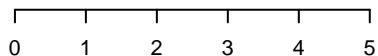


Fox_Nvec_vc1.1_XM_032383717.2

fraction genes in fg and bg

GTP_EFTU_D2	p=2.5E-02	n=5
GTP_EFTU	p=3.0E-02	n=5
2Fe-2S_thioredx	p=1.2E-01	n=1
AA_kinase	p=1.2E-01	n=1
AA_permease_2	p=1.2E-01	n=3
Aa_trans	p=1.2E-01	n=3
AAA	p=1.2E-01	n=5
AHD	p=1.2E-01	n=1
Alg14	p=1.2E-01	n=1
Archease	p=1.2E-01	n=1
ASF1_hist_chap	p=1.2E-01	n=1
Avl9	p=1.2E-01	n=1
AZUL	p=1.2E-01	n=1
B3_4	p=1.2E-01	n=1
B5	p=1.2E-01	n=1
BACK	p=1.2E-01	n=6
BTB	p=1.2E-01	n=6
bZIP_1	p=1.2E-01	n=3
bZIP_2	p=1.2E-01	n=3
CAP-ZIP_m	p=1.2E-01	n=1
CBF_beta	p=1.2E-01	n=1
CBFD_NFYB_HMF	p=1.2E-01	n=3
CFAP298	p=1.2E-01	n=1
CMS1	p=1.2E-01	n=1
CSN5_C	p=1.2E-01	n=1
CTU2	p=1.2E-01	n=1
CUPID	p=1.2E-01	n=1
DNA_gyraseB	p=1.2E-01	n=1
DNA_pol_A	p=1.2E-01	n=1
DNA_primase_Irg	p=1.2E-01	n=1

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



-log10(p)

n=403/379 input genes with annotations



fraction