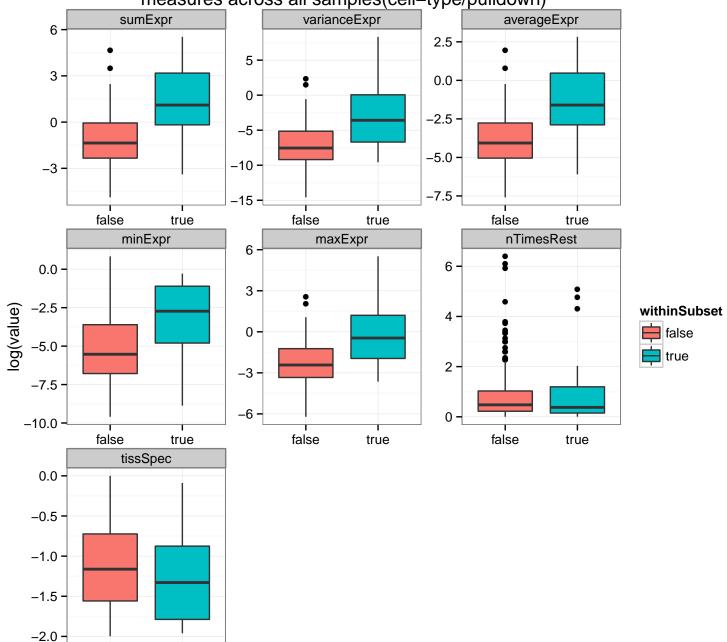
IncRNA group = IDRlessthan0\_1 ::: data cols = Inpa ( 16 / 231 ) = (func/total IncRNA) ::: biotype = processed\_transcript measures across all samples(cell-type/pulldown)



value of facet label

false

true