

Ncol_Nvec_vc1.1_XM_001627423.3

fraction genes in fg and bg

BTB_2	p=4.9E-02	n=9
lon_trans_2	p=4.9E-02	n=9
IP_trans	p=1.1E-01	n=3
40S_SA_C	p=1.7E-01	n=1
AA_permease_C	p=1.7E-01	n=2
ADAM_CR_2	p=1.7E-01	n=1
AF-4	p=1.7E-01	n=1
AF-4_C	p=1.7E-01	n=1
AICARFT_IMPCHas	p=1.7E-01	n=1
Anticodon_1	p=1.7E-01	n=1
AP3B1_C	p=1.7E-01	n=1
APP_amyloid	p=1.7E-01	n=1
APP_Cu_bd	p=1.7E-01	n=1
APP_E2	p=1.7E-01	n=1
APP_N	p=1.7E-01	n=1
ATP_synt_H	p=1.7E-01	n=1
B12D	p=1.7E-01	n=1
BACK	p=1.7E-01	n=7
BTB	p=1.7E-01	n=9
CaM_bdg_C0	p=1.7E-01	n=1
CCDC158	p=1.7E-01	n=1
CDC50	p=1.7E-01	n=1
CDK5_activator	p=1.7E-01	n=1
CDV3	p=1.7E-01	n=1
CEBP_ZZ	p=1.7E-01	n=1
CENP-T_C	p=1.7E-01	n=1
CKAP2_C	p=1.7E-01	n=1
CLU	p=1.7E-01	n=1
CLU_N	p=1.7E-01	n=1
cNMP_binding	p=1.7E-01	n=4

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

 $-\log_{10}(p)$

n=472/509 input genes with annotations



fraction