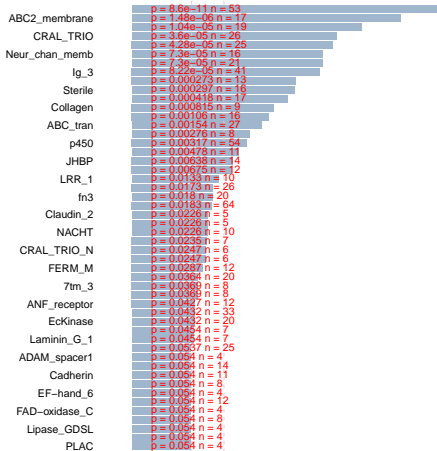


ALL.RUN-SNO_difpos domain



log(p)

n = 3010 genes | p adjust BH TRUE