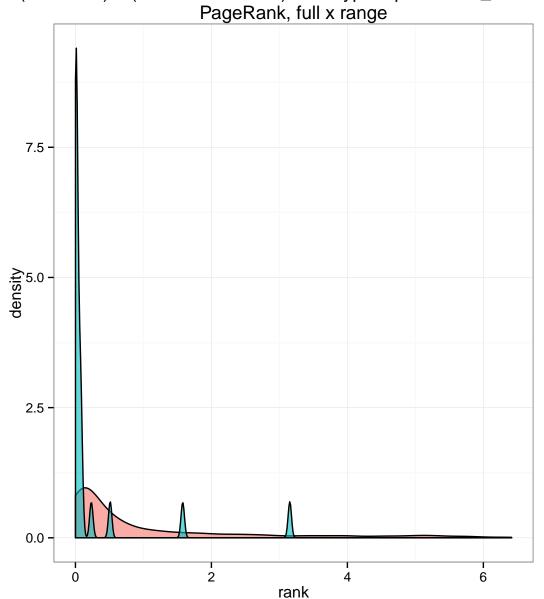
IncRNA group = allLncRNA ::: data cols = Inpa (23 / 962) = (func/total IncRNA) ::: biotype = processed_transcript PageRank, full x range



factor(label)