IncRNA group = allLncRNA ::: data cols = bothPullDowns (87 / 6104) = (func/total IncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds 0 800 -600 400 200 factor(label) 0 0 1 40 30 20 10 0 0.0 0.3 0.6 0.9

logRank

count