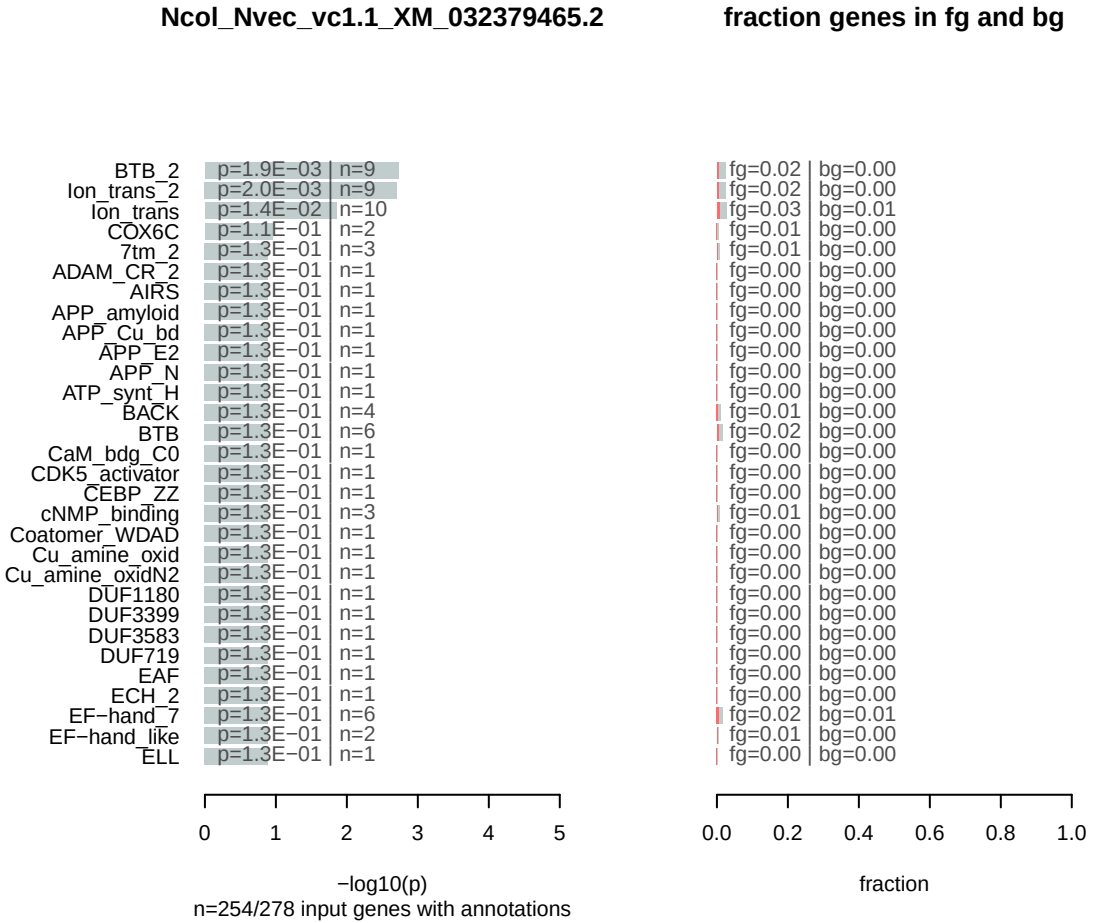
NcoI_Nvec_vc1.1_XM_032379465.2
fraction genes in fg and bg
BTB_2 p=1.9E−03 n=9 fg=0.02 bg=0.00
Ion_trans_2 p=2.0E−03 n=9 fg=0.02 bg=0.00
Ion_trans p=1.4E−02 n=10 fg=0.03 bg=0.01
COX6C p=1.1E−01 n=2 fg=0.01 bg=0.00
7tm_2 p=1.3E−01 n=3 fg=0.01 bg=0.00
ADAM_CR_2 p=1.3E−01 n=1 fg=0.00 bg=0.00
AIRS p=1.3E−01 n=1 fg=0.00 bg=0.00
APP_amyloid p=1.3E−01 n=1 fg=0.00 bg=0.00
APP_Cu_bd p=1.3E−01 n=1 fg=0.00 bg=0.00
APP_E2 p=1.3E−01 n=1 fg=0.00 bg=0.00
APP_N p=1.3E−01 n=1 fg=0.00 bg=0.00
ATP_synt_H p=1.3E−01 n=1 fg=0.00 bg=0.00
BACK p=1.3E−01 n=4 fg=0.01 bg=0.00
BTB p=1.3E−01 n=6 fg=0.02 bg=0.00
CaM_bdg_C0 p=1.3E−01 n=1 fg=0.00 bg=0.00
CDK5_activator p=1.3E−01 n=1 fg=0.00 bg=0.00
CEBP_ZZ p=1.3E−01 n=1 fg=0.00 bg=0.00
cNMP_binding p=1.3E−01 n=3 fg=0.01 bg=0.00
Coatomer_WDAD p=1.3E−01 n=1 fg=0.00 bg=0.00
Cu_amine_oxid p=1.3E−01 n=1 fg=0.00 bg=0.00
Cu_amine_oxidN2 p=1.3E−01 n=1 fg=0.00 bg=0.00
DUF1180 p=1.3E−01 n=1 fg=0.00 bg=0.00
DUF3399 p=1.3E−01 n=1 fg=0.00 bg=0.00
DUF3583 p=1.3E−01 n=1 fg=0.00 bg=0.00
DUF719 p=1.3E−01 n=1 fg=0.00 bg=0.00
EAF p=1.3E−01 n=1 fg=0.00 bg=0.00
ECH_2 p=1.3E−01 n=1 fg=0.00 bg=0.00
EF−hand_7 p=1.3E−01 n=6 fg=0.02 bg=0.01
EF−hand_like p=1.3E−01 n=2 fg=0.01 bg=0.00
ELL p=1.3E−01 n=1 fg=0.00 bg=0.00
0 1 2 3 4 5
−log10(p)
0.0 0.2 0.4 0.6 0.8 1.0
fraction
n=254/278 input genes with annotations