

BAT2_N	p=9.5E-02	n=1
COMM_domain	p=9.5E-02	n=1
COX5B	p=9.5E-02	n=1
DUF1682	p=9.5E-02	n=1
DUF3337	p=9.5E-02	n=1
DUF4497	p=9.5E-02	n=1
Dynamitin	p=9.5E-02	n=1
Fanconi_C	p=9.5E-02	n=1
FPL	p=9.5E-02	n=1
FragX_IP	p=9.5E-02	n=1
GAF	p=9.5E-02	n=2
GCM	p=9.5E-02	n=1
GGACT	p=9.5E-02	n=1
Glyco_transf_41	p=9.5E-02	n=1
Gryzun-like	p=9.5E-02	n=1
HLH	p=9.5E-02	n=3
ig	p=9.5E-02	n=2
IMD	p=9.5E-02	n=1
Ion_trans_2	p=9.5E-02	n=4
Mak16	p=9.5E-02	n=1
Med11	p=9.5E-02	n=1
Mgm101p	p=9.5E-02	n=1
Mitoc_L55	p=9.5E-02	n=1
PAS	p=9.5E-02	n=2
PAS_11	p=9.5E-02	n=2
PC_rep	p=9.5E-02	n=1
PDEase_I	p=9.5E-02	n=2
PGM_PMM_I	p=9.5E-02	n=1
PGM_PMM_II	p=9.5E-02	n=1
PGM_PMM_III	p=9.5E-02	n=1

fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.02	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.01	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00
fg=0.00	bg=0.00

 $-\log_{10}(p)$

n=191/170 input genes with annotations



fraction