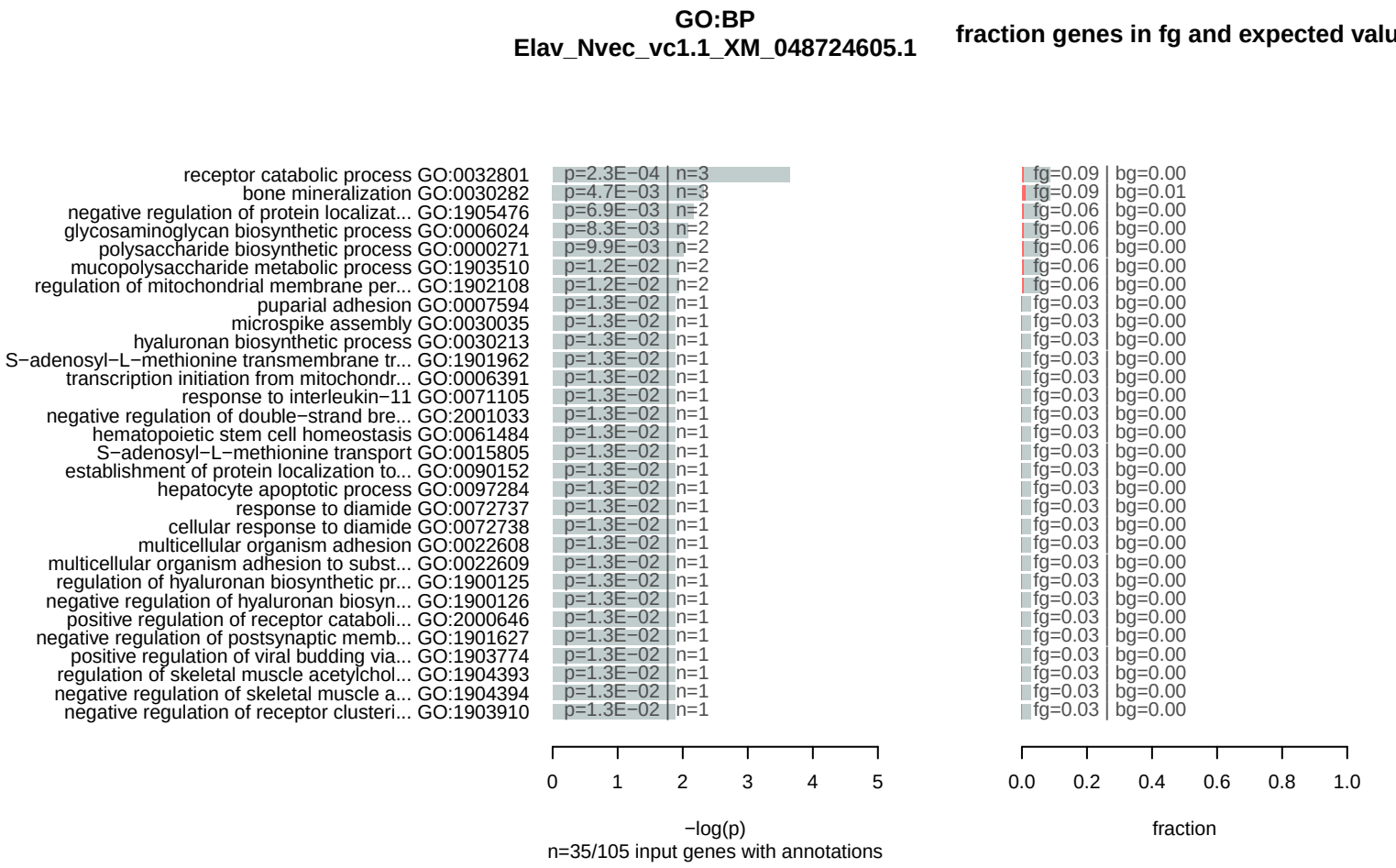
GO:BP
Elav_Nvec_vc1.1_XM_048724605.1
fraction genes in fg and expected valu
receptor catabolic process GO:0032801 p=2.3E−04 n=3 fg=0.09 bg=0.00
bone mineralization GO:0030282 p=4.7E−03 n=3 fg=0.09 bg=0.01
negative regulation of protein localizat... GO:1905476 p=6.9E−03 n=2 fg=0.06 bg=0.00
glycosaminoglycan biosynthetic process GO:0006024 p=8.3E−03 n=2 fg=0.06 bg=0.00
polysaccharide biosynthetic process GO:0000271 p=9.9E−03 n=2 fg=0.06 bg=0.00
mucopolysaccharide metabolic process GO:1903510 p=1.2E−02 n=2 fg=0.06 bg=0.00
regulation of mitochondrial membrane per... GO:1902108 p=1.2E−02 n=2 fg=0.06 bg=0.00
puparial adhesion GO:0007594 p=1.3E−02 n=1 fg=0.03 bg=0.00
microspike assembly GO:0030035 p=1.3E−02 n=1 fg=0.03 bg=0.00
hyaluronan biosynthetic process GO:0030213 p=1.3E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:1901962 p=1.3E−02 n=1 fg=0.03 bg=0.00
transcription initiation from mitochondr... GO:0006391 p=1.3E−02 n=1 fg=0.03 bg=0.00
response to interleukin−11 GO:0071105 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of double−strand bre... GO:2001033 p=1.3E−02 n=1 fg=0.03 bg=0.00
hematopoietic stem cell homeostasis GO:0061484 p=1.3E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transport GO:0015805 p=1.3E−02 n=1 fg=0.03 bg=0.00
establishment of protein localization to... GO:0090152 p=1.3E−02 n=1 fg=0.03 bg=0.00
hepatocyte apoptotic process GO:0097284 p=1.3E−02 n=1 fg=0.03 bg=0.00
response to diamide GO:0072737 p=1.3E−02 n=1 fg=0.03 bg=0.00
cellular response to diamide GO:0072738 p=1.3E−02 n=1 fg=0.03 bg=0.00
multicellular organism adhesion GO:0022608 p=1.3E−02 n=1 fg=0.03 bg=0.00
multicellular organism adhesion to subst... GO:0022609 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of hyaluronan biosynthetic pr... GO:1900125 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of hyaluronan biosyn... GO:1900126 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of receptor cataboli... GO:2000646 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of postsynaptic memb... GO:1901627 p=1.3E−02 n=1 fg=0.03 bg=0.00
positive regulation of viral budding via... GO:1903774 p=1.3E−02 n=1 fg=0.03 bg=0.00
regulation of skeletal muscle acetylchol... GO:1904393 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of skeletal muscle a... GO:1904394 p=1.3E−02 n=1 fg=0.03 bg=0.00
negative regulation of receptor clusteri... GO:1903910 p=1.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=35/105 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048724605.1
fraction genes in fg and expected valu
sulfotransferase activity GO:0008146 p=9.8E−04 n=2 fg=0.06 bg=0.00
arrestin family protein binding GO:1990763 p=1.6E−03 n=2 fg=0.06 bg=0.00
polyubiquitin modification−dependent pro... GO:0031593 p=1.0E−02 n=2 fg=0.06 bg=0.01
clathrin light chain binding GO:0032051 p=1.3E−02 n=1 fg=0.03 bg=0.00
translation elongation factor binding GO:0061770 p=1.3E−02 n=1 fg=0.03 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=1.3E−02 n=1 fg=0.03 bg=0.00
heparan sulfate 2−O−sulfotransferase act... GO:0004394 p=1.3E−02 n=1 fg=0.03 bg=0.00
heparan sulfate sulfotransferase activit... GO:0034483 p=1.3E−02 n=1 fg=0.03 bg=0.00
CXCR chemokine receptor binding GO:0045236 p=1.3E−02 n=1 fg=0.03 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=1.3E−02 n=1 fg=0.03 bg=0.00
sulfur compound transmembrane transporte... GO:1901682 p=1.6E−02 n=2 fg=0.06 bg=0.01
carbon−carbon lyase activity GO:0016830 p=1.8E−02 n=2 fg=0.06 bg=0.01
lyase activity GO:0016829 p=2.0E−02 n=3 fg=0.10 bg=0.02
mismatch repair complex binding GO:0032404 p=2.6E−02 n=1 fg=0.03 bg=0.00
MutLalpha complex binding GO:0032405 p=2.6E−02 n=1 fg=0.03 bg=0.00
3'−5'−exodeoxyribonuclease activity GO:0008296 p=2.6E−02 n=1 fg=0.03 bg=0.00
MutSalpha complex binding GO:0032407 p=2.6E−02 n=1 fg=0.03 bg=0.00
STAT family protein binding GO:0097677 p=2.6E−02 n=1 fg=0.03 bg=0.00
1−hydroxypyrene sulfotransferase activit... GO:0034930 p=2.6E−02 n=1 fg=0.03 bg=0.00
chemokine receptor binding GO:0042379 p=2.6E−02 n=1 fg=0.03 bg=0.00
thiamine pyrophosphate binding GO:0030976 p=2.6E−02 n=1 fg=0.03 bg=0.00
cystathionine beta−synthase activity GO:0004122 p=2.6E−02 n=1 fg=0.03 bg=0.00
cysteine synthase activity GO:0004124 p=2.6E−02 n=1 fg=0.03 bg=0.00
aryl sulfotransferase activity GO:0004062 p=2.6E−02 n=1 fg=0.03 bg=0.00
vitamin binding GO:0019842 p=3.3E−02 n=2 fg=0.06 bg=0.01
Wnt−activated receptor activity GO:0042813 p=3.9E−02 n=1 fg=0.03 bg=0.00
oxalate transmembrane transporter activi... GO:0019531 p=3.9E−02 n=1 fg=0.03 bg=0.00
sulfate transmembrane transporter activi... GO:0015116 p=3.9E−02 n=1 fg=0.03 bg=0.00
DNA photolyase activity GO:0003913 p=3.9E−02 n=1 fg=0.03 bg=0.00
formate transmembrane transporter activi... GO:0015499 p=3.9E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=31/105 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048724605.1
fraction genes in fg and expected valu
sperm connecting piece GO:0097224 p=1.1E−02 n=1 fg=0.03 bg=0.00
mitochondrial DNA−directed RNA polymeras... GO:0034245 p=1.1E−02 n=1 fg=0.03 bg=0.00
sperm cytoplasmic droplet GO:0097598 p=1.1E−02 n=1 fg=0.03 bg=0.00
clathrin complex GO:0071439 p=2.1E−02 n=1 fg=0.03 bg=0.00
Seh1−associated complex GO:0035859 p=2.1E−02 n=1 fg=0.03 bg=0.00
nuclear stress granule GO:0097165 p=2.1E−02 n=1 fg=0.03 bg=0.00
U2AF complex GO:0089701 p=2.1E−02 n=1 fg=0.03 bg=0.00
GATOR2 complex GO:0061700 p=2.1E−02 n=1 fg=0.03 bg=0.00
ESCRT I complex GO:0000813 p=2.1E−02 n=1 fg=0.03 bg=0.00
sorting endosome GO:0097443 p=2.1E−02 n=1 fg=0.03 bg=0.00
filopodium GO:0030175 p=2.3E−02 n=2 fg=0.07 bg=0.01
endolysosome membrane GO:0036020 p=3.2E−02 n=1 fg=0.03 bg=0.00
mitotic spindle microtubule GO:1990498 p=3.2E−02 n=1 fg=0.03 bg=0.00
endolysosome GO:0036019 p=3.2E−02 n=1 fg=0.03 bg=0.00
outer dynein arm GO:0036157 p=3.2E−02 n=1 fg=0.03 bg=0.00
ciliary rootlet GO:0035253 p=3.2E−02 n=1 fg=0.03 bg=0.00
trans−Golgi network membrane GO:0032588 p=4.5E−02 n=2 fg=0.07 bg=0.01
sperm flagellum GO:0036126 p=5.1E−02 n=2 fg=0.07 bg=0.01
sperm fibrous sheath GO:0035686 p=5.3E−02 n=1 fg=0.03 bg=0.00
intrinsic component of the cytoplasmic s... GO:0031235 p=5.3E−02 n=1 fg=0.03 bg=0.00
ciliary plasm GO:0097014 p=5.3E−02 n=2 fg=0.07 bg=0.01
cytoplasmic region GO:0099568 p=5.5E−02 n=4 fg=0.14 bg=0.05
9+2 motile cilium GO:0097729 p=5.6E−02 n=2 fg=0.07 bg=0.01
mitotic spindle GO:0072686 p=6.2E−02 n=2 fg=0.07 bg=0.01
filopodium membrane GO:0031527 p=6.3E−02 n=1 fg=0.03 bg=0.00
clathrin−coated endocytic vesicle membra... GO:0030669 p=6.3E−02 n=1 fg=0.03 bg=0.00
axonemal dynein complex GO:0005858 p=7.3E−02 n=1 fg=0.03 bg=0.00
proteasome regulatory particle, base sub... GO:0008540 p=7.3E−02 n=1 fg=0.03 bg=0.00
spliceosomal complex GO:0005681 p=8.0E−02 n=2 fg=0.07 bg=0.02
aggresome GO:0016235 p=8.3E−02 n=1 fg=0.03 bg=0.00
0 1 2 3 4 5
−log(p)
n=29/105 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction