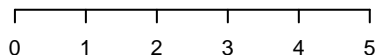


gc006

fraction genes in fg and bg

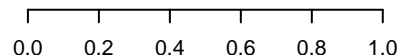
LRR_8	p=1.3E-16	n=17
7tm_1	p=3.9E-11	n=23
Ldl_recept_a	p=3.9E-02	n=2
7tm_3	p=4.9E-02	n=3
Calsequestrin	p=4.9E-02	n=1
CUB	p=4.9E-02	n=2
Vasohibin	p=4.9E-02	n=1
XK-related	p=4.9E-02	n=1
zf-TRAF	p=5.9E-02	n=1
ANF_receptor	p=6.8E-02	n=3
Peptidase_M13	p=7.3E-02	n=1
Peptidase_M13_N	p=7.3E-02	n=1
G-alpha	p=1.0E-01	n=1
LRR_1	p=1.0E-01	n=1
SRCR	p=1.0E-01	n=2
PARP_reg	p=1.1E-01	n=1
SAM_2	p=1.1E-01	n=1
zf-C3HC4_2	p=1.1E-01	n=1
EF-hand_5	p=1.3E-01	n=1
LRR_5	p=1.4E-01	n=1
DnaJ	p=1.8E-01	n=1
Kringle	p=1.8E-01	n=1
NCD3G	p=1.8E-01	n=1
PARP	p=1.8E-01	n=1
SAM_1	p=1.8E-01	n=1
TPR_7	p=1.8E-01	n=1
Homeodomain	p=2.0E-01	n=1
MAM	p=2.0E-01	n=1
TPR_12	p=2.3E-01	n=2
Lectin_C	p=2.3E-01	n=1

fg=0.21	bg=0.01
fg=0.29	bg=0.05
fg=0.03	bg=0.00
fg=0.04	bg=0.01
fg=0.01	bg=0.00
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fg=0.01	bg=0.00
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fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.01	bg=0.00



-log10(p)

n=34/82 input genes with annotations



fraction