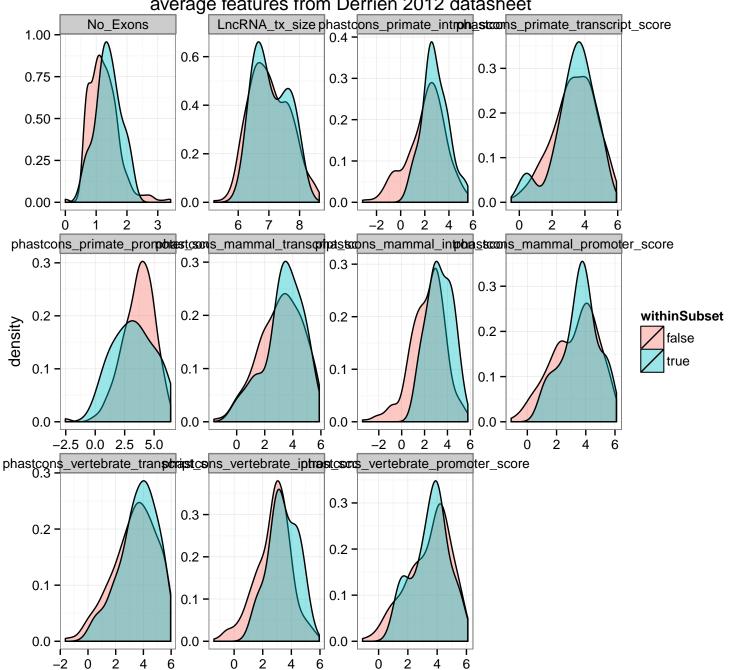
IncRNA group = allLncRNA ::: data cols = lpa
( 17 / 385 ) = (func/total lncRNA) ::: biotype = processed\_transcript
average features from Derrien 2012 datasheet



value of facet label