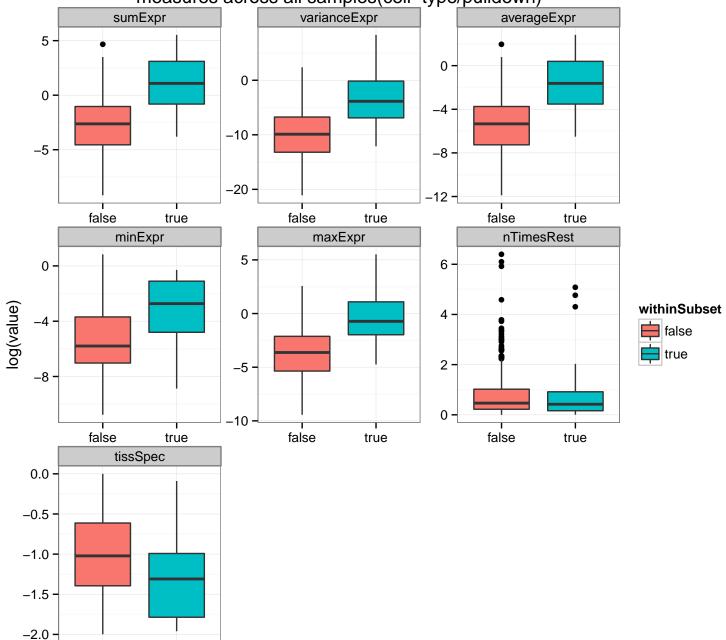
IncRNA group = allLncRNA ::: data cols = lpa
(17 / 385) = (func/total lncRNA) ::: biotype = processed_transcript
 measures across all samples(cell-type/pulldown)



value of facet label

false

true