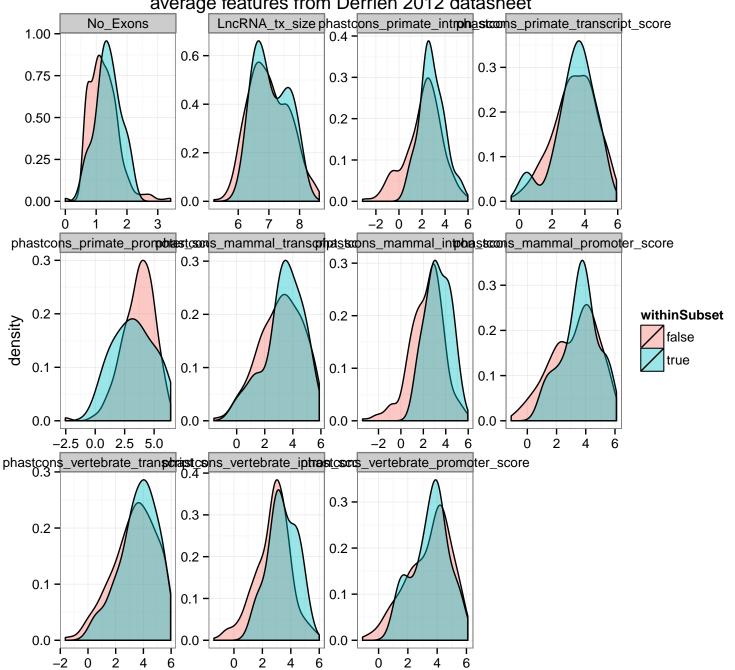
IncRNA group = allLncRNA ::: data cols = bothPullDowns (17 / 397) = (func/total IncRNA) ::: biotype = processed\_transcript average features from Derrien 2012 datasheet



value of facet label