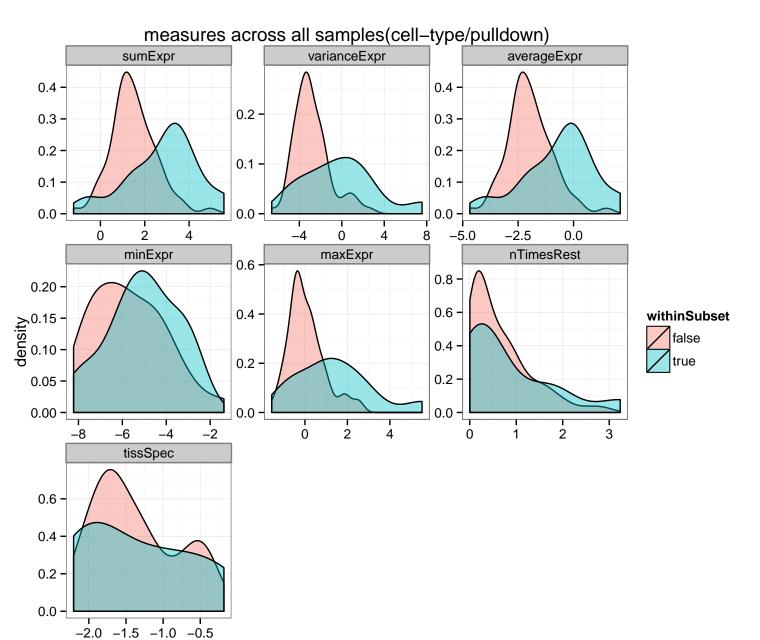
IncRNA group = IDRlessthan0_01 ::: data cols = bothPullDowns (11 / 79) = (func/total IncRNA) ::: biotype = processed_transcript subset =

11 IncRNAs out of 79 total IncRNAs



value of facet label