IncRNA group = allLncRNA ::: data cols = bothPullDowns (17/397) = (func/total lncRNA) ::: biotype = processed_transcript logRank, range = median +/- 2 ds 100 -75 -50 -25 · factor(label) 0 0 1 10 -5 -0 -0.25-0.500.00 0.25 0.50 0.75

logRank