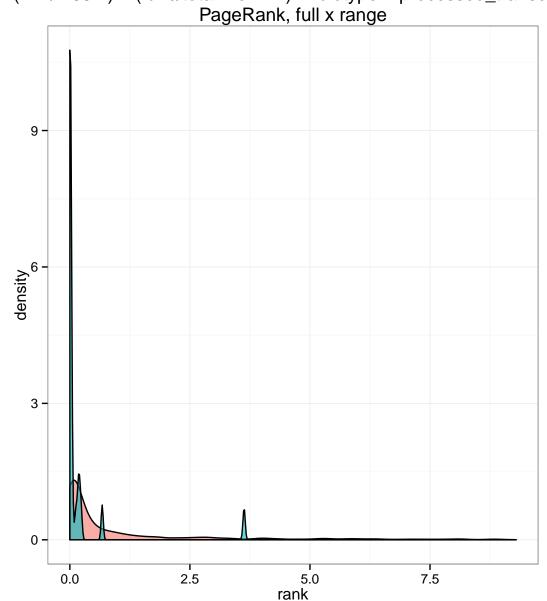
IncRNA group = allLncRNA ::: data cols = bothPullDowns (24 / 1031) = (func/total IncRNA) ::: biotype = processed_transcript



factor(label)