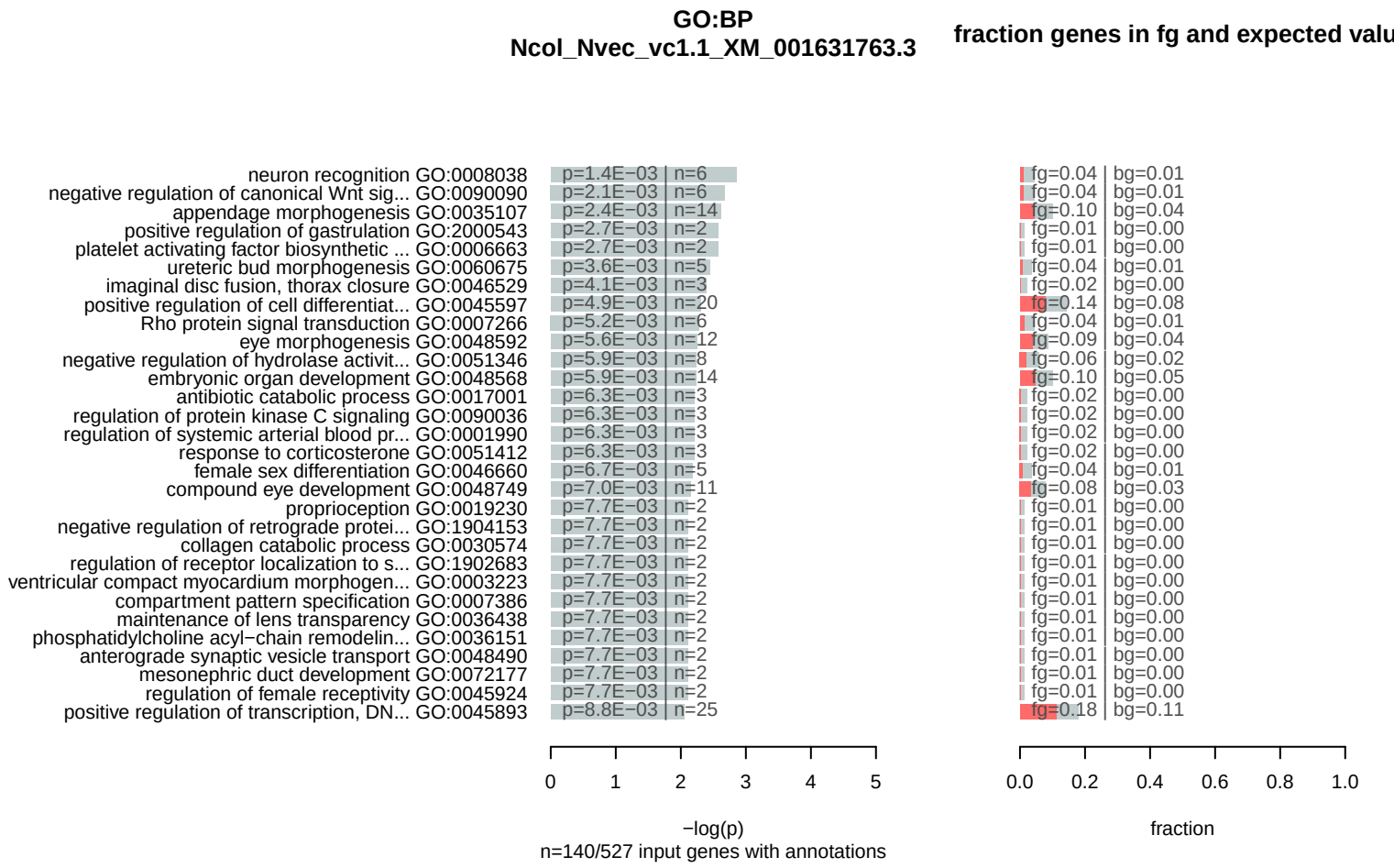
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fraction genes in fg and expected valu
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negative regulation of canonical Wnt sig... GO:0090090 p=2.1E−03 n=6 fg=0.04 bg=0.01
appendage morphogenesis GO:0035107 p=2.4E−03 n=14 fg=0.10 bg=0.04
positive regulation of gastrulation GO:2000543 p=2.7E−03 n=2 fg=0.01 bg=0.00
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imaginal disc fusion, thorax closure GO:0046529 p=4.1E−03 n=3 fg=0.02 bg=0.00
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Rho protein signal transduction GO:0007266 p=5.2E−03 n=6 fg=0.04 bg=0.01
eye morphogenesis GO:0048592 p=5.6E−03 n=12 fg=0.09 bg=0.04
negative regulation of hydrolase activit... GO:0051346 p=5.9E−03 n=8 fg=0.06 bg=0.02
embryonic organ development GO:0048568 p=5.9E−03 n=14 fg=0.10 bg=0.05
antibiotic catabolic process GO:0017001 p=6.3E−03 n=3 fg=0.02 bg=0.00
regulation of protein kinase C signaling GO:0090036 p=6.3E−03 n=3 fg=0.02 bg=0.00
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response to corticosterone GO:0051412 p=6.3E−03 n=3 fg=0.02 bg=0.00
female sex differentiation GO:0046660 p=6.7E−03 n=5 fg=0.04 bg=0.01
compound eye development GO:0048749 p=7.0E−03 n=11 fg=0.08 bg=0.03
proprioception GO:0019230 p=7.7E−03 n=2 fg=0.01 bg=0.00
negative regulation of retrograde protei... GO:1904153 p=7.7E−03 n=2 fg=0.01 bg=0.00
collagen catabolic process GO:0030574 p=7.7E−03 n=2 fg=0.01 bg=0.00
regulation of receptor localization to s... GO:1902683 p=7.7E−03 n=2 fg=0.01 bg=0.00
ventricular compact myocardium morphogen... GO:0003223 p=7.7E−03 n=2 fg=0.01 bg=0.00
compartment pattern specification GO:0007386 p=7.7E−03 n=2 fg=0.01 bg=0.00
maintenance of lens transparency GO:0036438 p=7.7E−03 n=2 fg=0.01 bg=0.00
phosphatidylcholine acyl−chain remodelin... GO:0036151 p=7.7E−03 n=2 fg=0.01 bg=0.00
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mesonephric duct development GO:0072177 p=7.7E−03 n=2 fg=0.01 bg=0.00
regulation of female receptivity GO:0045924 p=7.7E−03 n=2 fg=0.01 bg=0.00
positive regulation of transcription, DN... GO:0045893 p=8.8E−03 n=25 fg=0.18 bg=0.11
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n=140/527 input genes with annotations
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fraction
GO:MF
Ncol_Nvec_vc1.1_XM_001631763.3
fraction genes in fg and expected valu
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1−alkylglycerophosphocholine O−acetyltra... GO:0047192 p=2.9E−03 n=2 fg=0.02 bg=0.00
caspase binding GO:0089720 p=8.4E−03 n=2 fg=0.02 bg=0.00
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2−acylglycerol−3−phosphate O−acyltransfe... GO:0047144 p=8.4E−03 n=2 fg=0.02 bg=0.00
protease binding GO:0002020 p=1.6E−02 n=6 fg=0.05 bg=0.01
xylosyltransferase activity GO:0042285 p=1.6E−02 n=2 fg=0.02 bg=0.00
UDP−xylosyltransferase activity GO:0035252 p=1.6E−02 n=2 fg=0.02 bg=0.00
phosphotransferase activity, alcohol gro... GO:0016773 p=2.6E−02 n=14 fg=0.11 bg=0.06
transcription coactivator binding GO:0001223 p=2.6E−02 n=2 fg=0.02 bg=0.00
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transcription regulator activity GO:0140110 p=3.1E−02 n=20 fg=0.16 bg=0.10
DNA−binding transcription factor activit... GO:0003700 p=3.2E−02 n=15 fg=0.12 bg=0.07
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protein serine/threonine kinase activity GO:0004674 p=3.6E−02 n=10 fg=0.08 bg=0.04
1−acylglycerol−3−phosphate O−acyltransfe... GO:0003841 p=3.8E−02 n=2 fg=0.02 bg=0.00
DNA binding GO:0003677 p=4.3E−02 n=22 fg=0.17 bg=0.12
signaling receptor binding GO:0005102 p=4.4E−02 n=19 fg=0.15 bg=0.10
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acylglycerol O−acyltransferase activity GO:0016411 p=5.1E−02 n=2 fg=0.02 bg=0.00
ATPase−coupled ion transmembrane transpo... GO:0042625 p=5.1E−02 n=3 fg=0.02 bg=0.01
transcription coactivator activity GO:0003713 p=5.3E−02 n=8 fg=0.06 bg=0.03
neuregulin binding GO:0038132 p=5.4E−02 n=1 fg=0.01 bg=0.00
phosphatidylcholine transporter activity GO:0008525 p=5.4E−02 n=1 fg=0.01 bg=0.00
oxidative DNA demethylase activity GO:0035516 p=5.4E−02 n=1 fg=0.01 bg=0.00
semaphorin receptor binding GO:0030215 p=5.4E−02 n=1 fg=0.01 bg=0.00
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JUN kinase kinase activity GO:0008545 p=5.4E−02 n=1 fg=0.01 bg=0.00
neurotrophin binding GO:0043121 p=5.4E−02 n=1 fg=0.01 bg=0.00
tRNA 2'−phosphotransferase activity GO:0000215 p=5.4E−02 n=1 fg=0.01 bg=0.00
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−log(p)
n=128/527 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Ncol_Nvec_vc1.1_XM_001631763.3
fraction genes in fg and expected valu
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proximal dendrite GO:1990635 p=2.3E−02 n=2 fg=0.01 bg=0.00
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plasma membrane protein complex GO:0098797 p=3.8E−02 n=8 fg=0.06 bg=0.03
extracellular matrix GO:0031012 p=3.9E−02 n=4 fg=0.03 bg=0.01
cilium GO:0005929 p=4.0E−02 n=14 fg=0.10 bg=0.06
external encapsulating structure GO:0030312 p=4.4E−02 n=4 fg=0.03 bg=0.01
apical plasma membrane GO:0016324 p=4.5E−02 n=9 fg=0.07 bg=0.03
preribosome, small subunit precursor GO:0030688 p=4.5E−02 n=2 fg=0.01 bg=0.00
bounding membrane of organelle GO:0098588 p=5.0E−02 n=25 fg=0.18 bg=0.13
bleb GO:0032059 p=5.0E−02 n=1 fg=0.01 bg=0.00
core−binding factor complex GO:0016513 p=5.0E−02 n=1 fg=0.01 bg=0.00
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integrin alpha3−beta1 complex GO:0034667 p=5.0E−02 n=1 fg=0.01 bg=0.00
nascent polypeptide−associated complex GO:0005854 p=5.0E−02 n=1 fg=0.01 bg=0.00
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mitochondrial pyruvate dehydrogenase com... GO:0005967 p=5.0E−02 n=1 fg=0.01 bg=0.00
centralspindlin complex GO:0097149 p=5.0E−02 n=1 fg=0.01 bg=0.00
cyclin E1−CDK2 complex GO:0097134 p=5.0E−02 n=1 fg=0.01 bg=0.00
cyclin E2−CDK2 complex GO:0097135 p=5.0E−02 n=1 fg=0.01 bg=0.00
stereocilia ankle link GO:0002141 p=5.0E−02 n=1 fg=0.01 bg=0.00
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stereocilia coupling link GO:0002139 p=5.0E−02 n=1 fg=0.01 bg=0.00
USH2 complex GO:1990696 p=5.0E−02 n=1 fg=0.01 bg=0.00
proteasome storage granule GO:0034515 p=5.0E−02 n=1 fg=0.01 bg=0.00
AMPA glutamate receptor complex GO:0032281 p=5.0E−02 n=1 fg=0.01 bg=0.00
cytoplasmic side of plasma membrane GO:0009898 p=5.2E−02 n=6 fg=0.04 bg=0.02
proton−transporting V−type ATPase comple... GO:0033176 p=5.8E−02 n=2 fg=0.01 bg=0.00
contractile ring GO:0070938 p=5.8E−02 n=2 fg=0.01 bg=0.00
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−log(p)
n=136/527 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction