IncRNA group = IDRlessthan0\_1 ::: data cols = bothPullDowns (42 / 1363) = (func/total lncRNA) ::: biotype = lincProcTrans logRank, range = median +/- 2 ds 0 30 -20 -10 factor(label) conut 2.0 0 1 1.5 -1.0 -0.5 0.0 -0.4 0.6 8.0 1.0 0.2 logRank