IncRNA group = allLncRNA ::: data cols = bothPullDowns (91 / 6927) = (func/total IncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds 1250 1000 -750 -500 250 factor(label) 0 0 50 -40 30 20 10 0

0.3

logRank

0.6

0.0

count

-0.3