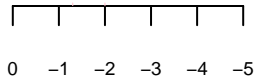
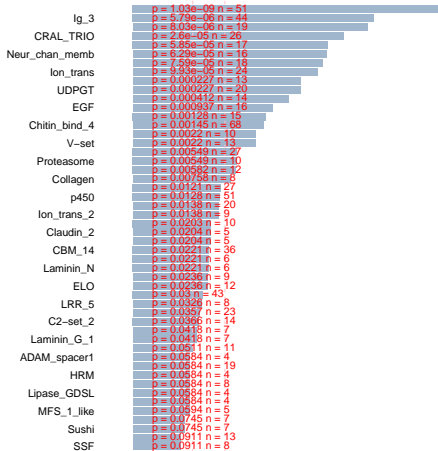


# ALL.RUN-SRO\_difpos domain



log(p)

n = 3077 genes | p adjust BH TRUE