lncRNA group = allLncRNA ::: data cols = lpa
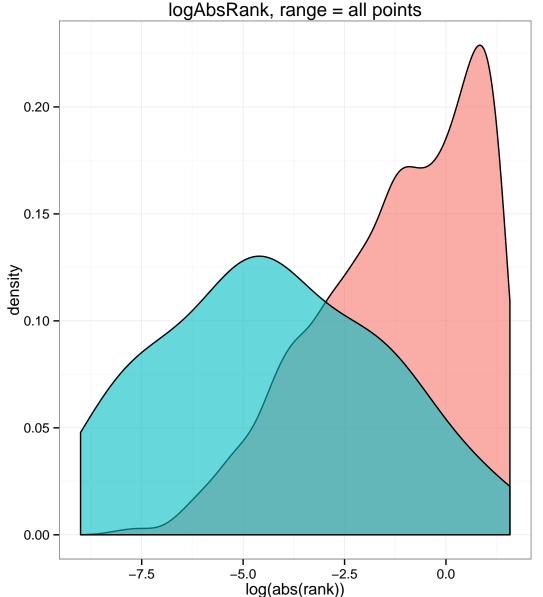(32 / 3068) = (func/total lncRNA) ::: biotype = lincRNA
logAbsRank, range = all points