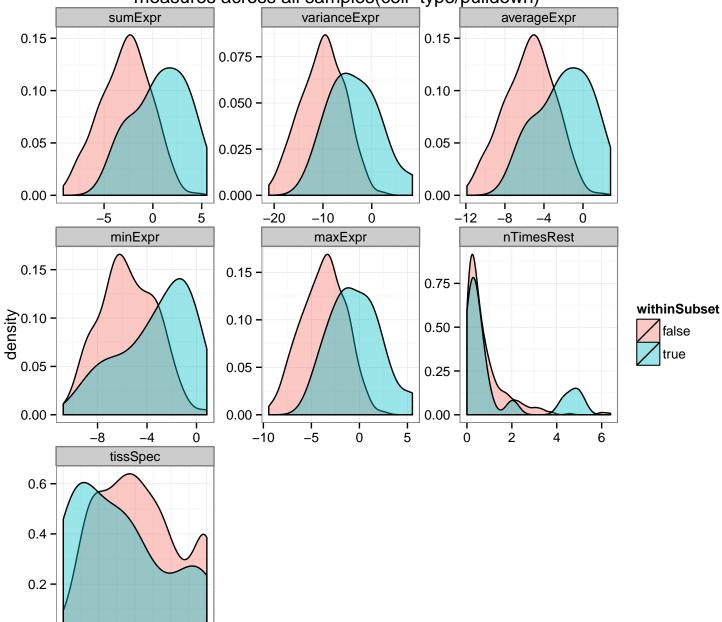
IncRNA group = allLncRNA ::: data cols = bothPullDowns
( 17 / 397 ) = (func/total IncRNA) ::: biotype = processed\_transcript
measures across all samples(cell-type/pulldown)



value of facet label

0.0

-2.0 -1.5 -1.0 -0.5