lncRNA group = allLncRNA ::: data cols = lnpa
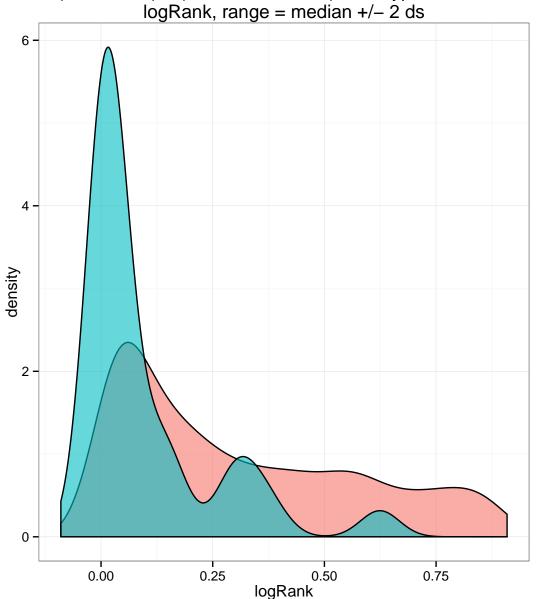(30 / 2632) = (func/total lncRNA) ::: biotype = lincRNA
logRank, range = median +/− 2 ds