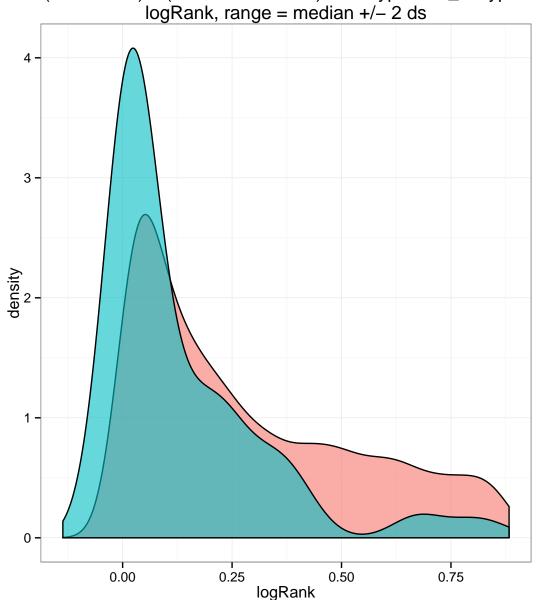
IncRNA group = allLncRNA ::: data cols = Inpa (86 / 5711) = (func/total IncRNA) ::: biotype = all_biotypes logRank, range = median +/- 2 ds



factor(label)