lncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns
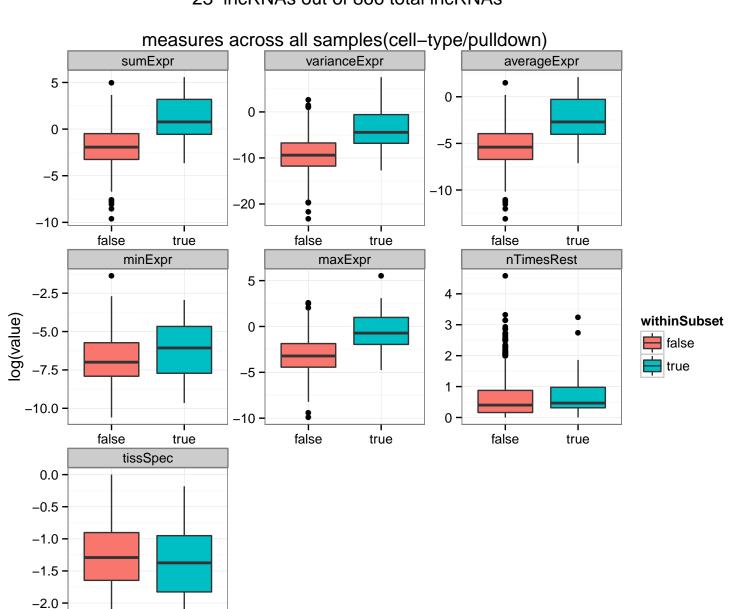## (23 / 866) = (func/total lncRNA) ::: biotype = processed_transcript
subset =
23 lncRNAs out of 866 total lncRNAs

measures across all samples(cell−type/pulldown)