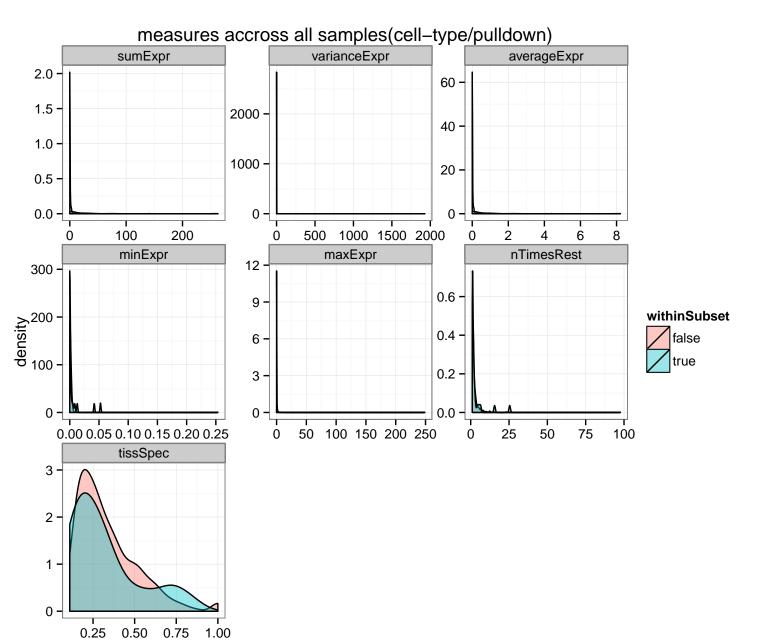
IncRNA group = allLncRNA ::: data cols = Inpa (23 / 962) = (func/total IncRNA) ::: biotype = processed_transcript subset = 23 IncRNAs out of 962 total IncRNAs



value of facet label