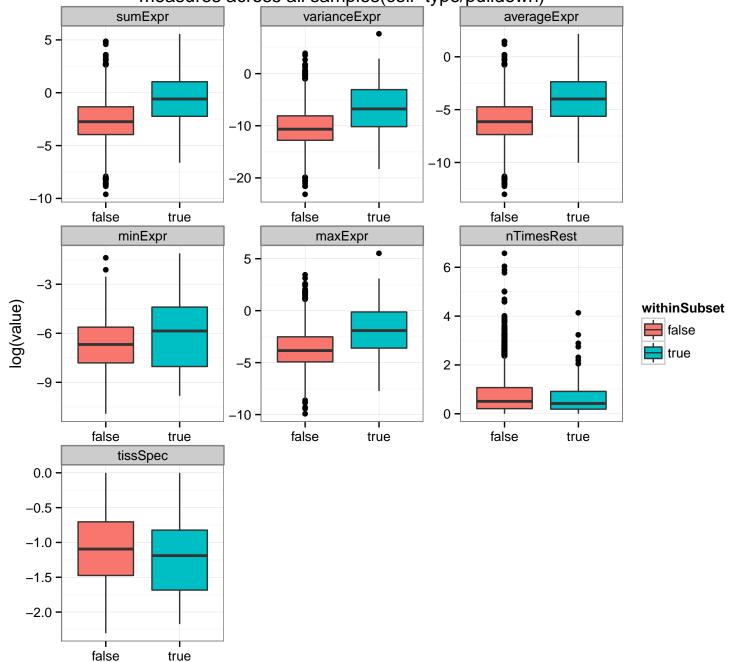
IncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (82 / 4643) = (func/total IncRNA) ::: biotype = all_biotypes measures across all samples(cell-type/pulldown)



value of facet label