IncRNA group = allLncRNA ::: data cols = bothPullDowns ( 49 / 3716 ) = (func/total IncRNA) ::: biotype = lincProcTrans PageRank, range = median +/- 2 ds 1000 -750 -500 -250 factor(label) 0 0 30 20 -10 -

0

rank

0 -