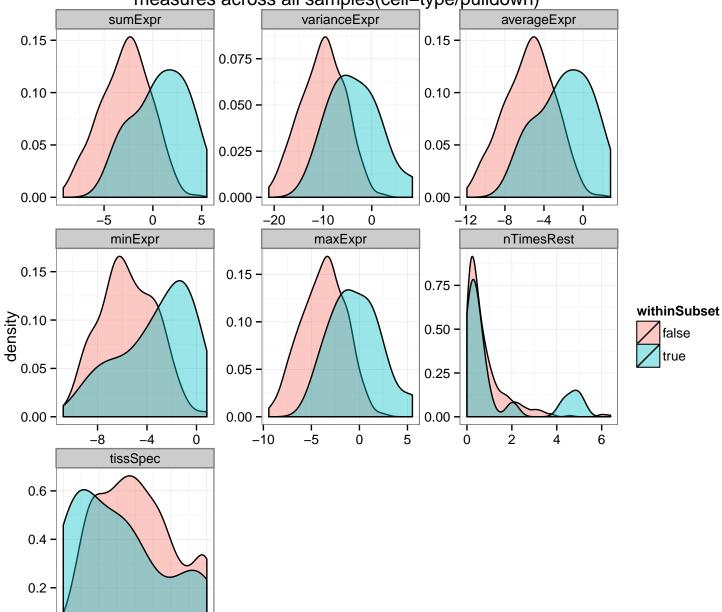lncRNA group = allLncRNA ::: data cols = lpa
(17 / 385) = (func/total lncRNA) ::: biotype = processed_transcript
measures across all samples(cell−type/pulldown)