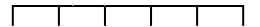
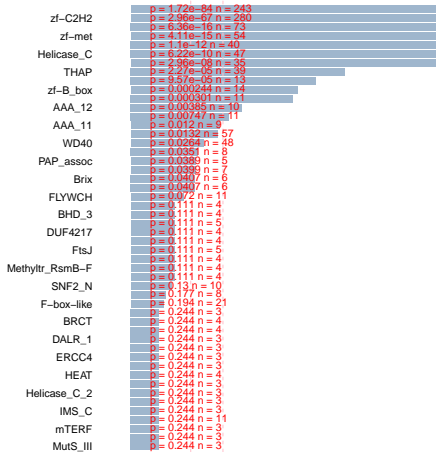


# ALL.RUN-SRO\_difneg domain



0 -1 -2 -3 -4 -5

log(p)

n = 2661 genes | p adjust BH TRUE