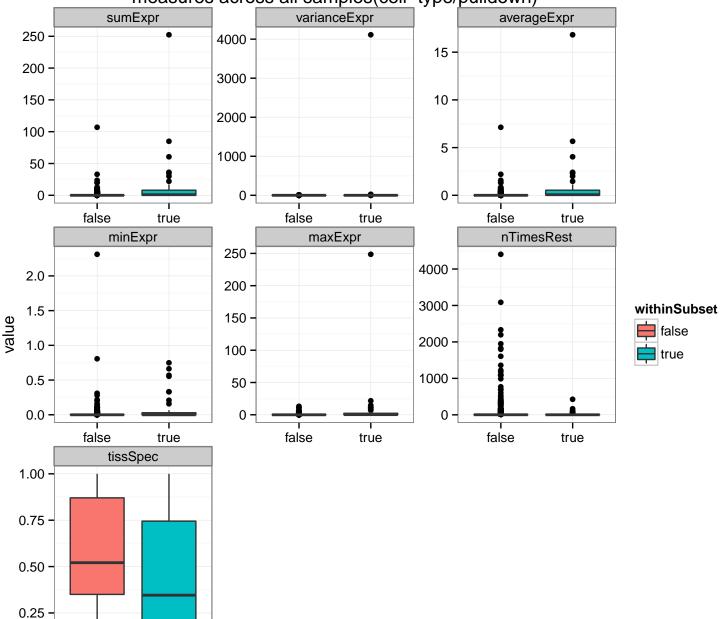lncRNA group = allLncRNA ::: data cols = lpa
(49 / 3453) = (func/total lncRNA) ::: biotype = lincProcTrans
measures across all samples(cell−type/pulldown)