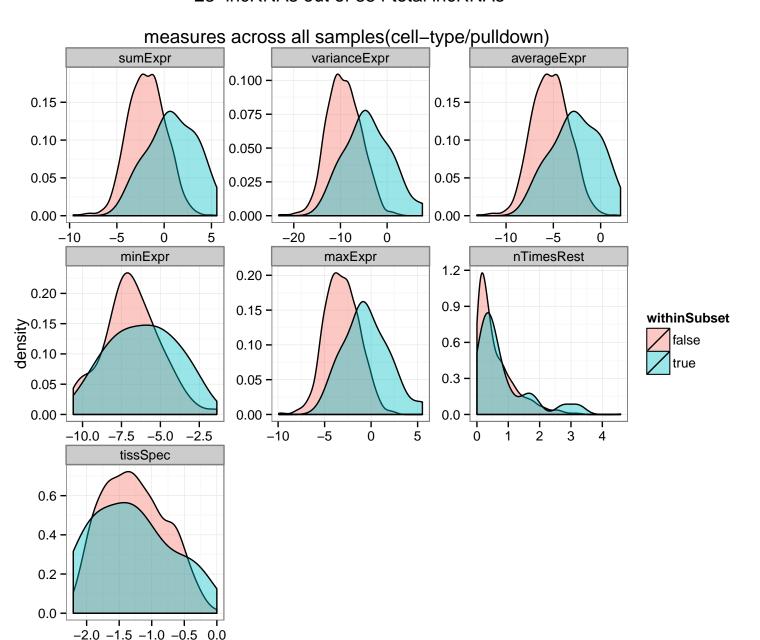
## IncRNA group = IDRlessthan0\_2 ::: data cols = Inpa ( 23 / 854 ) = (func/total IncRNA) ::: biotype = processed\_transcript subset = 23 IncRNAs out of 854 total IncRNAs



value of facet label