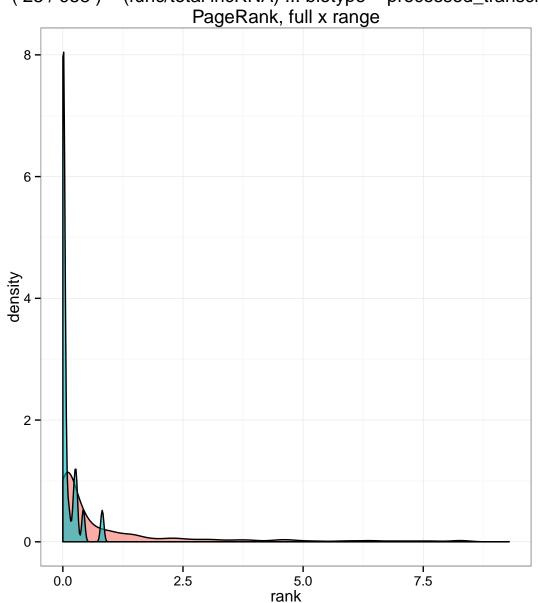lncRNA group = allLncRNA ::: data cols = lpa
(23 / 958) = (func/total lncRNA) ::: biotype = processed_transcript
PageRank, full x range