IncRNA group = allLncRNA ::: data cols = bothPullDowns $(88/6746) = (func/total IncRNA) ::: biotype = all_biotypes$ logRank, range = median +/- 2 ds 750 500 -250 · factor(label) 0 0 1 40 30 20 10 0 0.0 0.3 0.6 0.9 logRank

count