lncRNA group = allLncRNA ::: data cols = lpa
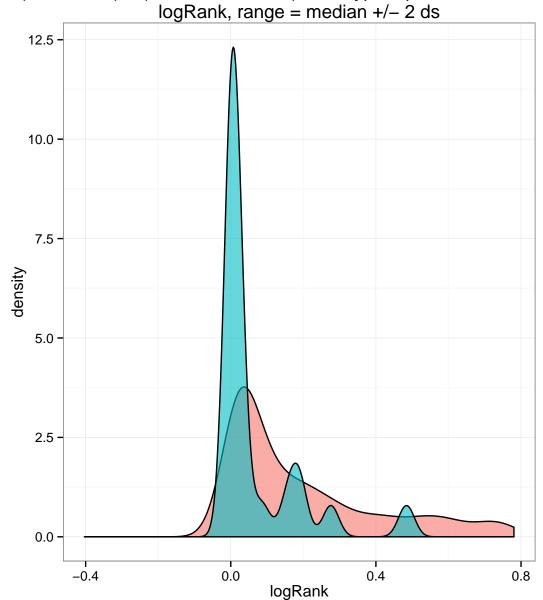( 24 / 1002 ) = (func/total lncRNA) ::: biotype = processed_transcript
logRank, range = median +/− 2 ds