

gc004

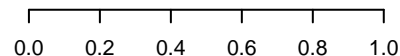
fraction genes in fg and bg

PDEase_I	p=3.5E-04	n=5
G-alpha	p=8.6E-04	n=4
bZIP_Maf	p=1.8E-03	n=3
GAF	p=6.7E-03	n=3
BTB_2	p=9.2E-03	n=3
bZIP_1	p=1.1E-02	n=3
NTP_transf_7	p=1.1E-02	n=2
cNMP_binding	p=1.5E-02	n=4
AC_N	p=3.6E-02	n=2
Atg8	p=3.6E-02	n=2
Guanylate_cyc	p=3.6E-02	n=4
TGFb_propeptide	p=3.6E-02	n=2
C2	p=3.6E-02	n=5
DnaJ_C	p=4.5E-02	n=2
RasGEF_N	p=4.5E-02	n=2
R1la	p=4.5E-02	n=2
Y_phosphatase	p=4.6E-02	n=3
zf-C2H2	p=4.8E-02	n=4
PAS_9	p=5.6E-02	n=2
Aida_C2	p=7.3E-02	n=1
API5	p=7.3E-02	n=1
APP_Cu_bd	p=7.3E-02	n=1
APP_E2	p=7.3E-02	n=1
APP_N	p=7.3E-02	n=1
BAG	p=7.3E-02	n=1
BTB_3	p=7.3E-02	n=1
BTG	p=7.3E-02	n=1
Cast	p=7.3E-02	n=1
CBF_beta	p=7.3E-02	n=1
Cul7	p=7.3E-02	n=1

fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
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fg=0.00	bg=0.00
fg=0.00	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=207/240 input genes with annotations



fraction