

ADP_ribosyl_GH	p=2.4E-01	n=1
BK_channel_a	p=2.4E-01	n=1
C1_1	p=2.4E-01	n=2
CaM_bdg_C0	p=2.4E-01	n=1
CCDC142	p=2.4E-01	n=1
CDK5_activator	p=2.4E-01	n=1
CEBP_ZZ	p=2.4E-01	n=1
CK_II_beta	p=2.4E-01	n=1
CS	p=2.4E-01	n=1
DUF4659	p=2.4E-01	n=1
DUF4745	p=2.4E-01	n=1
DUF758	p=2.4E-01	n=1
EamA	p=2.4E-01	n=1
ELM2	p=2.4E-01	n=2
ETS_PEA3_N	p=2.4E-01	n=1
FERM_M	p=2.4E-01	n=3
GAF_2	p=2.4E-01	n=1
GATA	p=2.4E-01	n=2
Glyco_hydro_2	p=2.4E-01	n=1
Glyco_hydro_2_C	p=2.4E-01	n=1
Glyco_hydro_2_N	p=2.4E-01	n=1
Hairy_orange	p=2.4E-01	n=1
Hist_deacetyl	p=2.4E-01	n=1
HJURP_C	p=2.4E-01	n=1
HLH	p=2.4E-01	n=4
HMG_box	p=2.4E-01	n=2
HSL_N	p=2.4E-01	n=1
HTH_Tnp_Tc5	p=2.4E-01	n=1
Integrin_b_cyt	p=2.4E-01	n=1
Integrin_B_tail	p=2.4E-01	n=1

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



$-\log_{10}(p)$
n=165/159 input genes with annotations



fraction