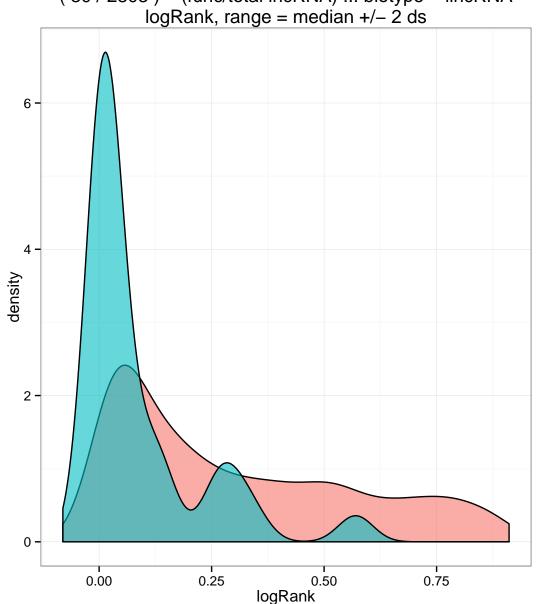
IncRNA group = allLncRNA ::: data cols = Inpa (30 / 2803) = (func/total lncRNA) ::: biotype = lincRNA logRank, range = median +/- 2 ds



factor(label)