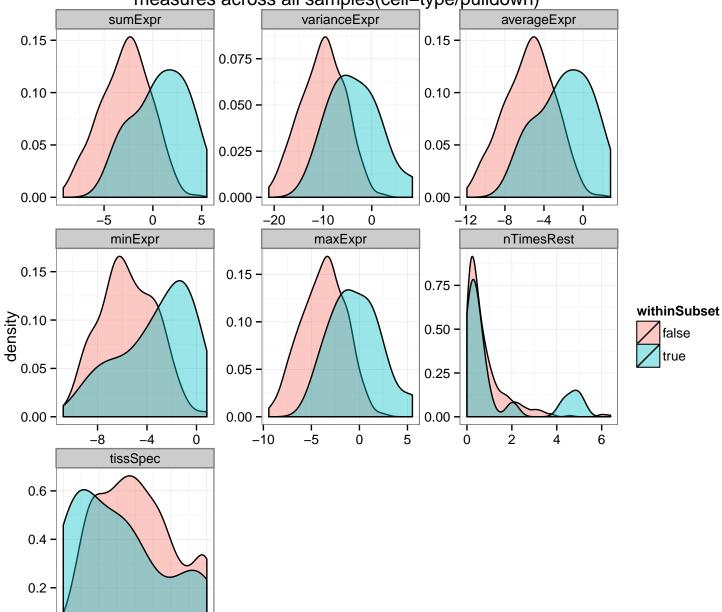
IncRNA group = allLncRNA ::: data cols = lpa
(17 / 385) = (func/total lncRNA) ::: biotype = processed_transcript
 measures across all samples(cell-type/pulldown)



value of facet label

0.0

-2.0 -1.5 -1.0 -0.5