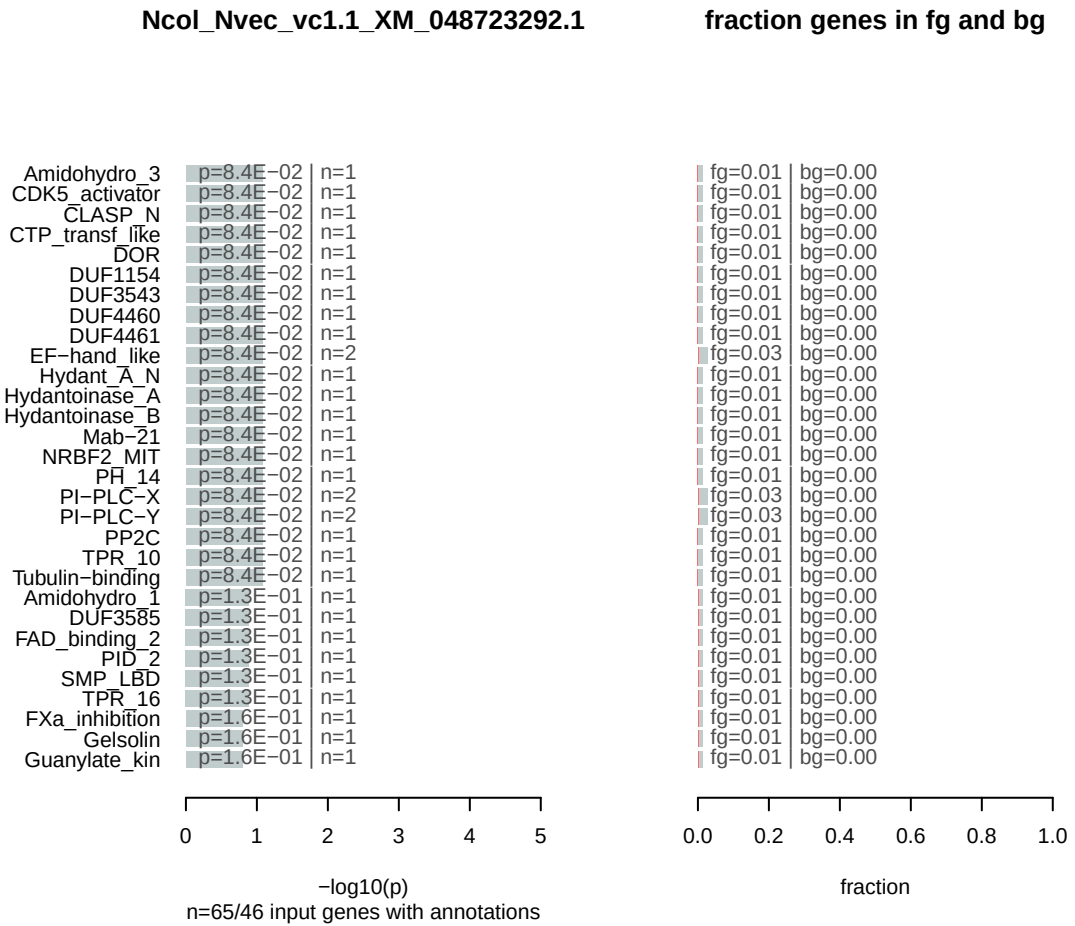
Ncol_Nvec_vc1.1_XM_048723292.1
fraction genes in fg and bg
Amidohydro_3 p=8.4E−02 n=1 fg=0.01 bg=0.00
CDK5_activator p=8.4E−02 n=1 fg=0.01 bg=0.00
CLASP_N p=8.4E−02 n=1 fg=0.01 bg=0.00
CTP_transf_like p=8.4E−02 n=1 fg=0.01 bg=0.00
DOR p=8.4E−02 n=1 fg=0.01 bg=0.00
DUF1154 p=8.4E−02 n=1 fg=0.01 bg=0.00
DUF3543 p=8.4E−02 n=1 fg=0.01 bg=0.00
DUF4460 p=8.4E−02 n=1 fg=0.01 bg=0.00
DUF4461 p=8.4E−02 n=1 fg=0.01 bg=0.00
EF−hand_like p=8.4E−02 n=2 fg=0.03 bg=0.00
Hydant_A_N p=8.4E−02 n=1 fg=0.01 bg=0.00
Hydantoinase_A p=8.4E−02 n=1 fg=0.01 bg=0.00
Hydantoinase_B p=8.4E−02 n=1 fg=0.01 bg=0.00
Mab−21 p=8.4E−02 n=1 fg=0.01 bg=0.00
NRBF2_MIT p=8.4E−02 n=1 fg=0.01 bg=0.00
PH_14 p=8.4E−02 n=1 fg=0.01 bg=0.00
PI−PLC−X p=8.4E−02 n=2 fg=0.03 bg=0.00
PI−PLC−Y p=8.4E−02 n=2 fg=0.03 bg=0.00
PP2C p=8.4E−02 n=1 fg=0.01 bg=0.00
TPR_10 p=8.4E−02 n=1 fg=0.01 bg=0.00
Tubulin−binding p=8.4E−02 n=1 fg=0.01 bg=0.00
Amidohydro_1 p=1.3E−01 n=1 fg=0.01 bg=0.00
DUF3585 p=1.3E−01 n=1 fg=0.01 bg=0.00
FAD_binding_2 p=1.3E−01 n=1 fg=0.01 bg=0.00
PID_2 p=1.3E−01 n=1 fg=0.01 bg=0.00
SMP_LBD p=1.3E−01 n=1 fg=0.01 bg=0.00
TPR_16 p=1.3E−01 n=1 fg=0.01 bg=0.00
FXa_inhibition p=1.6E−01 n=1 fg=0.01 bg=0.00
Gelsolin p=1.6E−01 n=1 fg=0.01 bg=0.00
Guanylate_kin p=1.6E−01 n=1 fg=0.01 bg=0.00
0 1 2 3 4 5
−log10(p)
n=65/46 input genes with annotations
0.0 0.2 0.4 0.6 0.8 1.0
fraction