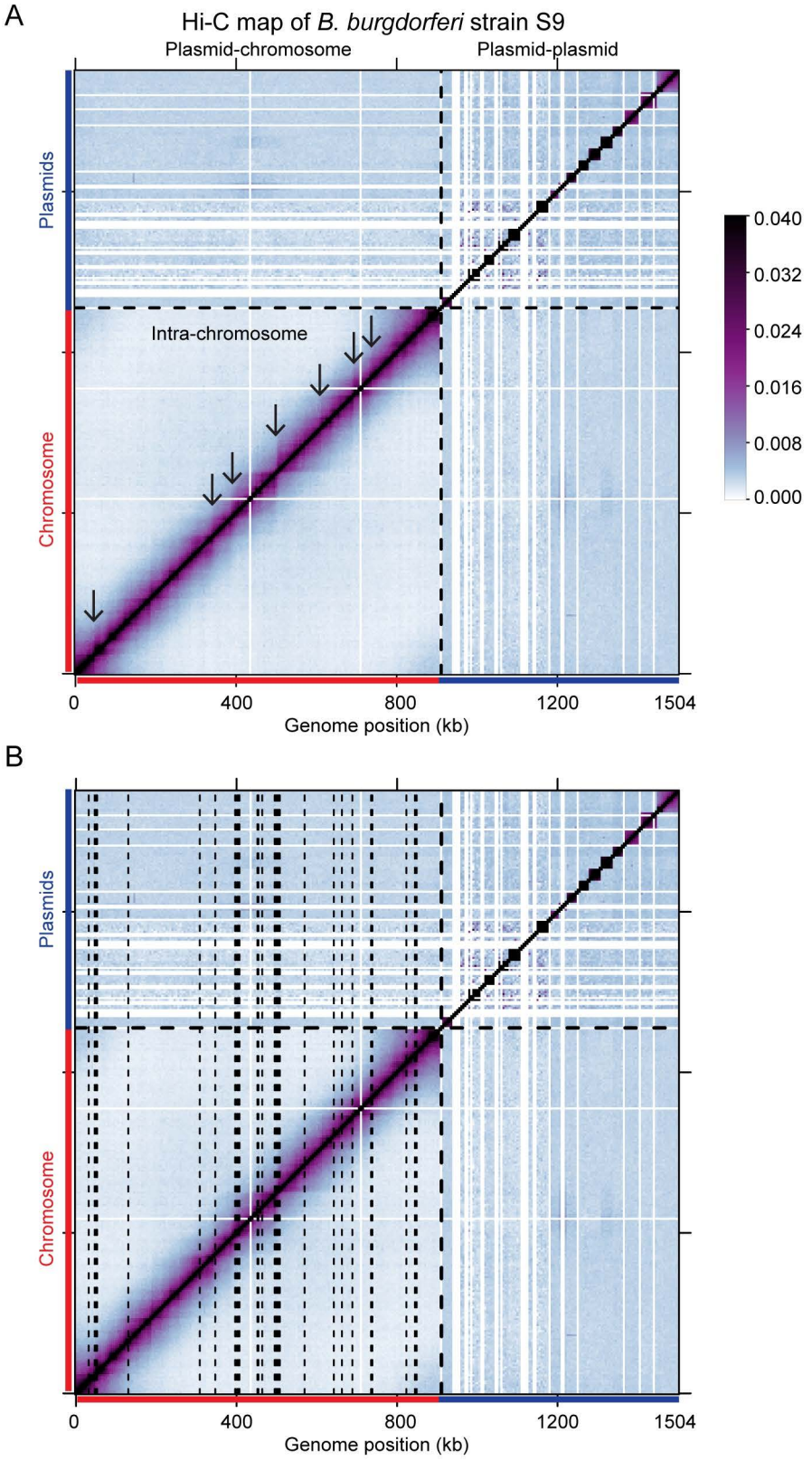
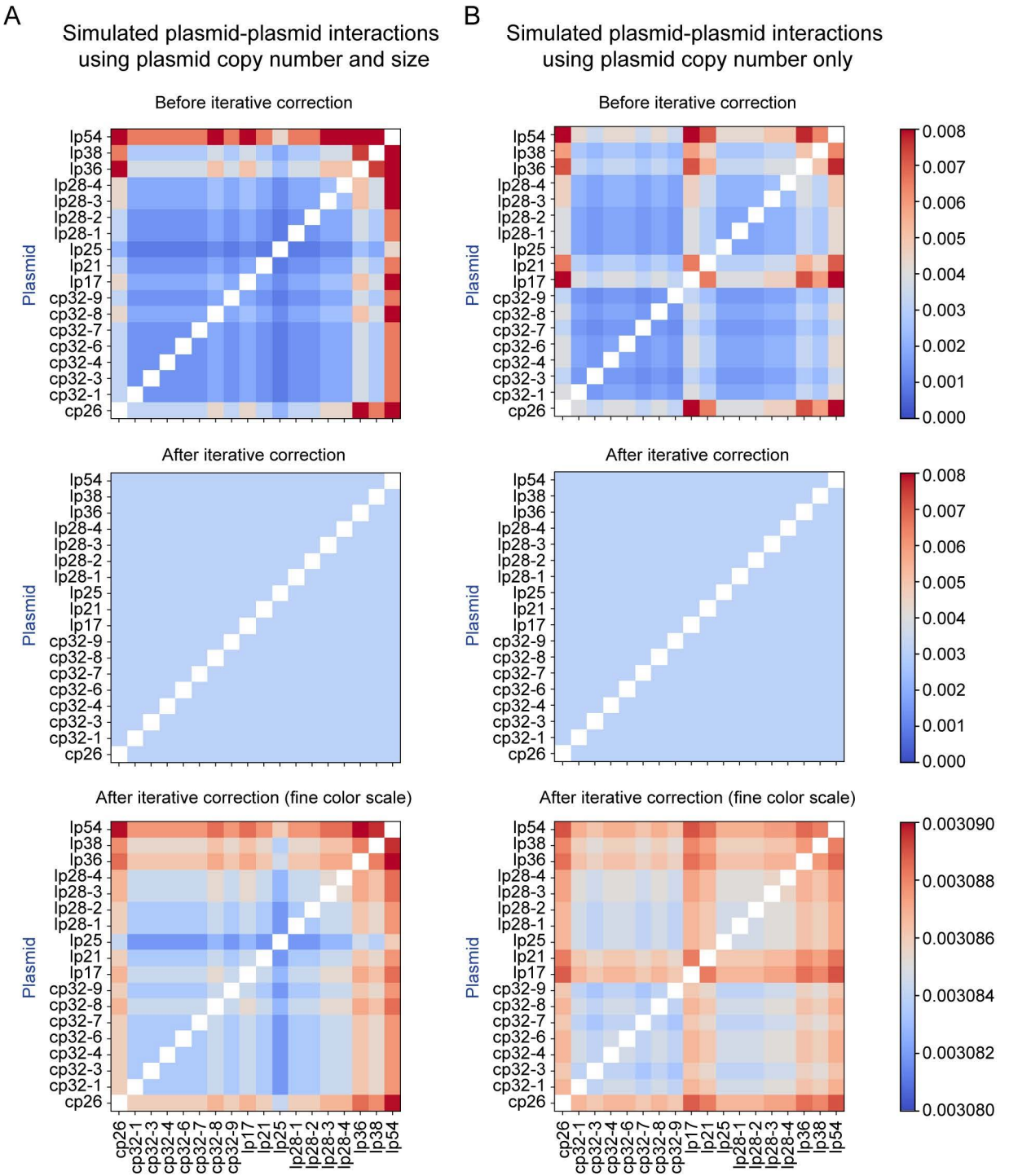

A
Hi-C map of B. burgdorferi strain S9
Plasmid-chromosome
Plasmid-plasmid
Plasmids
Chromosome
Intra-chromosome
0.040
0.032
0.024
0.016
0.008
0.000
0
400
800
1200
1504
Genome position (kb)
B
Plasmids
Chromosome
0
400
800
1200
1504
Genome position (kb)

S1 Fig. Hi-C interaction map of *B. burgdorferi* strain S9 shown in a different color scale.

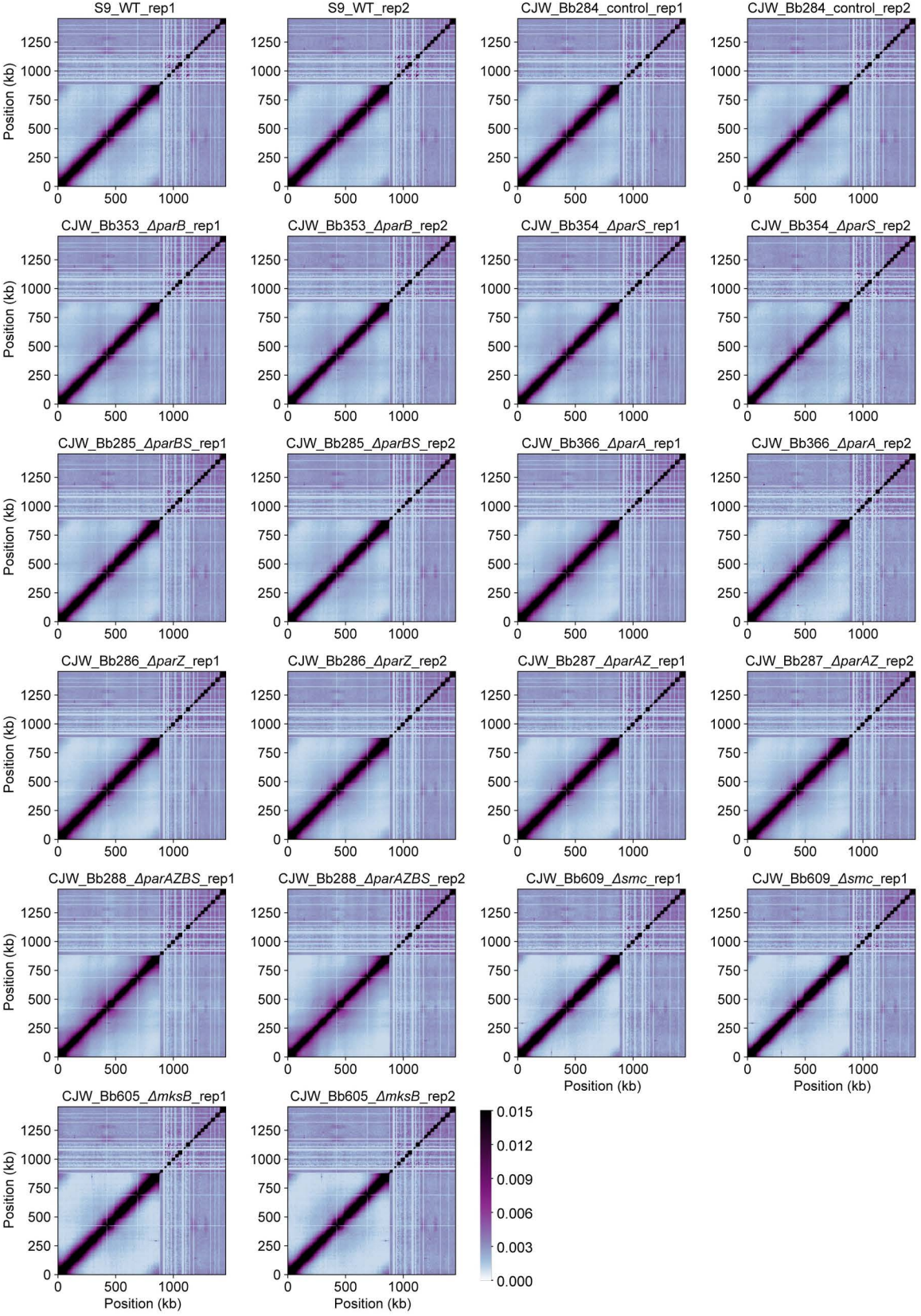
(A) To better show the intra-chromosomal interactions in **Fig 1B**, the normalized Hi-C interaction map is shown in a different color scale. Black arrows point to a few examples of strong CID boundaries that overlap with highly transcribed genes shown in (**B**). The color scale depicting Hi-C interaction scores in arbitrary units is shown at the right.

(B) The positions of the top 50 highly transcribed chromosomal genes found by RNA-seq [46] are indicated using fine black dotted lines. A recent study [46] published RNA-seq data of the *B. burgdorferi* B31-S9 strain grown in culture. We mapped the data to the *B. burgdorferi* B31 genome, calculated the number of transcripts per kilobase per million reads for each gene, and indicated the top 50 highly transcribed genes on the Hi-C map. Although the growth condition in our study was different from the RNA-seq study [46], strong CIDs boundaries (black arrows in **A**) largely overlap with highly transcribed genes.


A
Simulated plasmid-plasmid interactions using plasmid copy number and size
B
Simulated plasmid-plasmid interactions using plasmid copy number only
Before iterative correction
After iterative correction
After iterative correction (fine color scale)
Plasmid
lp54
lp38
lp36
lp28-4
lp28-3
lp28-2
lp28-1
lp25
lp21
lp17
cp32-9
cp32-8
cp32-7
cp32-6
cp32-4
cp32-3
cp32-1
cp26
0.008
0.007
0.006
0.005
0.004
0.003
0.002
0.001
0.000
0.003090
0.003088
0.003086
0.003084
0.003082
0.003080

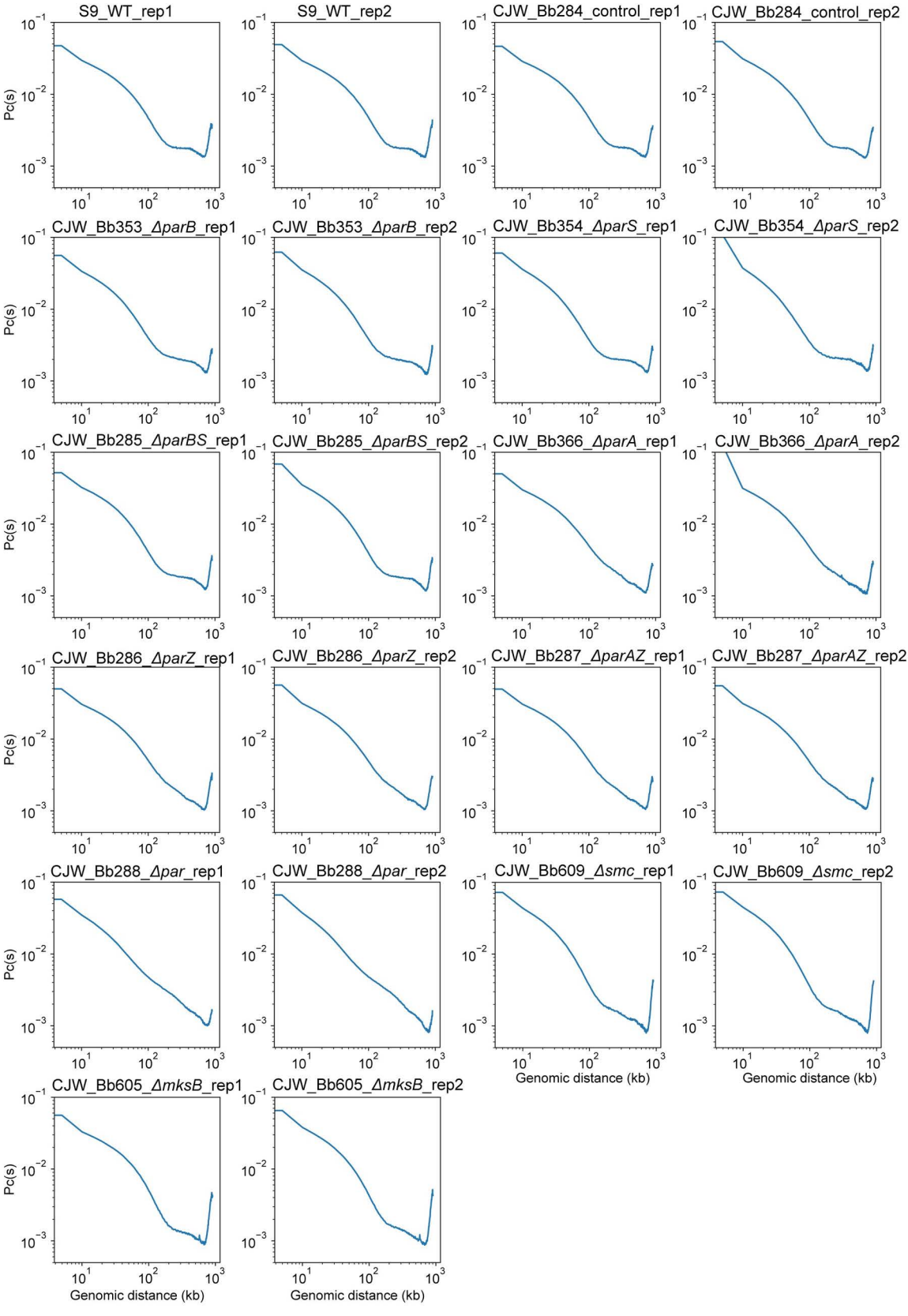
S2 Fig. Simulated plasmid-plasmid interaction frequencies.

The contact probability between plasmids was simulated under the assumptions that plasmids are randomly interacting, independent of one another, and are “well mixed” within the cytoplasm (see Materials and methods). The calculation was performed accounting for plasmid copy numbers and plasmid lengths together (**A**) or only plasmid copy numbers (**B**). Top panels, the raw contact frequency expected between plasmids without normalization. Middle panels, the simulated contact frequency after normalization using iterative correction. Bottom panels, the same as middle panels, but shown with a much finer color scale. The color scales depicting contact frequencies in arbitrary units are shown at the right. We note that there is residual resemblance between bottom and top panels, and in the bottom panel, the row or column sums do not appear to be the same. This is because the iterative correction procedure stops when the row and column sums approach 1 within a pre-defined error tolerance (see Materials and methods), but not exactly at 1.


S9_WT_rep1
S9_WT_rep2
CJW_Bb284_control_rep1
CJW_Bb284_control_rep2
CJW_Bb353_ΔparB_rep1
CJW_Bb353_ΔparB_rep2
CJW_Bb354_ΔparS_rep1
CJW_Bb354_ΔparS_rep2
CJW_Bb285_ΔparBS_rep1
CJW_Bb285_ΔparBS_rep2
CJW_Bb366_ΔparA_rep1
CJW_Bb366_ΔparA_rep2
CJW_Bb286_ΔparZ_rep1
CJW_Bb286_ΔparZ_rep2
CJW_Bb287_ΔparAZ_rep1
CJW_Bb287_ΔparAZ_rep2
CJW_Bb288_ΔparAZBS_rep1
CJW_Bb288_ΔparAZBS_rep2
CJW_Bb609_Δsmc_rep1
CJW_Bb609_Δsmc_rep1
CJW_Bb605_ΔmksB_rep1
CJW_Bb605_ΔmksB_rep2
Position (kb)
0
250
500
750
1000
1250
0.015
0.012
0.009
0.006
0.003
0.000

S3 Fig. Hi-C samples used in this study.

The normalized Hi-C interaction maps of all 22 experiments done for this study. The color scale depicting Hi-C interaction scores is shown at the bottom right.

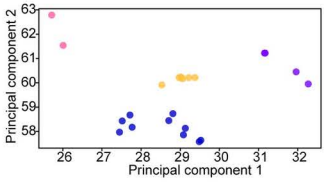

S9_WT_rep1
S9_WT_rep2
CJW_Bb284_control_rep1
CJW_Bb284_control_rep2
CJW_Bb353_ΔparB_rep1
CJW_Bb353_ΔparB_rep2
CJW_Bb354_ΔparS_rep1
CJW_Bb354_ΔparS_rep2
CJW_Bb285_ΔparBS_rep1
CJW_Bb285_ΔparBS_rep2
CJW_Bb366_ΔparA_rep1
CJW_Bb366_ΔparA_rep2
CJW_Bb286_ΔparZ_rep1
CJW_Bb286_ΔparZ_rep2
CJW_Bb287_ΔparAZ_rep1
CJW_Bb287_ΔparAZ_rep2
CJW_Bb288_Δpar_rep1
CJW_Bb288_Δpar_rep2
CJW_Bb609_Δsmc_rep1
CJW_Bb609_Δsmc_rep2
CJW_Bb605_ΔmksB_rep1
CJW_Bb605_ΔmksB_rep2
Pc(s)
Genomic distance (kb)

S4 Fig. Individual Pc(s) curves of all the samples analyzed in this study.
Pc(s) curves of all 22 Hi-C experiments done in this study. The x-axis indicates genomic distance while the y-axis shows averaged contact frequency. Only intra-chromosomal interactions were used to calculate the Pc(s) curves.

PCA with groups from K-means clustering on log(Pc(s)) curves

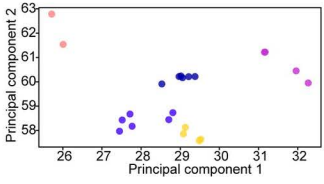
Components 1 and 2 explain 48% and 37% of the variance, respectively

4 clusters



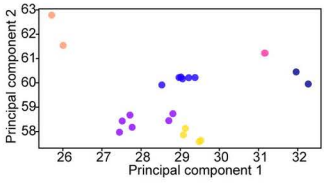
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep1, ΔparAZ_rep2, ΔparA_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔparS_rep1, WT_rep2, ΔparS_rep2, ΔparB_rep1, WT_rep1, ΔparBS_rep1, ΔparBS_rep2, control_rep2, control_rep1, ΔparB_rep2
Group: ΔmksB_rep1, ΔmksB_rep2, Δsmc_rep1, Δsmc_rep2

5 clusters



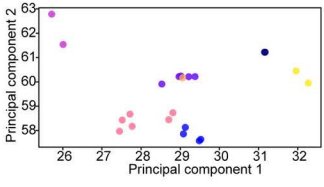
Group: ΔparS_rep1, ΔparS_rep2, ΔparB_rep1, ΔparBS_rep1, ΔparBS_rep2, ΔparB_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep1, ΔparAZ_rep2, ΔparA_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔmksB_rep1, ΔmksB_rep2, Δsmc_rep1, Δsmc_rep2

6 clusters



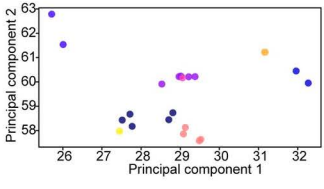
Group: ΔparS_rep1, ΔparS_rep2, ΔparB_rep1, ΔparBS_rep1, ΔparBS_rep2, ΔparB_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep1, ΔparAZ_rep2, ΔparA_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1

7 clusters



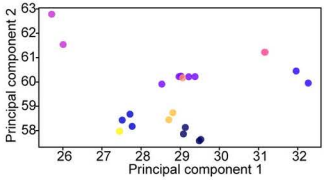
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparS_rep1, ΔparS_rep2, ΔparB_rep1, ΔparBS_rep1, ΔparBS_rep2, ΔparB_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparA_rep2

8 clusters



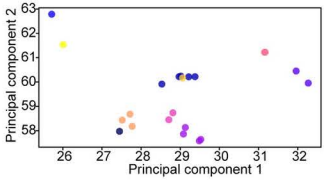
Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparBS_rep1, ΔparB_rep2, ΔparBS_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparA_rep2

9 clusters



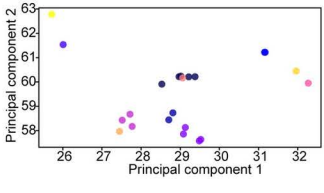
Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparB_rep2
Group: ΔparBS_rep1, ΔparBS_rep2
Group: ΔparA_rep2

10 clusters



Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparAZBS_rep1
Group: ΔmksB_rep1, ΔmksB_rep2
Group: ΔparAZBS_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparB_rep2
Group: ΔparBS_rep1, ΔparBS_rep2
Group: ΔparA_rep2

11 clusters



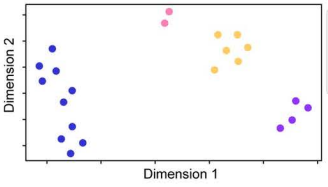
Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔmksB_rep1
Group: ΔparAZBS_rep1
Group: ΔmksB_rep2
Group: ΔparAZBS_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparB_rep2
Group: ΔparBS_rep1, ΔparBS_rep2
Group: ΔparA_rep2

S5 Fig. Principal Component Analysis (PCA) with groups from k-means clustering results.

To better visualize the results of the k-means clustering generated by the Silhouette method, we performed Principal Component Analysis (PCA) and labeled the clustering results (see Materials and methods). The plots with up to six clusters gave nicely visually segregated groups. Beyond six, the two-dimensional projections from PCA showed poor segregation of the data points, and biological replicates were separated to different groups.

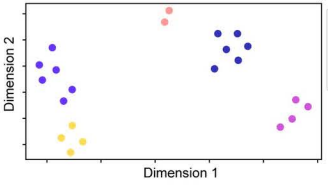
T-distributed stochastic neighbor embedding with groups from K-means clustering on log(Pc(s)) curves

4 clusters



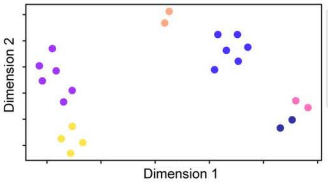
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep1, ΔparAZ_rep2, ΔparA_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔparS_rep1, WT_rep2, ΔparS_rep2, ΔparB_rep1, WT_rep1, ΔparBS_rep1, ΔparBS_rep2, control_rep2, control_rep1, ΔparB_rep2
Group: ΔmksB_rep1, ΔmksB_rep2, Δsmc_rep1, Δsmc_rep2

5 clusters



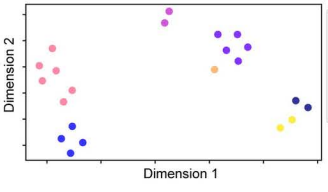
Group: ΔparS_rep1, ΔparS_rep2, ΔparB_rep1, ΔparBS_rep1, ΔparBS_rep2, ΔparB_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep1, ΔparAZ_rep2, ΔparA_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔmksB_rep1, ΔmksB_rep2, Δsmc_rep1, Δsmc_rep2

6 clusters



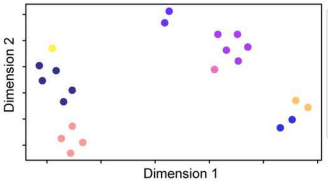
Group: ΔparS_rep1, ΔparS_rep2, ΔparB_rep1, ΔparBS_rep1, ΔparBS_rep2, ΔparB_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep1, ΔparAZ_rep2, ΔparA_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1

7 clusters



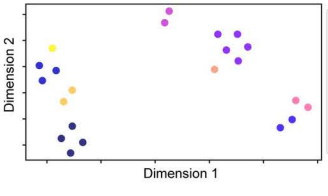
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparS_rep1, ΔparS_rep2, ΔparB_rep1, ΔparBS_rep1, ΔparBS_rep2, ΔparB_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparA_rep2

8 clusters



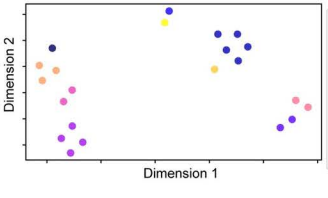
Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparBS_rep1, ΔparB_rep2, ΔparBS_rep2
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparA_rep2

9 clusters



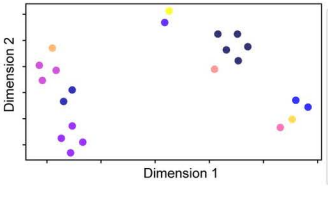
Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparAZBS_rep1, ΔparAZBS_rep2
Group: ΔmksB_rep1, ΔmksB_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparB_rep2
Group: ΔparBS_rep1, ΔparBS_rep2
Group: ΔparA_rep2

10 clusters



Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔparAZBS_rep1
Group: ΔmksB_rep1, ΔmksB_rep2
Group: ΔparAZBS_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparB_rep2
Group: ΔparBS_rep1, ΔparBS_rep2
Group: ΔparA_rep2

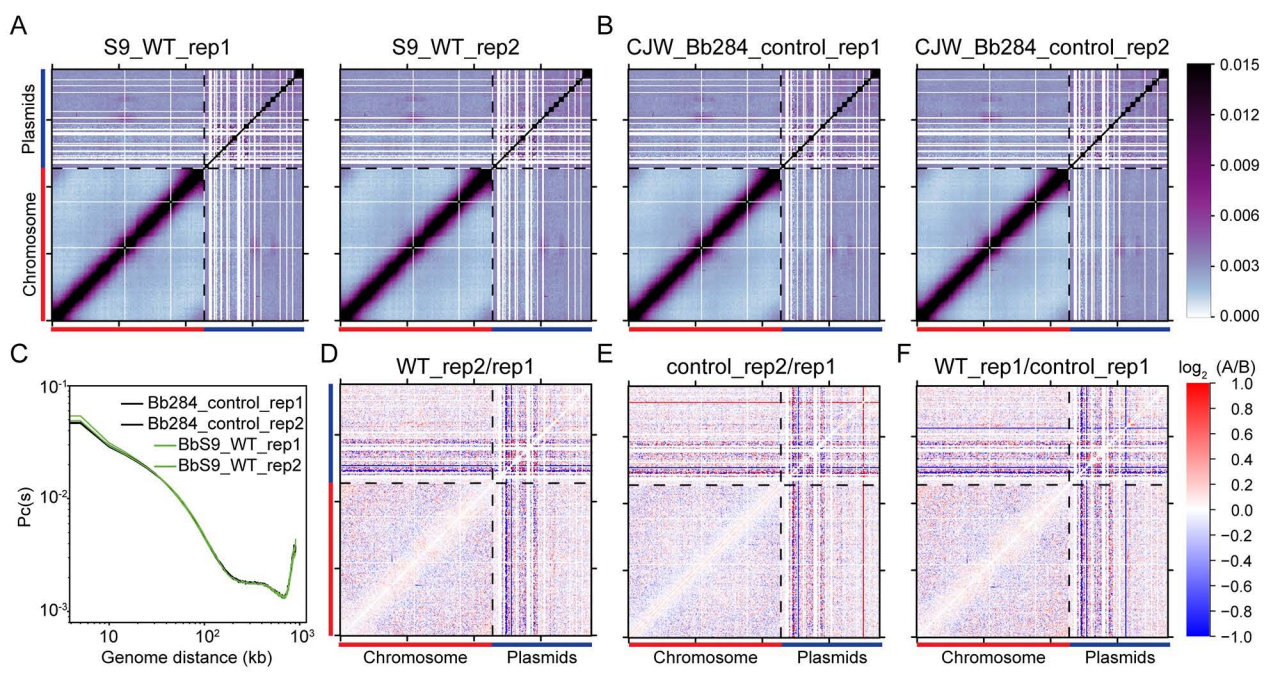
11 clusters



Group: ΔparS_rep2
Group: ΔparZ_rep2, ΔparA_rep1, ΔparZ_rep1, ΔparAZ_rep2, ΔparAZ_rep1
Group: ΔmksB_rep1
Group: ΔparAZBS_rep1
Group: ΔmksB_rep2
Group: ΔparAZBS_rep2
Group: Δsmc_rep1, Δsmc_rep2
Group: WT_rep1, WT_rep2, control_rep2, control_rep1
Group: ΔparS_rep1, ΔparB_rep1, ΔparB_rep2
Group: ΔparBS_rep1, ΔparBS_rep2
Group: ΔparA_rep2

S6 Fig. T-distributed stochastic neighbor embedding (t-SNE) with groups from k-means clustering results.

To better visualize the results of the k-means clustering generated by the Silhouette method, we performed t-distributed stochastic neighbor embedding (t-SNE) and labeled the clustering results (see Materials and methods). Similar to PCA, the plots with up to six clusters gave nicely visually segregated groups. Beyond six, the two-dimensional projections from t-SNE showed poor segregation of the data points, and biological replicates were separated to different groups.

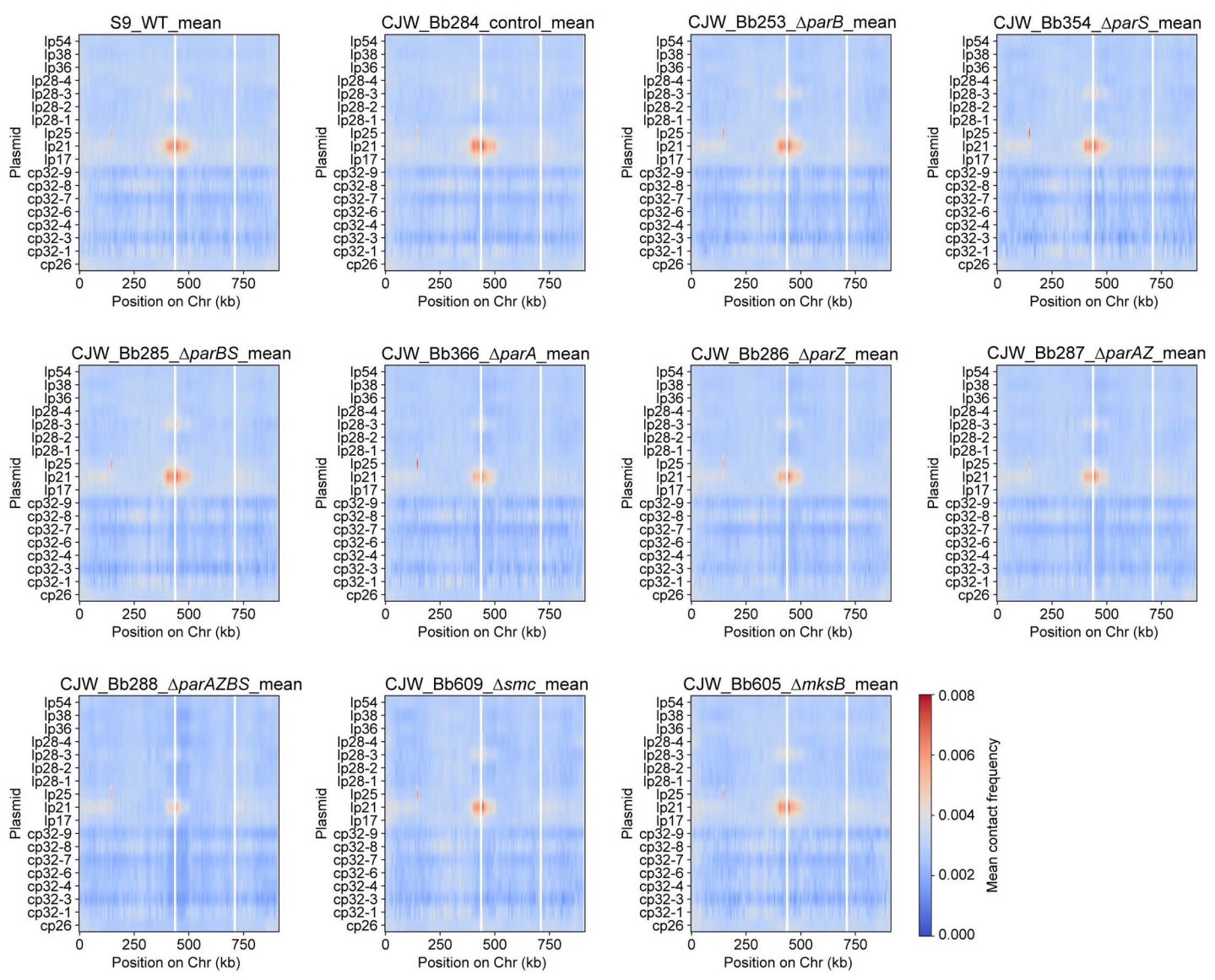

A
S9_WT_rep1
S9_WT_rep2
Plasmids
Chromosome
B
CJW_Bb284_control_rep1
CJW_Bb284_control_rep2
0.015
0.012
0.009
0.006
0.003
0.000
C
Bb284_control_rep1
Bb284_control_rep2
BbS9_WT_rep1
BbS9_WT_rep2
Pc(s)
Genome distance (kb)
D
WT_rep2/rep1
E
control_rep2/rep1
F
WT_rep1/control_rep1
log2 (A/B)
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
Chromosome
Plasmids

S7 Fig. Comparison of WT and control strains.

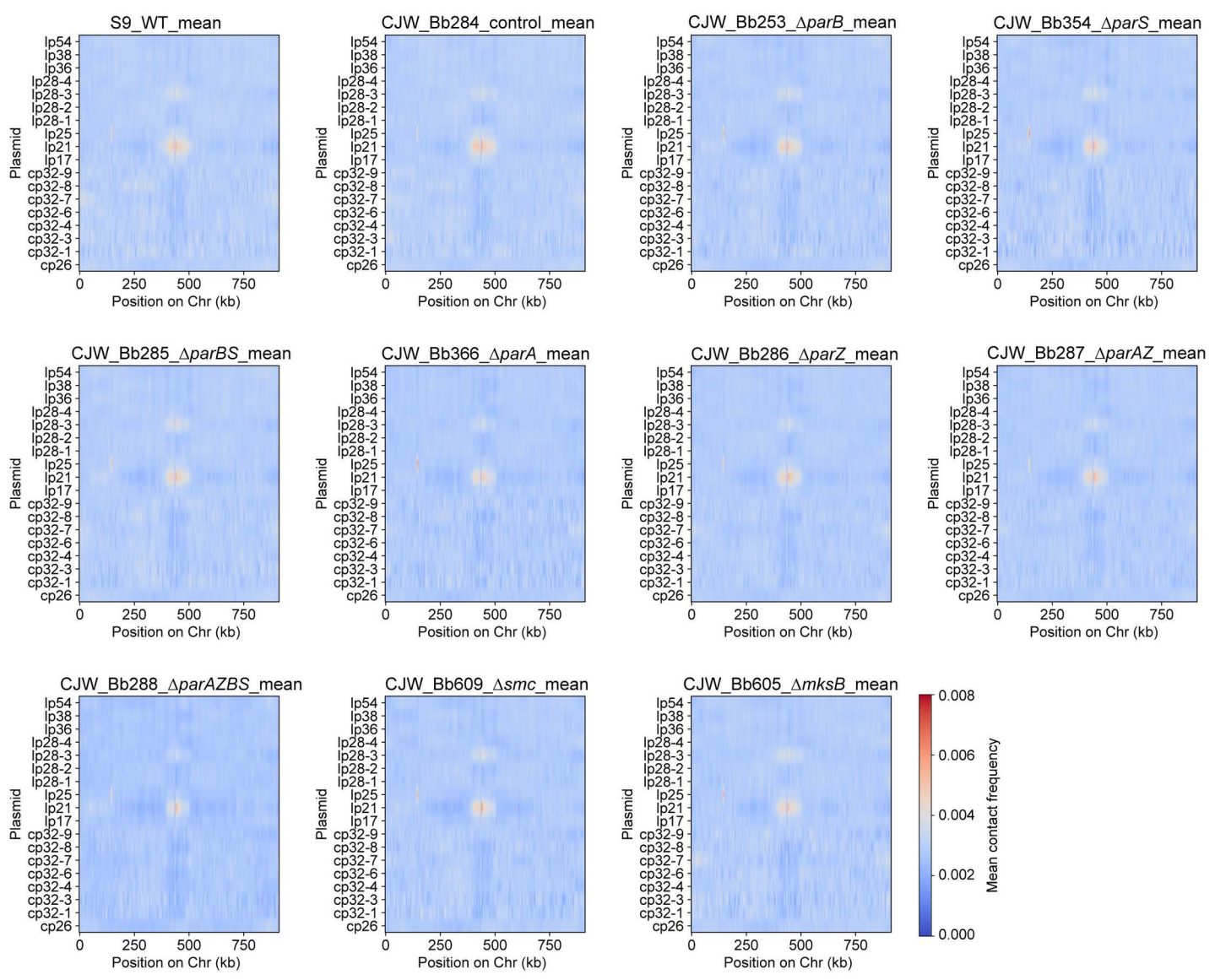
(A-B) Normalized Hi-C interaction maps of *B. burgdorferi* strains S9 (WT) and the control strain CJW_Bb284. Two biological replicates of each strain (rep1 and rep2) are shown. The color scale depicting Hi-C interaction scores in arbitrary units is shown at the right.

(C) Pc(s) curves of the four samples. Pc(s) curves show the averaged contact frequency between all pairs of loci on the chromosome separated by set distance (s). The x-axis indicates the genomic distance of separation in kb. The y-axis represents the averaged contact frequency. The curves were computed for data binned at 5 kb. Only intra-chromosomal interactions were used to calculate the Pc(s) curves.

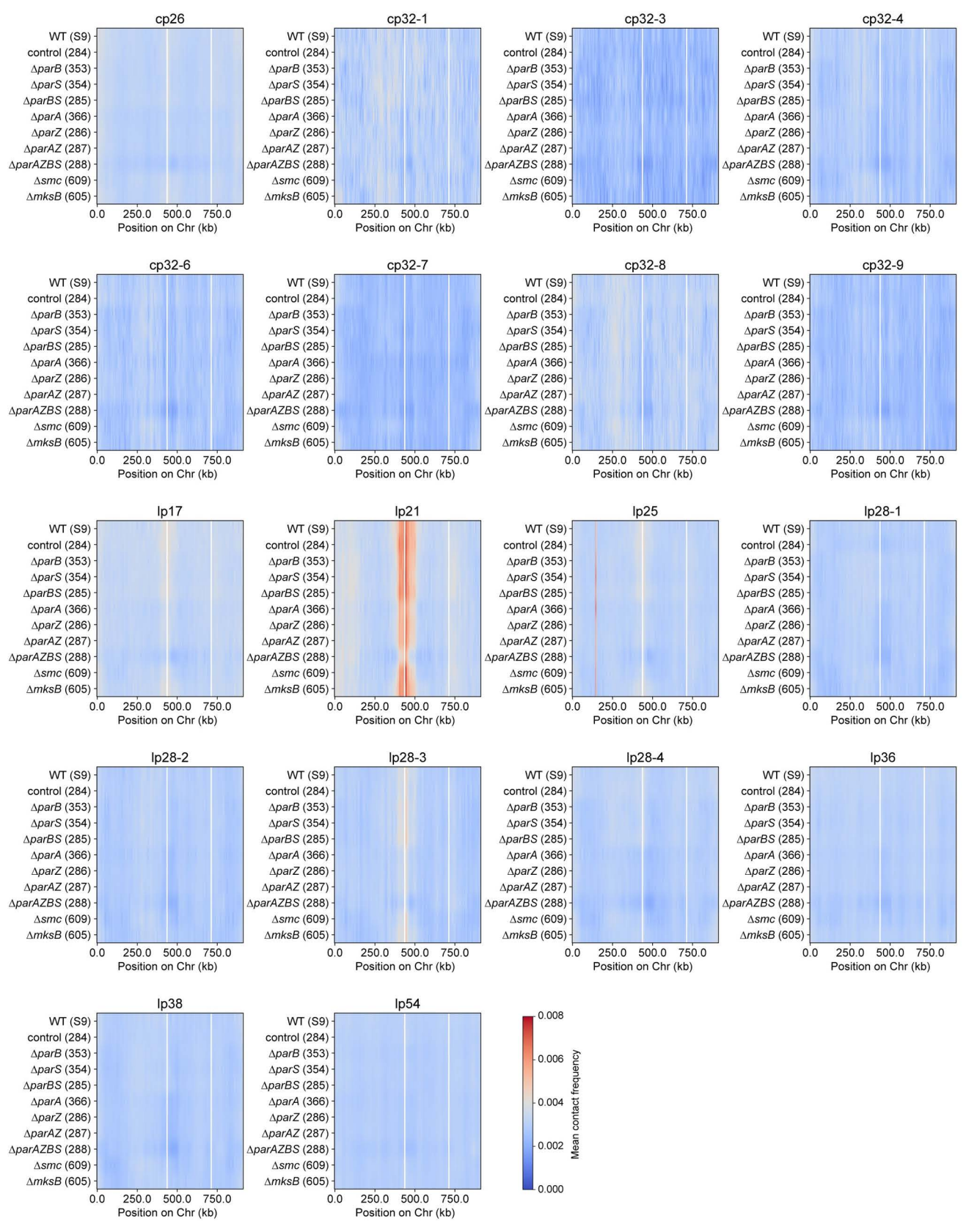
(D-F) Log_2 ratio plots comparing different Hi-C matrices. Log_2(matrix 1/matrix 2) was calculated and plotted in the heatmaps. The identities matrix 1/matrix 2 are shown at the top of each plot. The color scale is shown at the right of panel **(F)**.


S9_WT_mean
CJW_Bb284_control_mean
CJW_Bb253_ΔparB_mean
CJW_Bb354_ΔparS_mean
CJW_Bb285_ΔparBS_mean
CJW_Bb366_ΔparA_mean
CJW_Bb286_ΔparZ_mean
CJW_Bb287_ΔparAZ_mean
CJW_Bb288_ΔparAZBS_mean
CJW_Bb609_Δsmc_mean
CJW_Bb605_ΔmksB_mean
Plasmid
lp54
lp38
lp36
lp28-4
lp28-3
lp28-2
lp28-1
lp25
lp21
lp17
cp32-9
cp32-8
cp32-7
cp32-6
cp32-4
cp32-3
cp32-1
cp26
0
250
500
750
Position on Chr (kb)
0.008
0.006
0.004
0.002
0.000
Mean contact frequency

S8 Fig. Plasmid-chromosome interactions in different mutants.
Calculated plasmid-chromosome interaction frequencies are shown. The x-axis shows chromosome location in kb. The y-axis specifies the different plasmids analyzed. The color indicates the contact frequency between each plasmid and chromosome locus. Each graph plots the mean value of the two biological replicates shown in **S3 Fig**. Data are binned at 5-kb resolution. The data were normalized including all the interactions in the genome (i.e. intra-chromosomal, plasmid-chromosome and plasmid-plasmid interactions).

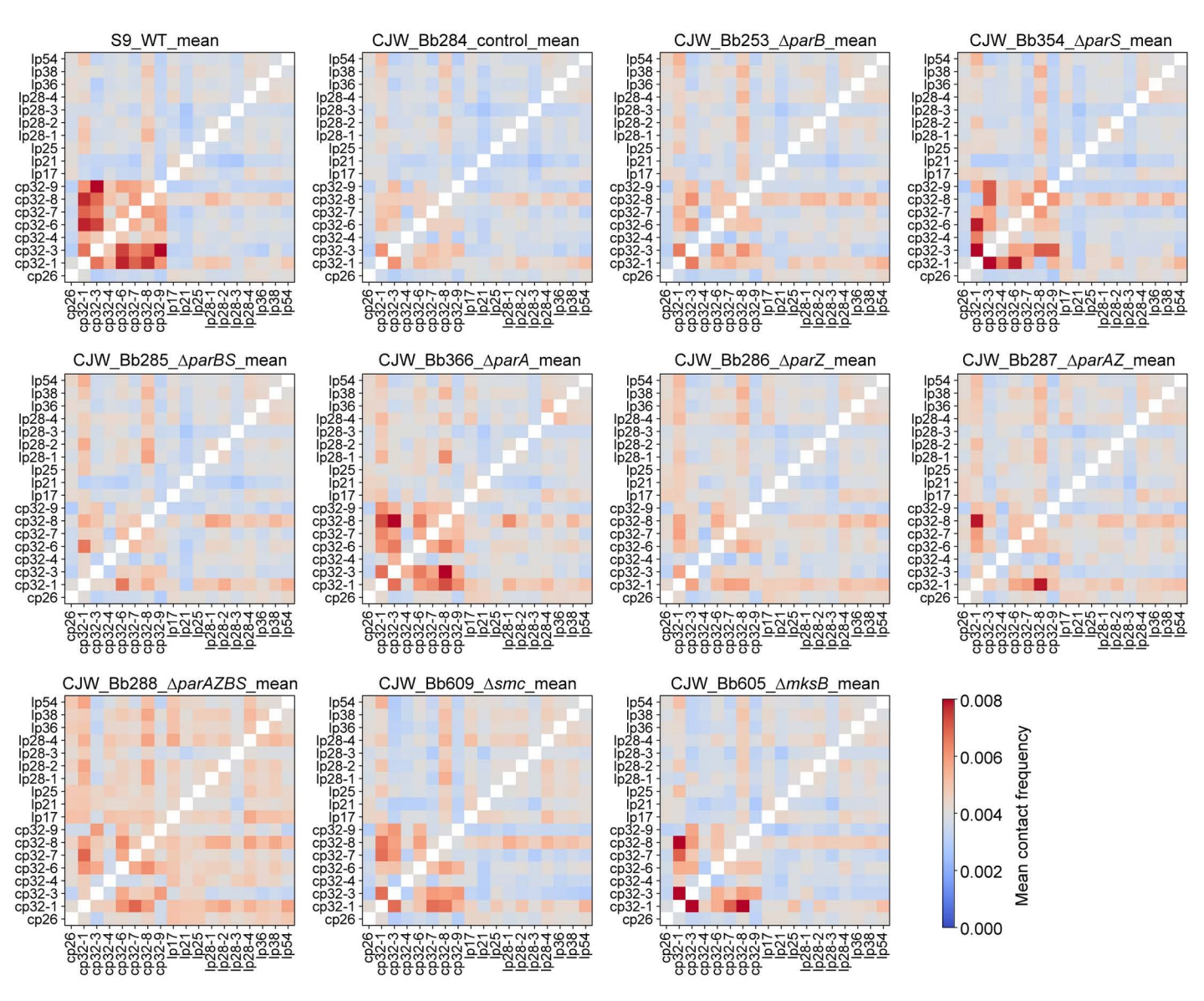

S9_WT_mean
CJW_Bb284_control_mean
CJW_Bb253_ΔparB_mean
CJW_Bb354_ΔparS_mean
CJW_Bb285_ΔparBS_mean
CJW_Bb366_ΔparA_mean
CJW_Bb286_ΔparZ_mean
CJW_Bb287_ΔparAZ_mean
CJW_Bb288_ΔparAZBS_mean
CJW_Bb609_Δsmc_mean
CJW_Bb605_ΔmksB_mean
Plasmid
lp54
lp38
lp36
lp28-4
lp28-3
lp28-2
lp28-1
lp25
lp21
lp17
cp32-9
cp32-8
cp32-7
cp32-6
cp32-4
cp32-3
cp32-1
cp26
0
250
500
750
Position on Chr (kb)
0.008
0.006
0.004
0.002
0.000
Mean contact frequency

S9 Fig. Renormalized plasmid-chromosome interactions in different mutants. Plasmid-chromosome interactions from **S8 Fig** were renormalized using iterative correction to remove the influence of intra-chromosomal and plasmid-plasmid interactions (see Materials and methods). The data were normalized such that each row had the same total score, and each column had the same total score.


cp26
cp32-1
cp32-3
cp32-4
cp32-6
cp32-7
cp32-8
cp32-9
lp17
lp21
lp25
lp28-1
lp28-2
lp28-3
lp28-4
lp36
lp38
lp54
WT (S9)
control (284)
ΔparB (353)
ΔparS (354)
ΔparBS (285)
ΔparA (366)
ΔparZ (286)
ΔparAZ (287)
ΔparAZBS (288)
Δsmc (609)
ΔmksB (605)
0.0
250.0
500.0
750.0
Position on Chr (kb)
0.008
0.006
0.004
0.002
0.000
Mean contact frequency

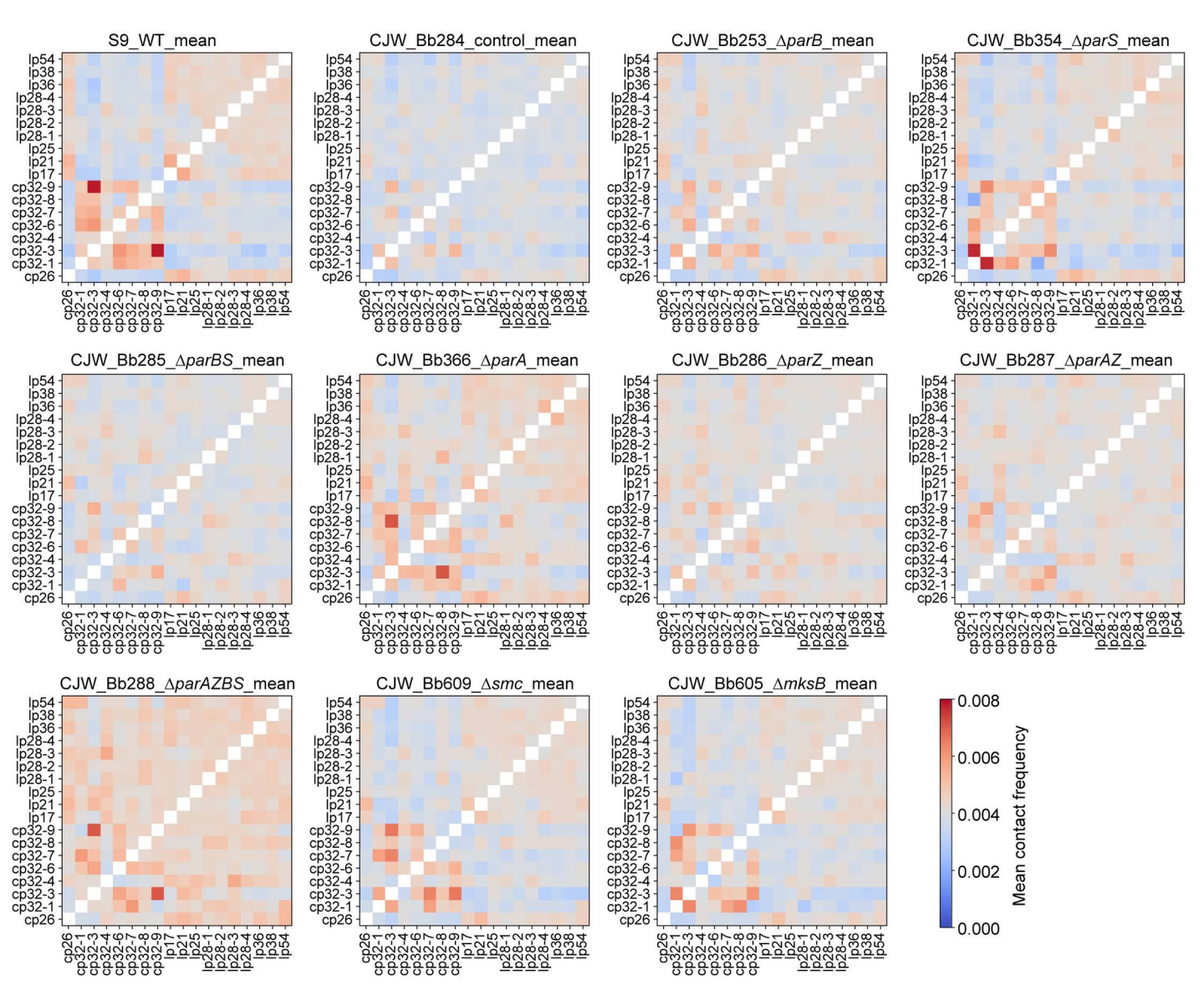
S10 Fig. Plasmid-chromosome interactions in different mutants organized by plasmids.

Calculated plasmid-chromosome interaction frequencies are shown. The x-axis shows the chromosome location in kb. The y-axis specifies the different mutants. The color indicates the contact frequency between each plasmid and chromosome locus. Each graph plots the mean value of the two biological replicates shown in **S3 Fig**. Data are binned at 5-kb resolution.


S9_WT_mean
CJW_Bb284_control_mean
CJW_Bb253_ΔparB_mean
CJW_Bb354_ΔparS_mean
CJW_Bb285_ΔparBS_mean
CJW_Bb366_ΔparA_mean
CJW_Bb286_ΔparZ_mean
CJW_Bb287_ΔparAZ_mean
CJW_Bb288_ΔparAZBS_mean
CJW_Bb609_Δsmc_mean
CJW_Bb605_ΔmksB_mean
lp54
lp38
lp36
lp28-4
lp28-3
lp28-2
lp28-1
lp25
lp21
lp17
cp32-9
cp32-8
cp32-7
cp32-6
cp32-4
cp32-3
cp32-1
cp26
0.008
0.006
0.004
0.002
0.000
Mean contact frequency

S11 Fig. Plasmid-plasmid interactions in different mutants.

Calculated plasmid-plasmid contact frequencies in different strains. The x- and y-axes indicate the plasmids analyzed. The color shows the computed contact frequency. Each graph plots the mean of the two biological replicates shown in **S3 Fig**. The data were normalized including all the interactions in the genome (i.e. intra-chromosomal, plasmid-chromosome and plasmid-plasmid interactions).


S9_WT_mean
CJW_Bb284_control_mean
CJW_Bb253_ΔparB_mean
CJW_Bb354_ΔparS_mean
CJW_Bb285_ΔparBS_mean
CJW_Bb366_ΔparA_mean
CJW_Bb286_ΔparZ_mean
CJW_Bb287_ΔparAZ_mean
CJW_Bb288_ΔparAZBS_mean
CJW_Bb609_Δsmc_mean
CJW_Bb605_ΔmksB_mean
lp54
lp38
lp36
lp28-4
lp28-3
lp28-2
lp28-1
lp25
lp21
lp17
cp32-9
cp32-8
cp32-7
cp32-6
cp32-4
cp32-3
cp32-1
cp26
0.008
0.006
0.004
0.002
0.000
Mean contact frequency

S12 Fig. Renormalized plasmid-plasmid interactions in different mutants.
Plasmid-plasmid contact frequencies from **S11 Fig** were renormalized without plasmid-chromosome interactions. The data were normalized such that each row had the same total score, and each column had the same total score.

S1 Table. Bacterial strains used in this study.

Strain	Genotype	Antibiotic resistance	Reference	Figure
S9	Transformable derivative of the *B. burgdorferi* type strain B31; lacks endogenous plasmids cp9, lp5, and lp56; also known as B31-A3-68-*Δbbe02::PflaB-aadA*	Sr	[1]	1-4, 5A-C, S1-S12
CJW_Bb284	S9-derived control strain; has gentamicin resistance cassette inserted between *parZ* and *parB*	Sr, Gm	[2]	5A-C, 6A, 6D-I, S3-S12
CJW_Bb285	S9-derived *ΔparBS* strain	Sr, Gm	[2]	5ABF, 7CF, S3-6, S8-12
CJW_Bb286	S9-derived *ΔparZ* strain	Sr, Gm	[2]	5ABG, 7HL, S3-6, S8-12
CJW_Bb287	S9-derived *ΔparAZ* strain	Sr, Gm	[2]	5ABG, 7IM, S3-6, S8-12
CJW_Bb288	S9-derived *ΔparAZBS* strain	Sr, Gm	[2]	5ABH, 7JN, S3-6, S8-12
CJW_Bb353	S9-derived *ΔparB* strain	Sr, Gm	[2]	5ABF, 7AD, S3-6, S8-12
CJW_Bb354	S9-derived *ΔparS* strain	Sr, Gm	[2]	5ABF, 7BE, S3-6, S8-12
CJW_Bb366	S9-derived *ΔparA* strain	Sr, Km	[2]	5ABG, 7GK, S3-6, S8-12
CJW_Bb605	S9-derived *ΔmksB* strain	Sr, Gm	This study	5ABE, 6CFI, S3-6, S8-12
CJW_Bb609	S9-derived *Δsmc* strain	Sr, Gm	[2]	5ABD, 6BEH, S3-6, S8-12

Sr, streptomycin resistance; Gm, gentamicin resistance; Km, kanamycin resistance.

References

1. Rego RO, Bestor A, Rosa PA. Defining the plasmid-borne restriction-modification systems of the Lyme disease spirochete Borrelia burgdorferi. J Bacteriol. 2011;193(5):1161-71. Epub 2011/01/05. doi: 10.1128/JB.01176-10. PubMed PMID: 21193609; PubMed Central PMCID: PMCPMC3067601.
2. Takacs CN, Wachter J, Xiang Y, Ren Z, Karaboja X, Scott M, et al. Polyploidy, regular patterning of genome copies, and unusual control of DNA partitioning in the Lyme disease spirochete. Nat Commun. 2022;13(1):7173. Epub 2022/12/01. doi: 10.1038/s41467-022-34876-4. PubMed PMID: 36450725; PubMed Central PMCID: PMCPMC9712426.

S2 Table. Plasmids used in this study.

Plasmid	Description	Reference
pΔmksB(gent)	Plasmid to make replace Δ*mksB* with gentamycin resistance gene	This study
pKIGent_parS^{P1}_phoU	Plasmid to insert *parS^{P1}* near *phoU*	[1]
pΔparA(kan)	Plasmid to delete *parA* from *B. burgdorferi* chromosome	[1]

Reference

1. Takacs CN, Wachter J, Xiang Y, Ren Z, Karaboja X, Scott M, et al. Polyploidy, regular patterning of genome copies, and unusual control of DNA partitioning in the Lyme disease spirochete. Nat Commun. 2022;13(1):7173. Epub 2022/12/01. doi: 10.1038/s41467-022-34876-4. PubMed PMID: 36450725; PubMed Central PMCID: PMCPMC9712426.

S3 Table. Oligonucleotides used in this study.

Oligo	Sequence
NT968	5'-tggtaccgagctcggatccgggatttcttttgcgttgtttggtagatctactacatgtcc-3'
NT969	5'-ttttgttttttttacccgggcccgattgtcttaaaagaagtgtatcgaaattcaactcatg-3'
NT970	5'-cttcttttaagacaatcgggcccgggtaaaaaaacaaaagatcctttaaaggatcttttg-3'
NT971	5'-tatgccaatttgtcgcccgcggttcaaggaagatttcctattaaggttgaacttaagagc-3'
NT972	5'-aatcttccttgaaccgcgggcgacaaattggcataatttcccatgtttcttatttgaagg-3'
NT973	5'-ctctagatgcatgcattgcaataacccaaaaagatataaccgcaaaagacaataatatgc-3'
NT974	5'-tctttttgggttattgcaatgcatgcatctagagggcccaattcgccctatagtgagtcg-3'
NT975	5'-aaacaacgcaaaagaaatcccggatccgagctcggtaccaagcttgatgcatagcttgag-3'

S4 Table. Next generation sequencing samples used in this study.

Sample name	Figure	Reference	Identifier	Numbers of nonduplicated double-side unique mapped reads
HiC_CJW_Bb284_rep1	5A-C, 6A, 6D-I, S3-S12	This study	GSM7056005	12,949,960
HiC_CJW_Bb284_rep2	5A-C, 6D-I, S3-S12	This study	GSM7056006	18,388,642
HiC_CJW_Bb285_rep1	5ABF, 7CF, S3-6, S8-12	This study	GSM7056007	15,384,363
HiC_CJW_Bb285_rep2	5ABF, S3-6, S8-12	This study	GSM7056008	17,196,945
HiC_CJW_Bb286_rep1	5ABG, 7HL, S3-6, S8-12	This study	GSM7056009	16,232,326
HiC_CJW_Bb286_rep2	5ABG, S3-6, S8-12	This study	GSM7056010	18,775,364
HiC_CJW_Bb287_rep1	5ABG, 7IM, S3-6, S8-12	This study	GSM7056011	14,421,014
HiC_CJW_Bb287_rep2	5ABG, S3-6, S8-12	This study	GSM7056012	16,560,484
HiC_CJW_Bb288_rep1	5ABH, 7JN, S3-6, S8-12	This study	GSM7056013	15,605,994
HiC_CJW_Bb288_rep2	5ABH, S3-6, S8-12	This study	GSM7056014	17,741,544
HiC_CJW_Bb353_rep1	5ABF, 7AD, S3-6, S8-12	This study	GSM7056015	15,306,050
HiC_CJW_Bb353_rep2	5ABF, S3-6, S8-12	This study	GSM7056016	13,407,970
HiC_CJW_Bb354_rep1	5ABF, 7BE, S3-6, S8-12	This study	GSM7056017	13,917,027
HiC_CJW_Bb354_rep2	5ABF, S3-6, S8-12	This study	GSM7056018	11,211,083
HiC_CJW_Bb366_rep1	5ABG, 7GK, S3-6, S8-12	This study	GSM7056019	15,375,430
HiC_CJW_Bb366_rep2	5ABG, S3-6, S8-12	This study	GSM7056020	10,765,224
HiC_CJW_Bb605_rep1	5ABE, 6I, S3-6, S8-12	This study	GSM7056021	8,440,508
HiC_CJW_Bb605_rep2	5ABE, 6CFI, S3-6, S8-12	This study	GSM7056022	9,953,656
HiC_CJW_Bb609_rep1	5ABD, 6BEH, S3-6, S8-12	This study	GSM7056023	9,798,914
HiC_CJW_Bb609_rep2	5ABD, 6H, S3-6, S8-12	This study	GSM7056024	11,279,804
HiC_CJW_S9WT_rep1	1-4, 5A-C, S1-S12	This study	GSM7056025	10,377,706
HiC_CJW_S9WT_rep2	5A-C, S1-S12	This study	GSM7056026	11,847,047