**Hi-C/3C-Seq experiments performed so far on bacteria**

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| Organism | Paper | Key observations, Features |
| *E. coli* | Cedric Cagliero, Ralph S. Grand, M. Beatrix Jones, Ding J. Jin and Justin M. O’Sullivan. **Genome conformation capture reveals that the Escherichia coli chromosome is organized by replication and transcription.** NAR, 2013 | **No replichores alignment.**  Nothing interesting, low level of information on maps.  20kb map, HhaI RE |
| *E. coli* | Virginia S. Lioy, Axel Cournac, Martial Marbouty, Stephane Duigou, Julien Mozziconacci, Olivier Espeli, Frederic Boccard, and Romain Koszul. **Multiscale Structuring of the E. coli Chromosome by Nucleoid-Associated and Condensin Proteins**. Cell, 2018 | **No replichores alignment.**  3C-Seq for wt exponential, wt stationary, ΔmatP, ΔmukB, ΔhupAB, Δfis, Δhns  2kb map, HpaII RE |
| *C. crescentus* | Mark A. Umbarger, Esteban Toro, Matthew A. Wright, Gregory J. Porreca, Davide Baù, Sun-Hae Hong, Michael J. Fero, Marc A. Marti-Renom, Harley H. McAdams, Lucy Shapiro, Job Dekker, and George M. Church. **The Three-Dimensional Architecture of a Bacterial Genome**. Molecular Cell, 2011 | **Pronounced replichores alignment.**  5C: ParS site and replichores alignment  13kb map, BglII |
| *C. crescentus* | Tung B.K. Le, Maxim V. Imakaev, Leonid A. Mirny, and Michael T. Laub. **High-resolution mapping of the spatial organization of a bacterial chromosome**. Science, 2013 | **Pronounced replichores alignment.**  Hi-C and RNA-Seq  10kb map, BglII or NcoI RE |
| *C. crescentus* | Tung BK Le & Michael T Laub. **Transcription rate and transcript length drive formation of chromosomal interaction domain boundaries**. The EMBO journal, 2016 | **Pronounced replichores alignment.**  Hi-C: transcription and CID boundaries.  10kb map, BglII or NcoI RE |
| *C. crescentus* | Ngat T. Tran, Michael T. Laub, and Tung B.K. Le. **SMC Progressively Aligns Chromosomal Arms**  **in Caulobacter crescentus but Is Antagonized**  **by Convergent Transcription**. Cell reports, 2017 | **Pronounced replichores alignment.**  Hi-C: role of ParS/ParB/SMC  10kb map, BglII RE |
| *B. subtilis* | Martial Marbouty, Antoine Le Gall, Diego I. Cattoni, Axel Cournac, Alan Koh, Jean-Bernard Fiche, Julien Mozziconacci, Heath Murray, Romain Koszul, and Marcelo Nollmann. **Condensin- and Replication-Mediated Bacterial Chromosome Folding and Origin Condensation Revealed by Hi-C and Super-resolution Imaging**. Molecular cell, 2015 | **Pronounced replichores alignment.**  Hi-C: role of ParS/ParB/SMC  4kb map, HpaII RE |
| *B. subtilis* | Xindan Wang, Tung B.K. Le, Bryan R. Lajoie, Job Dekker, Michael T. Laub, and David Z. Rudner. **Condensin promotes the juxtaposition of DNA flanking its loading site in Bacillus subtilis**. Genes & Development, 2015 | **Pronounced replichores alignment.**  Hi-C: role of ParS/ParB/SMC  10kb map, HindIII RE |
| *B. subtilis* | Xindan Wang, Hugo B. Brandao, Tung B. K. Le, Michael T. Laub, and David Z. Rudner. ***Bacillus subtilis* SMC complexes juxtapose chromosome arms as they travel from origin to terminus.** Science, 2017 | **Pronounced replichores alignment.**  Hi-C: role of ParS/ParB/SMC  10kb map, HindIII RE |
| *B. subtilis* | Xindan Wang, Anna C. Hughes, Hugo B. Brandao, Benjamin Walker, Carrie Lierz, Jared C. Cochran, Martha G. Oakley, Andrew C. Kruse, and David Z. Rudner. **In Vivo Evidence for ATPase-Dependent DNA Translocation by the Bacillus subtilis SMC Condensin Complex**. Molecular cell, 2018 | **Pronounced replichores alignment.**  Hi-C: ATPase role of SMC  10kb map, HindIII RE |
| *Mycoplasma pneumoniae* | Marie Trussart, Eva Yus, Sira Martinez, Davide Bau, Yuhei O. Tahara, Thomas Pengo, Michael Widjaja, Simon Kretschmer, Jim Swoger, Steven Djordjevic, Lynne Turnbull, Cynthia Whitchurch, Makoto Miyata, Marc A. Marti-Renom, Maria Lluch-Senar & Luis Serrano.  **Defined chromosome structure in the genome reduced bacterium Mycoplasma pneumoniae**. Nature communications, 2017 | **Faint replichores alignment.**  Hi-C: low level of information. SMC is encoded in the genome, but what is with ParB and ParS  10kb map, HindIII or HpaII RE |
| *1) Bacillus subtilis*  *2) Flavobacterium johnsoniae*  *3) Escherichia coli*  *4) Methanococcus maripaludis*  *5) Vibrio fischery* | Joshua N. Burton, Ivan Liachko, Maitreya J. Dunham, and Jay Shendure. **Species-Level Deconvolution of Metagenome Assemblies with Hi-C–Based Contact Probability Maps**. G3, 2014 | **1) Faint replichore alignment**  **2) Pronounced replichores alignment**  **3) No replichores alignment**  **4) No information on the map - very high noise**  **5) No information on the map - very high noise**  Hi-C: in general, low level of information.  Resolution is not applicable; HindIII or NcoI RE |
| *1) Escherichia coli*  *2) Bacillus subtilis*  *3) Vibrio cholerae*  *4) Aeromonas veronii* | Martial Marbouty, Axel Cournac, Jean-François Flot, Hervé Marie-Nelly, Julien Mozziconacci, Romain Koszul. **Metagenomic chromosome conformation capture (meta3C) unveils the diversity of chromosome organization in microorganisms**. eLIFE, 2014 | **1) No replichores alignment**  **2) Pronounced replichores alignment**  **3) Pronounced replichores alignment**  **4) Pronounced replichores alignment**  10kb map, HaeIII RE |
| *1) Clostridium*  *2) Desulfovibrio*  *3) Odoribacter*  *4) Prevotella*  *5) Lachnospiraceae* | Martial Marbouty, Lyam Baudry, Axel Cournac, Romain Koszul. **Scaffolding bacterial genomes and probing host-virus interactions in gut microbiome by proximity ligation (chromosome capture) assay**. Science advances, 2017 | **1) Pronounced replichores alignment**  **2) Pronounced replichores alignment**  **3) Pronounced replichores alignment**  **4) No replichores alignment**  **5) No replichores alignment**  10kb map |