fraction genes in fg and expected valu...
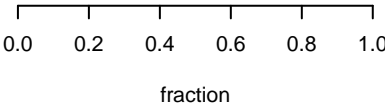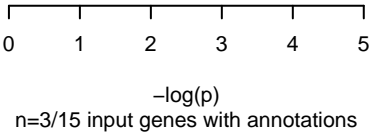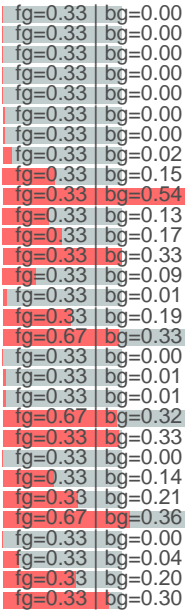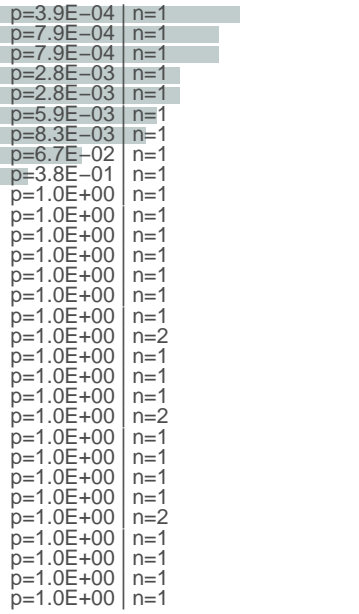
positive regulation of transcription fro... GO:0061400	p=3.9E−04 | n=1	fg=0.33 | bg=0.00
UDP catabolic process GO:0006256	p=7.9E−04 | n=1	fg=0.33 | bg=0.00
GDP catabolic process GO:0046712	p=7.9E−04 | n=1	fg=0.33 | bg=0.00
CTP metabolic process GO:0046036	p=2.8E−03 | n=1	fg=0.33 | bg=0.00
positive regulation of viral entry into ... GO:0046598	p=2.8E−03 | n=1	fg=0.33 | bg=0.00
protein autoprocessing GO:0016540	p=5.9E−03 | n=1	fg=0.33 | bg=0.00
nucleobase−containing small molecule cat... GO:0034656	p=8.3E−03 | n=1	fg=0.33 | bg=0.00
regulation of DNA−binding transcription ... GO:0051090	p=6.7E−02 | n=1	fg=0.33 | bg=0.02
regulation of molecular function GO:0065009	p=3.8E−01 | n=1	fg=0.33 | bg=0.15
regulation of cellular process GO:0050794	p=1.0E+00 | n=1	fg=0.33 | bg=0.54
regulation of transcription, DNA−templat... GO:0006355	p=1.0E+00 | n=1	fg=0.33 | bg=0.13
cellular catabolic process GO:0044248	p=1.0E+00 | n=1	fg=0.33 | bg=0.17
cellular biosynthetic process GO:0044249	p=1.0E+00 | n=1	fg=0.33 | bg=0.33
regulation of transcription by RNA polym... GO:0006357	p=1.0E+00 | n=1	fg=0.33 | bg=0.09
nucleoside diphosphate metabolic process GO:0009132	p=1.0E+00 | n=1	fg=0.33 | bg=0.01
regulation of biosynthetic process GO:0009889	p=1.0E+00 | n=1	fg=0.33 | bg=0.19
heterocycle metabolic process GO:0046483	p=1.0E+00 | n=2	fg=0.67 | bg=0.33
nucleoside diphosphate catabolic process GO:0009134	p=1.0E+00 | n=1	fg=0.33 | bg=0.00
purine nucleoside diphosphate metabolic ... GO:0009135	p=1.0E+00 | n=1	fg=0.33 | bg=0.01
ribonucleotide catabolic process GO:0009261	p=1.0E+00 | n=1	fg=0.33 | bg=0.01
gene expression GO:0010467	p=1.0E+00 | n=2	fg=0.67 | bg=0.32
protein metabolic process GO:0019538	p=1.0E+00 | n=1	fg=0.33 | bg=0.33
purine nucleoside diphosphate catabolic ... GO:0009137	p=1.0E+00 | n=1	fg=0.33 | bg=0.00
RNA biosynthetic process GO:0032774	p=1.0E+00 | n=1	fg=0.33 | bg=0.14
regulation of gene expression GO:0010468	p=1.0E+00 | n=1	fg=0.33 | bg=0.21
organic cyclic compound metabolic proces... GO:1901360	p=1.0E+00 | n=2	fg=0.67 | bg=0.36
pyrimidine nucleoside diphosphate metabo... GO:0009138	p=1.0E+00 | n=1	fg=0.33 | bg=0.00
organic cyclic compound catabolic proces... GO:1901361	p=1.0E+00 | n=1	fg=0.33 | bg=0.04
organic cyclic compound biosynthetic pro... GO:1901362	p=1.0E+00 | n=1	fg=0.33 | bg=0.20
regulation of macromolecule metabolic pr... GO:0060255	p=1.0E+00 | n=1	fg=0.33 | bg=0.30

0 1 2 3 4 5

−log(p)
n=3/15 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0

fraction

fraction genes in fg and expected valu...

CTPase activity GO:0043273	p=8.0E−04 | n=1	fg=0.33 | bg=0.00
cytidine−diphosphatase activity GO:0036384	p=8.0E−04 | n=1	fg=0.33 | bg=0.00
uridine−diphosphatase activity GO:0045134	p=1.6E−03 | n=1	fg=0.33 | bg=0.00
guanosine−diphosphatase activity GO:0044382	p=1.6E−03 | n=1	fg=0.33 | bg=0.00
scavenger receptor activity GO:0005044	p=2.8E−03 | n=1	fg=0.33 | bg=0.00
serine−type endopeptidase activity GO:0004252	p=2.4E−02 | n=1	fg=0.33 | bg=0.01
serine−type peptidase activity GO:0008236	p=2.8E−02 | n=1	fg=0.33 | bg=0.01
serine hydrolase activity GO:0017171	p=3.7E−02 | n=1	fg=0.33 | bg=0.01
DNA−binding transcription activator acti... GO:0001228	p=3.7E−02 | n=1	fg=0.33 | bg=0.01
DNA−binding transcription activator acti... GO:0001216	p=3.7E−02 | n=1	fg=0.33 | bg=0.01
endopeptidase activity GO:0004175	p=6.2E−02 | n=1	fg=0.33 | bg=0.02
DNA−binding transcription factor activit... GO:0000981	p=6.8E−02 | n=1	fg=0.33 | bg=0.02
RNA polymerase II cis−regulatory region ... GO:0000978	p=7.4E−02 | n=1	fg=0.33 | bg=0.03
DNA−binding transcription factor activit... GO:0003700	p=7.5E−02 | n=1	fg=0.33 | bg=0.03
cis−regulatory region sequence−specific ... GO:0000987	p=7.9E−02 | n=1	fg=0.33 | bg=0.03
RNA polymerase II transcription regulato... GO:0000977	p=8.8E−02 | n=1	fg=0.33 | bg=0.03
transcription cis−regulatory region bind... GO:0000976	p=1.1E−01 | n=1	fg=0.33 | bg=0.04
transcription regulatory region nucleic ... GO:0001067	p=1.1E−01 | n=1	fg=0.33 | bg=0.04
peptidase activity GO:0008233	p=1.1E−01 | n=1	fg=0.33 | bg=0.04
sequence−specific double−stranded DNA bi... GO:1990837	p=1.2E−01 | n=1	fg=0.33 | bg=0.04
double−stranded DNA binding GO:0003690	p=1.3E−01 | n=1	fg=0.33 | bg=0.05
sequence−specific DNA binding GO:0043565	p=1.3E−01 | n=1	fg=0.33 | bg=0.05
transcription regulator activity GO:0140110	p=1.5E−01 | n=1	fg=0.33 | bg=0.05
DNA binding GO:0003677	p=2.6E−01 | n=1	fg=0.33 | bg=0.09
hydrolase activity GO:0016787	p=2.9E−01 | n=2	fg=0.67 | bg=0.16
catalytic activity, acting on a protein GO:0140096	p=3.5E−01 | n=1	fg=0.33 | bg=0.14
nucleic acid binding GO:0003676	p=4.4E−01 | n=1	fg=0.33 | bg=0.18
catalytic activity GO:0003824	p=6.3E−01 | n=2	fg=0.67 | bg=0.39
heterocyclic compound binding GO:1901363	p=7.0E−01 | n=1	fg=0.33 | bg=0.33
organic cyclic compound binding GO:0097159	p=7.0E−01 | n=1	fg=0.33 | bg=0.33

0 1 2 3 4 5

−log(p)
n=3/15 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0
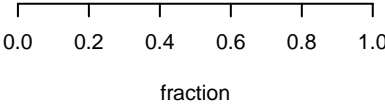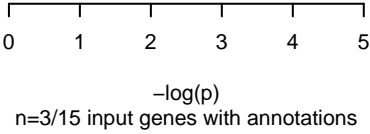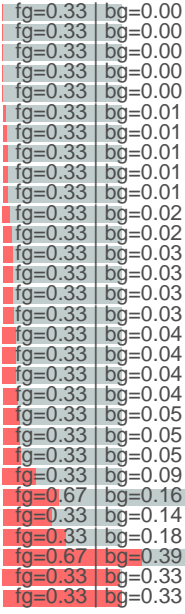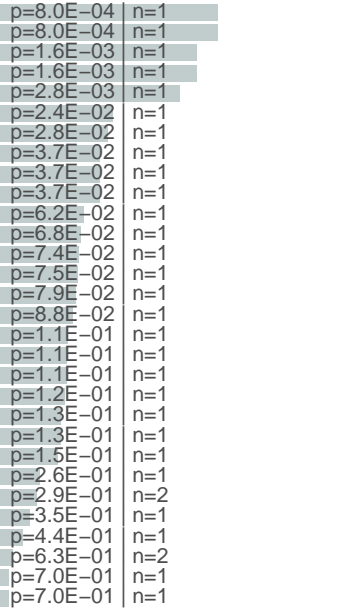
fraction

fraction genes in fg and expected valu...

granular component GO:0001652	p=7.9E−04 | n=1	fg=0.33 | bg=0.00
autophagosome membrane GO:0000421	p=1.1E−02 | n=1	fg=0.33 | bg=0.00
autophagosome GO:0005776	p=3.0E−02 | n=1	fg=0.33 | bg=0.01
vacuolar membrane GO:0005774	p=5.8E−02 | n=1	fg=0.33 | bg=0.02
Golgi membrane GO:0000139	p=6.5E−02 | n=1	fg=0.33 | bg=0.02
vacuole GO:0005773	p=1.4E−01 | n=1	fg=0.33 | bg=0.05
extracellular region GO:0005576	p=1.9E−01 | n=1	fg=0.33 | bg=0.07
bounding membrane of organelle GO:0098588	p=2.5E−01 | n=1	fg=0.33 | bg=0.09
Golgi apparatus GO:0005794	p=2.9E−01 | n=1	fg=0.33 | bg=0.11
nuclear lumen GO:0031981	p=4.6E−01 | n=2	fg=0.67 | bg=0.27
membrane GO:0016020	p=4.7E−01 | n=2	fg=0.67 | bg=0.48
organelle membrane GO:0031090	p=4.9E−01 | n=1	fg=0.33 | bg=0.20
intracellular membrane−bounded organelle GO:0043231	p=5.1E−01 | n=3	fg=1.00 | bg=0.72
intracellular organelle lumen GO:0070013	p=5.3E−01 | n=2	fg=0.67 | bg=0.31
organelle lumen GO:0043233	p=5.3E−01 | n=2	fg=0.67 | bg=0.31
membrane−enclosed lumen GO:0031974	p=5.3E−01 | n=2	fg=0.67 | bg=0.31
nucleoplasm GO:0005654	p=5.5E−01 | n=1	fg=0.33 | bg=0.23
membrane−bounded organelle GO:0043227	p=5.7E−01 | n=3	fg=1.00 | bg=0.75
plasma membrane GO:0005886	p=5.8E−01 | n=1	fg=0.33 | bg=0.25
intracellular organelle GO:0043229	p=6.0E−01 | n=3	fg=1.00 | bg=0.78
cell periphery GO:0071944	p=6.1E−01 | n=1	fg=0.33 | bg=0.27
endomembrane system GO:0012505	p=6.3E−01 | n=1	fg=0.33 | bg=0.28
organelle GO:0043226	p=6.3E−01 | n=3	fg=1.00 | bg=0.80
nucleus GO:0005634	p=6.7E−01 | n=2	fg=0.67 | bg=0.43
intracellular anatomical structure GO:0005622	p=7.3E−01 | n=3	fg=1.00 | bg=0.86
cellular anatomical entity GO:0110165	p=9.2E−01 | n=3	fg=1.00 | bg=0.96
cytoplasm GO:0005737	p=9.8E−01 | n=1	fg=0.33 | bg=0.73
non−membrane−bounded organelle GO:0043228	p=1.0E+00 | n=1	fg=0.33 | bg=0.29
nucleolus GO:0005730	p=1.0E+00 | n=1	fg=0.33 | bg=0.07
intracellular non−membrane−bounded organ... GO:0043232	p=1.0E+00 | n=1	fg=0.33 | bg=0.29

0 1 2 3 4 5

−log(p)
n=3/15 input genes with annotations

0.0 0.2 0.4 0.6 0.8 1.0

fraction