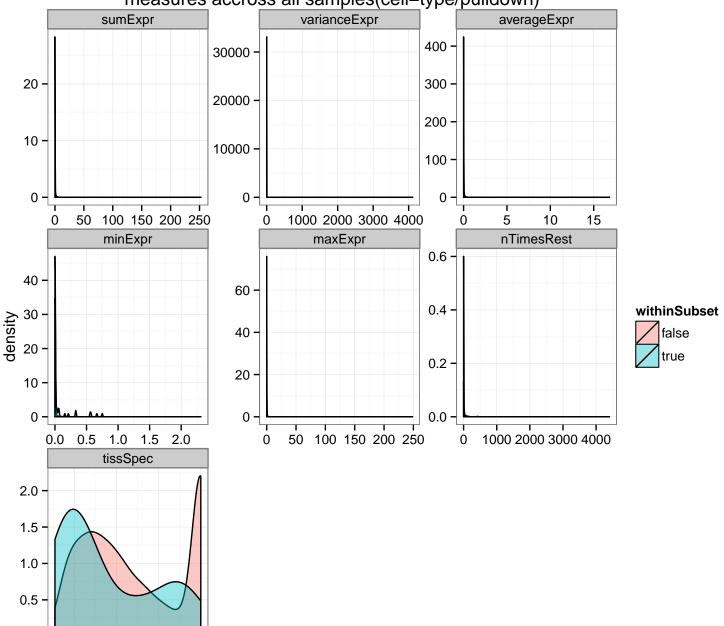
IncRNA group = allLncRNA ::: data cols = bothPullDowns (52 / 4177) = (func/total IncRNA) ::: biotype = remove_antisense measures accross all samples(cell-type/pulldown)



value of facet label

0.0

0.25

0.50

0.75

1.00