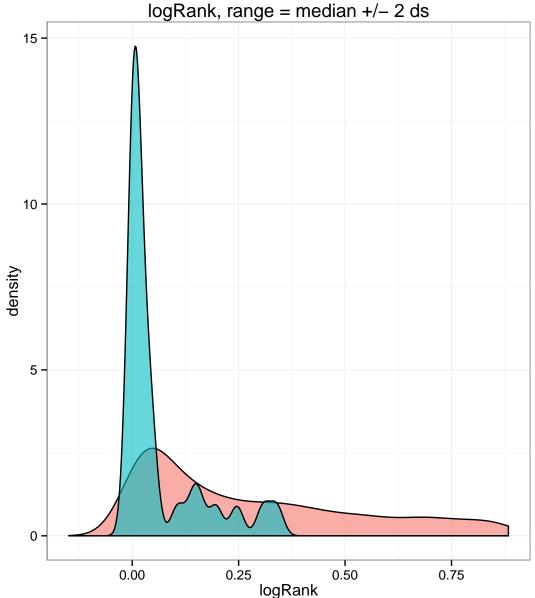
IncRNA group = allLncRNA ::: data cols = bothPullDowns (30 / 2851) = (func/total IncRNA) ::: biotype = lincRNA logRank, range = median +/- 2 ds



factor(label)