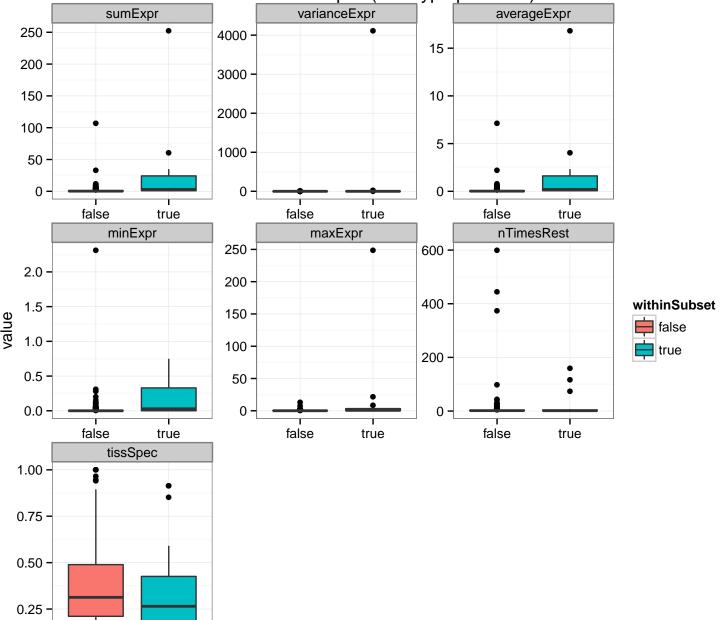lncRNA group = IDRlessthan0_1 ::: data cols = lpa
(16 / 232) = (func/total lncRNA) ::: biotype = processed_transcript
measures across all samples(cell−type/pulldown)