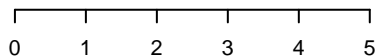


BK_channel_a	p=6.2E-02	n=1
Cbl_N	p=6.2E-02	n=1
Cbl_N2	p=6.2E-02	n=1
Cbl_N3	p=6.2E-02	n=1
CSRNP_N	p=6.2E-02	n=1
CUB	p=6.2E-02	n=2
ETS_PEA3_N	p=6.2E-02	n=1
FEZ	p=6.2E-02	n=1
FSA_C	p=6.2E-02	n=1
HTH_Tnp_Tc5	p=6.2E-02	n=1
Prok-RING_4	p=6.2E-02	n=1
Ric8	p=6.2E-02	n=1
STAS	p=6.2E-02	n=1
Sulfate_transp	p=6.2E-02	n=1
Tubulin	p=6.2E-02	n=2
Tubulin_C	p=6.2E-02	n=2
ARID	p=8.6E-02	n=1
CAP_GLY	p=8.6E-02	n=1
COesterase	p=8.6E-02	n=1
Ets	p=8.6E-02	n=1
F-box	p=8.6E-02	n=1
UPAR_LY6	p=8.6E-02	n=1
WW	p=8.6E-02	n=1
SH2	p=1.2E-01	n=1
SH3_9	p=1.2E-01	n=1
C2	p=1.4E-01	n=2
Peptidase_M13	p=1.4E-01	n=1
Peptidase_M13_N	p=1.4E-01	n=1
PI3_PI4_kinase	p=1.4E-01	n=1
PI-PLC-X	p=1.5E-01	n=1



-log10(p)

n=47/41 input genes with annotations

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=0.04	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=0.04	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=0.04	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



fraction