lncRNA group = IDRlessthan0_2 ::: data cols = lpa (82 / 5045) = (func/total lncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds 0 500 -400 -300 -200 -100 factor(label) 0 0 1 30 20 10 -0

0.50

logRank

0.75

0.25

0.00

count