

## gc011a

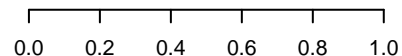
## fraction genes in fg and bg

7tm_1	p=1.6E-03	n=9
LRR_8	p=4.1E-03	n=4
Cys_knot	p=1.2E-02	n=1
DUF21	p=1.2E-02	n=1
Homeodomain	p=1.2E-02	n=2
SIX1_SD	p=1.2E-02	n=1
DAN	p=2.1E-02	n=1
Prominin	p=2.7E-02	n=1
7tm_2	p=6.2E-02	n=2
7tm_3	p=6.2E-02	n=2
ANF_receptor	p=6.2E-02	n=2
Astacin	p=6.2E-02	n=1
CBS	p=6.2E-02	n=1
Laminin_G_3	p=6.2E-02	n=1
LIM	p=6.2E-02	n=1
Roc	p=6.2E-02	n=1
Asp	p=6.2E-02	n=1
HMG_box	p=6.7E-02	n=1
IgGfc_binding	p=9.5E-02	n=1
NCD3G	p=1.0E-01	n=1
GAIN	p=1.4E-01	n=1
COR	p=1.4E-01	n=1
Lectin_C	p=1.7E-01	n=1
GPS	p=2.0E-01	n=1
Death	p=2.6E-01	n=1
TPR_12	p=3.9E-01	n=1
WD40	p=3.9E-01	n=1

fg=0.21	bg=0.04
fg=0.10	bg=0.01
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.05	bg=0.01
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=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.01
fg=0.02	bg=0.01
fg=0.02	bg=0.01

-log<sub>10</sub>(p)

n=27/58 input genes with annotations



fraction