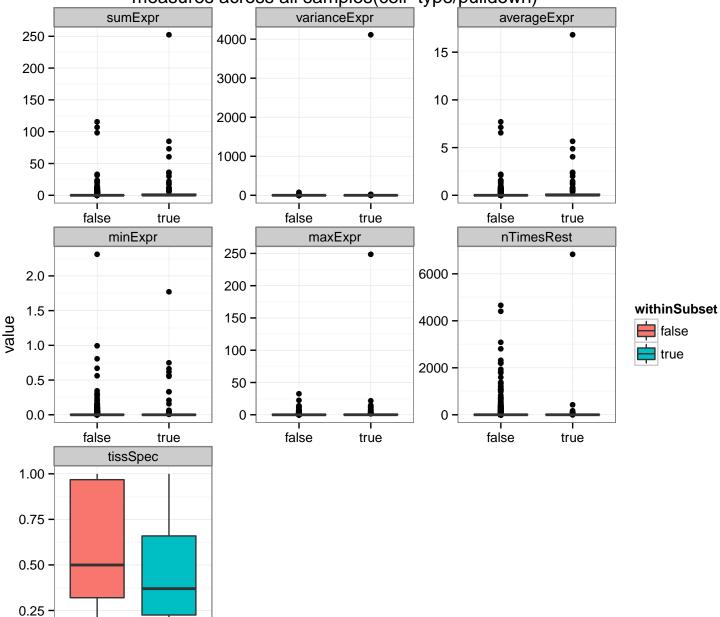
IncRNA group = allLncRNA ::: data cols = bothPullDowns (91 / 6927) = (func/total IncRNA) ::: biotype = all\_biotypes measures across all samples(cell-type/pulldown)



value of facet label

false

true