Supplemental Data. Nicolas et al. (2009). Genetic regulation of meiotic crossovers between related genomes in *Brassica napus* haploids and hybrids
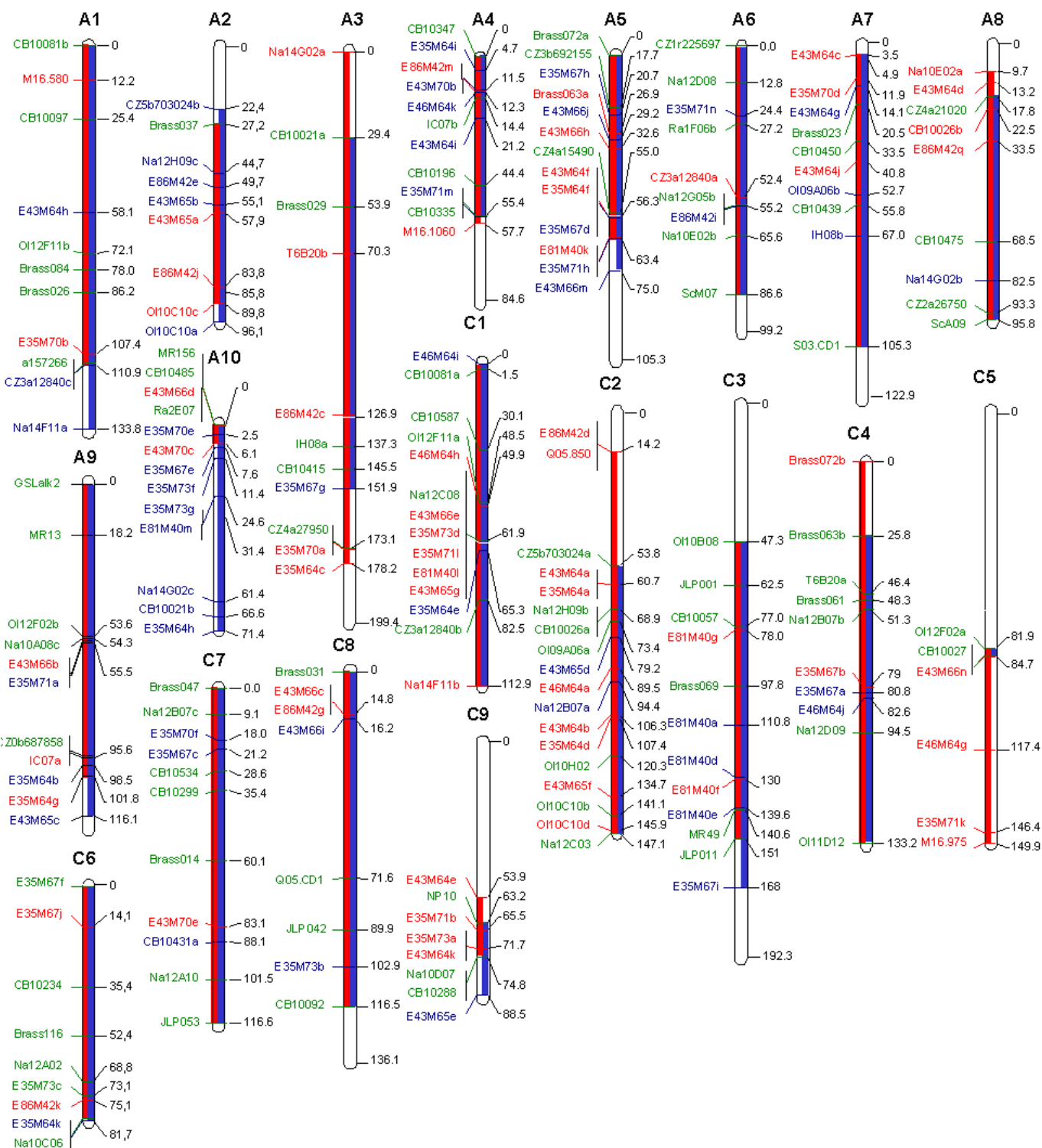

Figure S1: Localization of the markers used in this study and coverage of the frame map established for each linkage group by Delourme *et al.* (2006)

We used the chromosome/linkage group nomenclature that was recently proposed as a reference by the Multinational Brassica Genome Project Steering Committee where *B. napus* N1-N19 nomenclature is replaced by A1-A10 and C1-C9 designations (http://www.brassica.info/information/lg_assigments.htm); see Delourme et al. (2006) for correspondence to former DY maps). Marker names are indicated on the left of each linkage group. Details about markers are given in the supplemental data set. Codominant markers are indicated in green. Dominant markers are indicated either in red or in blue depending on whether they were amplified from *Darmor-bzh* or *Yudal*, respectively. The extent of linkage group coverage is indicated for each linkage group by a line (the red one indicates *Darmor bzh* and the blue indicates *Yudal*).
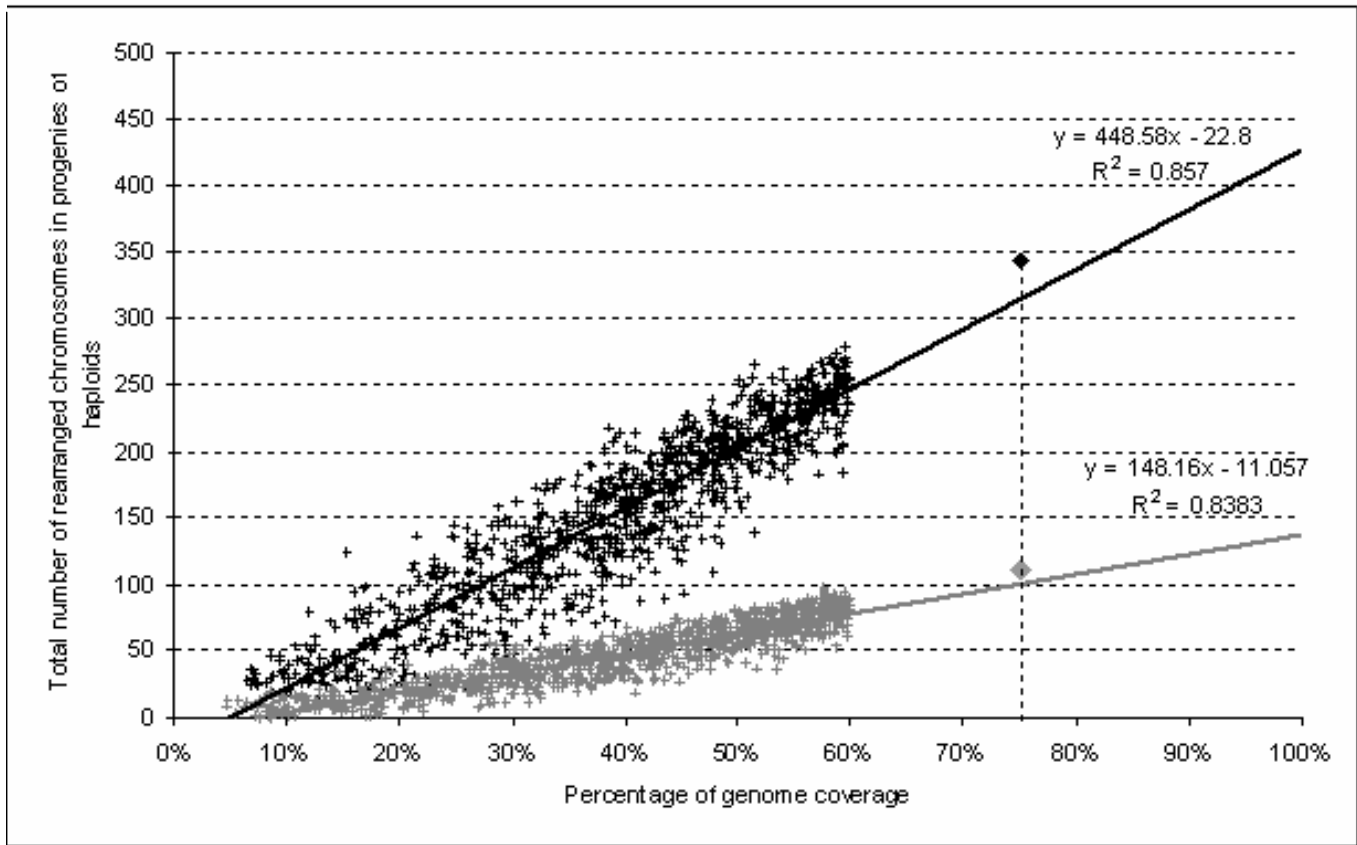
Figure S2: Resampling-based estimation of the relationship between genome coverage and the number of rearranged chromosomes detected in the progenies of *Darmor-bzh* or *Yudal* haploids

For each genotype, random sample sets of loci (N=1500) were simulated by considering 5% to 50% of loci that were genotyped at random; the proportion of genome covered and the number of targeted rearrangements were determined for each simulated sample set and plotted. Simple regression models were fitted and used to approximate the relationships between genome coverage and the number of rearrangements detected in the progenies of *Darmor-bzh* or *Yudal* haploids, respectively. As a control, we compared the total numbers of rearrangements observed in the two progenies (represented by ♦ for *Darmor-bzh* and ♦ for *Yudal*) with 75% genome coverage with the predictions from the regression functions: a total of 342 and 111 rearrangements were observed in the progenies of *Darmor-bzh* or *Yudal* haploids while our regression functions predicted 314 and 100 rearrangements, respectively.