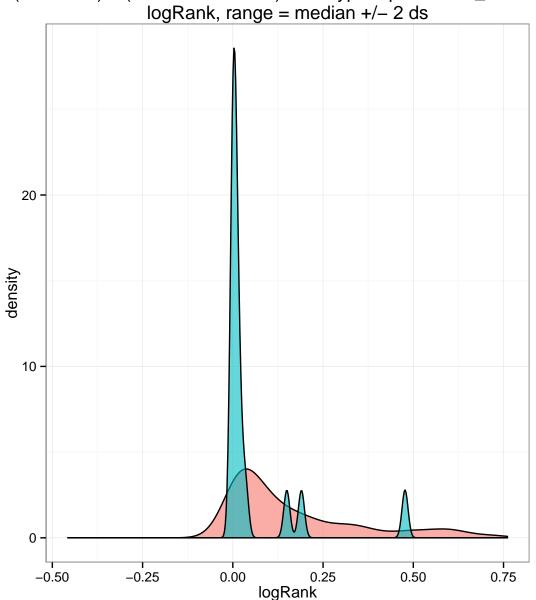
IncRNA group = allLncRNA ::: data cols = bothPullDowns (17 / 397) = (func/total IncRNA) ::: biotype = processed_transcript logRank, range = median +/- 2 ds



factor(label)