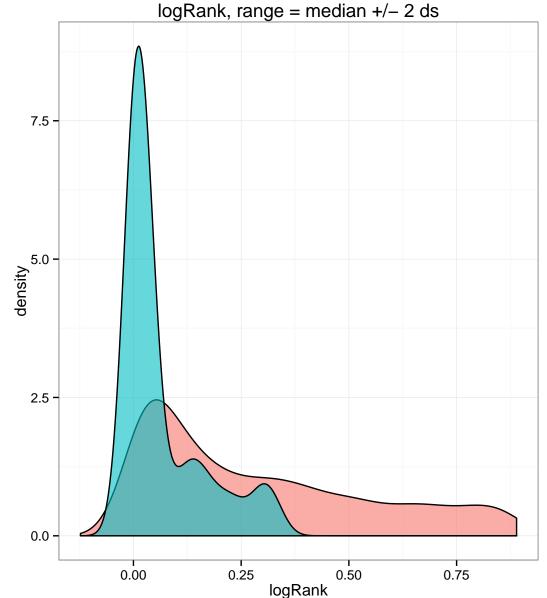
IncRNA group = allLncRNA ::: data cols = bothPullDowns (27 / 2546) = (func/total IncRNA) ::: biotype = lincRNA logRank, range = median +/- 2 ds



factor(label)