lncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (47 / 2369) = (func/total lncRNA) ::: biotype = lincProcTrans logRank, range = median +/- 2 ds 150 -100 -50 factor(label) 0 0 1 20 15 -10 -5 · 0 -0.25 0.50 0.00 0.75 logRank

count