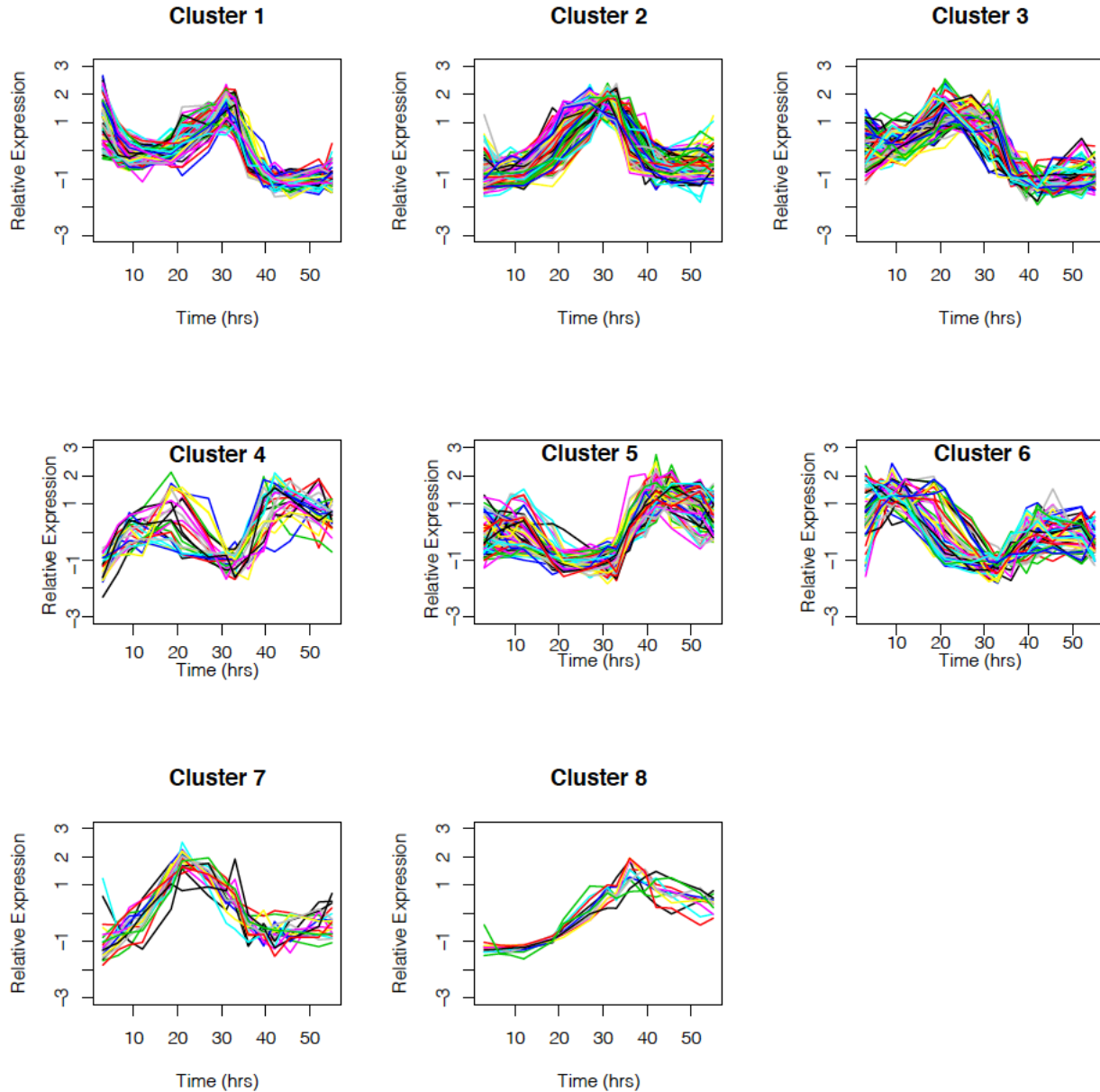
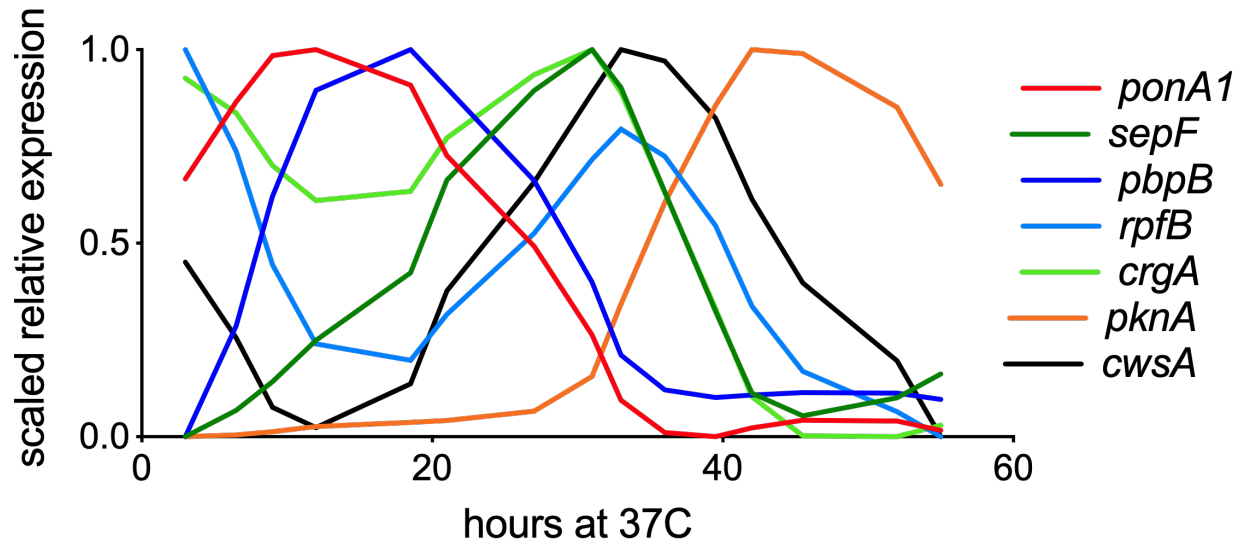


**Figure S1. Transcriptional compartmentalization of the *Mycobacterium tuberculosis* cell cycle. Related to Figure 2. (A)** Hierarchical clustering of genes in *Mtbcos* (log transformed DESeq normalized counts, centered around the mean, similarity metric: centered correlation, clustering method: centroid linkage). X axis: hours at 37°C. **(B)** Performance of the GP smoothing analysis. Expression profile of the DNA polymerase *poIA* is shown. Data from two replicates (yellow and blue dashed lines), GP smooth fit (solid blue line) and sinusoidal fit (pink dotted line) are shown. Y axis: Relative expression (DESeq normalized value for each time point divided by the mean *poIA* expression value across all time points). X axis: hours at 37°C.



**Figure S2. Periodic gene expression during *Mycobacterium tuberculosis* cell cycle progression. Related to Figure 2E.** 485 periodically expressed genes in *Mtbcos* grouped into eight clusters. Y axis: Relative expression (standard normalized DESeq counts - each value is subtracted by the mean for that gene across time and then divided by the standard deviation). X axis: Hours post release into permissive temperature. Distance matrix: Euclidean. Clustering method: Hierarchical.



**Figure S3. Genes with known roles in cell division expressed around the cytokinesis window. Related to Figure 3A.** Scaled relative expression (GP smoothed, DESeq normalized read counts for each time point divided by the mean value for that gene across time, then scaled) of 7/13 known cytokinesis genes. The other six genes are shown in Figure 3A.

### Supplemental Reference

- S1. Zhou, B., Schrader, J.M., Kalogeraki, V.S., Abeliuk, E., Dinh, C.B., Pham, J.Q., Cui, Z.Z., Dill, D.L., McAdams, H.H., and Shapiro, L. (2015). The Global Regulatory Architecture of Transcription during the *Caulobacter* Cell Cycle. *PLOS Genet.* 11, e1004831.