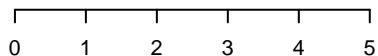


5-nucleotidase	p=9.6E-02	n=1
A_deaminase	p=9.6E-02	n=1
AA_permease_2	p=9.6E-02	n=3
AA_permease_C	p=9.6E-02	n=3
Anoct_dimer	p=9.6E-02	n=2
ARA70	p=9.6E-02	n=1
ArfGap	p=9.6E-02	n=2
B12-binding_2	p=9.6E-02	n=1
Calponin	p=9.6E-02	n=1
Calx-beta	p=9.6E-02	n=2
CH_2	p=9.6E-02	n=2
CLN3	p=9.6E-02	n=2
COMPASS-Shg1	p=9.6E-02	n=1
DAZAP2	p=9.6E-02	n=1
DDE_Tnp_4	p=9.6E-02	n=2
DUF3105	p=9.6E-02	n=1
DUF4502	p=9.6E-02	n=1
DUF4503	p=9.6E-02	n=1
EHN	p=9.6E-02	n=1
eIF-3_zeta	p=9.6E-02	n=1
EPTP	p=9.6E-02	n=1
ETF_alpha	p=9.6E-02	n=1
FACT-Spt16_Nlob	p=9.6E-02	n=1
FAM92	p=9.6E-02	n=1
Forkhead	p=9.6E-02	n=3
Gcd10p	p=9.6E-02	n=1
Headcase	p=9.6E-02	n=1
HECA	p=9.6E-02	n=1
HSNSD	p=9.6E-02	n=1
IER	p=9.6E-02	n=1

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-log<sub>10</sub>(p)  
n=309/289 input genes with annotations



fraction