

gc004

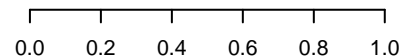
fraction genes in fg and bg

G-alpha	p=4.5E-03	n=4
bZIP_Maf	p=6.0E-03	n=3
Guanylate_cyc	p=6.6E-03	n=6
C2	p=8.8E-03	n=7
BTB_2	p=2.0E-02	n=3
Ca_chan_IQ	p=2.2E-02	n=2
C1_1	p=2.6E-02	n=4
HNOBA	p=2.6E-02	n=4
bZIP_1	p=3.0E-02	n=3
cNMP_binding	p=3.0E-02	n=4
zf-C2H2	p=3.0E-02	n=5
STPPase_N	p=3.3E-02	n=2
AC_N	p=4.1E-02	n=2
Atg8	p=4.1E-02	n=2
FYVE_2	p=4.1E-02	n=2
PDEase_I	p=4.1E-02	n=3
Pkinase	p=4.1E-02	n=11
RGS	p=4.1E-02	n=3
Rlla	p=4.1E-02	n=2
Hydrolase_4	p=6.3E-02	n=2
Acylphosphatase	p=6.6E-02	n=1
AF-4_C	p=6.6E-02	n=1
Aida_C2	p=6.6E-02	n=1
APP_Cu_bd	p=6.6E-02	n=1
APP_E2	p=6.6E-02	n=1
APP_N	p=6.6E-02	n=1
Band_7	p=6.6E-02	n=2
BTB_3	p=6.6E-02	n=1
BTG	p=6.6E-02	n=1
CaMKII_AD	p=6.6E-02	n=1

fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
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fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00

 $-\log_{10}(p)$ 

n=250/311 input genes with annotations



fraction