lncRNA group = IDRlessthan0_1 ::: data cols = lpa
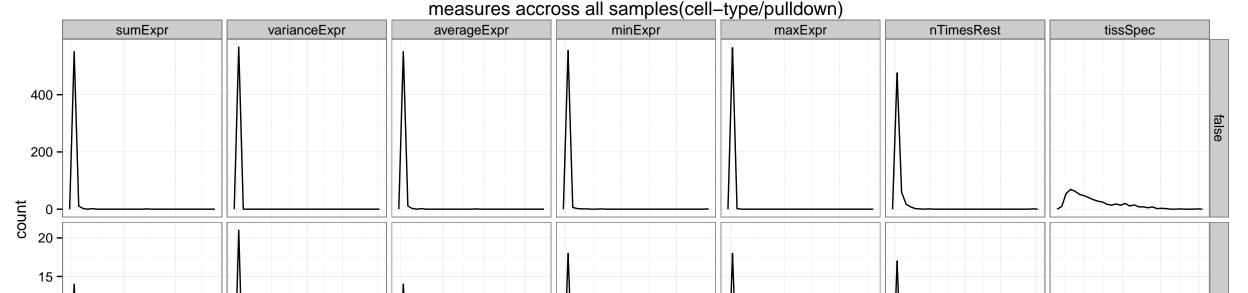(22 / 588) = (func/total lncRNA) ::: biotype = processed_transcript
subset =
22 lncRNAs out of 588 total lncRNAs

measures accross all samples(cell−type/pulldown)