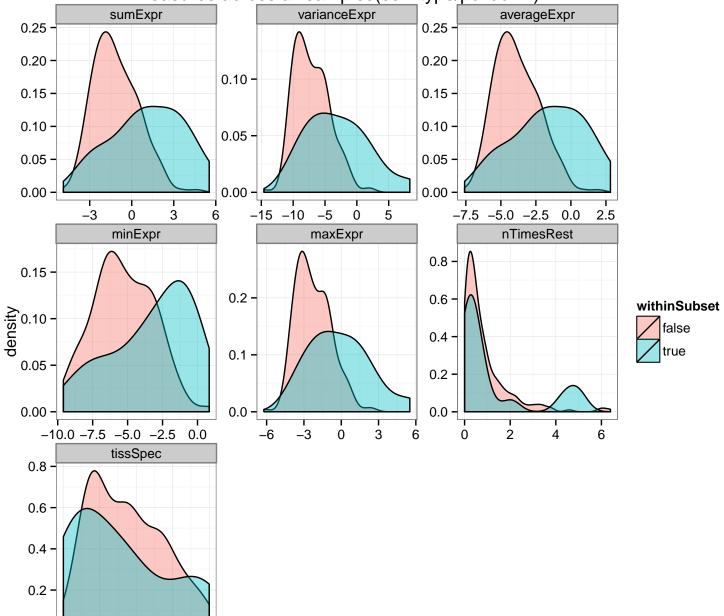
IncRNA group = IDRIessthan0_1 ::: data cols = bothPullDowns (16 / 232) = (func/total IncRNA) ::: biotype = processed_transcript measures across all samples(cell-type/pulldown)



value of facet label

0.0

-2.0 -1.5 -1.0 -0.5