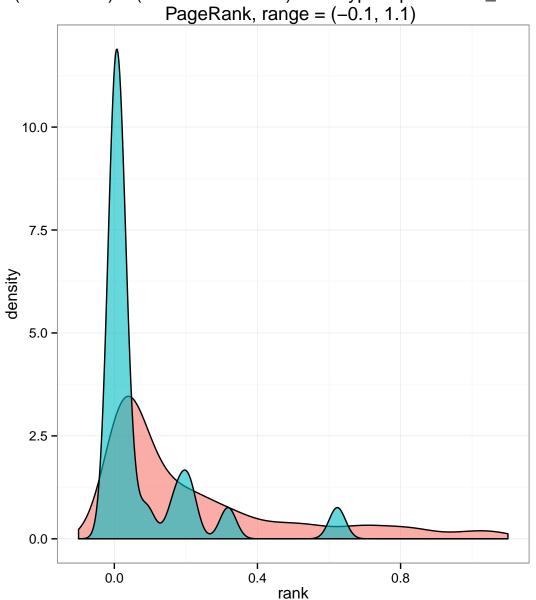
IncRNA group = allLncRNA ::: data cols = lpa (24 / 1002) = (func/total lncRNA) ::: biotype = processed_transcript PageRank_range = (-0.1, 1.1)



factor(label)