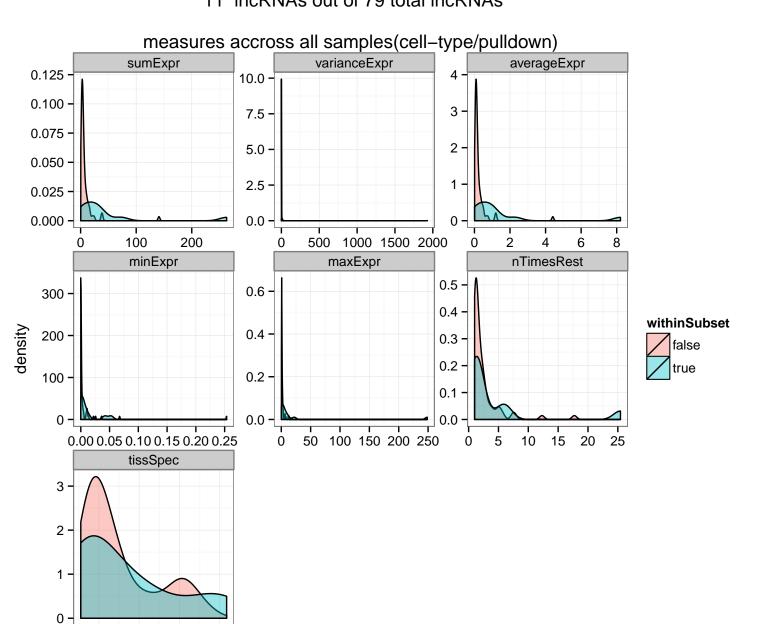lncRNA group = IDRlessthan0_01 ::: data cols = bothPullDowns
(11 / 79) = (func/total lncRNA) ::: biotype = processed_transcript
subset =
11 lncRNAs out of 79 total lncRNAs