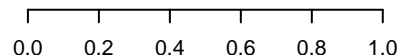


Ax_dynein_light	p=4.9E-02	n=2
Fz	p=6.0E-02	n=3
Frizzled	p=7.2E-02	n=2
Ribosomal_S15	p=7.2E-02	n=2
AA_permease_2	p=7.9E-02	n=2
AA_permease_C	p=7.9E-02	n=2
ALG11_N	p=7.9E-02	n=1
Aminotran_5	p=7.9E-02	n=2
BNIP3	p=7.9E-02	n=1
CEBP_ZZ	p=7.9E-02	n=1
CHAT	p=7.9E-02	n=2
COLFI	p=7.9E-02	n=1
DIM1	p=7.9E-02	n=1
DUF1325	p=7.9E-02	n=1
DUF3689	p=7.9E-02	n=1
ETC_C1_NDUFA4	p=7.9E-02	n=1
FAM117	p=7.9E-02	n=1
GCV_H	p=7.9E-02	n=1
HS1_rep	p=7.9E-02	n=1
I-set	p=7.9E-02	n=4
Ins145_P3_rec	p=7.9E-02	n=1
Lipin_mid	p=7.9E-02	n=1
Lipin_N	p=7.9E-02	n=1
LNS2	p=7.9E-02	n=1
Med13_C	p=7.9E-02	n=1
MID_MedPIWI	p=7.9E-02	n=1
PIG-X	p=7.9E-02	n=1
RanGAP1_C	p=7.9E-02	n=1
Rho_Binding	p=7.9E-02	n=1
RIH_assoc	p=7.9E-02	n=1

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-log<sub>10</sub>(p)

n=176/164 input genes with annotations



fraction