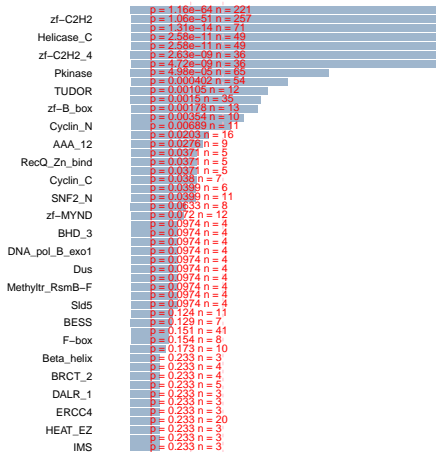


ALL.RUN-SNO_difneg domain



log(p)

n = 2666 genes | p adjust BH TRUE