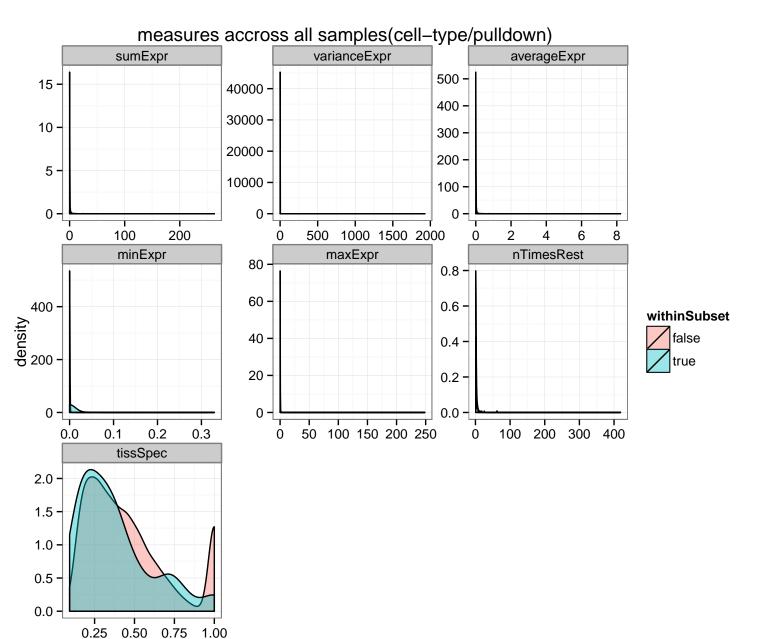
IncRNA group = allLncRNA ::: data cols = bothPullDowns (92 / 7622) = (func/total IncRNA) ::: biotype = all_biotypes subset = 92 IncRNAs out of 7622 total IncRNAs



value of facet label