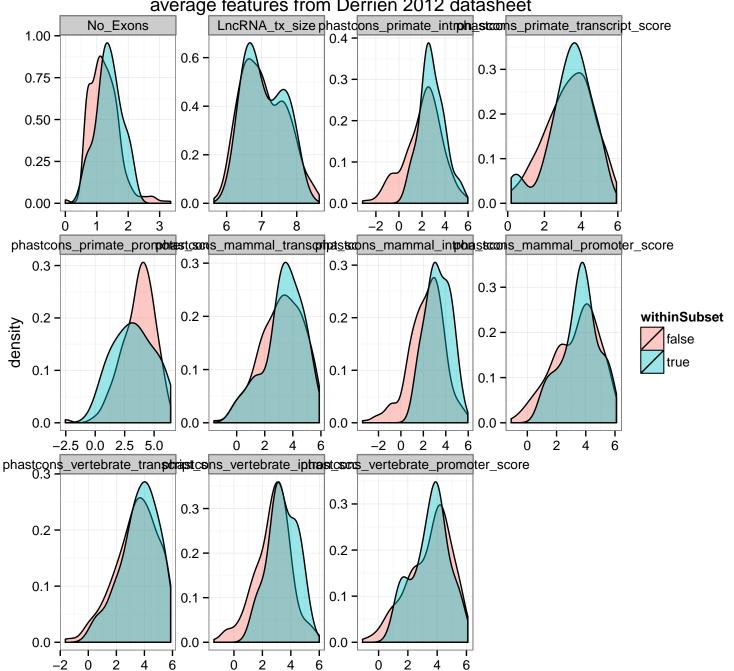
IncRNA group = IDRlessthan0_2 ::: data cols = bothPullDowns (17 / 331) = (func/total IncRNA) ::: biotype = processed_transcript average features from Derrien 2012 datasheet



value of facet label