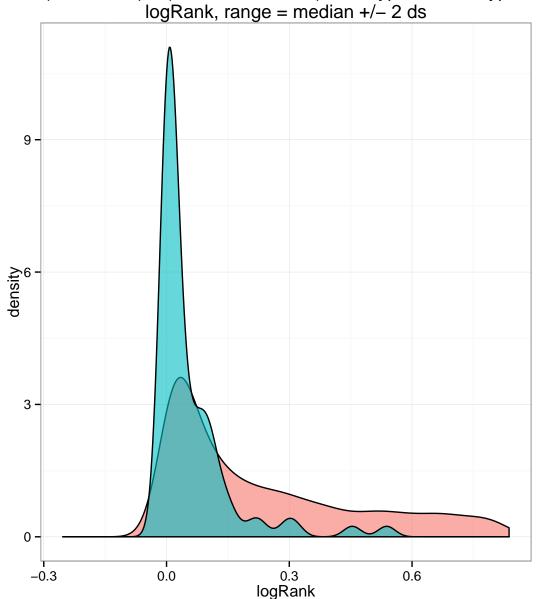
IncRNA group = allLncRNA ::: data cols = bothPullDowns (91 / 6927) = (func/total IncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds



factor(label)