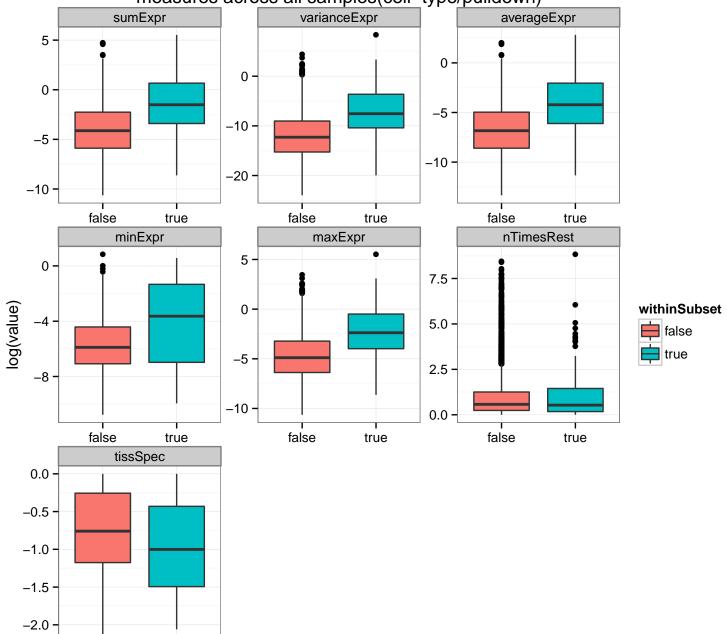lncRNA group = allLncRNA ::: data cols = lpa
(90 / 6451) = (func/total lncRNA) ::: biotype = all_biotypes
measures across all samples(cell−type/pulldown)