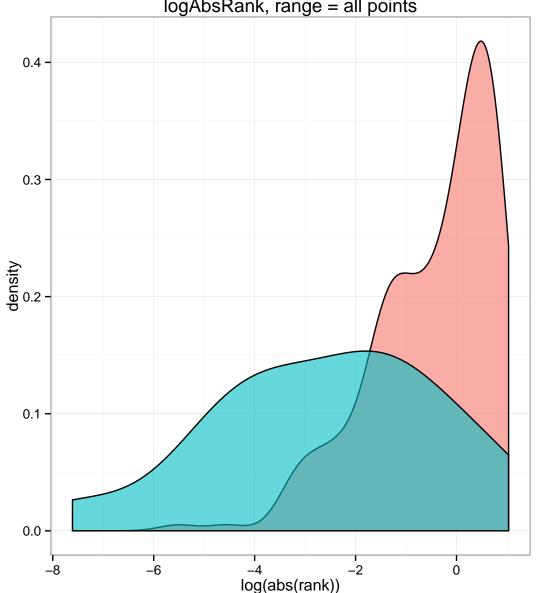lncRNA group = IDRlessthan0_1 ::: data cols = bothPullDowns
(16 / 232) = (func/total lncRNA) ::: biotype = processed_transcript
logAbsRank, range = all points