GO:BP
Fox_Nvec_v1g93844

fraction genes in fg and expected valu

outer ear morphogenesis GO:0042473	p=3.1E−04 | n=2	fg=0.11 | bg=0.00
regulation of extracellular matrix disas... GO:0010715	p=6.2E−04 | n=2	fg=0.11 | bg=0.00
otic vesicle morphogenesis GO:0071600	p=1.0E−03 | n=2	fg=0.11 | bg=0.00
middle ear morphogenesis GO:0042474	p=1.5E−03 | n=2	fg=0.11 | bg=0.00
negative regulation of cell fate specifi... GO:0009996	p=1.5E−03 | n=2	fg=0.11 | bg=0.00
pole cell migration GO:0007280	p=1.5E−03 | n=2	fg=0.11 | bg=0.00
morphogenesis of an epithelial fold GO:0060571	p=2.1E−03 | n=2	fg=0.11 | bg=0.00
ectodermal placode morphogenesis GO:0071697	p=2.1E−03 | n=2	fg=0.11 | bg=0.00
regulation of collagen metabolic process GO:0010712	p=2.1E−03 | n=2	fg=0.11 | bg=0.00
salivary gland morphogenesis GO:0007435	p=2.2E−03 | n=3	fg=0.16 | bg=0.01
regulation of animal organ formation GO:0003156	p=3.6E−03 | n=2	fg=0.11 | bg=0.00
regulation of extrinsic apoptotic signal... GO:2001239	p=3.6E−03 | n=2	fg=0.11 | bg=0.00
mesodermal cell fate specification GO:0007501	p=3.6E−03 | n=2	fg=0.11 | bg=0.00
positive regulation of secretion by cell GO:1903532	p=3.7E−03 | n=4	fg=0.21 | bg=0.04
positive regulation of DNA repair GO:0045739	p=5.4E−03 | n=2	fg=0.11 | bg=0.01
establishment of vesicle localization GO:0051650	p=5.9E−03 | n=4	fg=0.21 | bg=0.04
eye−antennal disc morphogenesis GO:0007455	p=6.5E−03 | n=2	fg=0.11 | bg=0.01
wound healing GO:0042060	p=7.2E−03 | n=4	fg=0.21 | bg=0.04
regulation of gastrulation GO:0010470	p=7.6E−03 | n=2	fg=0.11 | bg=0.01
somatic muscle development GO:0007525	p=7.6E−03 | n=2	fg=0.11 | bg=0.01
vitamin metabolic process GO:0006766	p=1.0E−02 | n=2	fg=0.11 | bg=0.01
embryonic body morphogenesis GO:0010172	p=1.0E−02 | n=2	fg=0.11 | bg=0.01
regulation of basement membrane organiza... GO:0110011	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
tRNA transcription GO:0009304	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
cardiac cell fate specification GO:0060912	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
antigen processing and presentation via ... GO:0002475	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
negative regulation of nuclease activity GO:0032074	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
tRNA demethylation GO:1990983	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
regulation of hypoxia−induced intrinsic ... GO:1903297	p=1.0E−02 | n=1	fg=0.05 | bg=0.00
negative regulation of hypoxia−induced i... GO:1903298	p=1.0E−02 | n=1	fg=0.05 | bg=0.00

0   1   2   3   4   5

−log(p)
n=19/92 input genes with annotations

0.0   0.2   0.4   0.6   0.8   1.0

fraction

GO:MF
Fox_Nvec_v1g93844

fraction genes in fg and expected valu

G−protein alpha−subunit binding GO:0001965	p=1.6E−03 | n=2	fg=0.12 | bg=0.00
endoribonuclease inhibitor activity GO:0060698	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
nuclease inhibitor activity GO:0140721	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
ribonuclease inhibitor activity GO:0008428	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
protein tyrosine phosphatase activity, m... GO:0030946	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
methylcytosine dioxygenase activity GO:0070579	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
proteinase activated receptor binding GO:0031871	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
dystroglycan binding GO:0002162	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
tRNA demethylase activity GO:1990984	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
L−malate dehydrogenase activity GO:0030060	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
oxidative RNA demethylase activity GO:0035515	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
propionyl−CoA carboxylase activity GO:0004658	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
CoA carboxylase activity GO:0016421	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
kinetochore binding GO:0043515	p=1.1E−02 | n=1	fg=0.06 | bg=0.00
heparan−alpha−glucosaminide N−acetyltran... GO:0015019	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
DNA−N1−methyladenine dioxygenase activit... GO:0043734	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
GDP−dissociation inhibitor activity GO:0005092	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
ubiquitin−protein transferase activator ... GO:0097027	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
malic enzyme activity GO:0004470	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
ligase activity, forming carbon−carbon b... GO:0016885	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
malate dehydrogenase activity GO:0016615	p=2.1E−02 | n=1	fg=0.06 | bg=0.00
fibroblast growth factor−activated recep... GO:0005007	p=3.2E−02 | n=1	fg=0.06 | bg=0.00
tumor necrosis factor receptor binding GO:0005164	p=3.2E−02 | n=1	fg=0.06 | bg=0.00
NAD binding GO:0051287	p=3.2E−02 | n=1	fg=0.06 | bg=0.00
ubiquitin−protein transferase regulator ... GO:0055106	p=3.2E−02 | n=1	fg=0.06 | bg=0.00
DNA−(apurinic or apyrimidinic site) endo... GO:0003906	p=3.2E−02 | n=1	fg=0.06 | bg=0.00
receptor−receptor interaction GO:0090722	p=3.2E−02 | n=1	fg=0.06 | bg=0.00
molecular function regulator activity GO:0098772	p=4.1E−02 | n=5	fg=0.29 | bg=0.12
GTP−dependent protein binding GO:0030742	p=4.2E−02 | n=1	fg=0.06 | bg=0.00
chemoattractant activity GO:0042056	p=4.2E−02 | n=1	fg=0.06 | bg=0.00

0   1   2   3   4   5

−log(p)
n=17/92 input genes with annotations

0.0   0.2   0.4   0.6   0.8   1.0

fraction

GO:CC
Fox_Nvec_v1g93844

fraction genes in fg and expected valu

trans−Golgi network GO:0005802	p=4.4E−03 | n=4	fg=0.21 | bg=0.04
nuclear outer membrane GO:0005640	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
cortical microtubule plus−end GO:1903754	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
cytoplasmic microtubule plus−end GO:1904511	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
lumenal side of Golgi membrane GO:0098547	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
centrosomal corona GO:0031592	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
cortical microtubule GO:0055028	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
RNA polymerase III transcription regulat... GO:0090576	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
transcription factor TFIIIC complex GO:0000127	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
AP−3 adaptor complex GO:0030123	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
cortical microtubule cytoskeleton GO:0030981	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
Flemming body GO:0090543	p=1.1E−02 | n=1	fg=0.05 | bg=0.00
intracellular vesicle GO:0097708	p=1.2E−02 | n=8	fg=0.42 | bg=0.18
cytoplasmic vesicle GO:0031410	p=1.2E−02 | n=8	fg=0.42 | bg=0.18
vesicle GO:0031982	p=1.7E−02 | n=8	fg=0.42 | bg=0.19
extracellular space GO:0005615	p=1.8E−02 | n=3	fg=0.16 | bg=0.03
endosome GO:0005768	p=2.1E−02 | n=5	fg=0.26 | bg=0.09
extrinsic component of Golgi membrane GO:0090498	p=2.1E−02 | n=1	fg=0.05 | bg=0.00
nuclear chromosome GO:0000228	p=3.1E−02 | n=3	fg=0.16 | bg=0.04
microtubule plus−end GO:0035371	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
NuRD complex GO:0016581	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
intercalary heterochromatin GO:0005725	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
endoplasmic reticulum exit site GO:0070971	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
CHD−type complex GO:0090545	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
PRC1 complex GO:0035102	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
kinetochore microtubule GO:0005828	p=3.1E−02 | n=1	fg=0.05 | bg=0.00
extracellular region GO:0005576	p=3.8E−02 | n=4	fg=0.21 | bg=0.07
cell cortex GO:0005938	p=4.0E−02 | n=3	fg=0.16 | bg=0.04
myelin sheath GO:0043209	p=4.1E−02 | n=2	fg=0.11 | bg=0.02
basal cortex GO:0045180	p=4.1E−02 | n=1	fg=0.05 | bg=0.00

0   1   2   3   4   5

−log(p)
n=19/92 input genes with annotations

0.0   0.2   0.4   0.6   0.8   1.0

fraction