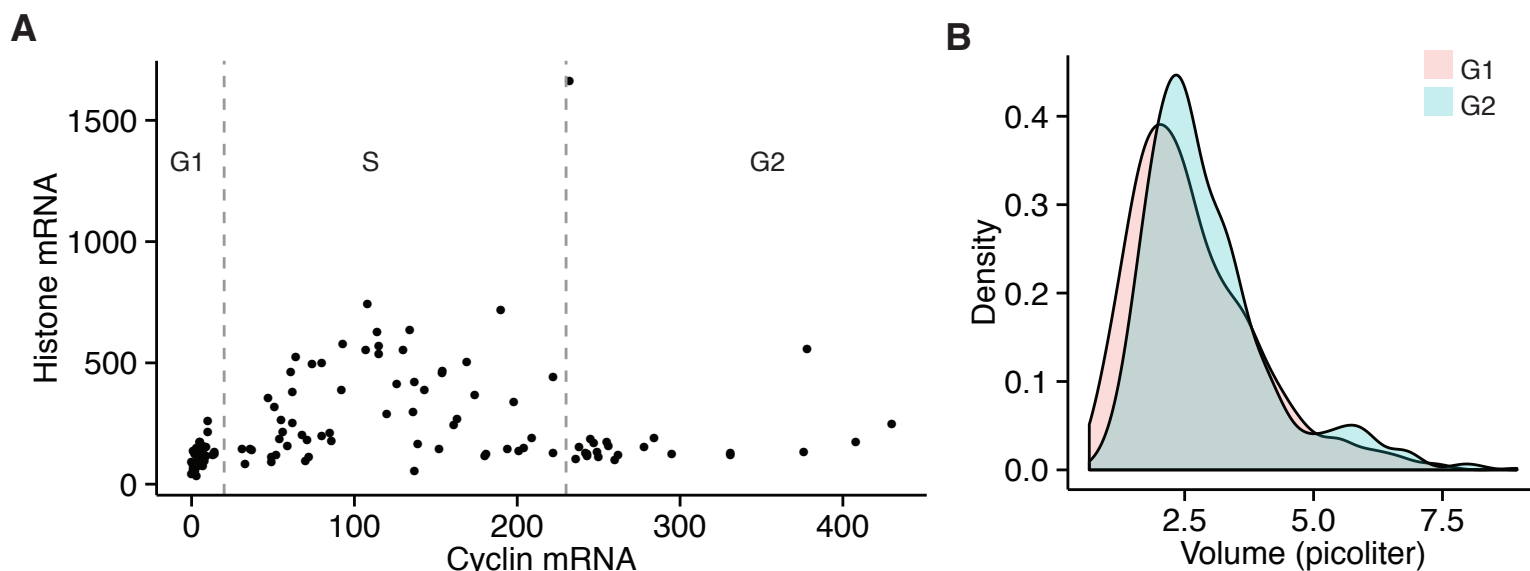# Supplementary Figure 6

Supplementary Fig. 6. Cell cycle characterization.

A. We simultaneously measured *CCNA2* and *HIST1H4E* mRNA by RNA FISH to precisely determine cell cycle position. Each data point is a single cell measurement. *CCNA2* is highly expressed in S and G2, but not G1. *HIST1H4E* is highly expressed only in S phase. Cells with low *CCNA2* and *HIST1H4E* are in G1 (cutoff = 20 *CCNA2* mRNA), cells with mid-range *CCNA2* and high *HIST1H4E* are in S, and cells with high *CCNA2* and low *HIST1H4E* are in G2 (cutoff = 230 *CCNA2* mRNA). We determined thresholds for all samples using this method. Data shown are from one of four biological replicates.

B. Volume distributions in G1 and G2. We determine cell cycle position using *CCNA2*. We note that G2 cells are larger than G1 cells, but only 10% larger on average, possibly due to non-linearities in growth over the course of the cell cycle. n = 841 cells in G1, 191 cells in G2.