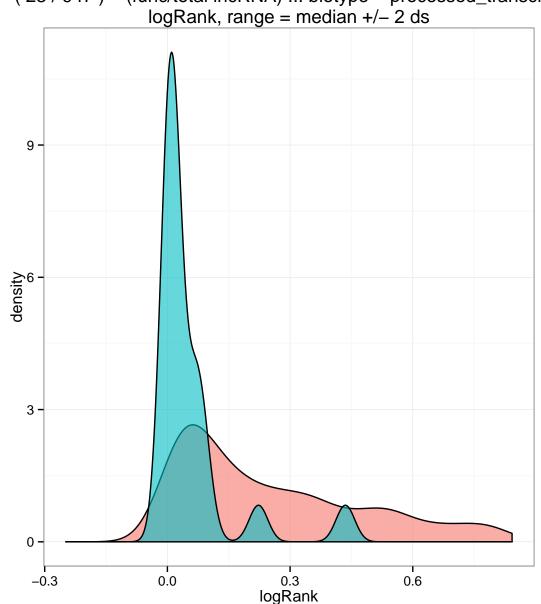
IncRNA group = allLncRNA ::: data cols = Inpa (23 / 947) = (func/total IncRNA) ::: biotype = processed_transcript logRank_range = median +/- 2 ds



factor(label)