IncRNA group = allLncRNA ::: data cols = lpa (87 / 5951) = (func/total lncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds 1000 750 500 250 factor(label) 0 0 40 30 20 10 0 0.3 0.0 0.6 0.9 logRank

count