IncRNA group = allLncRNA ::: data cols = lpa (91 / 7106) = (func/total lncRNA) ::: biotype = all\_biotypes logRank, range = median +/- 2 ds 1200 800 400 factor(label) 0 0 40 30 20 10 0 0.3 0.0 0.6 0.9 logRank