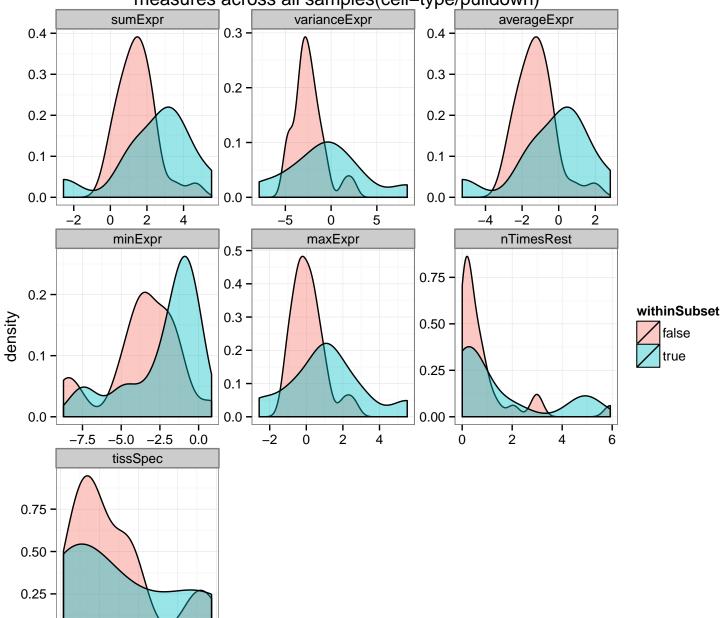
IncRNA group = IDRlessthan0_01 ::: data cols = bothPullDowns (10 / 37) = (func/total IncRNA) ::: biotype = processed_transcript measures across all samples(cell-type/pulldown)



value of facet label

0.00

-1.5 -1.0 -0.5