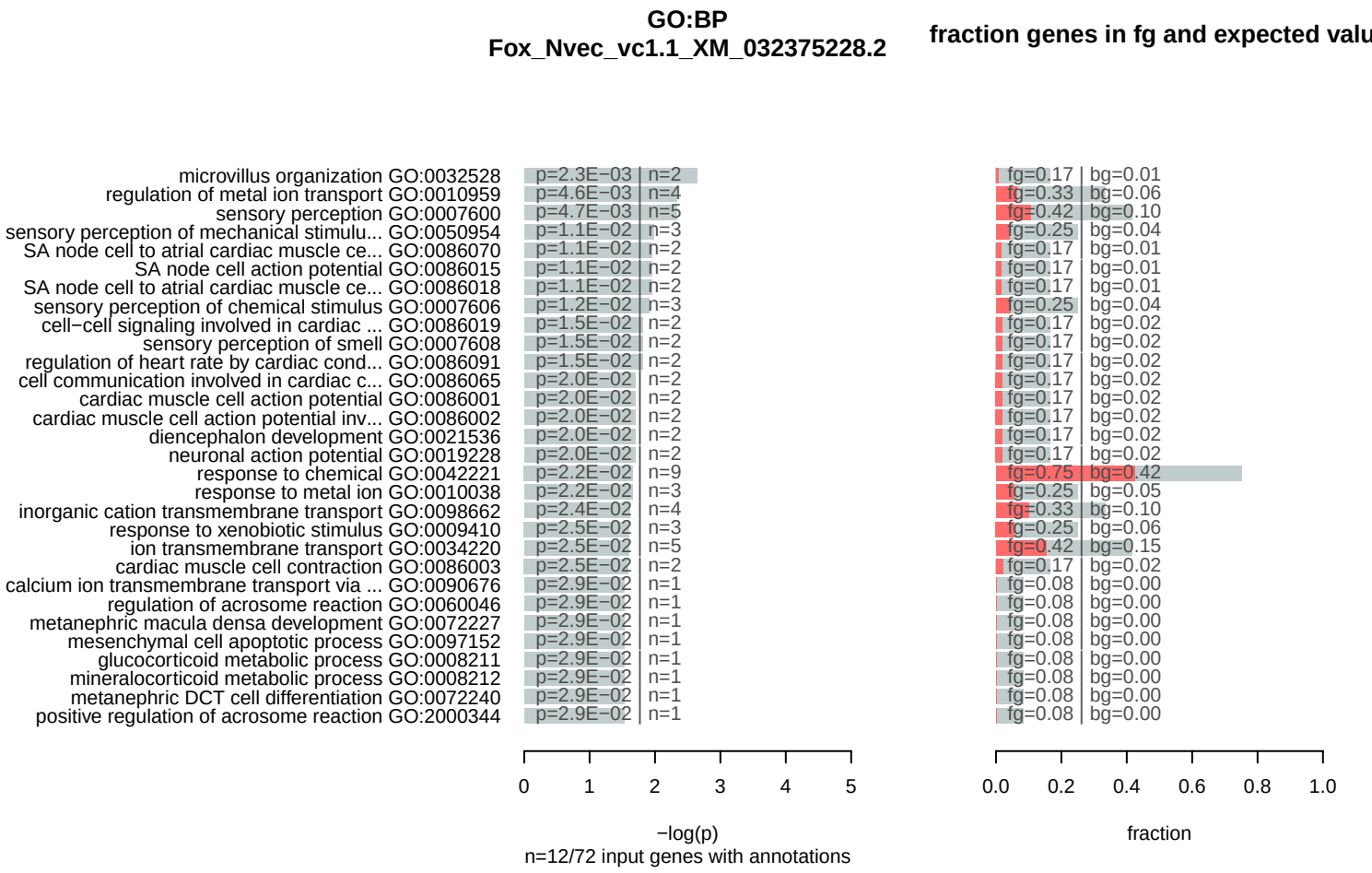
GO:BP
Fox_Nvec_vc1.1_XM_032375228.2
fraction genes in fg and expected valu
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regulation of metal ion transport GO:0010959 p=4.6E−03 n=4 fg=0.33 bg=0.06
sensory perception GO:0007600 p=4.7E−03 n=5 fg=0.42 bg=0.10
sensory perception of mechanical stimulu... GO:0050954 p=1.1E−02 n=3 fg=0.25 bg=0.04
SA node cell to atrial cardiac muscle ce... GO:0086070 p=1.1E−02 n=2 fg=0.17 bg=0.01
SA node cell action potential GO:0086015 p=1.1E−02 n=2 fg=0.17 bg=0.01
SA node cell to atrial cardiac muscle ce... GO:0086018 p=1.1E−02 n=2 fg=0.17 bg=0.01
sensory perception of chemical stimulus GO:0007606 p=1.2E−02 n=3 fg=0.25 bg=0.04
cell−cell signaling involved in cardiac ... GO:0086019 p=1.5E−02 n=2 fg=0.17 bg=0.02
sensory perception of smell GO:0007608 p=1.5E−02 n=2 fg=0.17 bg=0.02
regulation of heart rate by cardiac cond... GO:0086091 p=1.5E−02 n=2 fg=0.17 bg=0.02
cell communication involved in cardiac c... GO:0086065 p=2.0E−02 n=2 fg=0.17 bg=0.02
cardiac muscle cell action potential GO:0086001 p=2.0E−02 n=2 fg=0.17 bg=0.02
cardiac muscle cell action potential inv... GO:0086002 p=2.0E−02 n=2 fg=0.17 bg=0.02
diencephalon development GO:0021536 p=2.0E−02 n=2 fg=0.17 bg=0.02
neuronal action potential GO:0019228 p=2.0E−02 n=2 fg=0.17 bg=0.02
response to chemical GO:0042221 p=2.2E−02 n=9 fg=0.75 bg=0.42
response to metal ion GO:0010038 p=2.2E−02 n=3 fg=0.25 bg=0.05
inorganic cation transmembrane transport GO:0098662 p=2.4E−02 n=4 fg=0.33 bg=0.10
response to xenobiotic stimulus GO:0009410 p=2.5E−02 n=3 fg=0.25 bg=0.06
ion transmembrane transport GO:0034220 p=2.5E−02 n=5 fg=0.42 bg=0.15
cardiac muscle cell contraction GO:0086003 p=2.5E−02 n=2 fg=0.17 bg=0.02
calcium ion transmembrane transport via ... GO:0090676 p=2.9E−02 n=1 fg=0.08 bg=0.00
regulation of acrosome reaction GO:0060046 p=2.9E−02 n=1 fg=0.08 bg=0.00
metanephric macula densa development GO:0072227 p=2.9E−02 n=1 fg=0.08 bg=0.00
mesenchymal cell apoptotic process GO:0097152 p=2.9E−02 n=1 fg=0.08 bg=0.00
glucocorticoid metabolic process GO:0008211 p=2.9E−02 n=1 fg=0.08 bg=0.00
mineralocorticoid metabolic process GO:0008212 p=2.9E−02 n=1 fg=0.08 bg=0.00
metanephric DCT cell differentiation GO:0072240 p=2.9E−02 n=1 fg=0.08 bg=0.00
positive regulation of acrosome reaction GO:2000344 p=2.9E−02 n=1 fg=0.08 bg=0.00
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n=12/72 input genes with annotations
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fraction
GO:MF
Fox_Nvec_vc1.1_XM_032375228.2
fraction genes in fg and expected valu
transmembrane transporter activity GO:0022857 p=1.8E−02 n=5 fg=0.42 bg=0.14
transporter activity GO:0005215 p=2.8E−02 n=5 fg=0.42 bg=0.16
organophosphate ester transmembrane tran... GO:0015605 p=3.3E−02 n=1 fg=0.08 bg=0.00
aminophospholipid flippase activity GO:0015247 p=3.3E−02 n=1 fg=0.08 bg=0.00
nickel cation binding GO:0016151 p=3.3E−02 n=1 fg=0.08 bg=0.00
voltage−gated calcium channel activity i... GO:0086056 p=3.3E−02 n=1 fg=0.08 bg=0.00
voltage−gated calcium channel activity i... GO:0086059 p=3.3E−02 n=1 fg=0.08 bg=0.00
voltage−gated calcium channel activity i... GO:0086007 p=3.3E−02 n=1 fg=0.08 bg=0.00
carbonate dehydratase activity GO:0004089 p=3.3E−02 n=1 fg=0.08 bg=0.00
carbon−oxygen lyase activity GO:0016835 p=3.3E−02 n=1 fg=0.08 bg=0.00
hydro−lyase activity GO:0016836 p=3.3E−02 n=1 fg=0.08 bg=0.00
phosphatidylglycerol binding GO:1901611 p=3.3E−02 n=1 fg=0.08 bg=0.00
cardiolipin binding GO:1901612 p=3.3E−02 n=1 fg=0.08 bg=0.00
calmodulin−activated 3',5'−cyclic−GMP ph... GO:0048101 p=3.3E−02 n=1 fg=0.08 bg=0.00
ATPase−coupled intramembrane lipid trans... GO:0140326 p=3.3E−02 n=1 fg=0.08 bg=0.00
flippase activity GO:0140327 p=3.3E−02 n=1 fg=0.08 bg=0.00
ecdysis−triggering hormone receptor acti... GO:0042654 p=3.3E−02 n=1 fg=0.08 bg=0.00
calmodulin−activated dual specificity 3'... GO:0004117 p=3.3E−02 n=1 fg=0.08 bg=0.00
scaffold protein binding GO:0097110 p=3.9E−02 n=2 fg=0.17 bg=0.03
cation channel activity GO:0005261 p=4.6E−02 n=3 fg=0.25 bg=0.07
potassium ion transmembrane transporter ... GO:0015079 p=5.5E−02 n=2 fg=0.17 bg=0.03
potassium channel activity GO:0005267 p=5.5E−02 n=2 fg=0.17 bg=0.03
metal ion transmembrane transporter acti... GO:0046873 p=5.6E−02 n=3 fg=0.25 bg=0.08
ion transmembrane transporter activity GO:0015075 p=5.9E−02 n=4 fg=0.33 bg=0.13
ribosome binding GO:0043022 p=6.5E−02 n=1 fg=0.08 bg=0.01
minor groove of adenine−thymine−rich DNA... GO:0003680 p=6.5E−02 n=1 fg=0.08 bg=0.01
intramembrane lipid transporter activity GO:0140303 p=6.5E−02 n=1 fg=0.08 bg=0.01
low voltage−gated calcium channel activi... GO:0008332 p=6.5E−02 n=1 fg=0.08 bg=0.01
DNA secondary structure binding GO:0000217 p=6.5E−02 n=1 fg=0.08 bg=0.01
voltage−gated cation channel activity GO:0022843 p=7.3E−02 n=2 fg=0.17 bg=0.04
0 1 2 3 4 5
−log(p)
n=12/72 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction
GO:CC
Fox_Nvec_vc1.1_XM_032375228.2
fraction genes in fg and expected valu
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perikaryon GO:0043204 p=2.8E−02 n=2 fg=0.14 bg=0.02
integral component of membrane GO:0016021 p=3.5E−02 n=7 fg=0.50 bg=0.25
cytoplasmic vesicle membrane GO:0030659 p=3.7E−02 n=4 fg=0.29 bg=0.10
vesicle membrane GO:0012506 p=3.7E−02 n=4 fg=0.29 bg=0.10
cilium GO:0005929 p=3.9E−02 n=3 fg=0.21 bg=0.06
integral component of plasma membrane GO:0005887 p=4.0E−02 n=5 fg=0.36 bg=0.15
endocytic vesicle GO:0030139 p=4.3E−02 n=2 fg=0.14 bg=0.02
intrinsic component of membrane GO:0031224 p=4.5E−02 n=7 fg=0.50 bg=0.26
intrinsic component of plasma membrane GO:0031226 p=5.5E−02 n=5 fg=0.36 bg=0.16
specific granule GO:0042581 p=6.9E−02 n=1 fg=0.07 bg=0.01
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phagocytic vesicle membrane GO:0030670 p=6.9E−02 n=1 fg=0.07 bg=0.01
specific granule membrane GO:0035579 p=6.9E−02 n=1 fg=0.07 bg=0.01
stereocilium GO:0032420 p=6.9E−02 n=1 fg=0.07 bg=0.01
stereocilium bundle GO:0032421 p=6.9E−02 n=1 fg=0.07 bg=0.01
cation channel complex GO:0034703 p=9.1E−02 n=2 fg=0.14 bg=0.04
phagocytic vesicle GO:0045335 p=1.0E−01 n=1 fg=0.07 bg=0.01
rough endoplasmic reticulum GO:0005791 p=1.0E−01 n=1 fg=0.07 bg=0.01
ciliary membrane GO:0060170 p=1.0E−01 n=1 fg=0.07 bg=0.01
tertiary granule GO:0070820 p=1.0E−01 n=1 fg=0.07 bg=0.01
tertiary granule membrane GO:0070821 p=1.0E−01 n=1 fg=0.07 bg=0.01
sensory dendrite GO:0071683 p=1.0E−01 n=1 fg=0.07 bg=0.01
transmembrane transporter complex GO:1902495 p=1.0E−01 n=2 fg=0.14 bg=0.04
ion channel complex GO:0034702 p=1.0E−01 n=2 fg=0.14 bg=0.04
transporter complex GO:1990351 p=1.0E−01 n=2 fg=0.14 bg=0.04
intrinsic component of organelle membran... GO:0031300 p=1.2E−01 n=2 fg=0.14 bg=0.04
integral component of organelle membrane GO:0031301 p=1.2E−01 n=2 fg=0.14 bg=0.04
acrosomal vesicle GO:0001669 p=1.3E−01 n=1 fg=0.07 bg=0.01
brush border membrane GO:0031526 p=1.3E−01 n=1 fg=0.07 bg=0.01
0 1 2 3 4 5
−log(p)
n=14/72 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction