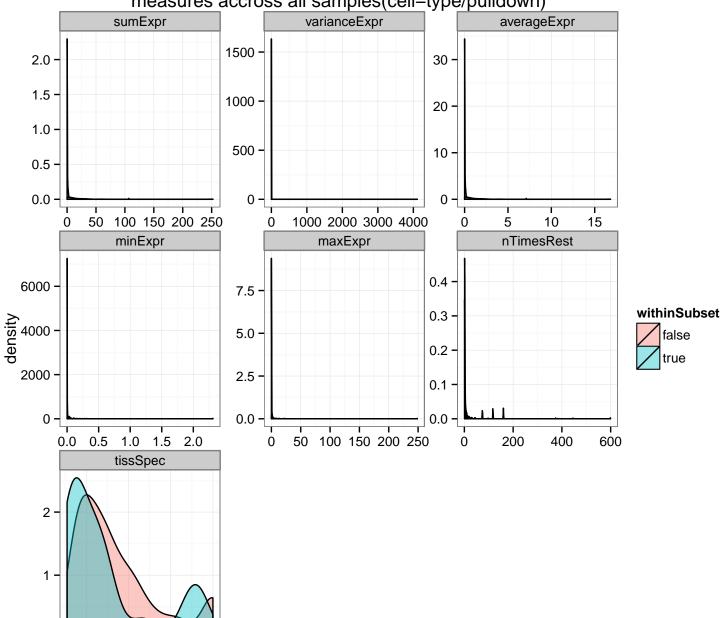
IncRNA group = allLncRNA ::: data cols = Ipa
(17 / 385) = (func/total IncRNA) ::: biotype = processed_transcript
measures accross all samples(cell-type/pulldown)



value of facet label

0

0.25

0.50

0.75

1.00