GO:BP
Fox_Nvec_vc1.1_XM_032376608.2

fraction genes in fg and expected value

GO term	p-value	n	fg	bg
positive regulation of gene expression GO:0010628	p=3.3E−05	n=35	fg=0.30	bg=0.15
regulation of cellular macromolecule bio... GO:2000112	p=8.1E−05	n=47	fg=0.40	bg=0.24
positive regulation of transcription by ... GO:0045944	p=1.7E−04	n=26	fg=0.22	bg=0.08
somatic stem cell population maintenance GO:0035019	p=1.9E−04	n=6	fg=0.05	bg=0.01
cellular response to retinoic acid GO:0071300	p=2.1E−04	n=5	fg=0.04	bg=0.01
epidermis morphogenesis GO:0048730	p=2.1E−04	n=5	fg=0.04	bg=0.01
positive regulation of programmed cell d... GO:0043068	p=2.8E−04	n=17	fg=0.15	bg=0.06
detection of temperature stimulus involv... GO:0050965	p=3.6E−04	n=4	fg=0.03	bg=0.00
respiratory system development GO:0060541	p=5.8E−04	n=11	fg=0.09	bg=0.03
beta−catenin−TCF complex assembly GO:1904837	p=7.4E−04	n=3	fg=0.03	bg=0.00
epithelial cell apoptotic process GO:1904019	p=7.6E−04	n=5	fg=0.04	bg=0.01
transforming growth factor beta receptor... GO:0007179	p=8.4E−04	n=7	fg=0.06	bg=0.01
cellular response to glucose starvation GO:0042149	p=8.7E−04	n=4	fg=0.03	bg=0.00
negative regulation of cell population p... GO:0008285	p=9.4E−04	n=15	fg=0.13	bg=0.05
negative regulation of hemopoiesis GO:1903707	p=1.0E−03	n=6	fg=0.05	bg=0.01
imaginal disc−derived wing morphogenesis GO:0007476	p=1.2E−03	n=10	fg=0.09	bg=0.03
lens morphogenesis in camera−type eye GO:0002089	p=1.4E−03	n=3	fg=0.03	bg=0.00
response to cycloheximide GO:0046898	p=1.4E−03	n=3	fg=0.03	bg=0.00
positive regulation of protein serine/th... GO:0071902	p=1.5E−03	n=9	fg=0.08	bg=0.02
hair follicle development GO:0001942	p=1.6E−03	n=5	fg=0.04	bg=0.01
artery morphogenesis GO:0048844	p=1.8E−03	n=4	fg=0.03	bg=0.00
response to mechanical stimulus GO:0009612	p=1.8E−03	n=9	fg=0.08	bg=0.02
liver development GO:0001889	p=2.1E−03	n=7	fg=0.06	bg=0.02
cellular response to cAMP GO:0071320	p=2.4E−03	n=4	fg=0.03	bg=0.01
regulation of hematopoietic stem cell di... GO:1902036	p=2.4E−03	n=4	fg=0.03	bg=0.01
regulation of calcium ion import GO:0090279	p=2.4E−03	n=3	fg=0.03	bg=0.00
labyrinthine layer morphogenesis GO:0060713	p=2.4E−03	n=3	fg=0.03	bg=0.00
cellular response to ethanol GO:0071361	p=2.4E−03	n=3	fg=0.03	bg=0.00
response to fungicide GO:0060992	p=2.4E−03	n=3	fg=0.03	bg=0.00
positive regulation of transcription of ... GO:0007221	p=2.4E−03	n=3	fg=0.03	bg=0.00
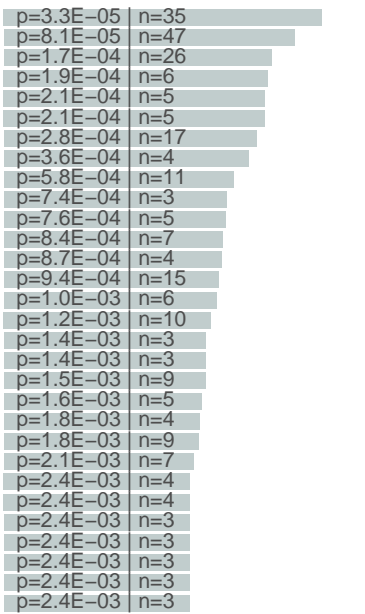
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n=117/425 input genes with annotations
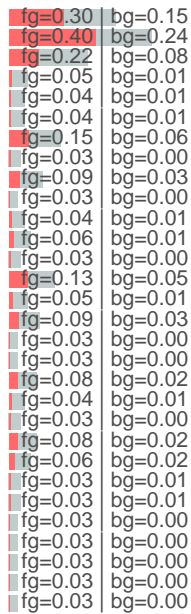
fraction

GO:MF
Fox_Nvec_vc1.1_XM_032376608.2

fraction genes in fg and expected value

GO term	p-value	n	fg	bg
transcription coregulator binding GO:0001221	p=4.3E−04	n=4	fg=0.04	bg=0.00
protein heterodimerization activity GO:0046982	p=9.8E−04	n=15	fg=0.14	bg=0.06
Wnt−protein binding GO:0017147	p=1.7E−03	n=3	fg=0.03	bg=0.00
coreceptor activity GO:0015026	p=1.7E−03	n=3	fg=0.03	bg=0.00
transcription coactivator activity GO:0003713	p=2.1E−03	n=10	fg=0.09	bg=0.03
calcium−release channel activity GO:0015278	p=2.8E−03	n=3	fg=0.03	bg=0.00
E−box binding GO:0070888	p=2.9E−03	n=4	fg=0.04	bg=0.01
DNA−binding transcription activator acti... GO:0001228	p=5.6E−03	n=9	fg=0.08	bg=0.03
DNA−binding transcription factor activit... GO:0003700	p=5.7E−03	n=19	fg=0.18	bg=0.07
oxidoreductase activity, acting on the C... GO:0016899	p=6.0E−03	n=2	fg=0.02	bg=0.00
inosine kinase activity GO:0008906	p=6.0E−03	n=2	fg=0.02	bg=0.00
phosphoenolpyruvate carboxykinase (GTP) ... GO:0004613	p=6.0E−03	n=2	fg=0.02	bg=0.00
voltage−gated calcium channel activity GO:0005245	p=8.8E−03	n=3	fg=0.03	bg=0.00
transcription cis−regulatory region bind... GO:0000976	p=9.8E−03	n=14	fg=0.13	bg=0.05
protein dimerization activity GO:0046983	p=1.1E−02	n=29	fg=0.27	bg=0.13
RNA polymerase II transcription regulato... GO:0000977	p=1.1E−02	n=13	fg=0.12	bg=0.04
fibroblast growth factor−activated recep... GO:0005007	p=1.2E−02	n=2	fg=0.02	bg=0.00
lactate dehydrogenase activity GO:0004457	p=1.2E−02	n=2	fg=0.02	bg=0.00
DNA binding domain binding GO:0050692	p=1.2E−02	n=2	fg=0.02	bg=0.00
ion gated channel activity GO:0022839	p=1.2E−02	n=7	fg=0.06	bg=0.02
nucleobase−containing compound kinase ac... GO:0019205	p=1.5E−02	n=3	fg=0.03	bg=0.01
cis−regulatory region sequence−specific ... GO:0000987	p=1.6E−02	n=11	fg=0.10	bg=0.03
RNA polymerase II cis−regulatory region ... GO:0000978	p=1.6E−02	n=11	fg=0.10	bg=0.03
heat shock protein binding GO:0031072	p=1.8E−02	n=6	fg=0.06	bg=0.02
nucleoside diphosphate kinase activity GO:0004550	p=1.9E−02	n=2	fg=0.02	bg=0.00
epinephrine binding GO:0051379	p=1.9E−02	n=2	fg=0.02	bg=0.00
catecholamine binding GO:1901338	p=1.9E−02	n=2	fg=0.02	bg=0.00
transcription coactivator binding GO:0001223	p=1.9E−02	n=2	fg=0.02	bg=0.00
actin monomer binding GO:0003785	p=1.9E−02	n=2	fg=0.02	bg=0.00
alcohol binding GO:0043178	p=1.9E−02	n=3	fg=0.03	bg=0.01
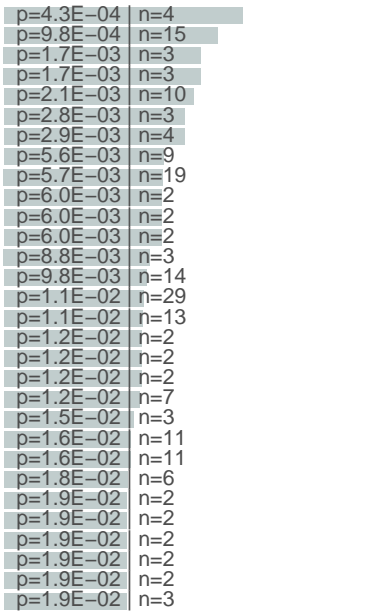
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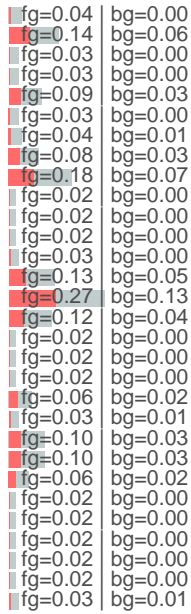
fraction

GO:CC
Fox_Nvec_vc1.1_XM_032376608.2

fraction genes in fg and expected value

GO term	p-value	n	fg	bg
chromatin GO:0000785	p=3.4E−04	n=15	fg=0.13	bg=0.05
beta−catenin−TCF complex GO:1990907	p=5.5E−03	n=2	fg=0.02	bg=0.00
receptor complex GO:0043235	p=9.9E−03	n=6	fg=0.05	bg=0.02
nuclear body GO:0016604	p=1.1E−02	n=14	fg=0.12	bg=0.06
basolateral plasma membrane GO:0016323	p=1.7E−02	n=7	fg=0.06	bg=0.02
basal plasma membrane GO:0009925	p=1.7E−02	n=7	fg=0.06	bg=0.02
intrinsic component of the cytoplasmic s... GO:0031235	p=1.7E−02	n=2	fg=0.02	bg=0.00
perinuclear endoplasmic reticulum GO:0097038	p=1.7E−02	n=2	fg=0.02	bg=0.00
Golgi cis cisterna GO:0000137	p=1.7E−02	n=2	fg=0.02	bg=0.00
transport vesicle GO:0030133	p=1.9E−02	n=9	fg=0.08	bg=0.03
cell surface GO:0009986	p=2.3E−02	n=9	fg=0.08	bg=0.04
tight junction GO:0070160	p=3.0E−02	n=3	fg=0.03	bg=0.01
basal part of cell GO:0045178	p=3.3E−02	n=7	fg=0.06	bg=0.03
side of membrane GO:0098552	p=4.3E−02	n=8	fg=0.07	bg=0.03
integrin alpha4−beta7 complex GO:0034669	p=4.4E−02	n=1	fg=0.01	bg=0.00
Scrib−APC−beta−catenin complex GO:0034750	p=4.4E−02	n=1	fg=0.01	bg=0.00
catenin−TCF7L2 complex GO:0071664	p=4.4E−02	n=1	fg=0.01	bg=0.00
condensin complex GO:0000796	p=4.4E−02	n=1	fg=0.01	bg=0.00
apoptosome GO:0043293	p=4.4E−02	n=1	fg=0.01	bg=0.00
smooth septate junction GO:0005920	p=4.4E−02	n=1	fg=0.01	bg=0.00
fascia adherens GO:0005916	p=4.4E−02	n=1	fg=0.01	bg=0.00
polycystin complex GO:0002133	p=4.4E−02	n=1	fg=0.01	bg=0.00
axonemal basal plate GO:0097541	p=4.4E−02	n=1	fg=0.01	bg=0.00
beta−catenin−TCF7L2 complex GO:0070369	p=4.4E−02	n=1	fg=0.01	bg=0.00
nucleoplasm GO:0005654	p=4.4E−02	n=43	fg=0.36	bg=0.29
nuclear chromosome GO:0000228	p=4.6E−02	n=10	fg=0.09	bg=0.05
nucleus GO:0005634	p=4.8E−02	n=69	fg=0.58	bg=0.50
cell cortex GO:0005938	p=5.1E−02	n=8	fg=0.07	bg=0.03
transcription regulator complex GO:0005667	p=5.4E−02	n=10	fg=0.08	bg=0.04
MLL1 complex GO:0071339	p=5.6E−02	n=2	fg=0.02	bg=0.00
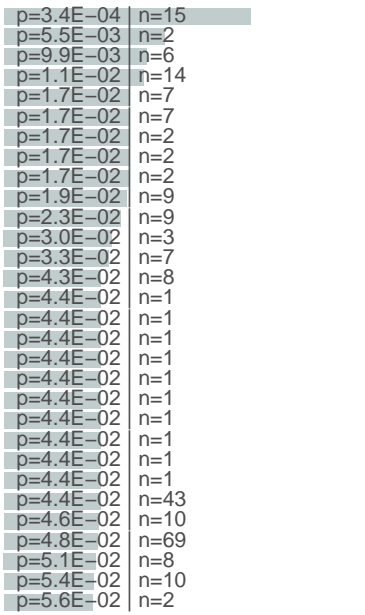
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n=118/425 input genes with annotations

fraction