lncRNA group = allLncRNA ::: data cols = lnpa
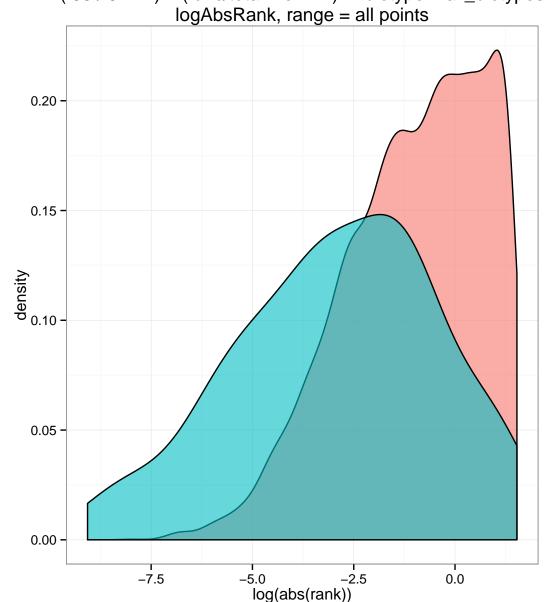(86 / 5711) = (func/total lncRNA) ::: biotype = all_biotypes
logAbsRank, range = all points