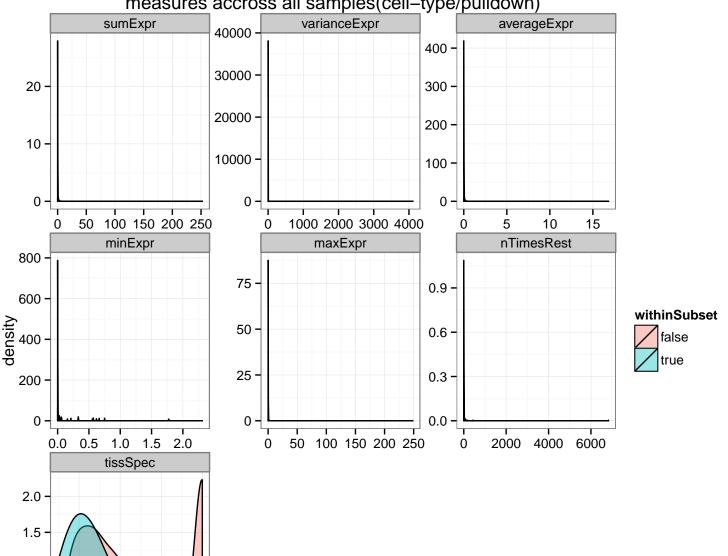
IncRNA group = allLncRNA ::: data cols = bothPullDowns (91 / 6927) = (func/total IncRNA) ::: biotype = all_biotypes measures accross all samples(cell-type/pulldown)



value of facet label

1.0

0.5

0.0

0.25

0.50

0.75

1.00