IncRNA group = allLncRNA ::: data cols = bothPullDowns (52 / 4503) = (func/total lncRNA) ::: biotype = remove_antisense logRank, range = median +/- 2 ds 600 -400 200 factor(label) 0 count 0 30 20 10 0

0.3

logRank

0.6

0.9

0.0