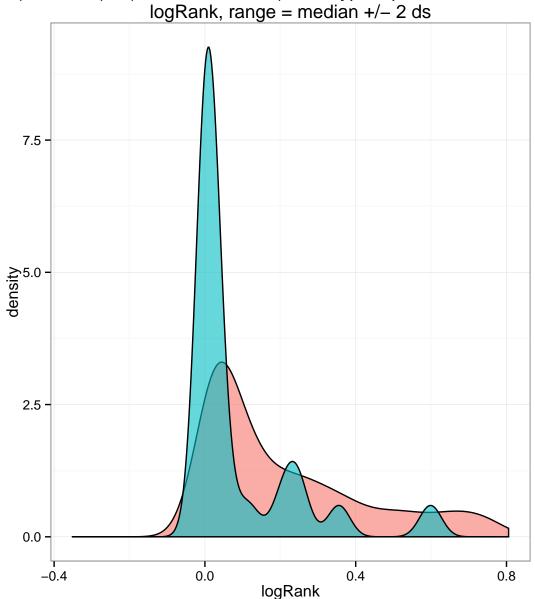
IncRNA group = allLncRNA ::: data cols = Ipa (23 / 958) = (func/total IncRNA) ::: biotype = processed_transcript logRank, range = median +/- 2 ds



factor(label)