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Global Linkage Map Connects Meiotic Centromere Function to Chromosome Size in Budding Yeast

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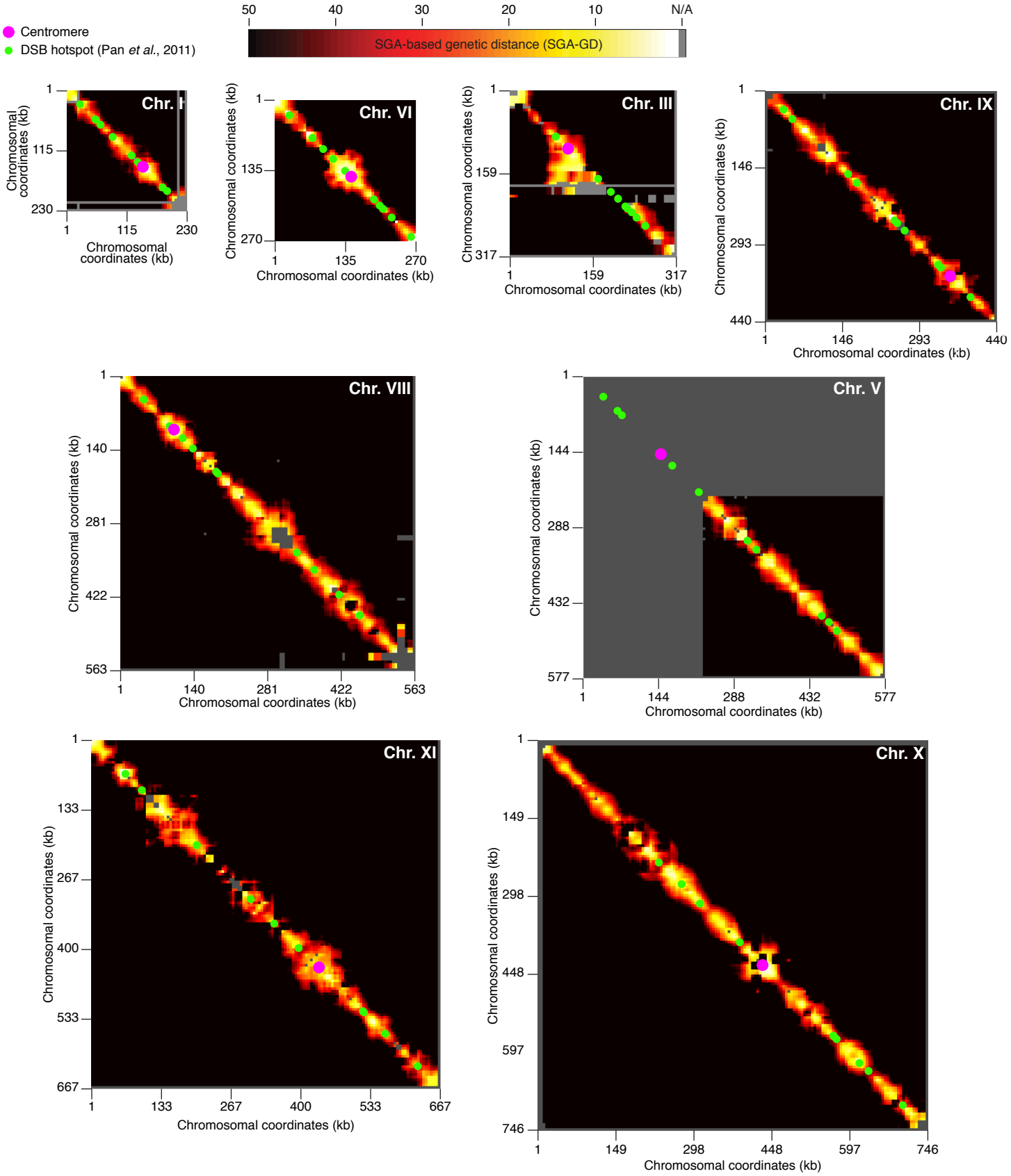
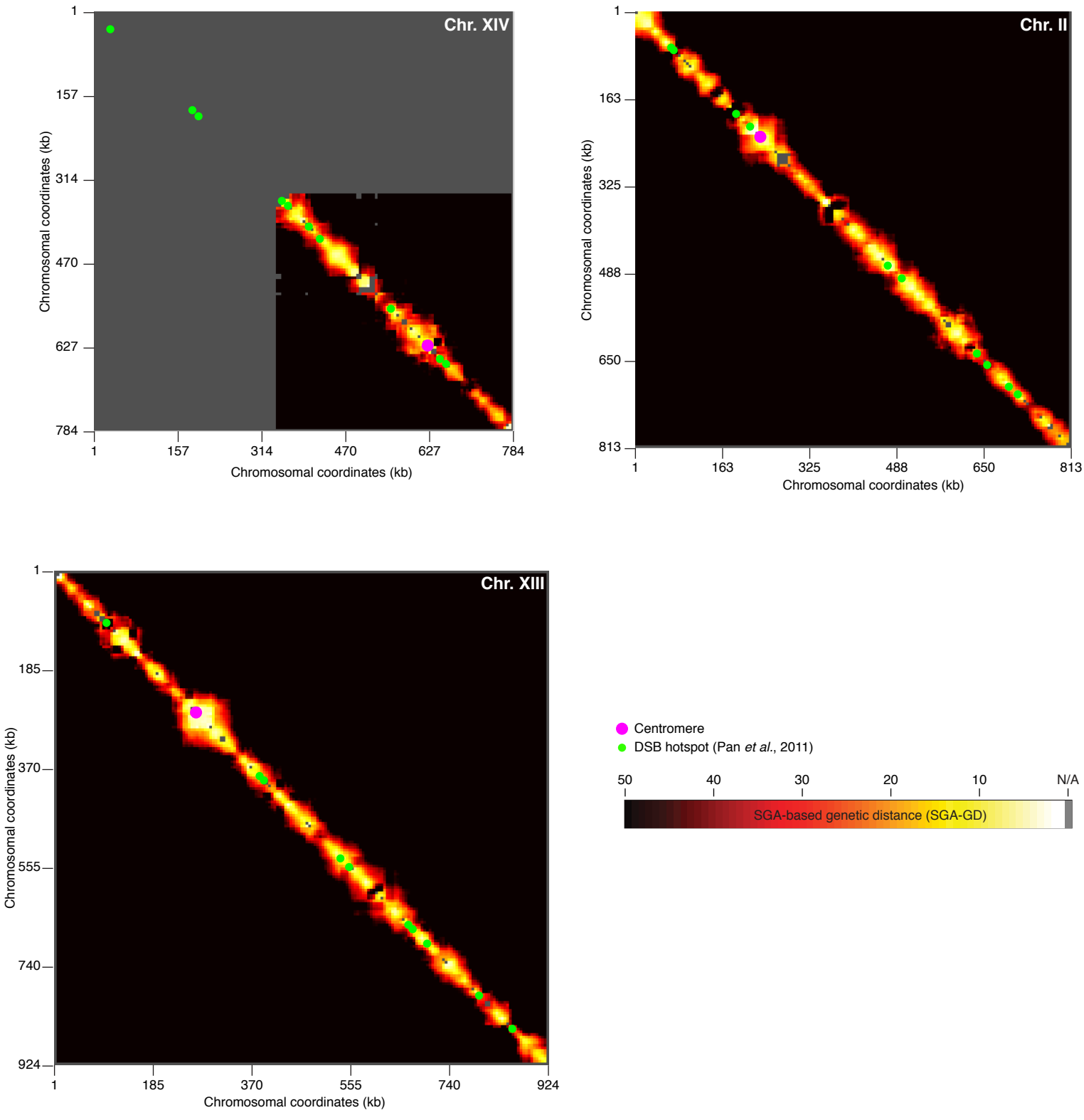
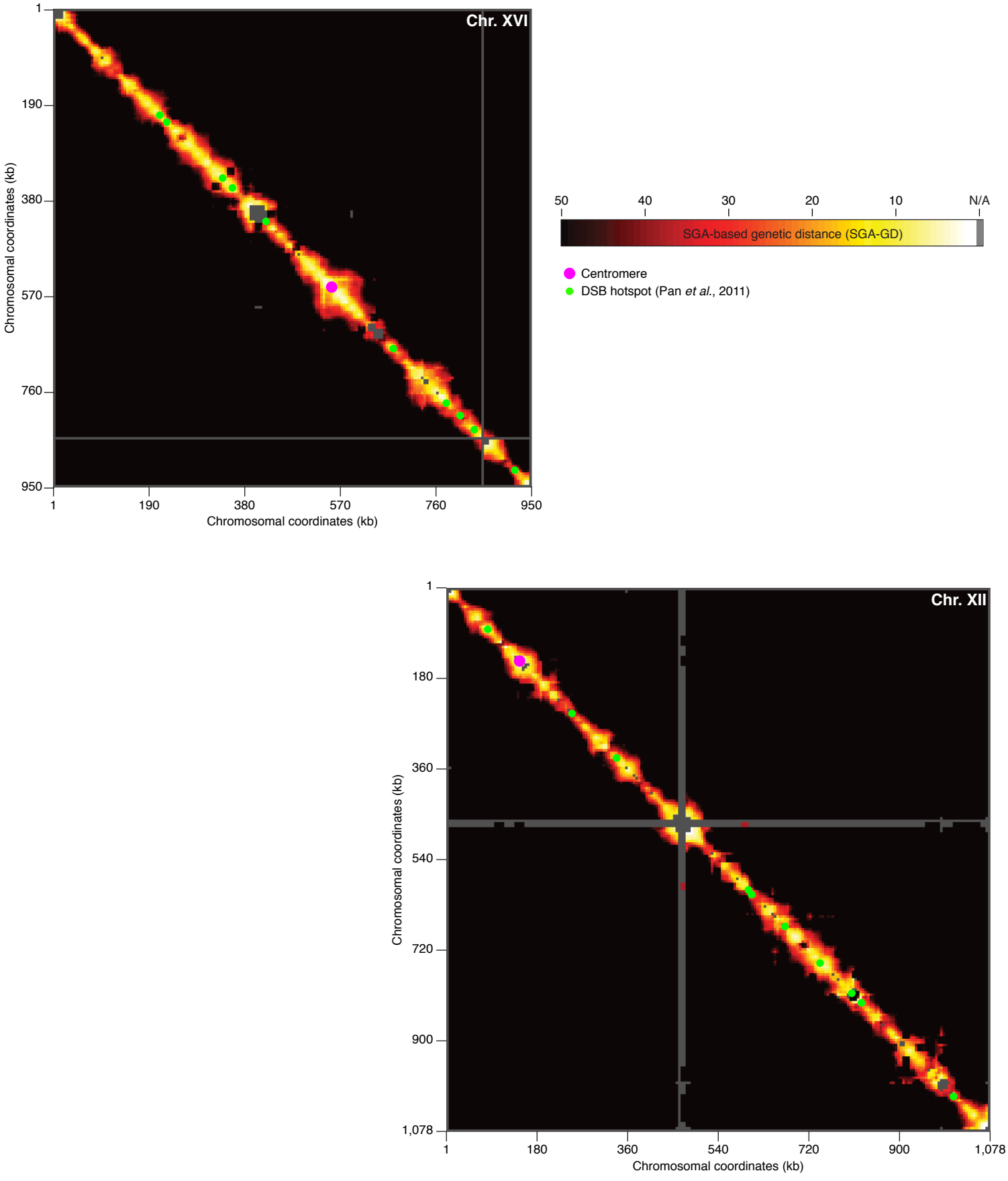
Figure S1 (A) A genetic linkage map for each chromosome was constructed as described in Methods and visualized as a heatmap. The horizontal and the vertical axes of the heatmap represent chromosomal coordinates; a third dimension indicating the SGA-based genetic distance (SGA-GD) between the corresponding chromosomal regions is represented by the intensity of color of each point in the image. Grey corresponds to missing data due to the experimental constrains of the SGA method (Methods). Each chromosome is drawn to scale. Purple dots represent centromeres. Green dots correspond to the top 10 highest double-strand break hotspots as reported by Pan et al., 2011.



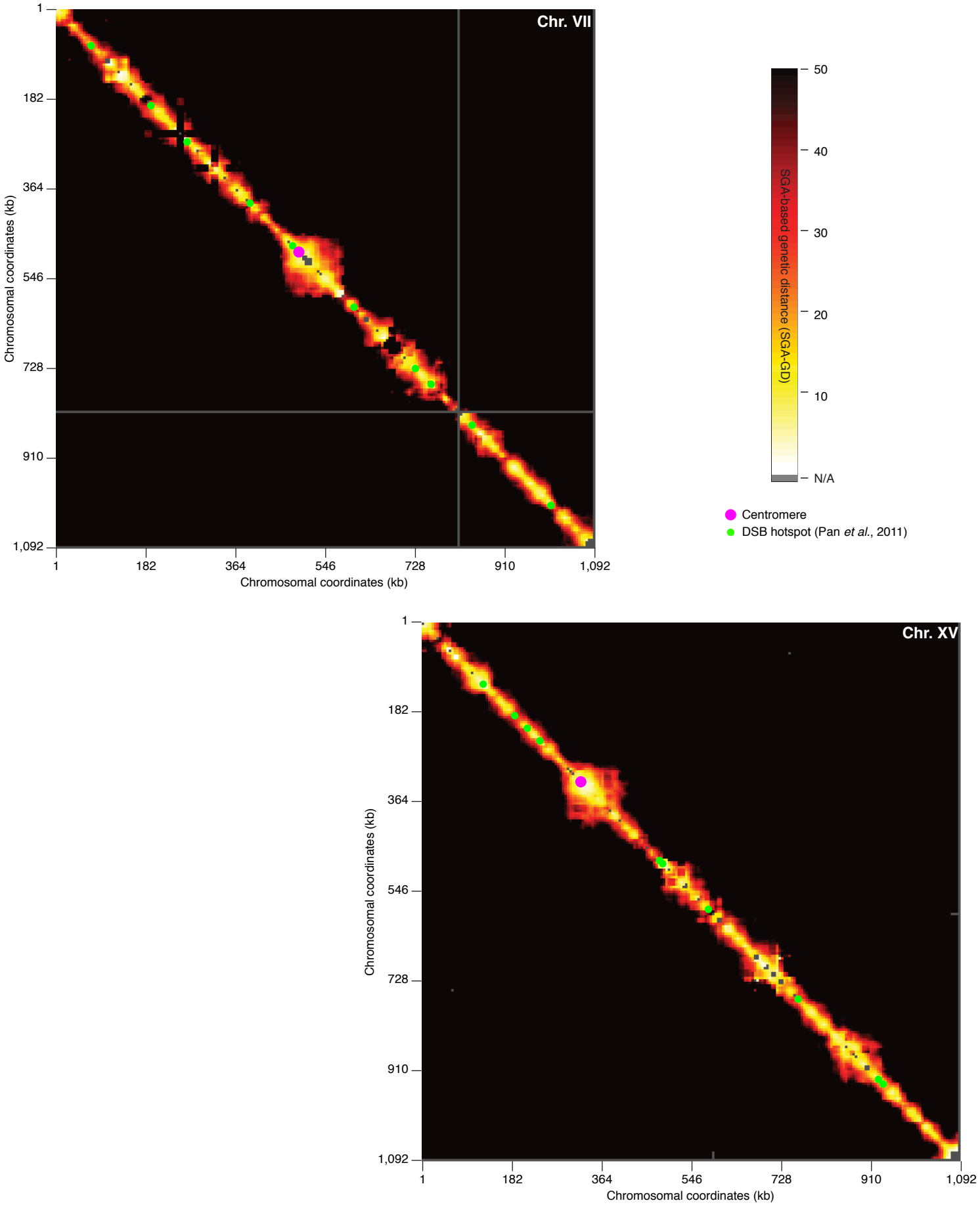
B


Chr. XIV
Chromosomal coordinates (kb)
1
157
314
470
627
784
Chr. II
Chromosomal coordinates (kb)
1
163
325
488
650
813
Chr. XIII
Chromosomal coordinates (kb)
1
185
370
555
740
924
Centromere
DSB hotspot (Pan et al., 2011)
50
40
30
20
10
N/A
SGA-based genetic distance (SGA-GD)

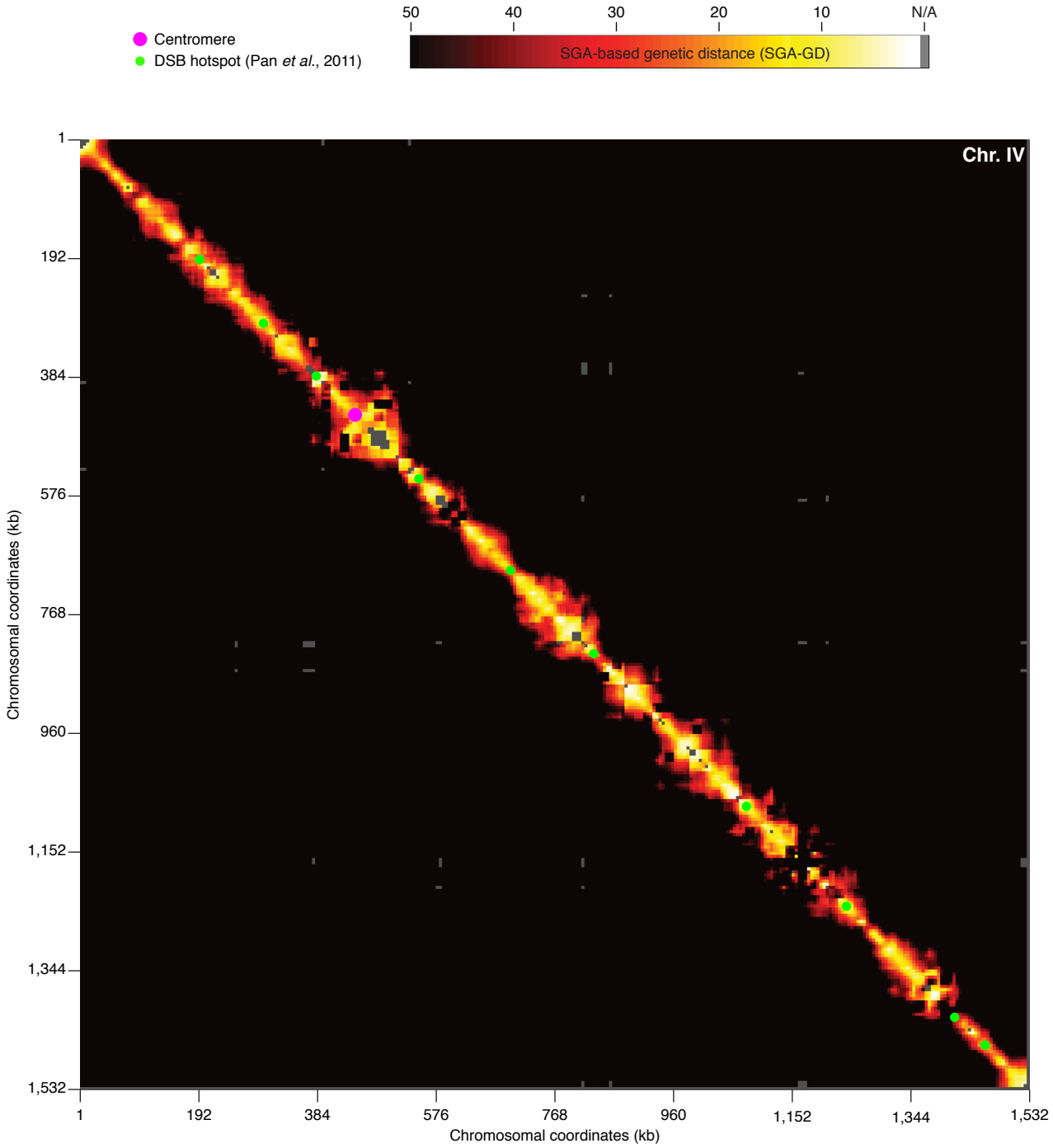
C

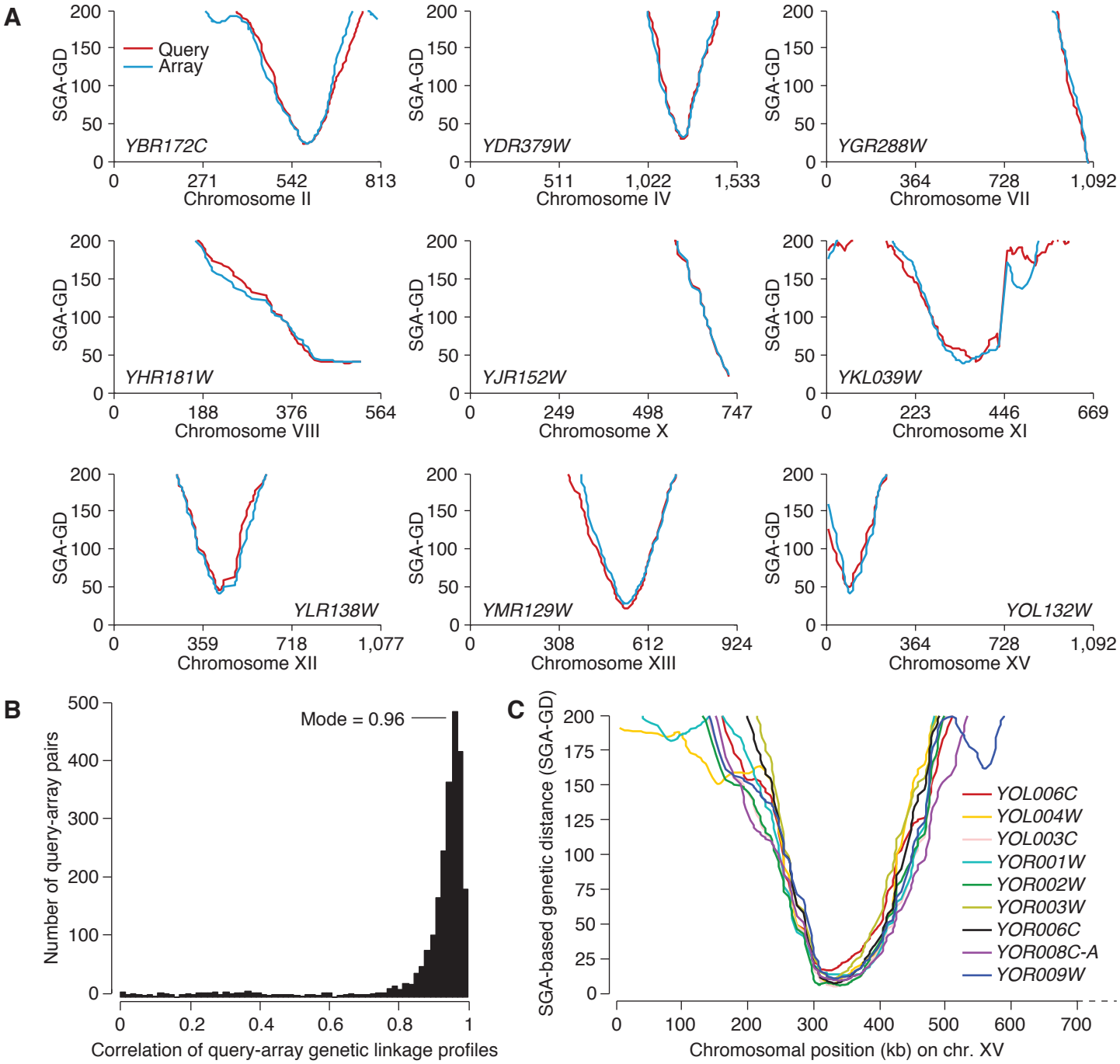

Chr. XVI
Chromosomal coordinates (kb)
1
190
380
570
760
950
Chromosomal coordinates (kb)
50
40
30
20
10
N/A
SGA-based genetic distance (SGA-GD)
Centromere
DSB hotspot (Pan et al., 2011)
Chr. XII
Chromosomal coordinates (kb)
1
180
360
540
720
900
1,078
Chromosomal coordinates (kb)

D


Chr. VII
Chromosomal coordinates (kb)
1
182
364
546
728
910
1,092
SGA-based genetic distance (SGA-GD)
50
40
30
20
10
N/A
Centromere
DSB hotspot (Pan et al., 2011)
Chr. XV
Chromosomal coordinates (kb)

E


Centromere
DSB hotspot (Pan *et al.*, 2011)
50
40
30
20
10
N/A
SGA-based genetic distance (SGA-GD)
Chr. IV
Chromosomal coordinates (kb)
1
192
384
576
768
960
1,152
1,344
1,532
Chromosomal coordinates (kb)



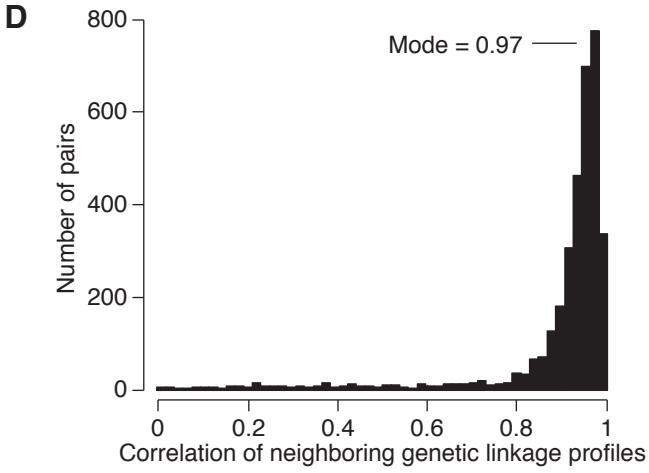


Figure S2 (A) Examples of genetic linkage profiles of query and array mutants involving the same genomic locus. A genetic linkage profile is defined as the set of genetic distances, measured in SGA-GD (Methods), between a given locus and all other loci present on the same chromosome. The reproducibility of genetic linkage profiles is assessed by systematically comparing two independent experiments: in one experiment, the locus of interest has been deleted using the *natMX4* selectable marker ("query" mutant); in the other experiment, the locus of interest has been deleted using the *kanMX* selectable marker ("array" mutant). **(B)** Distribution of Pearson correlation coefficients among the genetic linkage profiles of ~2,800 query-array mutant pairs. Each pair corresponds to two independent experiments for a given genomic locus. **(C)** Genetic linkage profiles for 9 consecutive genes located on chromosome XV. Consecutive loci are expected to have similar genetic linkage profiles because they are likely to experience similar local recombination rates. **(D)** Distribution of Pearson correlation coefficients for ~3,700 pairs of genetic linkage profiles involving consecutive genomic loci.

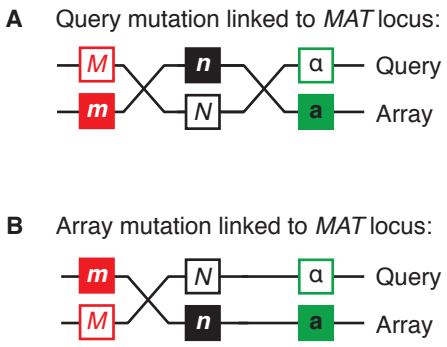


Figure S3 Chromosome III carries the yeast mating type locus (*MAT*), which determines the mating type of a yeast haploid cell and distinguishes array and query mutants, which are *MAT***a** and *MAT*α, respectively. Since SGA selects specifically for *MAT***a** meiotic progeny, a query mutant *n* (**A**, filled black square), located between gene *M* (**A**, empty red square) and the *MAT* locus (**A**, empty green square), requires a double recombination event to acquire both the array mutation *m* (**A**, filled red square) and the *MAT***a** information (**A**, filled green square). The array mutant *n*, however, (**B**, filled black square), being already linked to *MAT***a**, only requires one recombination event to acquire query mutation *m* (**B**, filled red square). As a result, query and array mutants linked to the *MAT* locus show different degrees of linkage to nearby genes, and averaging their genetic linkage maps would conceal the true recombination activity occurring within the region.

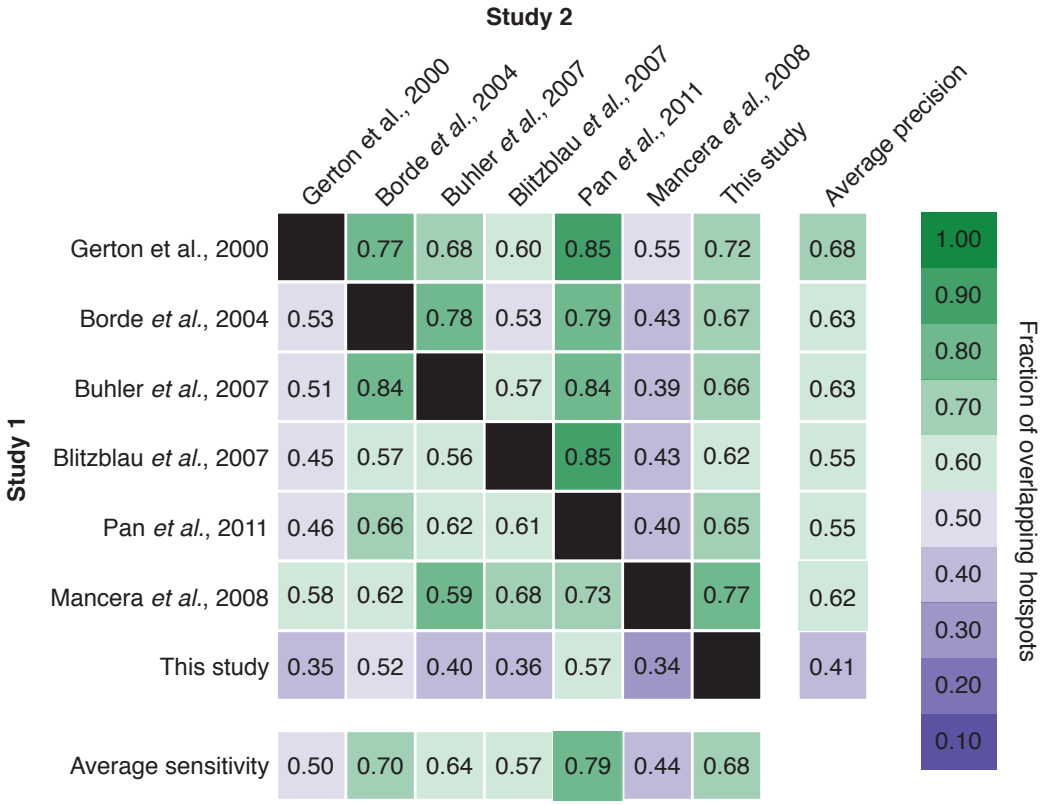


Figure S4 The overlap between any two datasets is visualized as a heatmap/table, where colors and numbers reflect the fraction of hotspots identified by study 1 (row labels) that are located within 10 kb from a hotspot identified by study 2 (column labels). For example, of all hotspots identified by Gerton *et al.* (row label), 77% were also identified by Borde *et al.* (column label), and, vice versa, of all hotspots identified by Borde *et al.* (row label), 53% were also identified by Gerton *et al.* (column label).

Significant / Not significant	Centromere linkage				Overall linkage (control)			
	All chromosomes		All chrs., excl. 4 smallest		All chromosomes		All chrs., excl. 4 smallest	
	R	*p-val*	*R*	*p-val*	*R*	*p-val*	*R*	*p-val*
This study	0.77	0.01	0.66	0.03	0.74	0.001	0.44	0.15
SGD	0.70	0.002	0.42	0.17	0.64	0.008	0.05	0.87
Gerton *et al.*, 2000	0.78	0.0003	0.74	0.006	0.46	0.08	–0.07	0.82
Borde *et al.*, 2004	0.79	0.001	0.92	0.0002	0.25	0.34	0.04	0.89
Buhler *et al.*, 2007	0.63	0.04	0.72	0.03	0.33	0.22	0.15	0.64
Blitzblau *et al.*, 2007	0.59	0.02	0.67	0.02	0.62	0.01	0.11	0.74

Figure S5 Pearson correlation coefficients and the corresponding significance p-values were computed between chromosome size and centromere-proximal recombination reported by several published studies, as described in Methods.

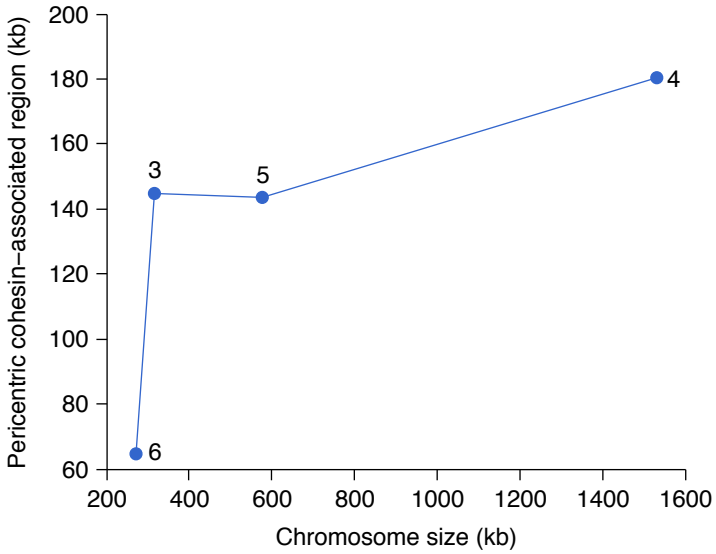


Figure S6 Relationship between chromosome size and centromere-associated cohesin clustering, measured from data reported previously (Kugou et al. 2009). Data relative to 1.5 hours after induction of meiosis are shown. Each data point corresponds to a chromosome, labeled by the number. Pearson correlation coefficient is R = 0.73 but not significant (p-value < 0.27).

Table S1 Data sources for large-scale recombination and cohesin binding studies

Publication	**Data source**
(Gerton *et al.* 2000)	Table 1
(Borde *et al.* 2004)	Table S2
(Buhler *et al.* 2007)	Table S5 (5X background)
(Blitzblau *et al.* 2007)	Table S2
(Mancera *et al.* 2008)	Supplementary information 2: hot_spots.txt
(Pan *et al.* 2011)	Table S2 (signal intensity > 1000)
(Glynn *et al.* 2004)	Mitotic cohesin subunit (Scc1/Mcd1): Supplementary dataset 8 Meiotic cohesin subunit (Rec8): Supplementary dataset 9
(Kiburz *et al.* 2005)	Supp Raw Data.doc
(Kugou *et al.* 2009)	http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8422

File S1

SGA-based genetic distances

Available for download at http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.007377/-/DC1

A set of 16 files, one for each chromosome, contain the SGA-based genetic distances (SGA-GD; Methods) for the indicated loci. Rows and columns correspond to query and array mutants, respectively. Multiple experiments, involving the same query locus, appear as duplicated rows in each file.

Supplementary references

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