lncRNA group = IDRlessthan0_01 ::: data cols = lnpa
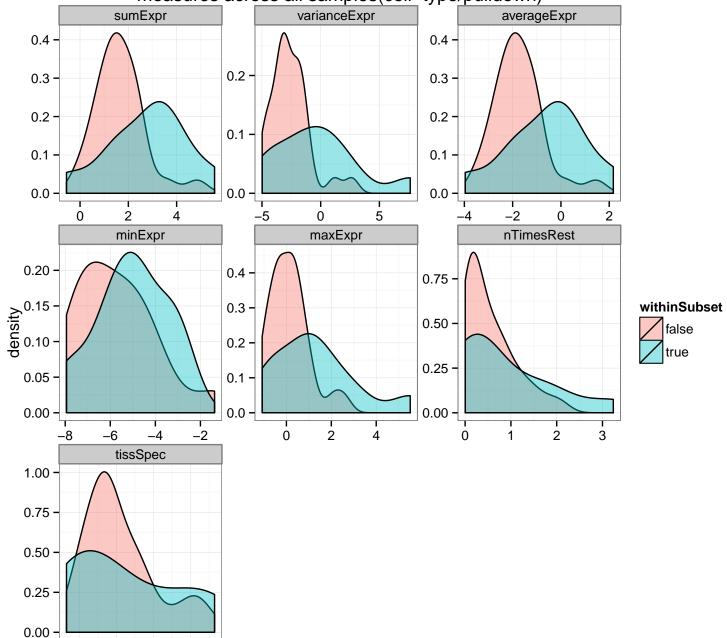(10 / 37) = (func/total lncRNA) ::: biotype = processed_transcript
measures across all samples(cell−type/pulldown)