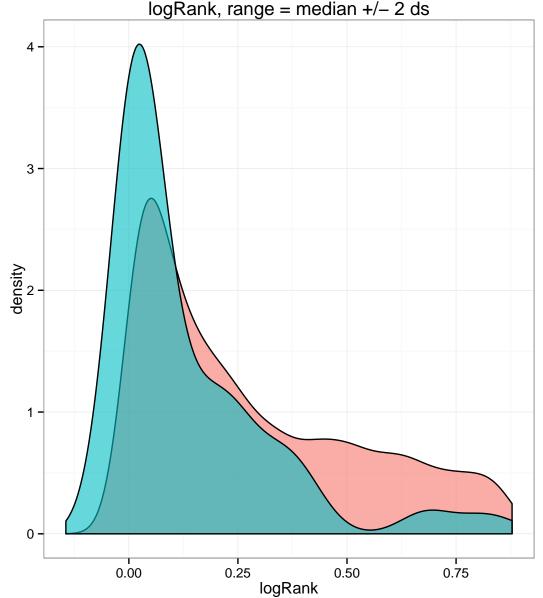lncRNA group = allLncRNA ::: data cols = lnpa
(87 / 6320) = (func/total lncRNA) ::: biotype = all_biotypes
logRank, range = median +/− 2 ds