Supplementary: Polymer architecture orchestrates the segregation and spatial organization of replicating *E. coli* chromosomes in slow growth.

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I.. ARC-0: LOCI DISTRIBUTION ALONG CYLINDER LONG-AXIS POST REPLICATION

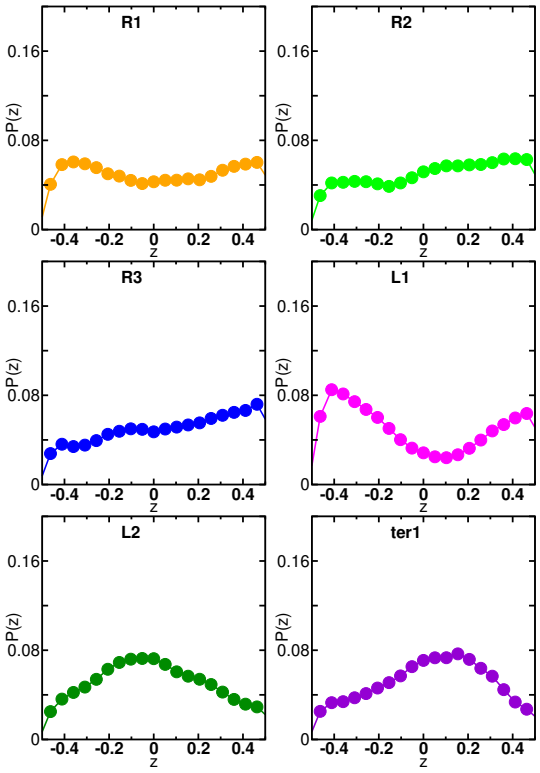

Figure S1. **Distribution of positions of loci along cylinder long axis post replication : Arc-0 architecture** The data shows the probability distribution of the monomers corresponding to the (a) R1, (b)R2, (c)R3, (d)L1, (e) L2 and (f) ter1 loci along the cylinder long axis for architecture Arc-0. The probability distributions in (a), (b), (c), (d), (e) and (f)) have been calculated from 20 independent runs post replication, from $10 - 15 \times 10^7$ MCS.

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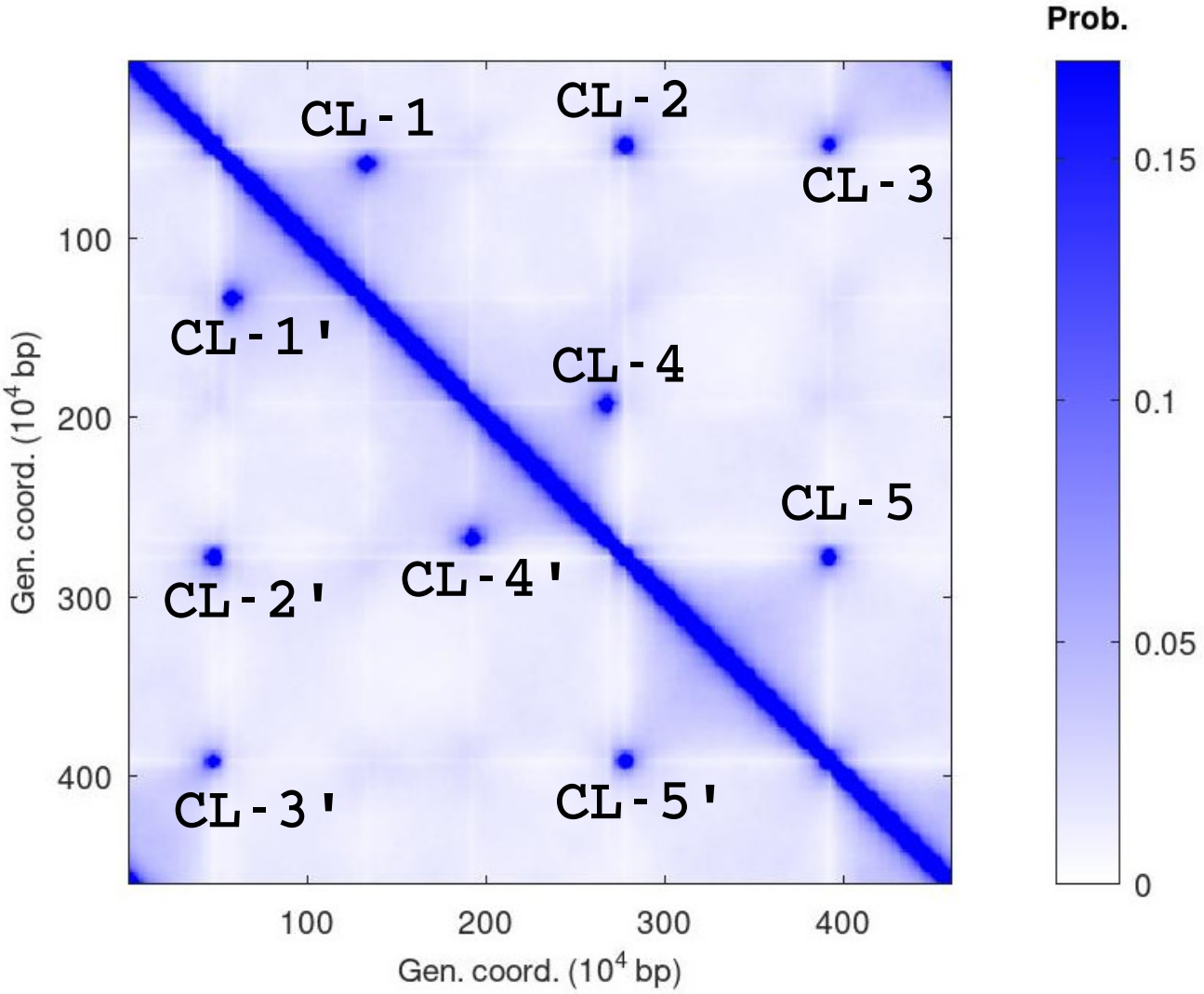

Figure S2. Contact map generated from simulations with CLs marked. The CLs with the primed indices are the "mirror" CLs present due to the symmetry of the contact map, i.e a CL with coordinates (x,y) has another corresponding bright spot with coordinate (y,x). We indicate these via the primed indices. Note that while we use only 4 CLs, we show here 5 CLs. This is because due to the CLs between monomer pairs (1,125) and (1,375), there is an "effective" CL created between monomer pairs (125,375).

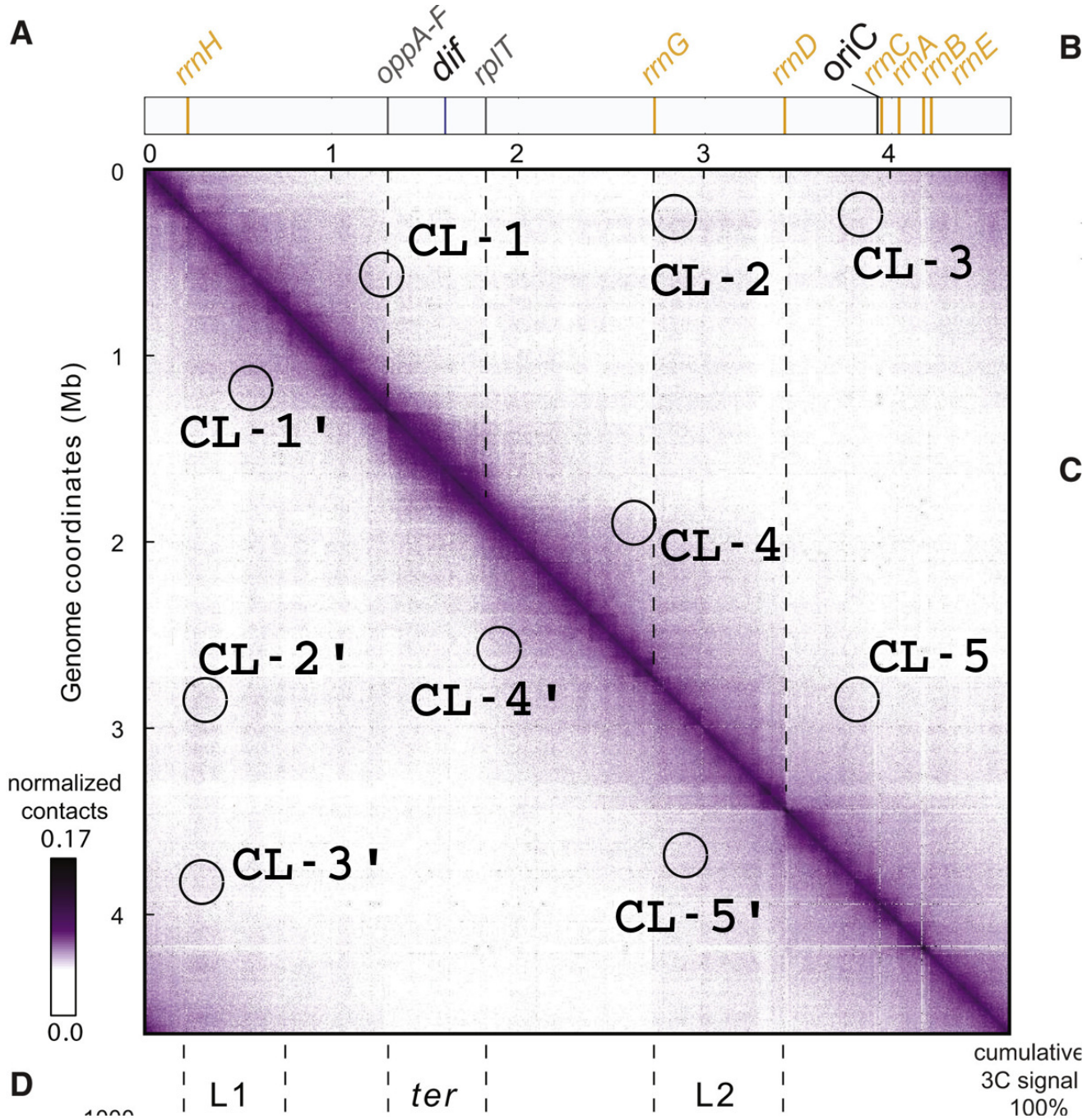

Figure S3. Contact map generated from Hi-C experiments with our additional cross-links (CLs) used in simulations, marked as CL-1,2,3 4,5. One can see that the sites of cross-linking have purple dots indicating high contact frequencies. Subsequently we provide the zoomed images of these CL-sites.

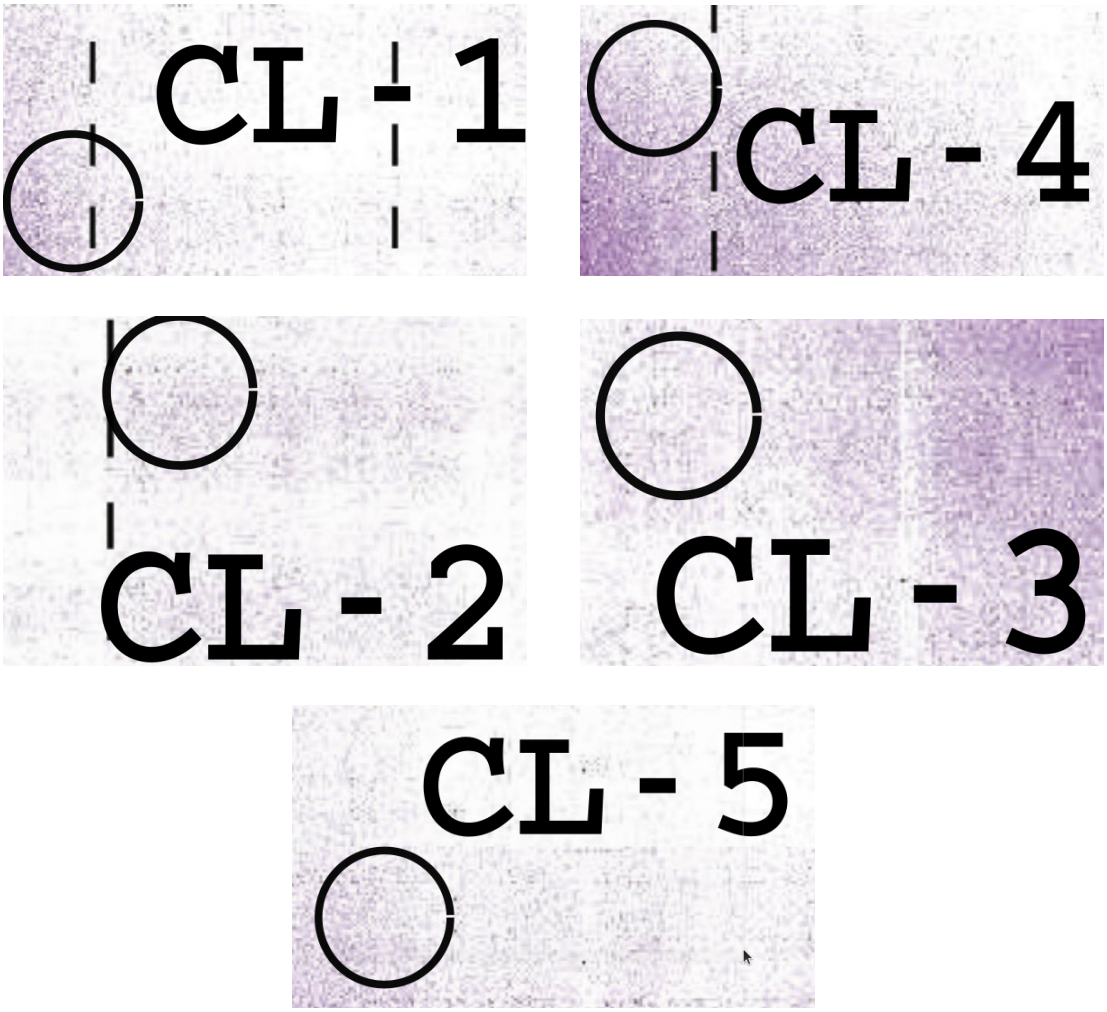

Figure S4. Zoomed images at the positions of the CLs (used in simulations) in the experimental HI-C map.These images have been generated by screen capture after zooming in to Fig.S3. We find that at the sites of the CLs (enclosed within open circles) there are grey/purple spots indicating high contact probabilities. We do not look at the zoomed images of the primed CLs indicated in Fig.S3 since due to the symmetry of the contact map they are equivalent to the unprimed CLs.

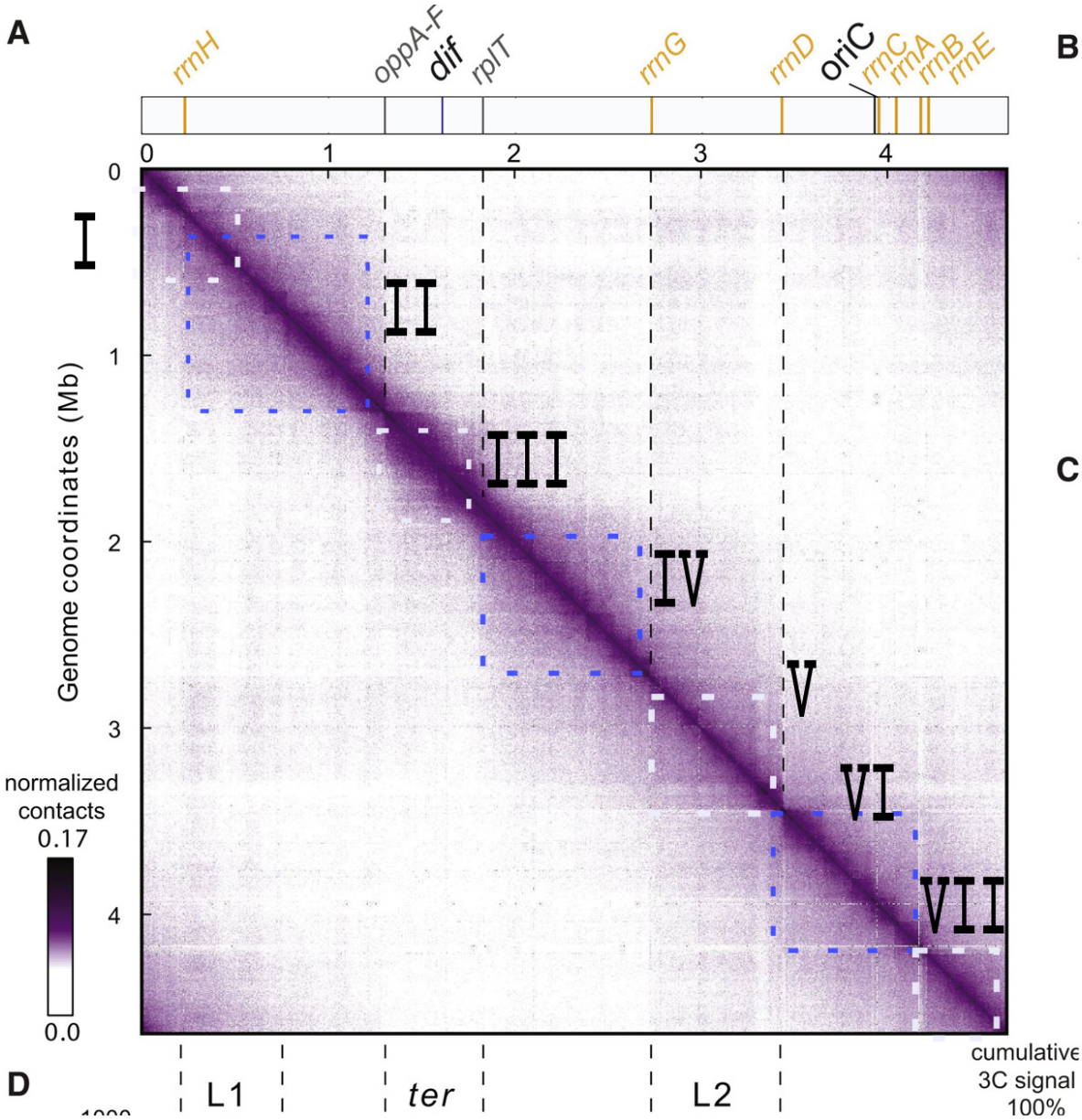

Figure S5. Contact map generated from Hi-C experiments reproduced from [1] with square patches of higher contact probabilities marked for aid of visualization. We have also shown the same Hi-C map in Fig.10 of the main manuscript.

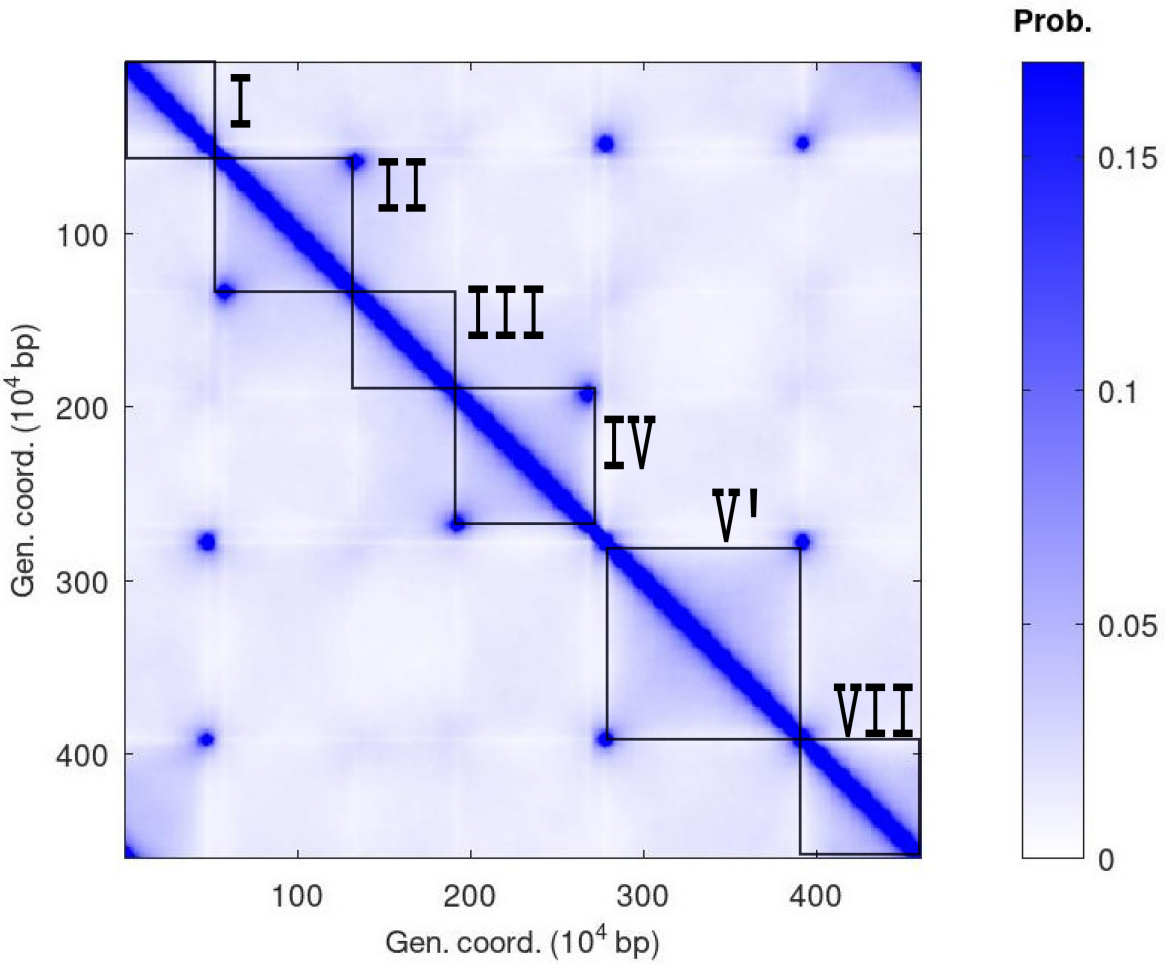

Figure S6. Contact map generated from simulations with bright square patches as a guide to the eye, to facilitate comparison with Fig.S5. We note that the unprimed regions (regions I-IV and region VII) are in fair agreement with the corresponding regions in the experimental contact map shown in Fig.S5. The primed region marked as V' is not similar to the region marked as V in Fig.S5. We also note the following:
We obtain a prominent ter macrodomain (region III) in the simulated contact map which arises spontaneously and is very similar to the ter macrodomain in the experimental contact map (region III).
The ter MD is more prominent in the experimental Hi- map. This is because the protein MatP is known to condense the ter region [2]. We have not incorporated this in the simulations.
The region marked as region V and VI in the experimental contact map shown in Fig.S5, does not feature in the simulated contact map,refer Fig.S6. However there is a bright patch marked as V' which is present in the simulated contact map.
A more detailed simulation model with additional CLs which further organizes region V' into smaller loops, is required to obtain a match with region V and VI. We however do not incorporate this in our model as the model is minimal in nature and only establishes the principles of entropic organization in bacterial chromosomes.

II.. MOVIE

We have uploaded a movie file where the unreplicated DNA with 500 monomers is shown in blue inside a cylinder of length $17.5a$ and diameter $7a$. During replication pink monomers of daughter DNA-2 get added and simultaneously the length of the confining cylinder keeps increasing to finally attain a aspect ratio of $1:5$. Finally, we see two segregated DNA-1 and DNA-2 polymers in two halves of the cylinder. The two *oriC*s are shown in red and the *dif-ter* is shown in yellow. The sizes of the *oriC*s and the *dif-ter* locus have been deliberately enlarged for aid of visualization. Note that the polymer architecture changes to the Arc-2 architecture after the replication of the 125th (and simultaneoulsy the 375th) monomer which occurs at $\sim 25s$ in the movie. The ter transition (change of ori-ori-ter configuration to the ori-ter-ori) configuration occurs at $\sim 47s$. Post the ter transition the *dif-ter* locus continues to fluctuate around the mid-cell position which is as seen in-vivo.

[1] Virginia S. Lioy, Axel Cournac, Martial Marbouty, Stéphane Duigou, Julien Mozziconacci, Olivier Espéli, Frédéric Boccard, and Romain Koszul. Multiscale structuring of the e. coli chromosome by nucleoid-associated and condensin proteins. *Cell*, 172(4):771–783.e18, February 2018.

[2] Virginia S. Lioy, Axel Cournac, Martial Marbouty, Stéphane Duigou, Julien Mozziconacci, Olivier Espéli, Frédéric Boccard, and Romain Koszul. Multiscale structuring of the e. coli chromosome by nucleoid-associated and condensin proteins. *Cell*, 172(4):771–783.e18, 2018.