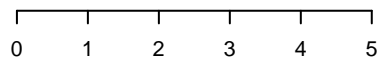


Elav_Nvec_vc1.1_XM_001630131.3

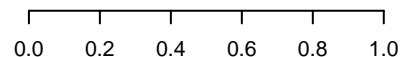
fraction genes in fg and bg

BtpA	p=7.2E-02	n=1
CaM_bdg_C0	p=7.2E-02	n=1
CKAP2_C	p=7.2E-02	n=1
Complex1_51K	p=7.2E-02	n=1
DIM1	p=7.2E-02	n=1
DTC	p=7.2E-02	n=1
DUF1682	p=7.2E-02	n=1
DUF3591	p=7.2E-02	n=1
eIF-3_zeta	p=7.2E-02	n=1
ETC_C1_NDUFA4	p=7.2E-02	n=1
FAM117	p=7.2E-02	n=1
Fz	p=7.2E-02	n=2
HD_3	p=7.2E-02	n=1
Kringle	p=7.2E-02	n=2
Lipin_mid	p=7.2E-02	n=1
Lipin_N	p=7.2E-02	n=1
LNS2	p=7.2E-02	n=1
Mago_nashi	p=7.2E-02	n=1
Med23	p=7.2E-02	n=1
Meiosis_expr	p=7.2E-02	n=1
Myotub-related	p=7.2E-02	n=2
NADH_4Fe-4S	p=7.2E-02	n=1
Nucleoporin_FG2	p=7.2E-02	n=1
Nup153	p=7.2E-02	n=1
PALP	p=7.2E-02	n=2
PBC	p=7.2E-02	n=1
Peptidase_C98	p=7.2E-02	n=1
Pirin	p=7.2E-02	n=1
Pirin_C	p=7.2E-02	n=1
RanGAP1_C	p=7.2E-02	n=1

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



$-\log_{10}(p)$
n=192/171 input genes with annotations



fraction