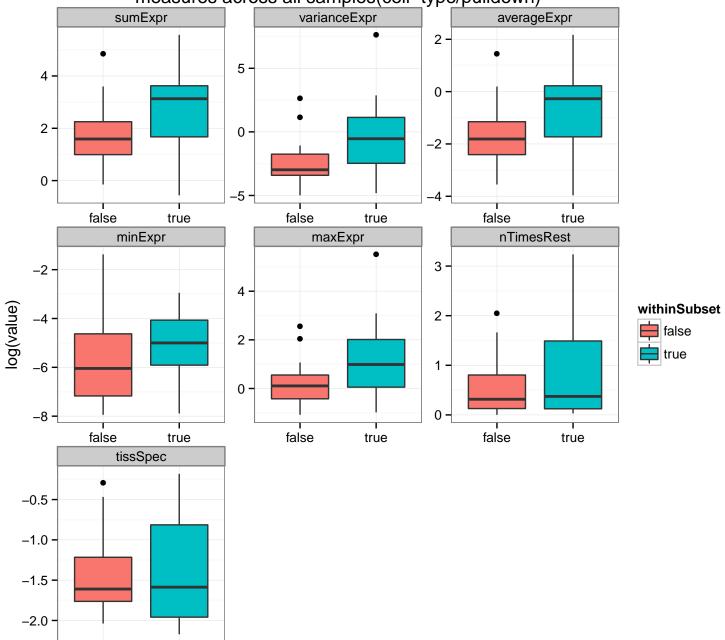
IncRNA group = IDRlessthan0\_01 ::: data cols = bothPullDowns ( 10 / 37 ) = (func/total IncRNA) ::: biotype = processed\_transcript measures across all samples(cell-type/pulldown)



value of facet label

false

true