SUPPORTING INFORMATION CONTENTS

Supporting Movie Legends

Movie S1 - Min pattern initiation under constant flow.

Movie S2 - Transition from wave- to oscillation-mode during constant flow.

Movie S3 - Min spiral without flow.

Movie S4 - Min pattern initiation on an SLB without cardiolipin.

Movie S5 - Min spiral on an SLB without cardiolipin.

Movie S6 - Wave trains of Min proteins on SLB made of PC and PS phospholipid.

Supporting Figures and Legends

Fig. S1 - Transition from wave- to oscillation-mode during constant flow.

Fig. S2 - MinE concentration effects on Min spirals on *E. coli* lipid and mSLB.

Fig. S3 - Lipid composition and salt concentration effects on MinD ATPase activity.

MOVIE LEGENDS

Note from the authors: For short duration movies, we suggest looping during playback.

Movie S1. Min pattern initiation under constant flow. A MinD (green) /MinE (red) initiation center breaking asymmetrically into an upstream travelling wave on an *E.coli* lipid SLB. GFP-MinD (1 μM) and 1.5 μM MinE (mixed 1:19 with MinE-Alexa 647) were preincubated with 2.5 mM ATP and infused into the flowcell at a constant flow rate of 1 μl/min from left to right. Movie is 100 times faster than real time. Panel areas are 66 x 66 μm.

Movie S2. Transition from wave- to oscillation-mode during constant flow. Under constant 1 μl/min flow, MinD (green) / MinE (red) waves propagate upstream until a downstream wave catches up to the tail end of an upstream wave. The pattern then switched to a surface concentration oscillation of MinD and MinE over a broad area of the SLB. Movie is 150 times faster than real time. Panel areas are 66 x 66 μm.

Movie S3. Typical Min spiral without flow. Several minutes after flow stoppage, MinD (green) and MinE (red) formed highly regular and spiraling wave trains. Movie is 150 times faster than real time. Panel areas are 98 x 98 μm.

Movie S4. Min pattern initiation on an SLB without cardiolipin. A MinD (green) / MinE (red) initiation center breaking asymmetrically into an upstream travelling wave on an mSLB. Movie is 150 times faster than real time. Panel areas are 98 x 98 μm.

Movie S5. Min spiral on an SLB without cardiolipin. Several minutes after flow stoppage, MinD (green) and MinE (red) formed highly regular and spiraling wave trains on an mSLB. Movie is 150 times faster than real time. Panel areas are 98 x 98 μm.

Movie S6. Wave trains of Min proteins on an SLB made of PC and PS phospholipid. Movie is 150 times faster than real time. Panel areas are 66 x 66 μm.

SUPPORTING FIGURES

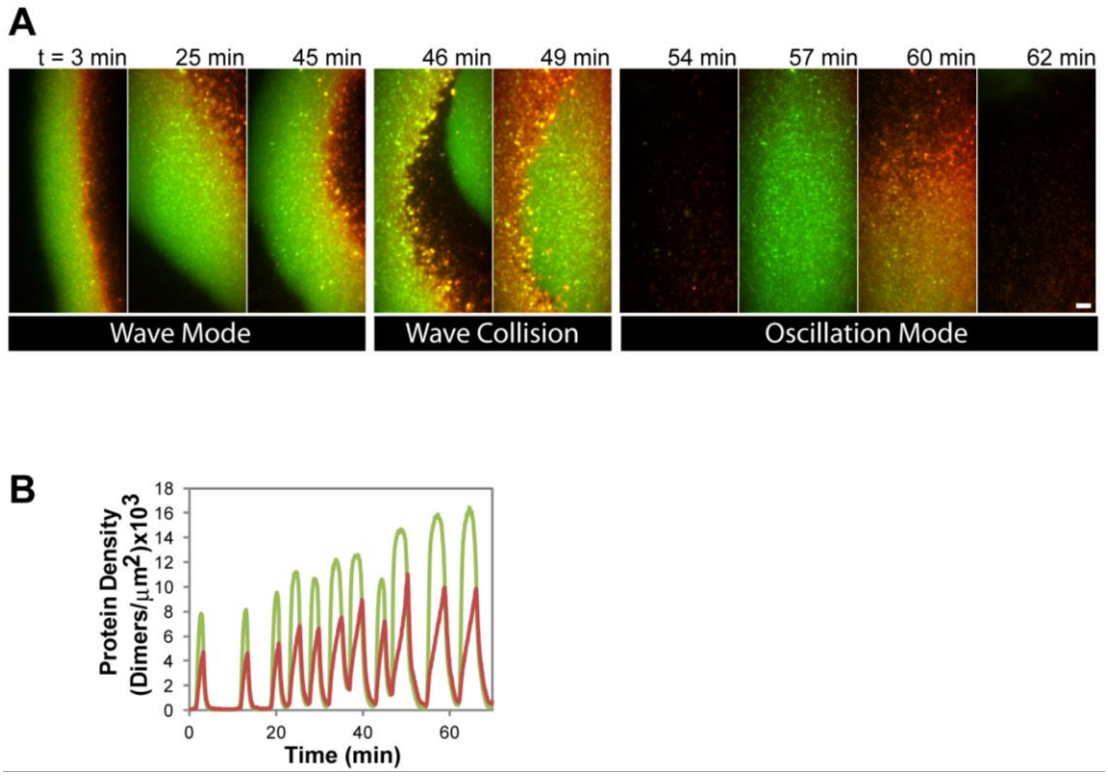

Figure S1. Transition from wave- to oscillation-mode during constant flow. (**A**) A time-lapse image series showing several waves propagating upstream (t = 3 to 45 min) until a downstream waves caught up to the tail end of an upstream wave (t = 46 to 49 min). At this point, the pattern switched to a surface concentration oscillation of bilayer-bound MinD and MinE over a broad area of the SLB (t = 54 to 62 min). This oscillation-mode persisted for hours while flow was maintained at 1 μl/min from left to right. Scale bar 5 μm. (**B**) Time-course of MinD (green) and MinE (red) protein densities at a fixed location within the flowcell shown in **A**. Time zero is when flow was initiated. See also Movie S2.

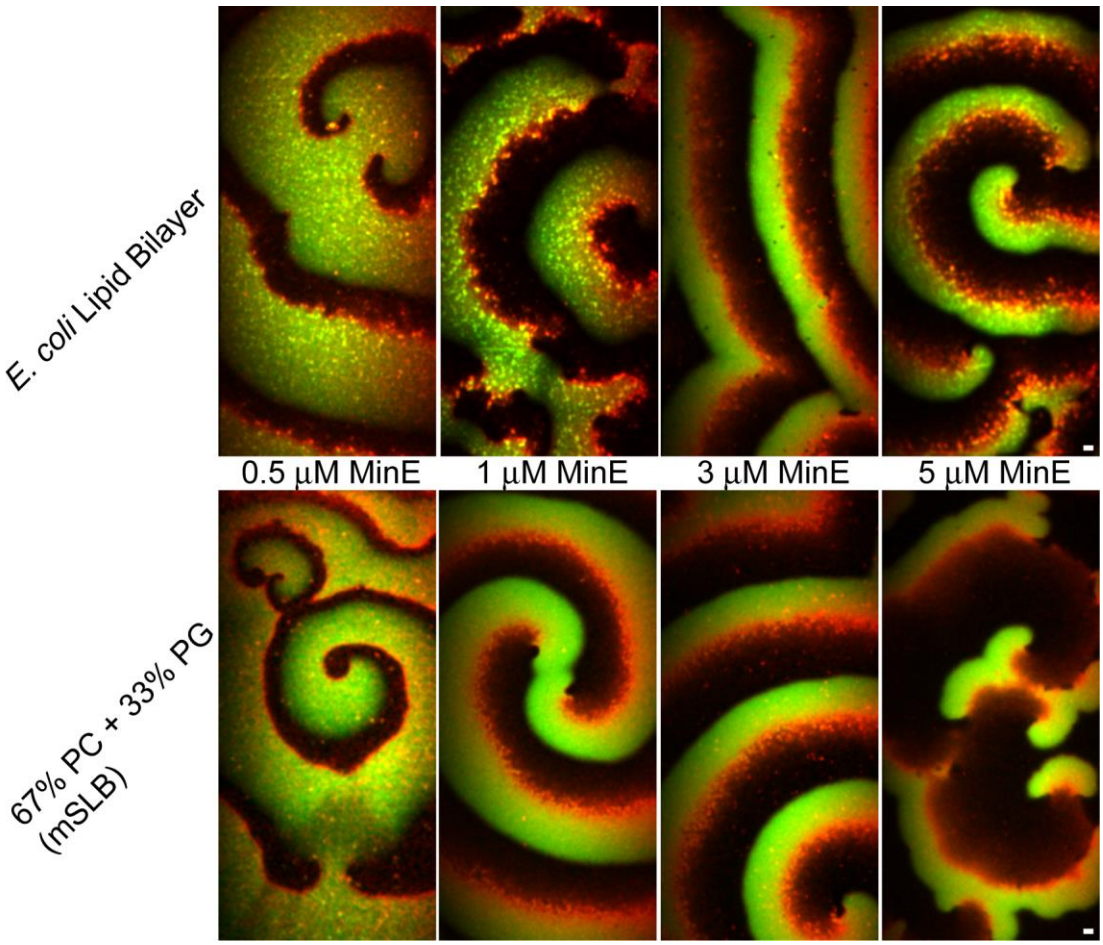

Figure S2. MinE concentration effects on Min spirals. Freeze frame images of Min spirals on *E. coli* lipid (top) and the mSLB without cardiolipin (bottom) at varying MinE concentrations. One micromolar GFP-MinD (green) and MinE (red; mixed 1:19 with MinE-Alexa 647) at the indicated concentration were preincubated with 2.5 mM ATP and infused into the flowcell. Several minutes after flow stoppage, MinD and MinE formed spiraling wave trains with band widths that narrowed with increasing MinE concentration. Scale bar 5 μm.

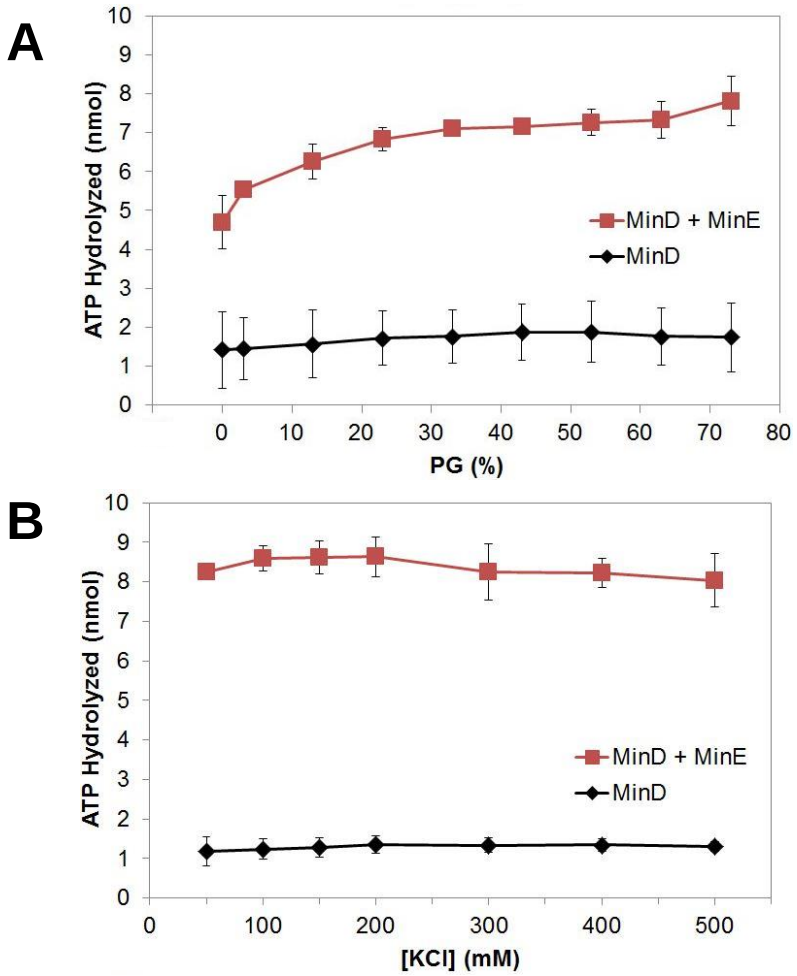

Figure S3. MinD ATPase activity at varying (A) liposome compositions and (B) salt concentrations. The ATPase activity of 5 μM MinD, with (red) or without (black) 5 μM MinE, was measured in 25 mM Tris-HCl (pH 7.4), 5 mM $MgCl_2$, 0.5 mg/ml lipid as small unilamellar vesicles, and 1 mM [γ-^{32}P]ATP (purified as described previously, Vecchiarelli *et al*., 2010). For **A**, the salt concentration in solution was held at 150 mM KCl. For **B**, the liposome composition was held at 67% PC + 33% PG (mSLB composition). Samples were incubated for 1 hr at 37 °C and analyzed by thin-layer chromatography as described previously (Fung *et al*., 2001). Error bars represent the SD for at least three independent experiments.

SUPPLEMENTARY REFERENCES

Fung, E., Bouet, J.Y., and Funnell, B.E. (2001) Probing the ATP-binding site of P1 ParA: partition and repression have different requirements for ATP binding and hydrolysis. *EMBO J* **20**: 4901–4911.

Vecchiarelli, A.G., Han, Y.W., Tan, X., Mizuuchi, M., Ghirlando, R., Biertumpfel, C., Funnell, B.E., and Mizuuchi, K. (2010) ATP control of dynamic P1 ParA–DNA interactions: a key role for the nucleoid in plasmid partition. *Mol Microbiol* **78**: 78–91.