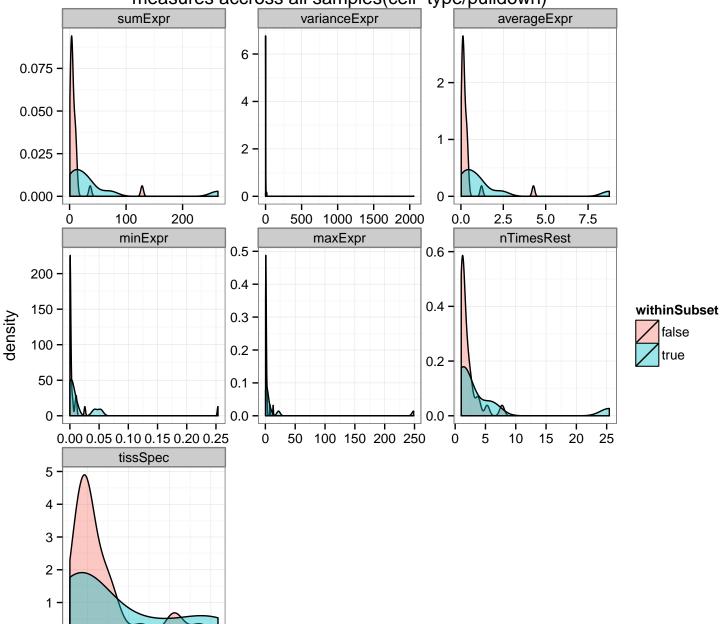
IncRNA group = IDRlessthan0\_01 ::: data cols = Inpa
( 10 / 37 ) = (func/total IncRNA) ::: biotype = processed\_transcript
 measures accross all samples(cell-type/pulldown)



value of facet label

0

0.2

0.4

0.6

8.0