Expanded View Figures

Figure EV1. Starvation induces a global change in locations of domain boundaries in *Caulobacter crescentus*.
Hi-C contact maps for intra-chromosomal arm interactions rotated 45° clockwise. Directional preference plots were used to assign domain boundaries (see Appendix Supplementary Materials and Methods). Leftward and rightward preferences are shown as green and red bars, respectively. Abrupt transitions from leftward to rightward preference correspond to chromosomal interaction domain boundaries. Vertical black and orange dashed lines indicate boundaries specific to growing or starved cells, respectively. The directional preference plot and "rpkm * transcript length" plot corresponding to each condition are shown beneath the Hi-C plots. For a complete tabulation of CID boundary locations, transcript lengths, and expression levels, see Dataset EV2.

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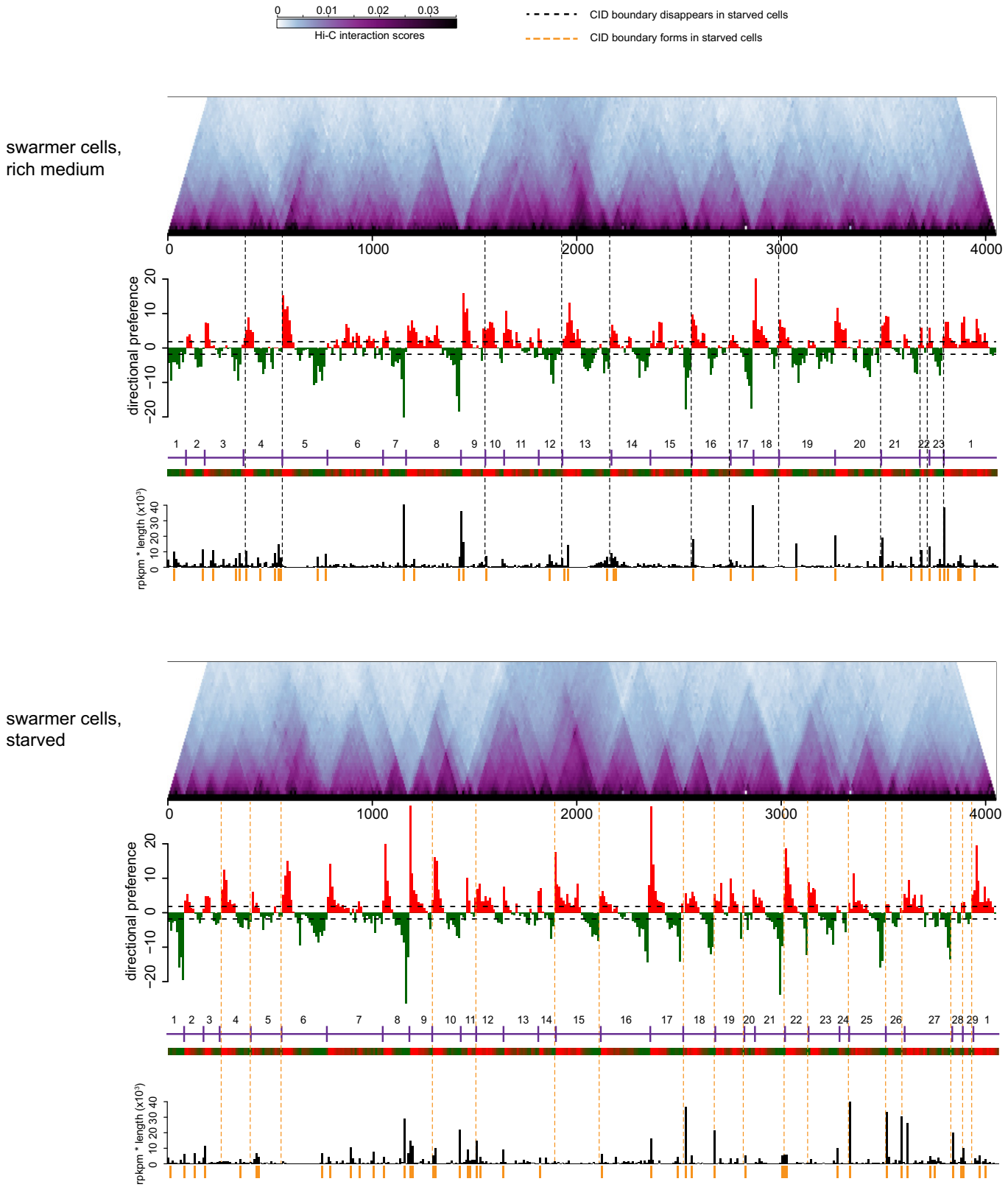

Figure EV1.

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Figure EV2. Expression levels and transcript lengths of wild-type *rsaA* and its derivatives.

A A schematic showing the location of RT–PCR products (green) examined for *rsaA* and the *ruvA* control. Transcripts are denoted as wavy red lines.
B RT–PCR products from RNA extracted from strains harboring the wild-type *rsaA* or the derivative indicated. Samples where no reverse transcriptase was added were included to control for genomic DNA contamination.
C Western blot of FLAG-tagged RsaA and its various derivatives indicated. Anti-FLAG primary antibody and anti-mouse secondary antibody were used.
D Contact probability plots showing interaction frequencies as a function of genomic distance for each strain examined by Hi-C in Figs 2 and 3.
E Expanded view of the region surrounding the site of insertion (dashed line) for each strain examined in Fig 2.

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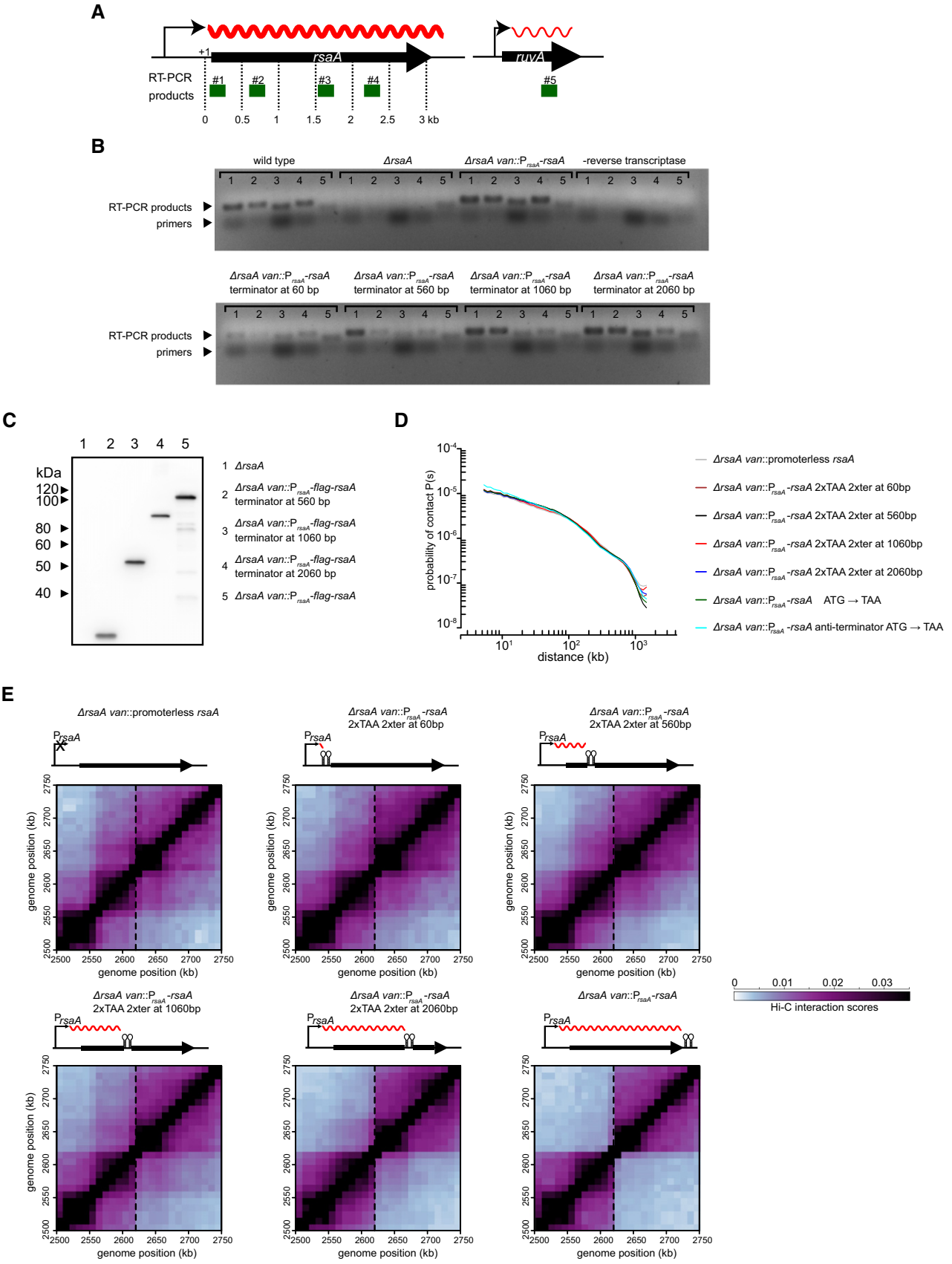

Figure EV2.

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Figure EV3. Expression levels and transcript lengths of *rsaA* variants.

A Independent repeats for the Hi-C maps in Fig 2 (right panel) and Fig 3 (left and center panels). A 1-Mbp region near the site of *rsaA* construct insertion (dashed line) is shown with the corresponding region of the directional preference plot below.

B Expanded view of the region surrounding the site of insertion (dashed line) for each strain examined in Fig 3.

C A schematic showing the location of RT–PCR products (green) examined for *rsaA* and a *ruvA* control locus. mRNA transcripts are denoted with wavy red lines.

D RT–PCR products from RNA extracted from a strain expressing wild-type *rsaA* or the derivative indicated. Wild-type samples where no reverse transcriptase was added were included to control for genomic DNA contamination.

E SDS–PAGE showing protein level after S-layer extraction by low pH for the strains indicated below. The position of RsaA on the gel is denoted by a black arrow.

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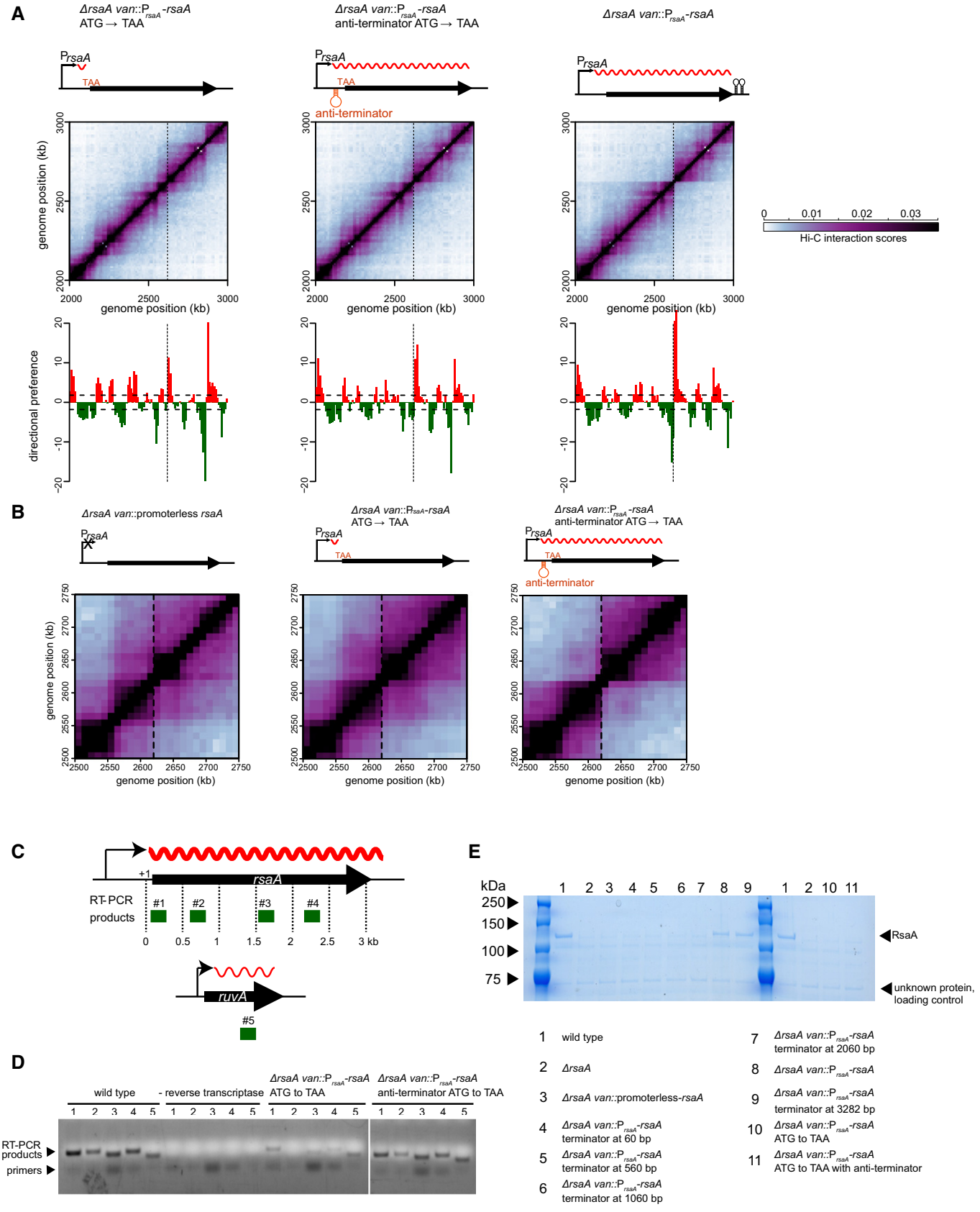

Figure EV3.

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Figure EV4. Hi-C analysis of elongated *Caulobacter* cells.

A Hi-C maps for cells depleted of DnaA for the times indicated. Only the top left half of each symmetric Hi-C map is shown with a region outlined shown as an inset along with a representative phase contrast micrograph of cells from each time point.

B Same as (A) but for cells overproducing CtrA(D51E)Δ3Ω.

C Same portion of the Hi-C maps shown in Fig 6A and B corresponding to the locations of loci examined by microscopy, but with directional preference plots below each panel.

D, E DNA–DNA contact probability P(s), plotted against genomic distance for (D) DnaA-depleted cells, or (E) cells overproducing CtrA(D51E)Δ3Ω at different time points after synchronization.

F, G Plots show the ratio of P(s) values at length scales up to 100 kb for locus–locus interactions within and between domains for (F) DnaA-depleted cells or (G) cells overproducing CtrA(D51E)Δ3Ω at different time points after synchronization.

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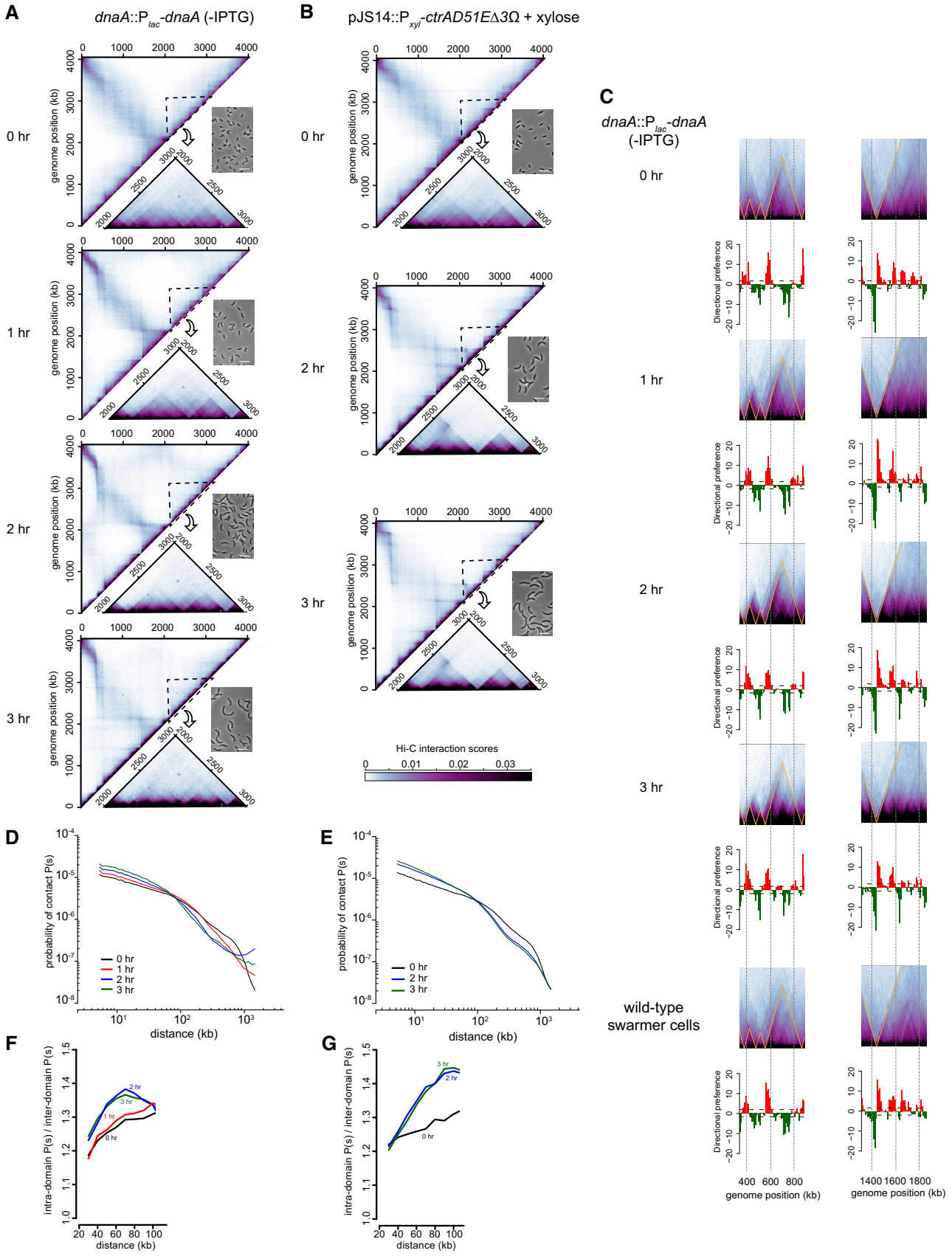

Figure EV4.

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