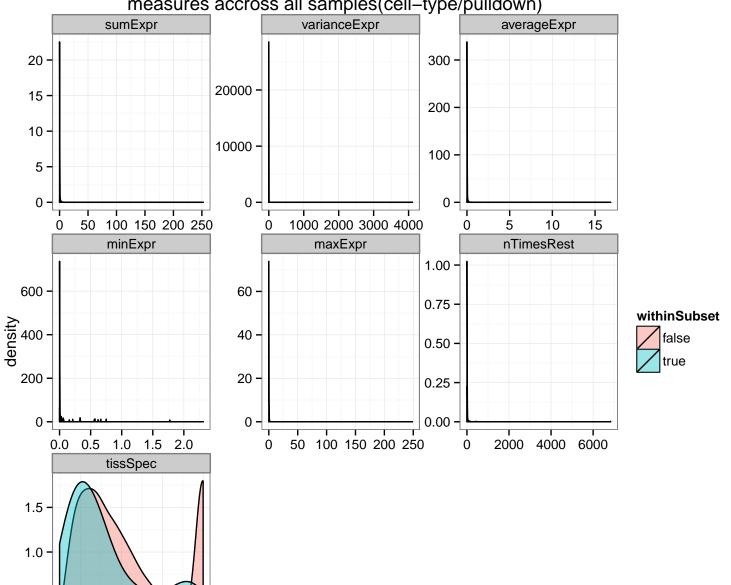
IncRNA group = allLncRNA ::: data cols = lpa (90 / 6451) = (func/total lncRNA) ::: biotype = all_biotypes measures accross all samples(cell-type/pulldown)



value of facet label

0.5

0.0

0.25

0.50

0.75

1.00