lncRNA group = allLncRNA ::: data cols = bothPullDowns
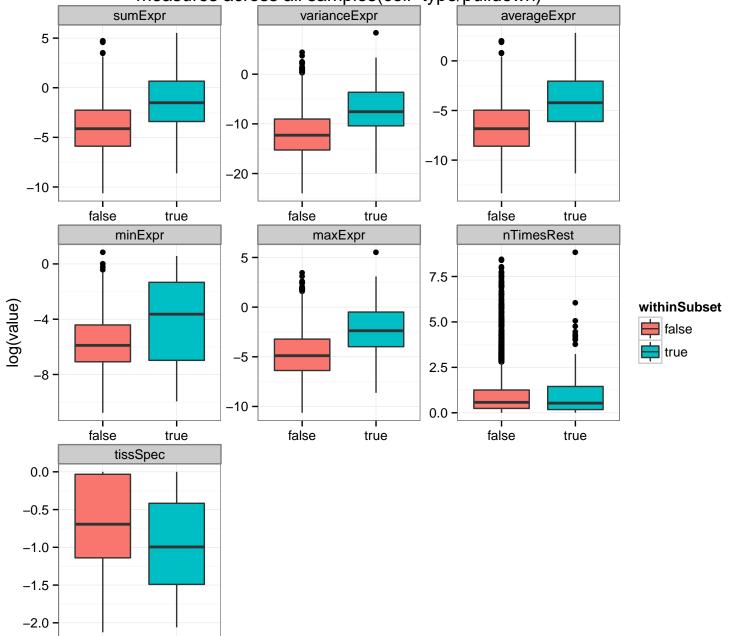(91 / 6927) = (func/total lncRNA) ::: biotype = all_biotypes
measures across all samples(cell−type/pulldown)