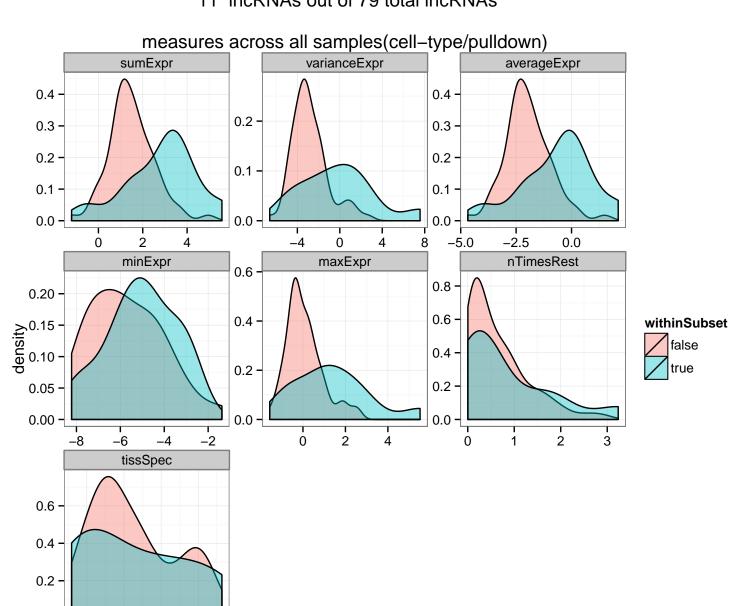# lncRNA group = IDRlessthan0_01 ::: data cols = lnpa
(11 / 79) = (func/total lncRNA) ::: biotype = processed_transcript
subset =
11 lncRNAs out of 79 total lncRNAs

measures across all samples(cell−type/pulldown)