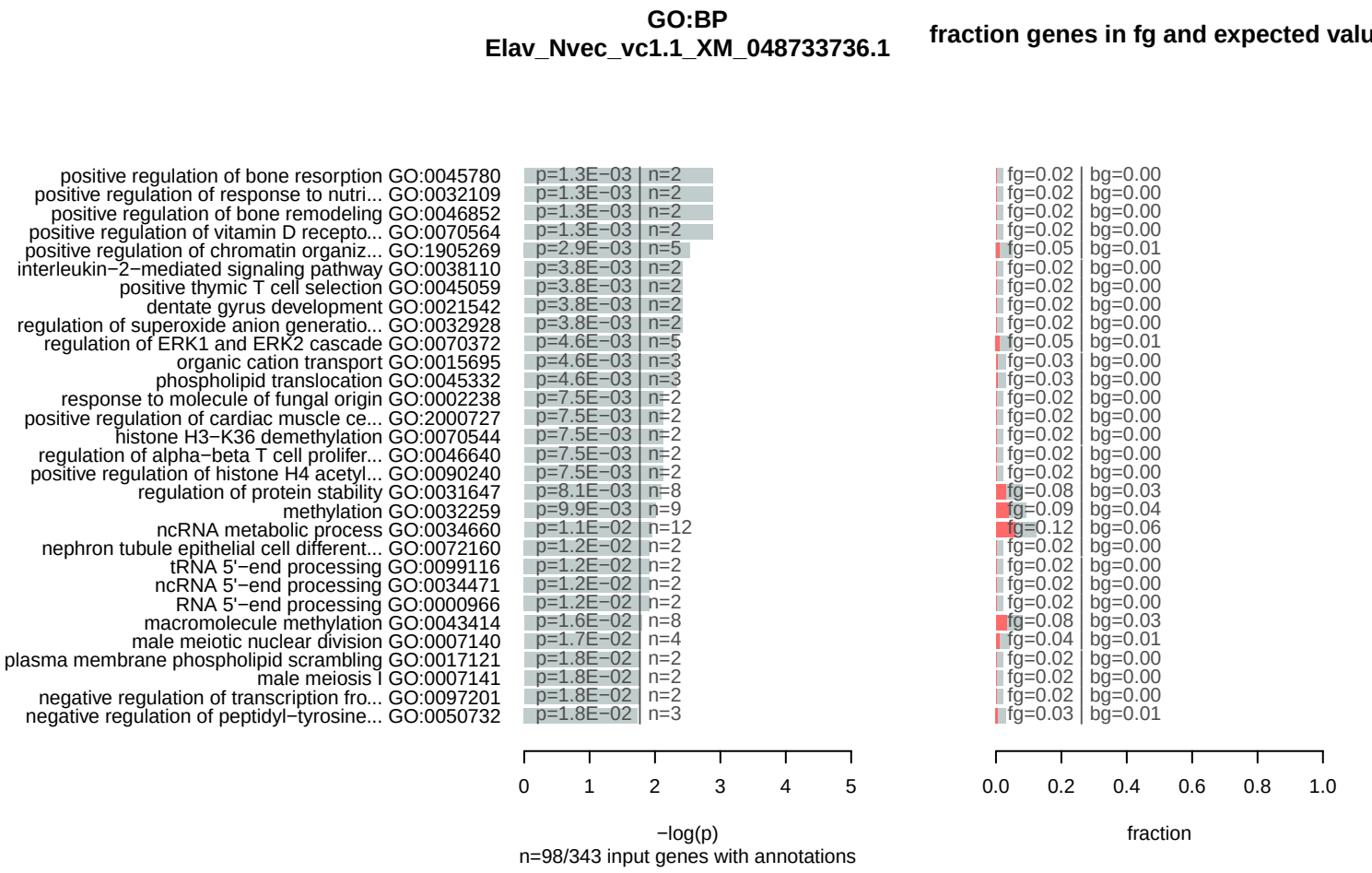
GO:BP
Elav_Nvec_vc1.1_XM_048733736.1
fraction genes in fg and expected valu
positive regulation of bone resorption GO:0045780 p=1.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of response to nutri... GO:0032109 p=1.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of bone remodeling GO:0046852 p=1.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of vitamin D recepto... GO:0070564 p=1.3E−03 n=2 fg=0.02 bg=0.00
positive regulation of chromatin organiz... GO:1905269 p=2.9E−03 n=5 fg=0.05 bg=0.01
interleukin−2−mediated signaling pathway GO:0038110 p=3.8E−03 n=2 fg=0.02 bg=0.00
positive thymic T cell selection GO:0045059 p=3.8E−03 n=2 fg=0.02 bg=0.00
dentate gyrus development GO:0021542 p=3.8E−03 n=2 fg=0.02 bg=0.00
regulation of superoxide anion generatio... GO:0032928 p=3.8E−03 n=2 fg=0.02 bg=0.00
regulation of ERK1 and ERK2 cascade GO:0070372 p=4.6E−03 n=5 fg=0.05 bg=0.01
organic cation transport GO:0015695 p=4.6E−03 n=3 fg=0.03 bg=0.00
phospholipid translocation GO:0045332 p=4.6E−03 n=3 fg=0.03 bg=0.00
response to molecule of fungal origin GO:0002238 p=7.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of cardiac muscle ce... GO:2000727 p=7.5E−03 n=2 fg=0.02 bg=0.00
histone H3−K36 demethylation GO:0070544 p=7.5E−03 n=2 fg=0.02 bg=0.00
regulation of alpha−beta T cell prolifer... GO:0046640 p=7.5E−03 n=2 fg=0.02 bg=0.00
positive regulation of histone H4 acetyl... GO:0090240 p=7.5E−03 n=2 fg=0.02 bg=0.00
regulation of protein stability GO:0031647 p=8.1E−03 n=8 fg=0.08 bg=0.03
methylation GO:0032259 p=9.9E−03 n=9 fg=0.09 bg=0.04
ncRNA metabolic process GO:0034660 p=1.1E−02 n=12 fg=0.12 bg=0.06
nephron tubule epithelial cell different... GO:0072160 p=1.2E−02 n=2 fg=0.02 bg=0.00
tRNA 5'−end processing GO:0099116 p=1.2E−02 n=2 fg=0.02 bg=0.00
ncRNA 5'−end processing GO:0034471 p=1.2E−02 n=2 fg=0.02 bg=0.00
RNA 5'−end processing GO:0000966 p=1.2E−02 n=2 fg=0.02 bg=0.00
macromolecule methylation GO:0043414 p=1.6E−02 n=8 fg=0.08 bg=0.03
male meiotic nuclear division GO:0007140 p=1.7E−02 n=4 fg=0.04 bg=0.01
plasma membrane phospholipid scrambling GO:0017121 p=1.8E−02 n=2 fg=0.02 bg=0.00
male meiosis I GO:0007141 p=1.8E−02 n=2 fg=0.02 bg=0.00
negative regulation of transcription fro... GO:0097201 p=1.8E−02 n=2 fg=0.02 bg=0.00
negative regulation of peptidyl−tyrosine... GO:0050732 p=1.8E−02 n=3 fg=0.03 bg=0.01
0 1 2 3 4 5
−log(p)
n=98/343 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:MF
Elav_Nvec_vc1.1_XM_048733736.1
fraction genes in fg and expected valu
G protein−coupled serotonin receptor bin... GO:0031821 p=1.4E−03 n=2 fg=0.02 bg=0.00
integrin binding GO:0005178 p=5.7E−03 n=4 fg=0.04 bg=0.01
histone H3−methyl−lysine−36 demethylase ... GO:0051864 p=8.0E−03 n=2 fg=0.02 bg=0.00
N−acetyltransferase activity GO:0008080 p=8.8E−03 n=3 fg=0.03 bg=0.01
phospholipid transporter activity GO:0005548 p=1.4E−02 n=3 fg=0.03 bg=0.01
lipid transporter activity GO:0005319 p=1.5E−02 n=4 fg=0.04 bg=0.01
organic cation transmembrane transporter... GO:0015101 p=1.9E−02 n=2 fg=0.02 bg=0.00
adrenergic receptor binding GO:0031690 p=2.6E−02 n=2 fg=0.02 bg=0.00
solute:anion antiporter activity GO:0140323 p=2.6E−02 n=2 fg=0.02 bg=0.00
anion:anion antiporter activity GO:0015301 p=2.6E−02 n=2 fg=0.02 bg=0.00
inorganic anion exchanger activity GO:0005452 p=2.6E−02 n=2 fg=0.02 bg=0.00
steroid hydroxylase activity GO:0008395 p=3.8E−02 n=1 fg=0.01 bg=0.00
mu−type opioid receptor binding GO:0031852 p=3.8E−02 n=1 fg=0.01 bg=0.00
1−alpha,25−dihydroxyvitamin D3 24−hydrox... GO:0030342 p=3.8E−02 n=1 fg=0.01 bg=0.00
vitamin D3 25−hydroxylase activity GO:0030343 p=3.8E−02 n=1 fg=0.01 bg=0.00
S−adenosyl−L−methionine transmembrane tr... GO:0000095 p=3.8E−02 n=1 fg=0.01 bg=0.00
platelet activating factor receptor bind... GO:0031859 p=3.8E−02 n=1 fg=0.01 bg=0.00
cholesterol 26−hydroxylase activity GO:0031073 p=3.8E−02 n=1 fg=0.01 bg=0.00
25−hydroxycholecalciferol−24−hydroxylase... GO:0008403 p=3.8E−02 n=1 fg=0.01 bg=0.00
oxidoreductase activity, acting on paire... GO:0016709 p=3.8E−02 n=1 fg=0.01 bg=0.00
alpha−1A adrenergic receptor binding GO:0031691 p=3.8E−02 n=1 fg=0.01 bg=0.00
5S rRNA primary transcript binding GO:0008098 p=3.8E−02 n=1 fg=0.01 bg=0.00
all−trans−retinol binding GO:1904768 p=3.8E−02 n=1 fg=0.01 bg=0.00
type 2A serotonin receptor binding GO:0031826 p=3.8E−02 n=1 fg=0.01 bg=0.00
all−trans retinol 3,4−desaturase activit... GO:0061896 p=3.8E−02 n=1 fg=0.01 bg=0.00
all−trans retinal 3,4−desaturase activit... GO:0061897 p=3.8E−02 n=1 fg=0.01 bg=0.00
all−trans retinoic acid 3,4−desaturase a... GO:0061898 p=3.8E−02 n=1 fg=0.01 bg=0.00
11−cis−retinal 3,4−desaturase activity GO:0061899 p=3.8E−02 n=1 fg=0.01 bg=0.00
RNA guanylyltransferase activity GO:0008192 p=3.8E−02 n=1 fg=0.01 bg=0.00
tRNA guanylyltransferase activity GO:0008193 p=3.8E−02 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log(p)
n=89/343 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Elav_Nvec_vc1.1_XM_048733736.1
fraction genes in fg and expected valu
chromatin GO:0000785 p=2.5E−03 n=12 fg=0.12 bg=0.05
Nebenkern GO:0016006 p=4.1E−03 n=2 fg=0.02 bg=0.00
PcG protein complex GO:0031519 p=1.1E−02 n=3 fg=0.03 bg=0.00
nuclear chromosome GO:0000228 p=1.8E−02 n=10 fg=0.10 bg=0.05
heterotrimeric G−protein complex GO:0005834 p=1.9E−02 n=2 fg=0.02 bg=0.00
GTPase complex GO:1905360 p=1.9E−02 n=2 fg=0.02 bg=0.00
nuclear lumen GO:0031981 p=2.9E−02 n=44 fg=0.44 bg=0.34
mitochondrion GO:0005739 p=3.5E−02 n=21 fg=0.21 bg=0.14
early endosome GO:0005769 p=3.6E−02 n=7 fg=0.07 bg=0.03
axonemal heterotrimeric kinesin−II compl... GO:0030993 p=3.7E−02 n=1 fg=0.01 bg=0.00
Kibra−Ex−Mer complex GO:0036375 p=3.7E−02 n=1 fg=0.01 bg=0.00
nuclear mitotic cohesin complex GO:0034990 p=3.7E−02 n=1 fg=0.01 bg=0.00
piP−body GO:0071547 p=3.7E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=3.7E−02 n=1 fg=0.01 bg=0.00
Sec61 translocon complex GO:0005784 p=3.7E−02 n=1 fg=0.01 bg=0.00
mitotic cohesin complex GO:0030892 p=3.7E−02 n=1 fg=0.01 bg=0.00
intrinsic component of endosome membrane GO:0031302 p=3.7E−02 n=1 fg=0.01 bg=0.00
kinesin II complex GO:0016939 p=3.7E−02 n=1 fg=0.01 bg=0.00
translocon complex GO:0071256 p=3.7E−02 n=1 fg=0.01 bg=0.00
immunoglobulin complex GO:0019814 p=3.7E−02 n=1 fg=0.01 bg=0.00
B cell receptor complex GO:0019815 p=3.7E−02 n=1 fg=0.01 bg=0.00
NatA complex GO:0031415 p=3.7E−02 n=1 fg=0.01 bg=0.00
extrinsic component of cytoplasmic side ... GO:0031234 p=4.1E−02 n=3 fg=0.03 bg=0.01
endosome GO:0005768 p=5.3E−02 n=12 fg=0.12 bg=0.07
heterochromatin GO:0000792 p=5.8E−02 n=3 fg=0.03 bg=0.01
ciliary tip GO:0097542 p=6.1E−02 n=2 fg=0.02 bg=0.00
mitotic spindle pole GO:0097431 p=6.1E−02 n=2 fg=0.02 bg=0.00
neuron projection cytoplasm GO:0120111 p=6.1E−02 n=2 fg=0.02 bg=0.00
plasma membrane protein complex GO:0098797 p=6.6E−02 n=6 fg=0.06 bg=0.03
non−motile cilium GO:0097730 p=7.0E−02 n=4 fg=0.04 bg=0.02
0 1 2 3 4 5
−log(p)
n=101/343 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction