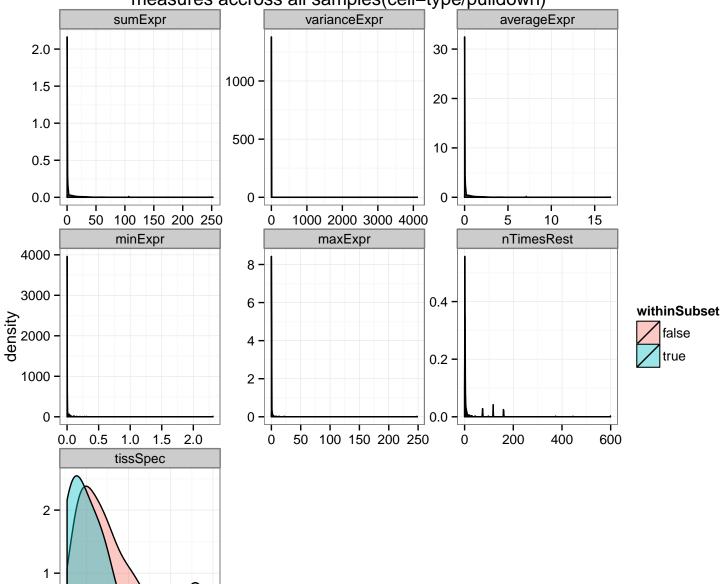
IncRNA group = allLncRNA ::: data cols = Inpa (17 / 372) = (func/total IncRNA) ::: biotype = processed_transcript measures accross all samples(cell-type/pulldown)



value of facet label

0

0.50

0.25

0.75

1.00