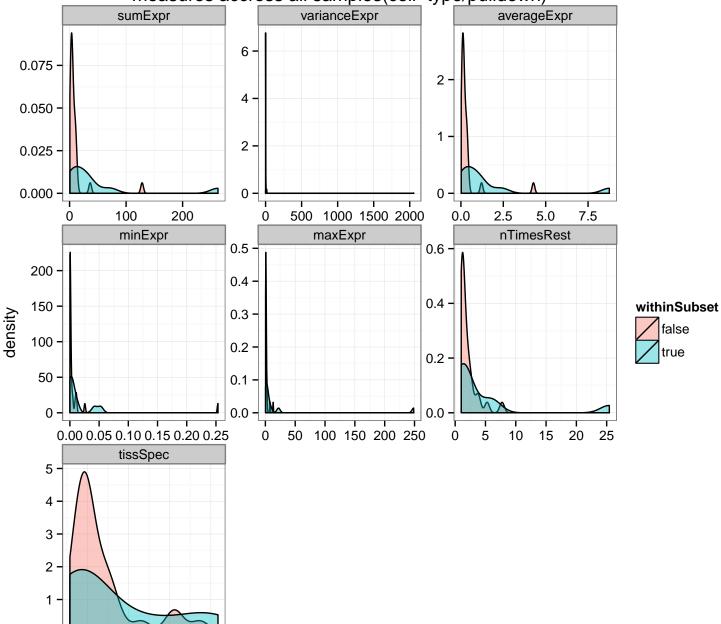
IncRNA group = IDRlessthan0_01 ::: data cols = bothPullDowns (10 / 37) = (func/total IncRNA) ::: biotype = processed_transcript measures accross all samples(cell-type/pulldown)



value of facet label

0

0.2

0.4

0.6

8.0