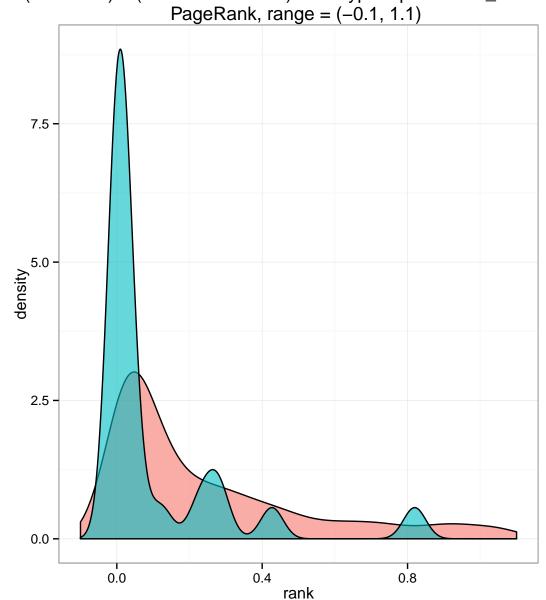
IncRNA group = allLncRNA ::: data cols = Ipa ( 23 / 958 ) = (func/total IncRNA) ::: biotype = processed\_transcript PageRank, range = (-0.1, 1.1)



factor(label)