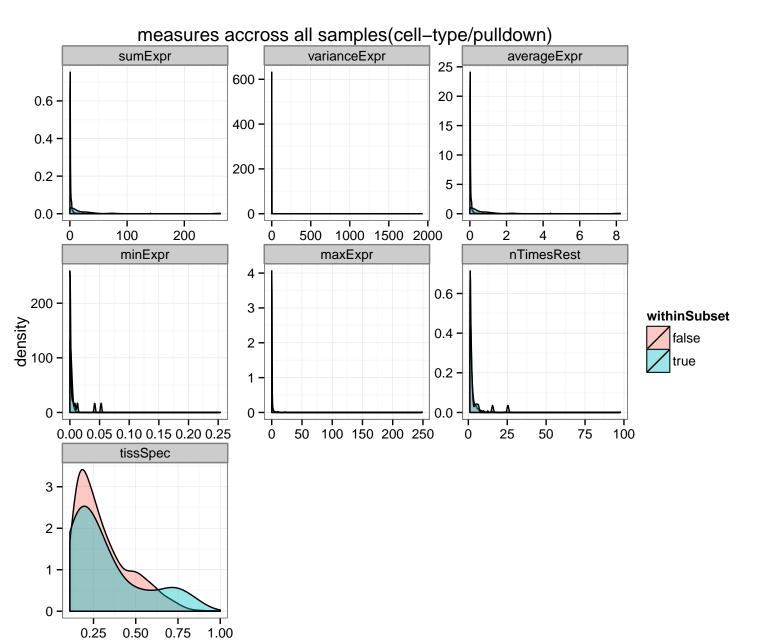
IncRNA group = IDRlessthan0_1 ::: data cols = lpa (22 / 588) = (func/total IncRNA) ::: biotype = processed_transcript subset = 22 IncRNAs out of 588 total IncRNAs



value of facet label