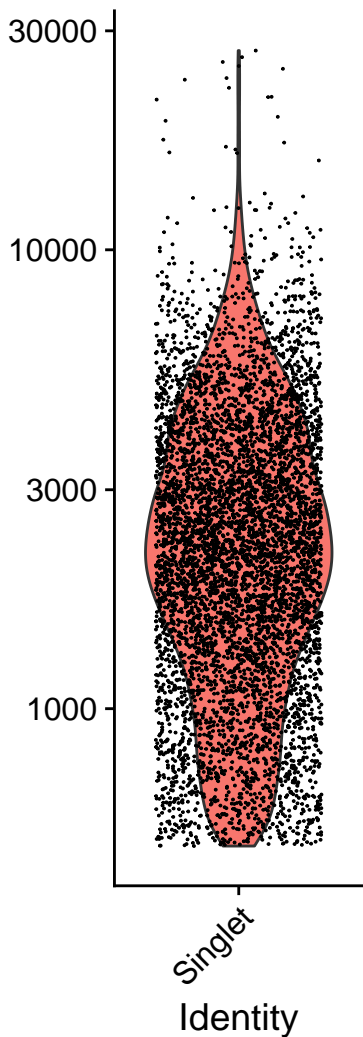
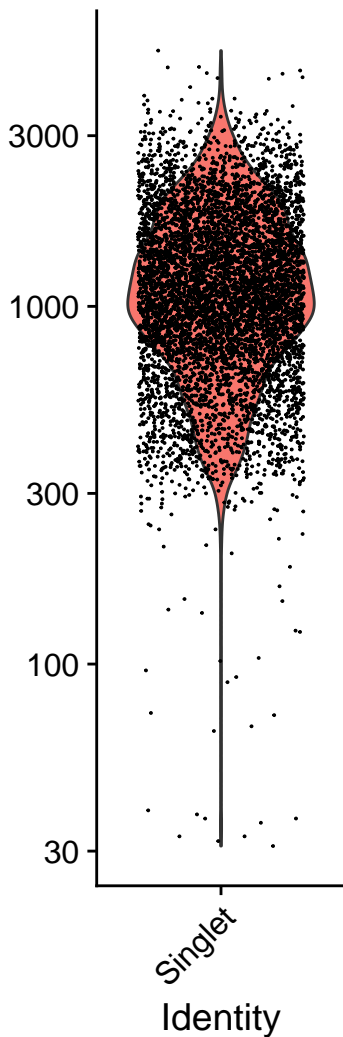


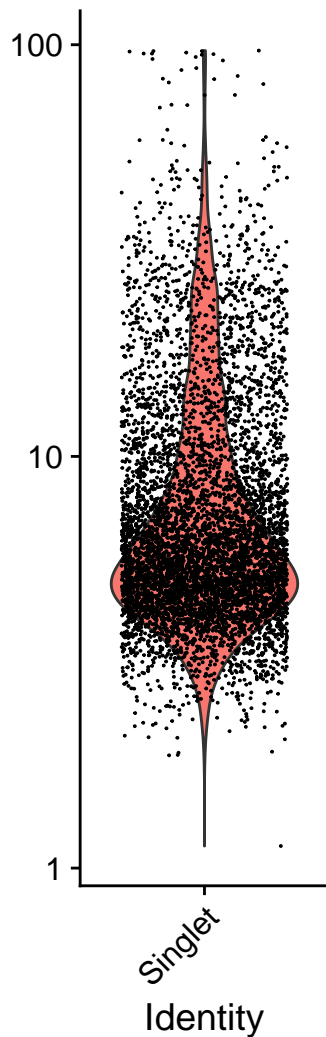
**nCount\_RNA**



**nFeature\_RNA**



**percent.mt**



# QC plot

Number of detected genes in function of number of UMI

