IncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (17/331) = (func/total lncRNA) ::: biotype = processed_transcript logRank, range = median +/- 2 ds 30 -20 -10 factor(label) 0 count 0 1 7.5 5.0 2.5

0.3

logRank

0.6

0.9

0.0

0.0