

ALMS_motif	p=1.4E-01	n=1
Aminotran_1_2	p=1.4E-01	n=2
AOX	p=1.4E-01	n=1
APP_amyloid	p=1.4E-01	n=1
APP_Cu_bd	p=1.4E-01	n=1
APP_E2	p=1.4E-01	n=1
APP_N	p=1.4E-01	n=1
ATG16	p=1.4E-01	n=1
CBM_21	p=1.4E-01	n=2
CCDC154	p=1.4E-01	n=1
CD20	p=1.4E-01	n=2
CLU	p=1.4E-01	n=1
CLU_N	p=1.4E-01	n=1
COMM_domain	p=1.4E-01	n=1
DNA_pol_B	p=1.4E-01	n=1
DNA_pol_B_exo1	p=1.4E-01	n=1
dsrm	p=1.4E-01	n=3
DUF1084	p=1.4E-01	n=1
DUF4200	p=1.4E-01	n=1
DUF4707	p=1.4E-01	n=1
DUF758	p=1.4E-01	n=1
Dynamitin	p=1.4E-01	n=1
ECH_1	p=1.4E-01	n=2
eIF3_p135	p=1.4E-01	n=1
ERG4_ERG24	p=1.4E-01	n=1
FAM117	p=1.4E-01	n=1
Fascin	p=1.4E-01	n=1
FEZ	p=1.4E-01	n=1
FH2	p=1.4E-01	n=2
Formin_GBD_N	p=1.4E-01	n=1

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=0.00	bg=0.00
fg=0.00	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
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



$-\log_{10}(p)$   
n=271/248 input genes with annotations



fraction