

Table S1. Genetic distances.

Interval	Chr	Starting position	Ending position	cM (Whole genome)	cM (Reporters)
<i>l1b</i>	1	3,905,441	5,755,618	4.9	6.6
<i>l1fg</i>	1	24,645,163	25,956,590	5.6	8.2
<i>l2f</i>	2	18,286,716	18,957,093	3.3	7.6
<i>420</i>	3	256,516	5,361,637	14.3	12.3
<i>CEN3</i>	3	11,115,724	16,520,560	10.2	11.9

Comparison of genetic distances in reporter intervals estimated from the whole-genome analysis presented in this study compared with those previously estimated from fluorescent reporters ([Ziolkowski et al. 2015](#)). Note that the estimates for the intervals *l1b*, *l1fg*, *l2f*, and *CEN3* are based on pollen reporters and represent male meiosis only. The whole genome data calculated from the study of crossovers (COs) in F₂ plants and the *420* interval in both datasets reflect sex-averaged genetic distances.

Table S2. Overlaps between CO intervals and structural variants

Variant type	Total Number	Number of overlaps with CO intervals (observed)	Mean number of overlaps with CO intervals (permuted)
Inversion	38	13*	246.4
Insertion	311	134*	231.8
Deletion	426	156*	238
Transpositions (Intrachromosomal)	102	113*	255.6
Translocations (Interchromosomal)	271	159*	297.8
Copy Number Variations	67	38	53.8

*p < 0.05 after 5000 permutations

Table S3. Crossover rates in flanking regions up- and downstream of structural variants

	50 kb CO rate (cM/Mb)	100 kb CO rate (cM/Mb)	200 kb CO rate (cM/Mb)
Genome mean	3.2	3.2	3.2
Inversion	3.4	3.6	3.8
Insertion	4.3	4.3	4.1
Deletion	4.3	4.2	4.1
Transposition (Interchromosomal)	3.7	3.8	4.1
Translocation (Intrachromosomal)	4.3	4.4	4.4
Copy Number Variation	4.4	4.2	4.0

Table S4. CO frequency in defense genes

Gene Annotation	Number of Genes	Number of Genes with COs	Proportion of Genes with COs
CNL	26	9	0.35
NB-ARC	15	6	0.4
NB-LRR	10	1	0.1
P-loop protein	6	0	0
Phloem protein	4	0	0
TIR-NBS	13	2	0.15
TIR family	20	5	0.25
TNL	87	29	0.33
Transmembrane receptors	4	1	0.25
Other	12	2	0.17

Table S5. CO Frequency of sequence motifs associated with a random subset of 2500 crossovers

Motif	Number	Percent
PolyA/T	2102	84.1
CTT/GAA	1141	45.6
CT/GA	943	37.0
CCN/GGN	304	12.2
PolyA/T or CTT/GAA	2292	91.7
All four motifs combined	2363	94.5