lncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns
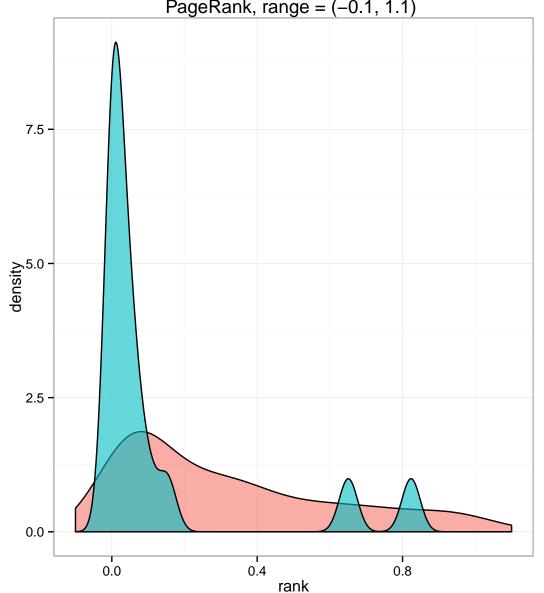(17 / 329) = (func/total lncRNA) ::: biotype = processed_transcript
PageRank, range = (−0.1, 1.1)