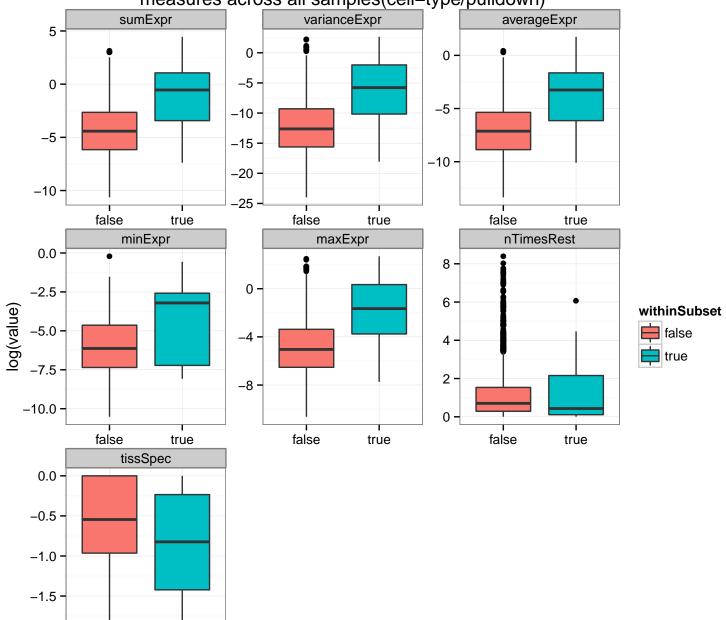
IncRNA group = allLncRNA ::: data cols = bothPullDowns
(32 / 3319) = (func/total IncRNA) ::: biotype = lincRNA
measures across all samples(cell-type/pulldown)
sumExpr varianceExpr averageExpr



value of facet label

-2.0

false

true