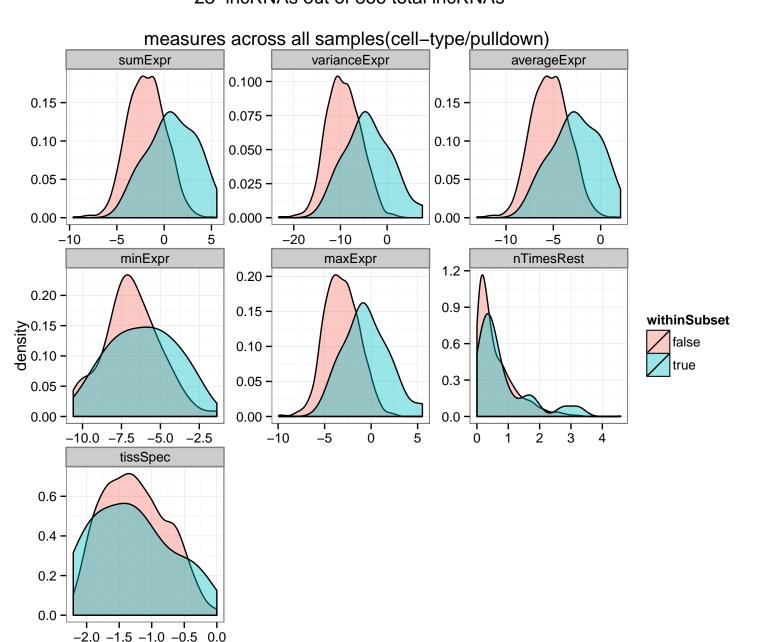
IncRNA group = IDRIessthan0_2 ::: data cols = bothPullDowns (23 / 866) = (func/total IncRNA) ::: biotype = processed_transcript subset = 23 IncRNAs out of 866 total IncRNAs



value of facet label