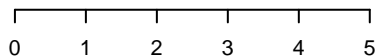


## Fox\_Nvec\_vc1.1\_XM\_032366790.2

## fraction genes in fg and bg

B12D	p=4.8E-02	n=1
BCL_N	p=4.8E-02	n=1
CDC50	p=4.8E-02	n=1
Cript	p=4.8E-02	n=1
DUF4200	p=4.8E-02	n=1
DUF4457	p=4.8E-02	n=1
DUF92	p=4.8E-02	n=1
EF-hand_8	p=4.8E-02	n=2
FAM219A	p=4.8E-02	n=1
GLTSCR1	p=4.8E-02	n=1
Hid1	p=4.8E-02	n=1
Hyd_WA	p=4.8E-02	n=1
KLRAQ	p=4.8E-02	n=1
Mg_trans_NIPA	p=4.8E-02	n=1
Na_Pi_cotrans	p=4.8E-02	n=1
NAGidase	p=4.8E-02	n=1
P66_CC	p=4.8E-02	n=1
PAW	p=4.8E-02	n=1
PDZ	p=4.8E-02	n=4
PDZ_5	p=4.8E-02	n=1
Perilipin	p=4.8E-02	n=1
PH_9	p=4.8E-02	n=1
RFX_DNA_binding	p=4.8E-02	n=2
Rlla	p=4.8E-02	n=2
TMEM189_B_dmain	p=4.8E-02	n=1
TMIE	p=4.8E-02	n=1
TTKRSYEDQ	p=4.8E-02	n=1
Pkinase_Tyr	p=5.6E-02	n=3
ALIX_LYPXL_bnd	p=6.1E-02	n=1
cNMP_binding	p=6.1E-02	n=2



-log<sub>10</sub>(p)  
n=101/88 input genes with annotations

fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
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fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.01
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.00
fg=0.02	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.01	bg=0.00
fg=0.03	bg=0.00
fg=0.01	bg=0.00
fg=0.02	bg=0.00



fraction