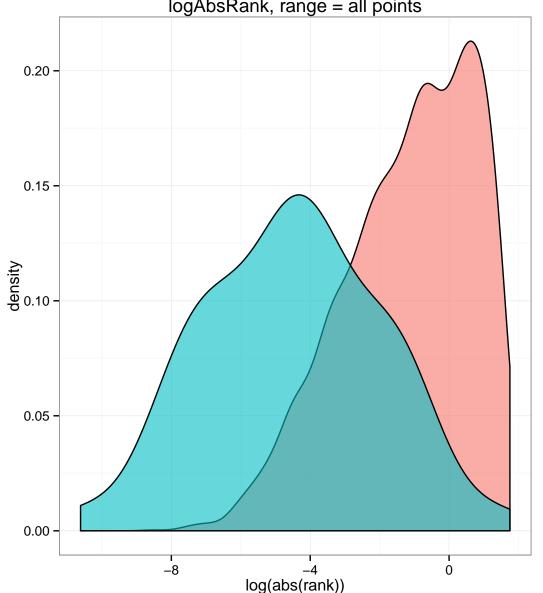
IncRNA group = allLncRNA ::: data cols = bothPullDowns (47 / 3223) = (func/total IncRNA) ::: biotype = lincProcTrans logAbsRank, range = all points



factor(label)