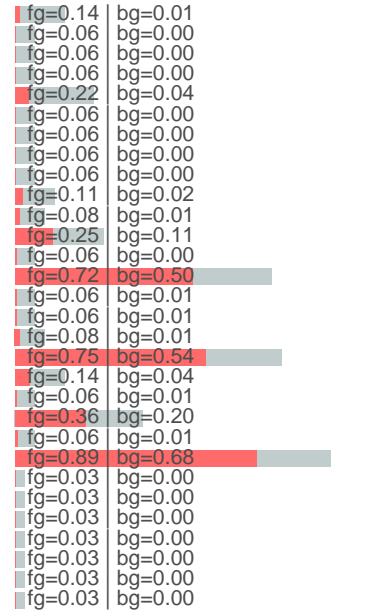
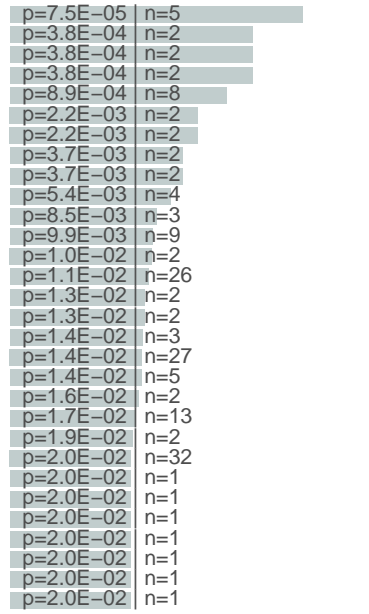


GO:BP  
Ncol\_Nvec\_vc1.1\_XM\_032373099.2

fraction genes in fg and expected value

potassium ion transmembrane transport	GO:0071805
granzyme-mediated apoptotic signaling pa...	GO:0008626
aggregation involved in sorocarp develop...	GO:0031152
aggregation of unicellular organisms	GO:0098630
regulation of membrane potential	GO:0042391
adherens junction maintenance	GO:0034334
glutamate receptor clustering	GO:0097688
regulation of protein homodimerization a...	GO:0043496
G protein-coupled receptor internalizati...	GO:0002031
cellular response to metal ion	GO:0071248
regulation of neurotransmitter secretion	GO:0046928
chemical homeostasis	GO:0048878
positive regulation of membrane potentia...	GO:0045838
anatomical structure development	GO:0048856
response to magnesium ion	GO:0032026
mitochondrial fusion	GO:0008053
receptor metabolic process	GO:0043112
developmental process	GO:0032502
divalent inorganic cation homeostasis	GO:0072507
magnesium ion homeostasis	GO:0010960
intracellular signal transduction	GO:0035556
autophagic cell death	GO:0048102
regulation of biological process	GO:0050789
histone H4-K20 dimethylation	GO:0034772
microspike assembly	GO:0030035
regulation of dauer entry	GO:1905909
dibasic protein processing	GO:0090472
smooth muscle cell-matrix adhesion	GO:0061302
sex determination, establishment of X:A ...	GO:0007540
keratinization	GO:0031424



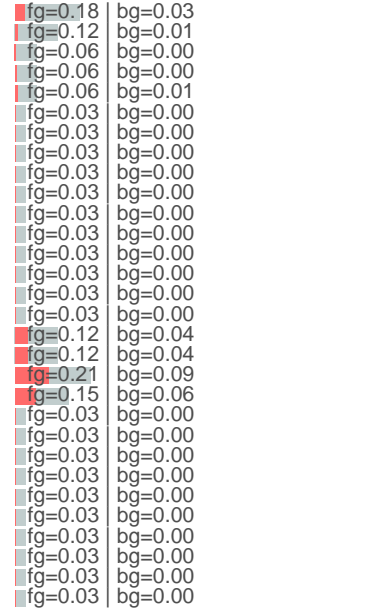
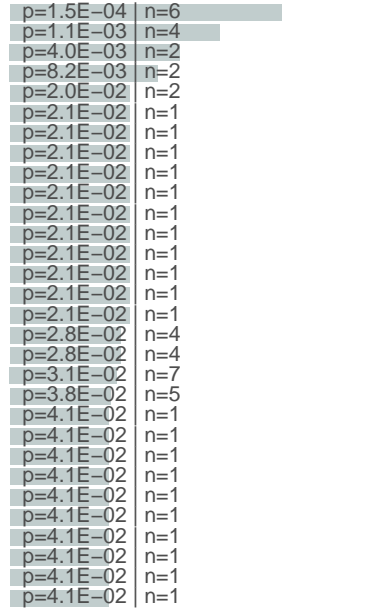
-log(p)  
n=36/175 input genes with annotations

fraction

GO:MF  
Ncol\_Nvec\_vc1.1\_XM\_032373099.2

fraction genes in fg and expected value

ion gated channel activity	GO:0022839
voltage-gated potassium channel activity	GO:0005249
solute:sodium symporter activity	GO:0015370
outward rectifier potassium channel acti...	GO:0015271
potassium channel regulator activity	GO:0015459
NEDD8 conjugating enzyme activity	GO:0061654
phosphate ion binding	GO:0042301
acid sphingomyelin phosphodiesterase act...	GO:0061750
nerve growth factor binding	GO:0048406
nucleoside transmembrane transporter act...	GO:0005337
sodium:phosphate symporter activity	GO:0005436
open rectifier potassium channel activit...	GO:0005252
S100 protein binding	GO:0044548
phorbol ester receptor activity	GO:0001565
neurotrophin binding	GO:0043121
intracellular sodium activated potassium...	GO:0005228
ubiquitin-like protein ligase activity	GO:0061659
ubiquitin protein ligase activity	GO:0061630
protein domain specific binding	GO:0019904
protein heterodimerization activity	GO:0046982
serine-type endopeptidase inhibitor acti...	GO:0004867
histone methyltransferase activity (H4-K...	GO:0042799
phosphatidic acid transfer activity	GO:1990050
phosphate ion transmembrane transporter ...	GO:0015114
platelet-activating factor acetyltransfe...	GO:0047179
caspase binding	GO:0089720
BH3 domain binding	GO:0051434
sphingomyelin phosphodiesterase activity	GO:0004767
high voltage-gated calcium channel activ...	GO:0008331
low voltage-gated calcium channel activi...	GO:0008332



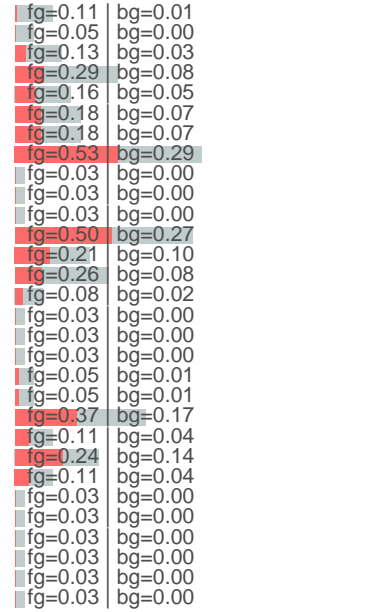
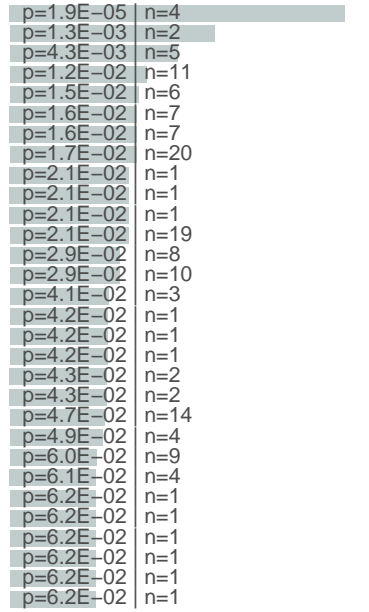
-log(p)  
n=33/175 input genes with annotations

fraction

GO:CC  
Ncol\_Nvec\_vc1.1\_XM\_032373099.2

fraction genes in fg and expected value

voltage-gated potassium channel complex	GO:0008076
lamellar body	GO:0042599
membrane raft	GO:0045121
intrinsic component of plasma membrane	GO:0031226
presynapse	GO:0098793
dendritic tree	GO:0097447
dendrite	GO:0030425
cell periphery	GO:0071944
phagolysosome membrane	GO:0061474
phagolysosome	GO:0032010
alveolar lamellar body	GO:0097208
plasma membrane	GO:0005886
synapse	GO:0045202
integral component of plasma membrane	GO:0005887
actin-based cell projection	GO:0098858
Lewy body	GO:0097413
trans-Golgi network transport vesicle me...	GO:0012510
growth cone filopodium	GO:1990812
main axon	GO:0044304
filopodium	GO:0030175
intrinsic component of membrane	GO:0031224
cell surface	GO:0009986
cell junction	GO:0030054
apical plasma membrane	GO:0016324
proximal dendrite	GO:1990635
muscle cell projection	GO:0036194
muscle cell projection membrane	GO:0036195
Bcl-2 family protein complex	GO:0097136
growth cone lamellipodium	GO:1990761
kinetochore microtubule	GO:0005828



-log(p)  
n=38/175 input genes with annotations

fraction