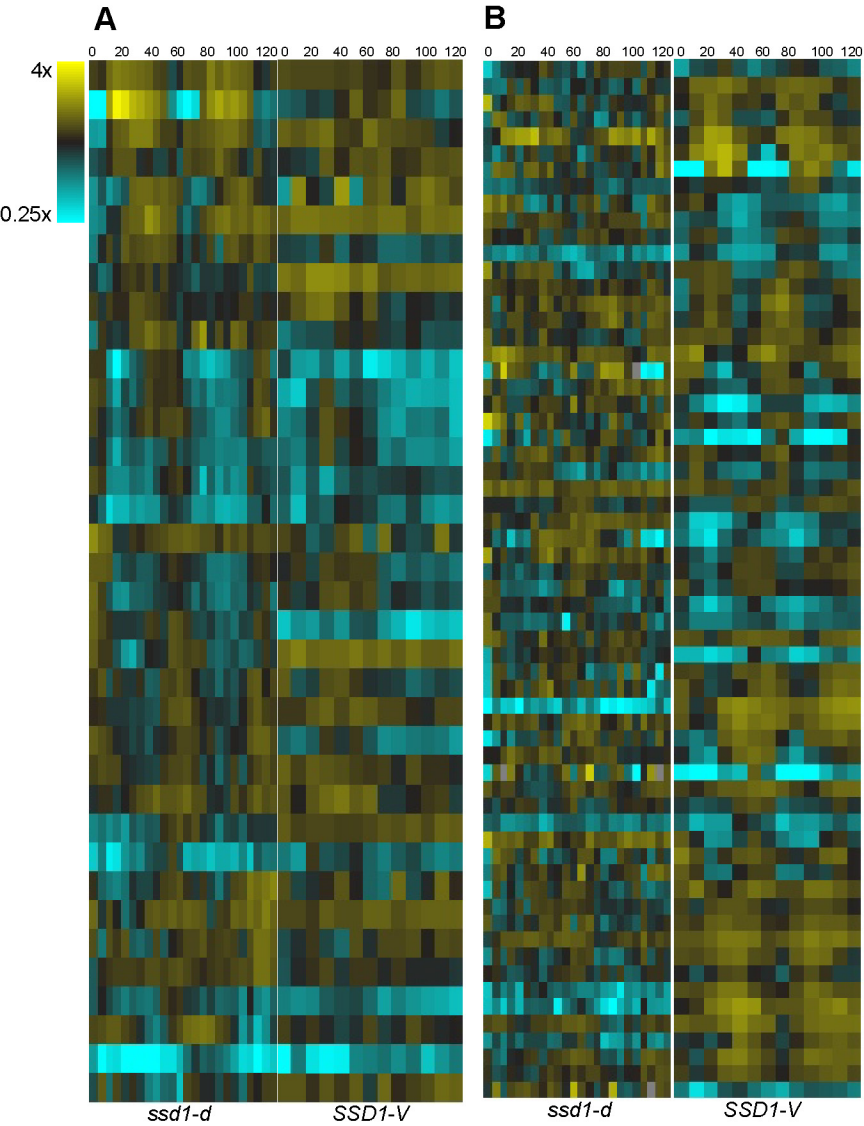
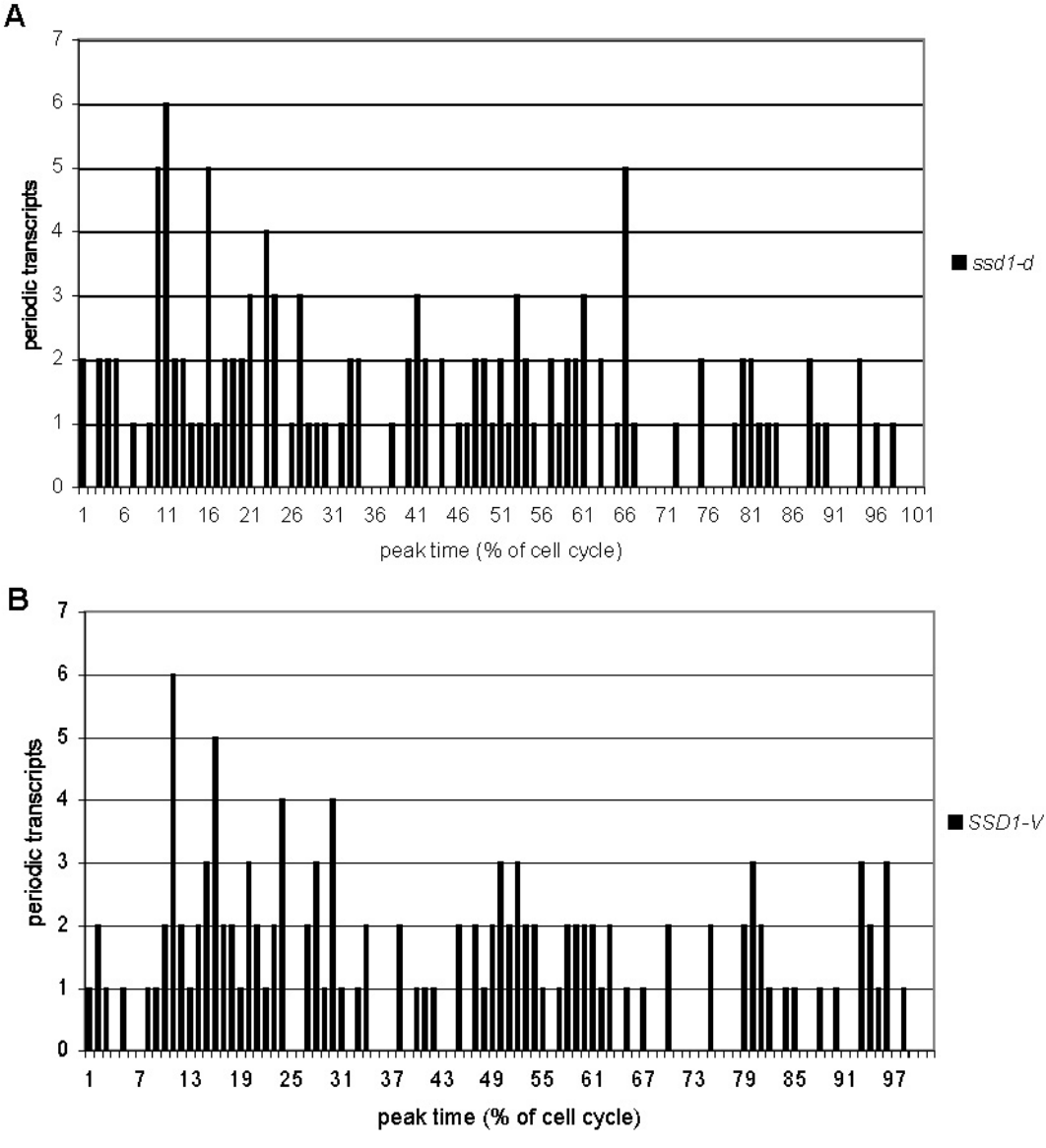
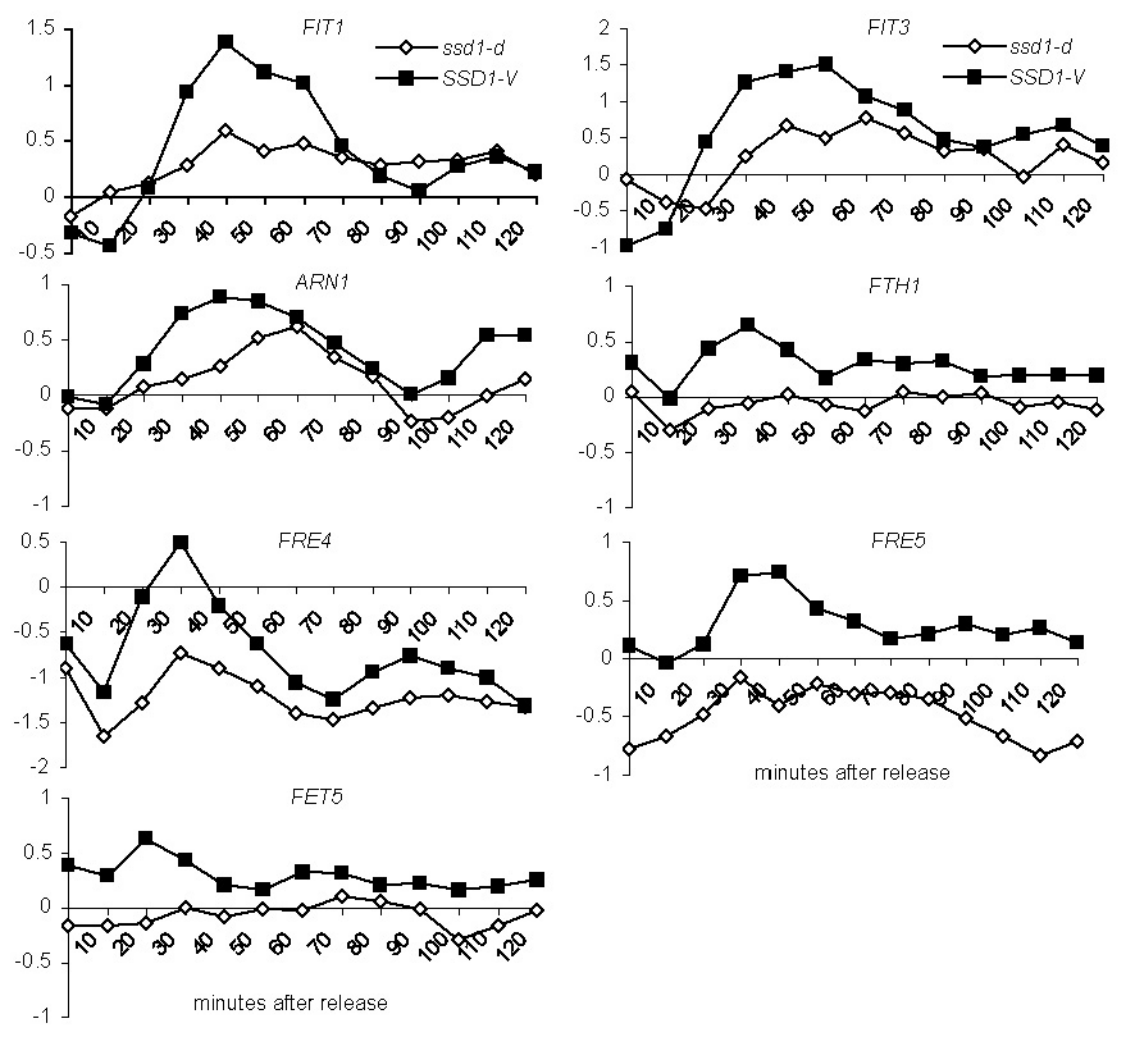
**Supplemental Figure 1**. Heat maps of 36 transcripts with high cycling score in *ssd1-d* and low cycling score in *SSD1-V* (left panel) and the 62 transcripts with low cycling score in *ssd1-d* high cycling score in *SSD1-V* (right panel). Time points are columns, genes are in rows. Zero time point is alpha factor arrest, then ten minute increments after release.

**Supplemental Figure 2.** Periodic transcripts that peak across the entire cell cycle are affected by *SSD1-V*. Histograms show the peak time distributions of differentially expressed genes. (A) Peak time distribution of the 125 differentially expressed genes that rank within the top 1000 cell cycle regulated transcripts in *ssd1-d* cells. (B) Peak time distribution of the 124 differentially expressed genes that rank within the top 1000 cell cycle regulated transcripts from *SSD1-V* cells.

**Supplemental Figure 3.** Iron transport and storage genes are up-regulated in *SSD1-V* cells. $Log_2$ ratios are plotted for each time point with the transcript level from an asynchronous population as the denominator. *ARN2*, *ARN3* (*SIT1*) and *ARN4* are also up-regulated in *SSD1-V*; data are not shown here because of their high homology with *ARN1*. *SSD1-V* (closed symbols) *ssd1-d* (open symbols).


A
B
0 20 40 60 80 100 120
4x
0.25x
ssd1-d
SSD1-V


A
periodic transcripts
peak time (% of cell cycle)
ssd1-d
B
periodic transcripts
peak time (% of cell cycle)
SSD1-V


FIT1
ssd1-d
SSD1-V
FIT3
ssd1-d
SSD1-V
ARN1
FTH1
FRE4
FRE5
FET5
minutes after release
minutes after release