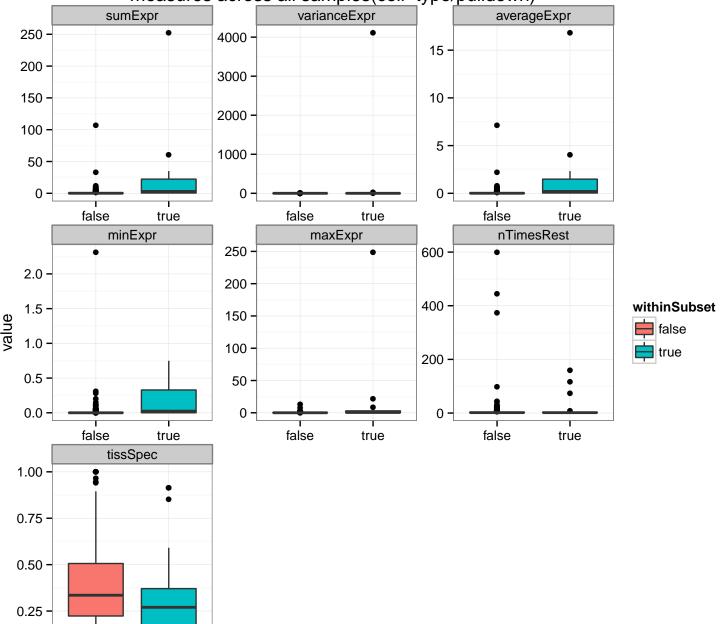
IncRNA group = IDRlessthan0_2 ::: data cols = Ipa
(17 / 328) = (func/total IncRNA) ::: biotype = processed_transcript
measures across all samples(cell-type/pulldown)



value of facet label

false

true