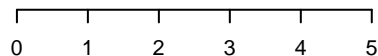


## gc023

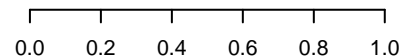
Aph-1	p=4.7E-02	n=1
API5	p=4.7E-02	n=1
ASCH	p=4.7E-02	n=1
C5-epim_C	p=4.7E-02	n=1
CD20	p=4.7E-02	n=2
DMAP_binding	p=4.7E-02	n=1
GDWWSH	p=4.7E-02	n=1
Glyco_hydro_85	p=4.7E-02	n=1
LMF1	p=4.7E-02	n=1
NOA36	p=4.7E-02	n=1
PDEase_I	p=4.7E-02	n=2
PID	p=4.7E-02	n=2
PIF1	p=4.7E-02	n=1
SH2	p=4.7E-02	n=3
STAR_dimer	p=4.7E-02	n=1
TF_AP-2	p=4.7E-02	n=1
TIG_plexin	p=4.7E-02	n=1
zf-C2HC5	p=4.7E-02	n=1
zf-C3HC4_4	p=4.7E-02	n=1
Cobalamin_bind	p=6.1E-02	n=1
DUF4203	p=6.1E-02	n=1
Erf4	p=6.1E-02	n=1
Glypican	p=6.1E-02	n=1
Linker_histone	p=6.1E-02	n=1
PET	p=6.1E-02	n=1
Plexin_cytopl	p=6.1E-02	n=1
SOXp	p=6.1E-02	n=1
TIG_2	p=6.1E-02	n=1
TPR_17	p=6.1E-02	n=1
SAM_1	p=6.5E-02	n=2



-log<sub>10</sub>(p)  
n=107/153 input genes with annotations

## fraction genes in fg and bg

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=0.02	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
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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
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=0.02	bg=0.00



fraction