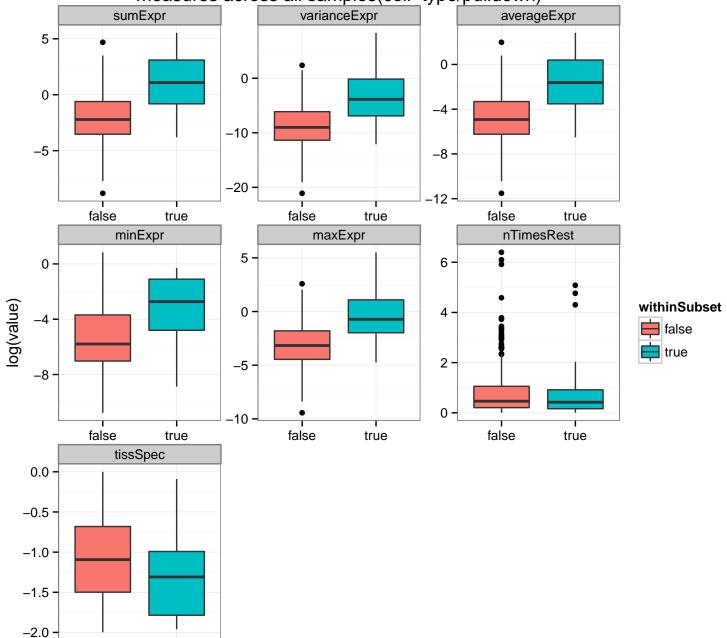lncRNA group = IDRlessthan0_2 ::: data cols = lpa
( 17 / 328 ) = (func/total lncRNA) ::: biotype = processed_transcript
measures across all samples(cell−type/pulldown)