

gc017

fraction genes in fg and bg

7tm_1	p=7.9E-05	n=11
7tm_3	p=2.0E-02	n=3
B12D	p=2.0E-02	n=1
c-SKI_SMAD_bind	p=2.0E-02	n=1
GSHPx	p=2.0E-02	n=1
Ion_trans_2	p=2.0E-02	n=1
Peptidase_C15	p=2.0E-02	n=1
VWC	p=2.0E-02	n=1
FAM124	p=2.4E-02	n=1
Ski_Sno	p=2.4E-02	n=1
Globin	p=2.9E-02	n=1
HMA	p=4.3E-02	n=1
VWD	p=4.3E-02	n=1
Pkinase_C	p=5.2E-02	n=1
ANF_receptor	p=5.6E-02	n=2
Hydrolase	p=5.6E-02	n=1
E1-E2_ATPase	p=7.5E-02	n=1
HNOBA	p=7.5E-02	n=1
Forkhead	p=7.9E-02	n=1
NCD3G	p=9.8E-02	n=1
Guanylate_cyc	p=1.0E-01	n=1
Abhydrolase_1	p=1.1E-01	n=1
Homeodomain	p=1.1E-01	n=1
GPS	p=1.2E-01	n=1
Lectin_C	p=1.4E-01	n=1
EF-hand_7	p=1.7E-01	n=1
7tm_2	p=1.9E-01	n=1
RRM_1	p=2.3E-01	n=1
Pkinase	p=4.0E-01	n=1

fg=0.26	bg=0.05
fg=0.07	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
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fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.01
fg=0.02	bg=0.01



-log10(p)

n=29/60 input genes with annotations



fraction