

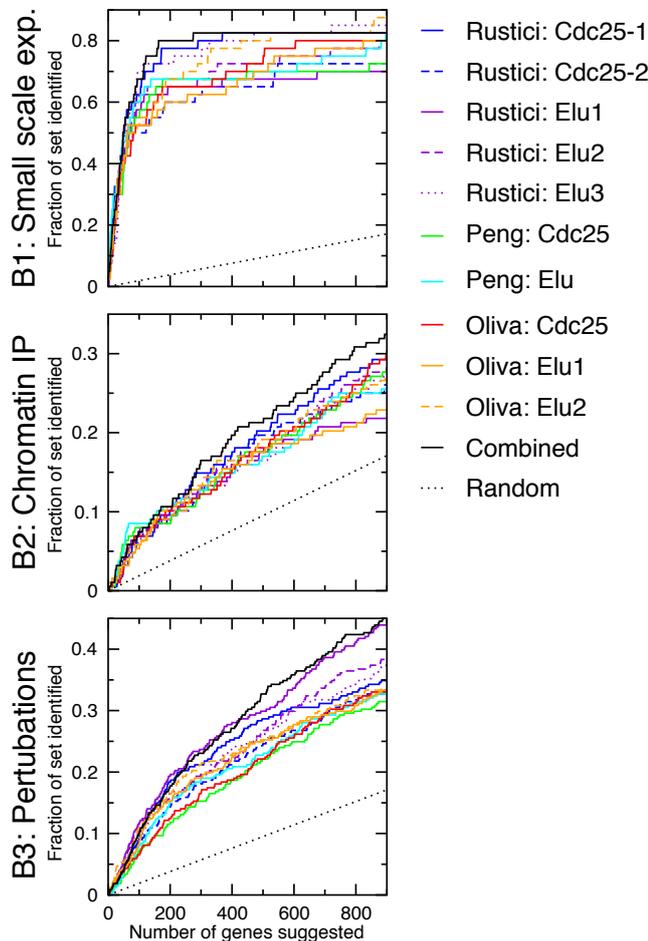
Supplementary Figures for:

The More the Merrier: Comparative Analysis of Microarray Studies on Cell Cycle-Regulated Genes in Fission Yeast

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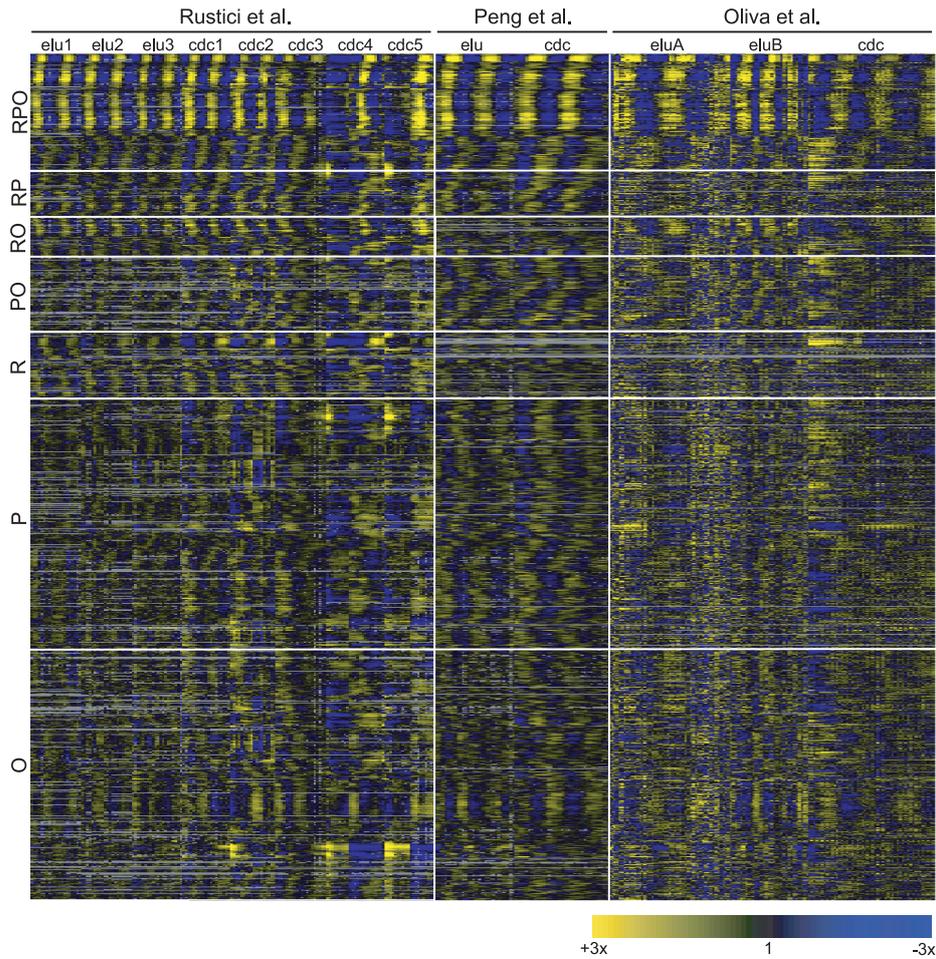
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Supplemental Figure 1



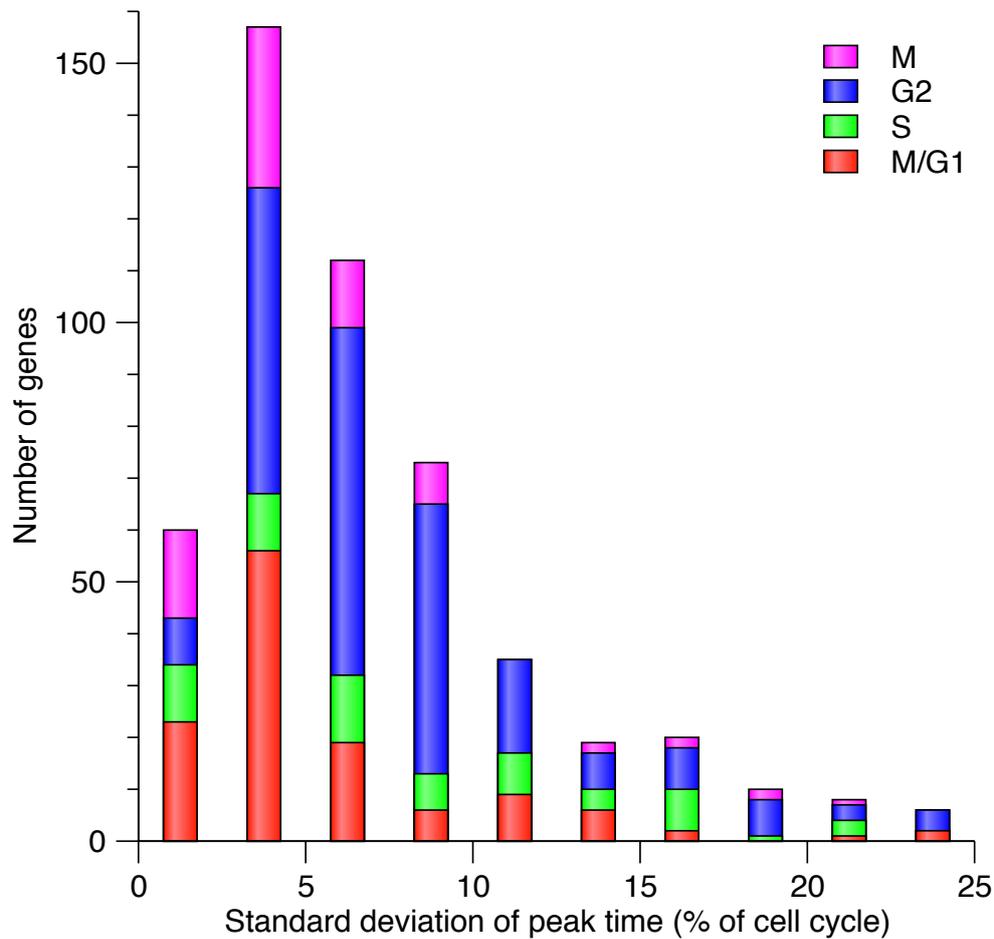
Supplemental Figure S1: **Benchmark analysis of individual experiments.** The fraction of genes retrieved from each benchmark set is plotted against the gene rank (number of genes suggested). A steeper curve is equivalent to a better correspondence with the independent evidence for cell-cycle regulation and thus with a better gene list. There are only minor difference in performance for the ten experiments, and the experiments seems to be of equal overall quality.

Supplemental Figure 2



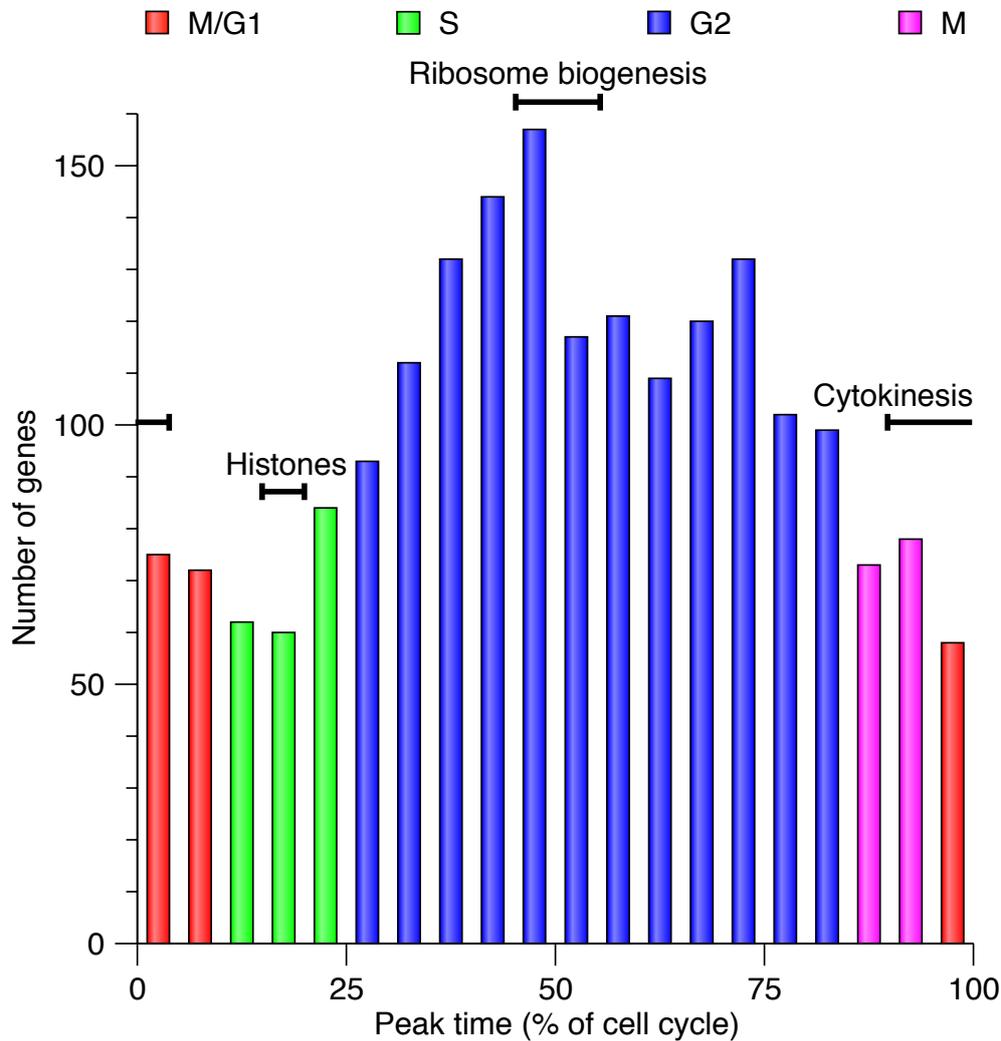
Supplemental Figure S2: **Cluster diagram of all genes identified as periodically expressed in at least one of the three microarray studies.** Horizontal rows represent the profiles of hierarchically clustered genes. RPO: 176 genes reported in all three papers (Rustici et al., 2004; Peng et al., 2005; Oliva et al., 2005); RP, RO, and PO: 243 genes reported in two of the three papers; R, P, and O: 863 genes reported in only one of the three papers (Figure 1B). Columns represent experimental timepoints of the timecourse experiments indicated. Experiments cdc1 to cdc5 refer to the following experiments of Rustici et al. (2004): *cdc25* block-release 1 and 2, *sep1Δ cdc25* block-release, elutriation and *cdc10* block-release, and elutriation and *cdc25* block-release, respectively. Only timecourse experiments that have been used to identify periodically expressed genes in the original studies are shown. The mRNA levels (fold change) at each timepoint relative to levels in unsynchronized cells are colour coded as indicated at the bottom, and missing data are shown in grey.

Supplemental Figure 3



Supplemental Figure S3: **Standard deviations of peak times.** The histogram of peak time standard deviation for the 500 highest ranking genes (colour-coded according to phases defined in Figure 5). Most genes appear to peak consistently across experiments, but genes peaking in S and G2 phases appear to have a larger spread on average. This is caused by the relative shift in S phase between *cdc25* and elutriation based arrest experiments (Figure 5). Furthermore, the long G2 phase and weakly regulated genes peaking during this stage are contributing to the larger deviation among G2 peaking genes.

Supplemental Figure 4



Supplemental Figure S4: **Histogram of peak times for the lowest scoring 2000 genes.** This histogram of average peak times for the lowest ranking 2000 genes shows a relative large fraction of genes peaking in early G2 phase as was also the case for the highest-ranking genes (Figure 6). However, the M-phase burst in transcription among the highest-ranking genes (Figure 6) cannot be seen among the lowest ranking genes indicating that only in early G2 phase may a global increase in transcription be present. The reason for this global distribution in low ranking genes is not known.