IncRNA group = allLncRNA ::: data cols = bothPullDowns (92 / 7622) = (func/total IncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds 1000 -500 factor(label) 0 0 50 -40 30 -20 10 -0 0.3 -0.30.0 0.6 logRank

count