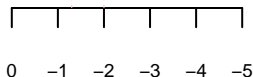
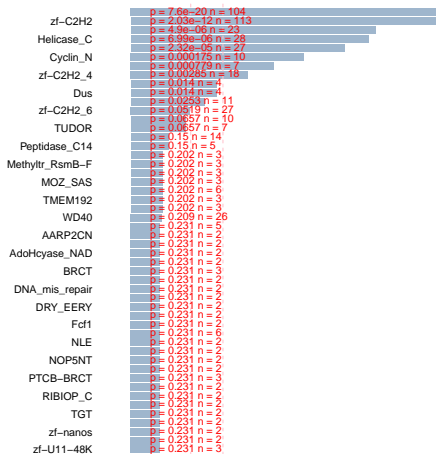


ALL.RUN-RFE_difneg domain



log(p)

n = 1480 genes | p adjust BH TRUE