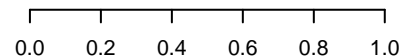


AA_permease_2	p=1.0E-01	n=3
ABC1	p=1.0E-01	n=2
Acyltransferase	p=1.0E-01	n=2
AP3D1	p=1.0E-01	n=1
ATP_synt_E	p=1.0E-01	n=1
BAT2_N	p=1.0E-01	n=1
CAP_N	p=1.0E-01	n=1
CBM_21	p=1.0E-01	n=2
CCDC74_C	p=1.0E-01	n=1
CCSAP	p=1.0E-01	n=1
CKAP2_C	p=1.0E-01	n=1
CoA_trans	p=1.0E-01	n=1
CybS	p=1.0E-01	n=1
Dimer_Tnp_hAT	p=1.0E-01	n=2
DUF2451	p=1.0E-01	n=1
DUF3689	p=1.0E-01	n=1
DUF4371	p=1.0E-01	n=2
DUF4464	p=1.0E-01	n=1
DUF5745	p=1.0E-01	n=1
E3_UbLigase_EDD	p=1.0E-01	n=1
F_actin_cap_B	p=1.0E-01	n=1
FANCI_HD1	p=1.0E-01	n=1
FANCI_HD2	p=1.0E-01	n=1
FANCI_S1	p=1.0E-01	n=1
FANCI_S1-cap	p=1.0E-01	n=1
FANCI_S2	p=1.0E-01	n=1
FANCI_S3	p=1.0E-01	n=1
FANCI_S4	p=1.0E-01	n=1
Filament	p=1.0E-01	n=1
Formyl_trans_C	p=1.0E-01	n=1

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



$-\log_{10}(p)$
n=320/279 input genes with annotations



fraction