sterol transporter activity | GO:0015248 | p=4.9E-02 | n=1 |
| ABC-type transporter activity | GO:0140359 | p=6.1E-02 | n=1 |

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|---------|---------|
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| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
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| fg=0.05 | bg=0.00 |
| fg=0.15 | bg=0.04 |
| fg=0.15 | bg=0.04 |
| fg=0.10 | bg=0.01 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
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| fg=0.05 | bg=0.00 |
| fg=0.20 | bg=0.07 |
| fg=0.10 | bg=0.02 |
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| fg=0.05 | bg=0.00 |
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| fg=0.05 | bg=0.00 |



GO:CC
Elav_Nvec_vc1.1_XM_032364605.2

fraction genes in fg and expected value

| | | | |
|---------------------------------------------|------------|-----------|------|
| endosome membrane | GO:0010008 | p=6.1E-03 | n=4 |
| recycling endosome | GO:0055037 | p=1.1E-02 | n=3 |
| telomerase holoenzyme complex | GO:0005697 | p=1.2E-02 | n=1 |
| photoreceptor outer segment membrane | GO:0042622 | p=2.4E-02 | n=1 |
| Wnt signalosome | GO:1990909 | p=2.4E-02 | n=1 |
| photoreceptor disc membrane | GO:0097381 | p=3.6E-02 | n=1 |
| RNA N6-methyladenosine methyltransferase... | GO:0036396 | p=3.6E-02 | n=1 |
| mRNA editing complex | GO:0045293 | p=3.6E-02 | n=1 |
| ubiquitin ligase complex | GO:0000151 | p=3.7E-02 | n=3 |
| side of membrane | GO:0098552 | p=4.3E-02 | n=3 |
| intrinsic component of the cytoplasmic s... | GO:0031235 | p=4.8E-02 | n=1 |
| plasma membrane | GO:0005886 | p=5.0E-02 | n=10 |
| protein phosphatase type 2A complex | GO:0000159 | p=5.9E-02 | n=1 |
| clathrin-coated endocytic vesicle membra... | GO:0030669 | p=7.1E-02 | n=1 |
| GTPase complex | GO:1905360 | p=7.1E-02 | n=1 |
| heterotrimeric G-protein complex | GO:0005834 | p=7.1E-02 | n=1 |
| cell periphery | GO:0071944 | p=7.4E-02 | n=10 |
| magnesium-dependent protein serine/threo... | GO:0005963 | p=8.2E-02 | n=1 |
| cytoplasmic side of plasma membrane | GO:0009898 | p=9.1E-02 | n=2 |
| site of double-strand break | GO:0035861 | p=9.3E-02 | n=1 |
| site of DNA damage | GO:0090734 | p=9.3E-02 | n=1 |
| azurophil granule membrane | GO:0035577 | p=9.3E-02 | n=1 |
| intrinsic component of plasma membrane | GO:0031226 | p=9.5E-02 | n=4 |
| recycling endosome membrane | GO:0055038 | p=1.0E-01 | n=1 |
| clathrin-coated endocytic vesicle | GO:0045334 | p=1.0E-01 | n=1 |
| voltage-gated potassium channel complex | GO:0008076 | p=1.0E-01 | n=1 |
| potassium channel complex | GO:0034705 | p=1.0E-01 | n=1 |
| cytoplasmic side of membrane | GO:0098562 | p=1.1E-01 | n=2 |
| intracellular protein-containing complex | GO:0140535 | p=1.1E-01 | n=4 |
| photoreceptor inner segment | GO:0001917 | p=1.3E-01 | n=1 |

| | |
|---------|---------|
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| fg=0.14 | bg=0.02 |
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| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.14 | bg=0.03 |
| fg=0.14 | bg=0.04 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.45 | bg=0.27 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.45 | bg=0.29 |
| fg=0.05 | bg=0.00 |
| fg=0.09 | bg=0.02 |
| fg=0.05 | bg=0.00 |
| fg=0.05 | bg=0.00 |
| fg=0.18 | bg=0.08 |
| fg=0.05 | bg=0.01 |
| fg=0.05 | bg=0.01 |
| fg=0.05 | bg=0.01 |
| fg=0.05 | bg=0.01 |
| fg=0.09 | bg=0.03 |
| fg=0.18 | bg=0.09 |
| fg=0.05 | bg=0.01 |

