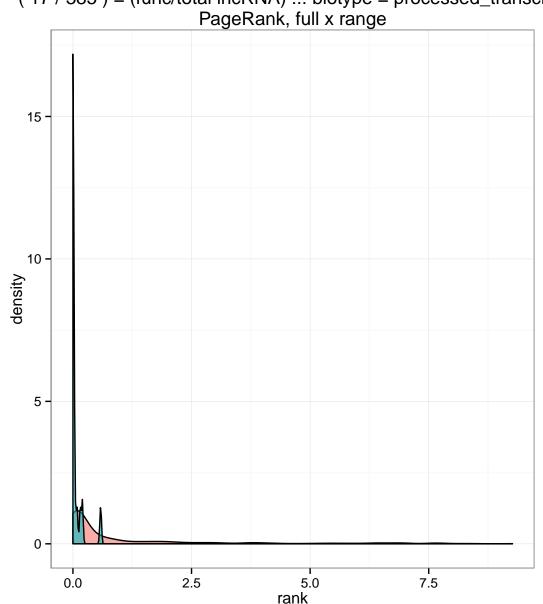lncRNA group = allLncRNA ::: data cols = lpa
(17 / 385) = (func/total lncRNA) ::: biotype = processed_transcript
PageRank, full x range