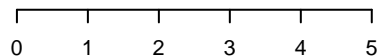


Elav_Nvec_vc1.1_XM_032366211.2

fraction genes in fg and bg

ABC_ATPase	p=8.3E-02	n=1
Acatn	p=8.3E-02	n=1
Apyrase	p=8.3E-02	n=1
ArfGap	p=8.3E-02	n=2
BAT2_N	p=8.3E-02	n=1
C1_2	p=8.3E-02	n=1
C1_4	p=8.3E-02	n=1
CLN3	p=8.3E-02	n=2
Cohesin_load	p=8.3E-02	n=1
Dak1	p=8.3E-02	n=1
Dak2	p=8.3E-02	n=1
DUF1180	p=8.3E-02	n=1
DUF2370	p=8.3E-02	n=1
DUF4611	p=8.3E-02	n=1
FF	p=8.3E-02	n=1
Glyco_hydro_56	p=8.3E-02	n=1
Glyoxalase_4	p=8.3E-02	n=1
GPS2_interact	p=8.3E-02	n=1
HLH	p=8.3E-02	n=3
HOOK	p=8.3E-02	n=1
IRK	p=8.3E-02	n=1
IRK_C	p=8.3E-02	n=1
malic	p=8.3E-02	n=1
Malic_M	p=8.3E-02	n=1
MamL-1	p=8.3E-02	n=1
Methyltr_RsmB-F	p=8.3E-02	n=1
Methyltr_RsmF_N	p=8.3E-02	n=1
Mito_carr	p=8.3E-02	n=3
Mst1_SARAH	p=8.3E-02	n=1
Na_Pi_cotrans	p=8.3E-02	n=1

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=0.01	bg=0.00
fg=0.00	bg=0.00
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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



$-\log_{10}(p)$
n=179/139 input genes with annotations



fraction