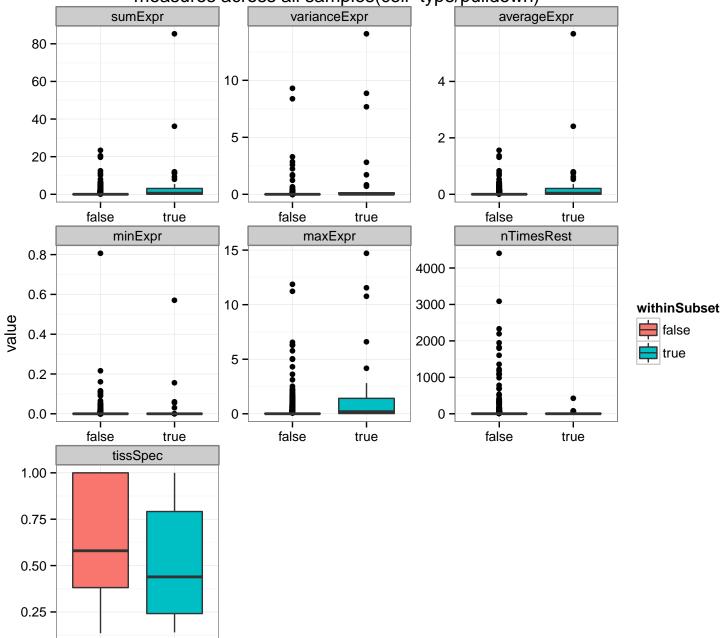
IncRNA group = allLncRNA ::: data cols = bothPullDowns (32 / 3319) = (func/total IncRNA) ::: biotype = lincRNA measures across all samples(cell-type/pulldown)



value of facet label

false

true