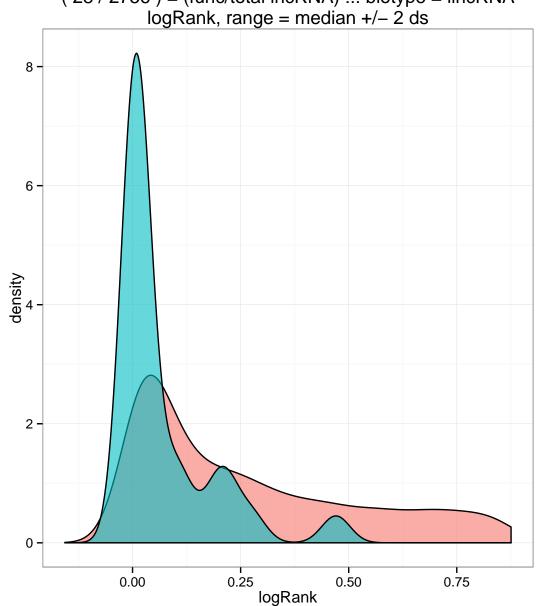
IncRNA group = allLncRNA ::: data cols = Ipa (28 / 2756) = (func/total IncRNA) ::: biotype = lincRNA logRank, range = median +/- 2 ds



factor(label)