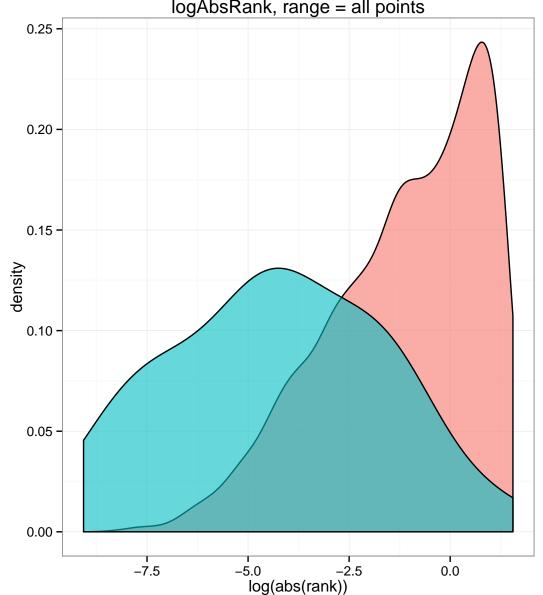
IncRNA group = allLncRNA ::: data cols = lpa
(28 / 2756) = (func/total IncRNA) ::: biotype = lincRNA
logAbsRank, range = all points



factor(label)