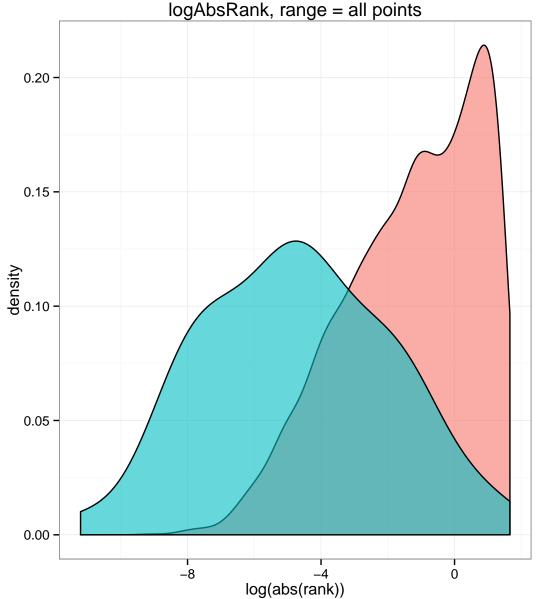
IncRNA group = allLncRNA ::: data cols = Ipa (49 / 3453) = (func/total IncRNA) ::: biotype = lincProcTrans logAbsRank, range = all points



factor(label)