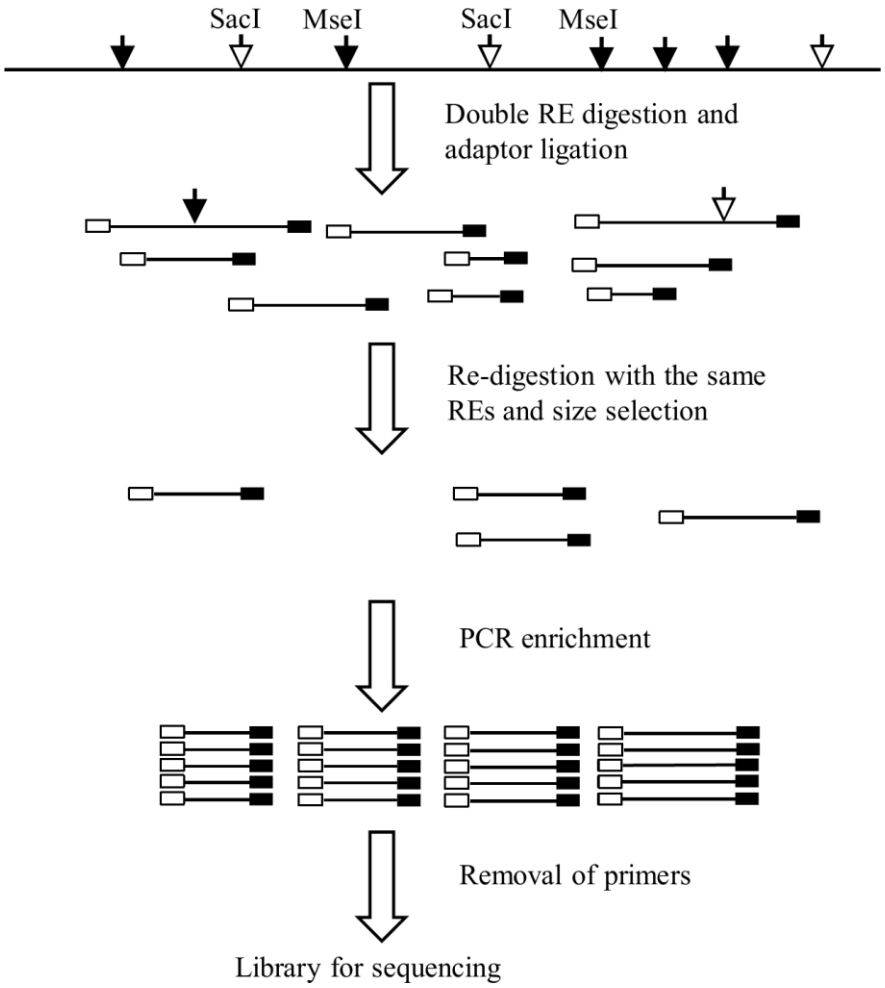


Figure S1. Flowchart for modified ddRADseq sequencing library construction.

The solid-headed and hollow-headed arrows indicate the SacI and MseI recognition site respectively. The horizontal lines represent the genomic sequence, and the solid and hollow boxes represent the Sac_AD and Mse_AD adaptor respectively.

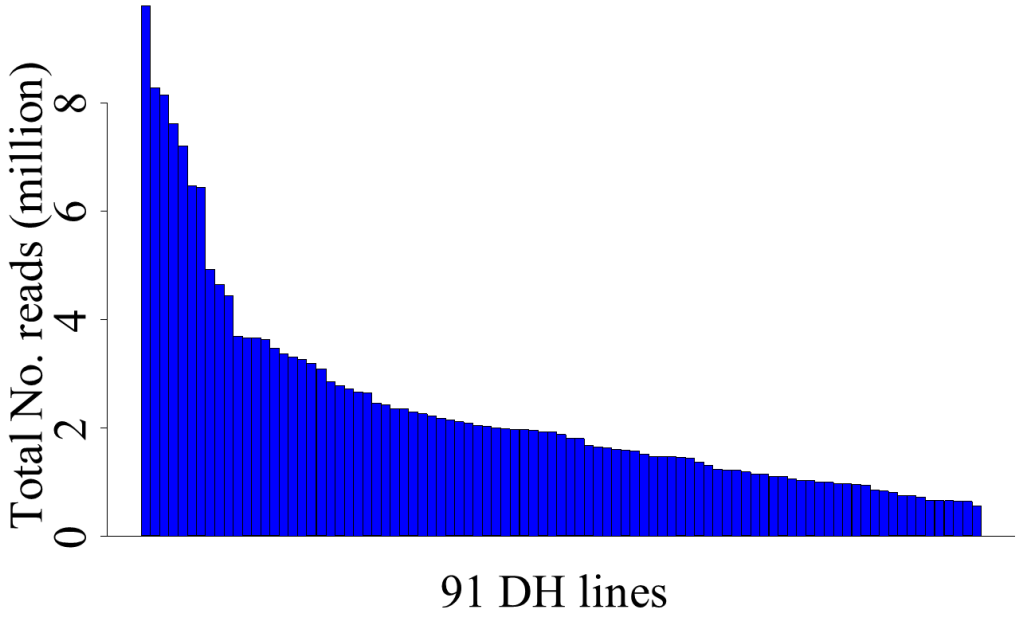


Figure S2. The number of Sequence reads of the 91 DH lines.

The lowest sequencing data is just 0.57 million reads, and the highest reach up to 9.79 million reads, with the average of 2.33 million reads.

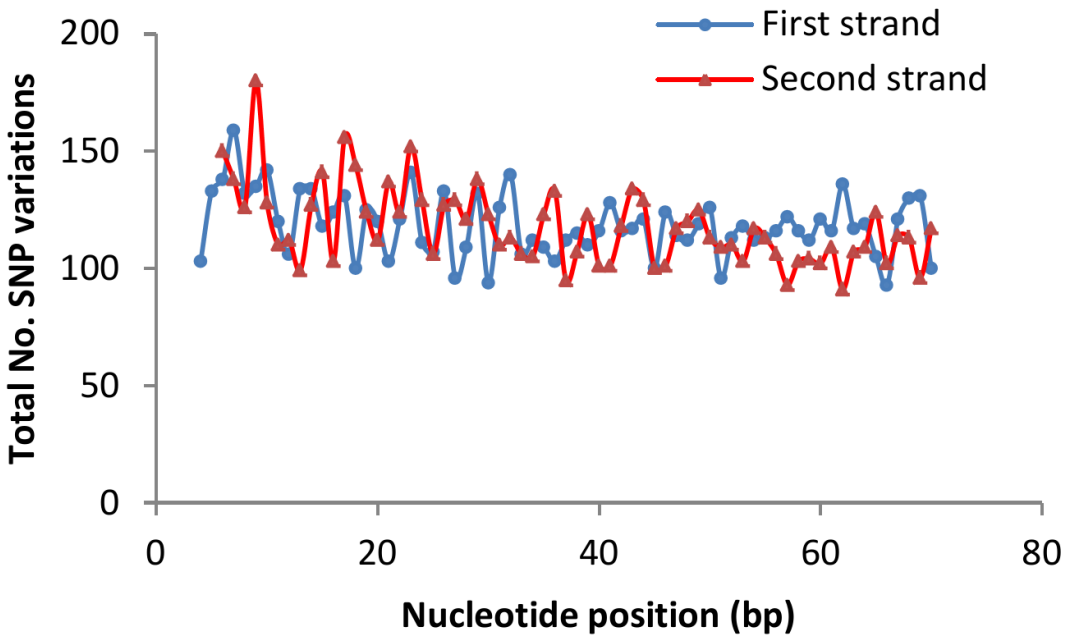
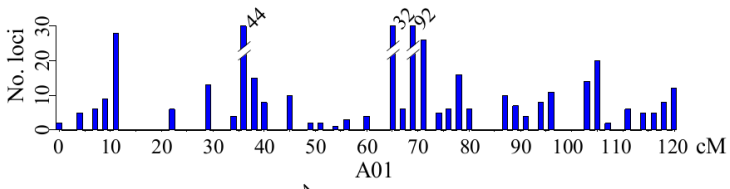
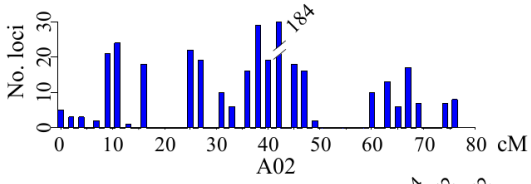
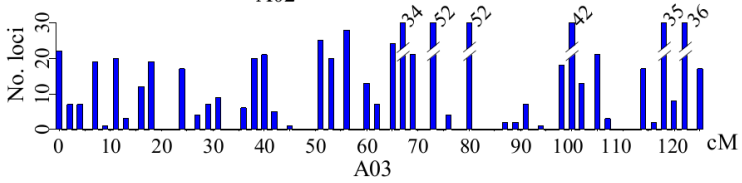
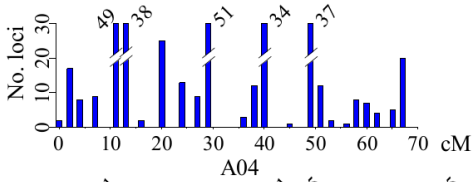


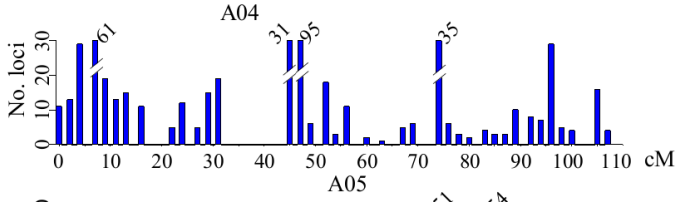
Figure S3. The distribution of the total number of SNP variations on each nucleotide position of each pair-end read.

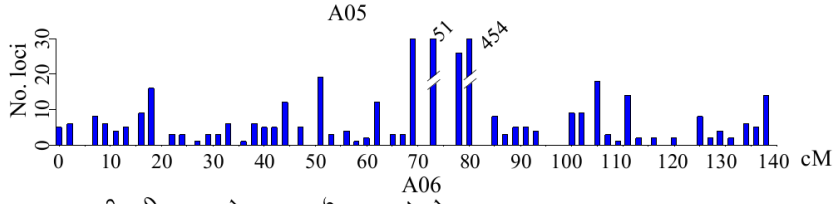

No. loci
0 10 20 30
44
32
62
0 10 20 30 40 50 60 70 80 90 100 110 120 cM
A01

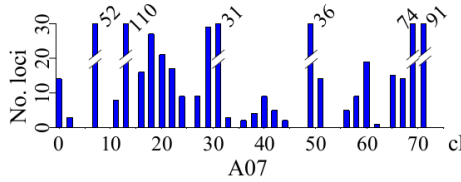

No. loci
0 10 20 30
184
0 10 20 30 40 50 60 70 80 cM
A02

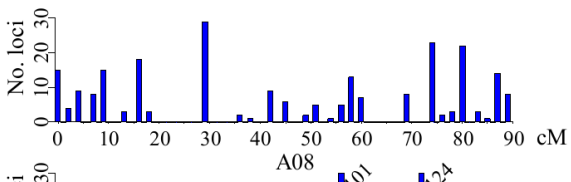

No. loci
0 10 20 30
34
52
52
42
35
36
0 10 20 30 40 50 60 70 80 90 100 110 120 cM
A03

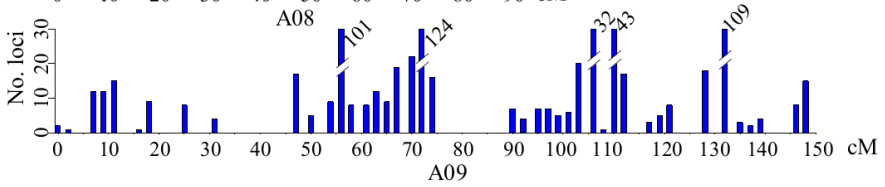

No. loci
0 10 20 30
49
38
51
34
37
0 10 20 30 40 50 60 70 cM
A04

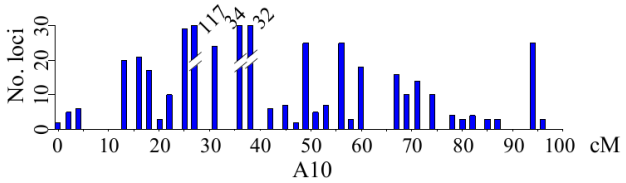

No. loci
0 10 20 30
61
31
95
35
0 10 20 30 40 50 60 70 80 90 100 110 cM
A05


No. loci
0 10 20 30
51
454
0 10 20 30 40 50 60 70 80 90 100 110 120 130 140 cM
A06


No. loci
0 10 20 30
52
110
31
36
74
91
0 10 20 30 40 50 60 70 cM
A07


No. loci
0 10 20 30
0 10 20 30 40 50 60 70 80 90 cM
A08


No. loci
0 10 20 30
101
124
32
43
109
0 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 cM
A09


No. loci
0 10 20 30
117
34
32
0 10 20 30 40 50 60 70 80 90 100 cM
A10

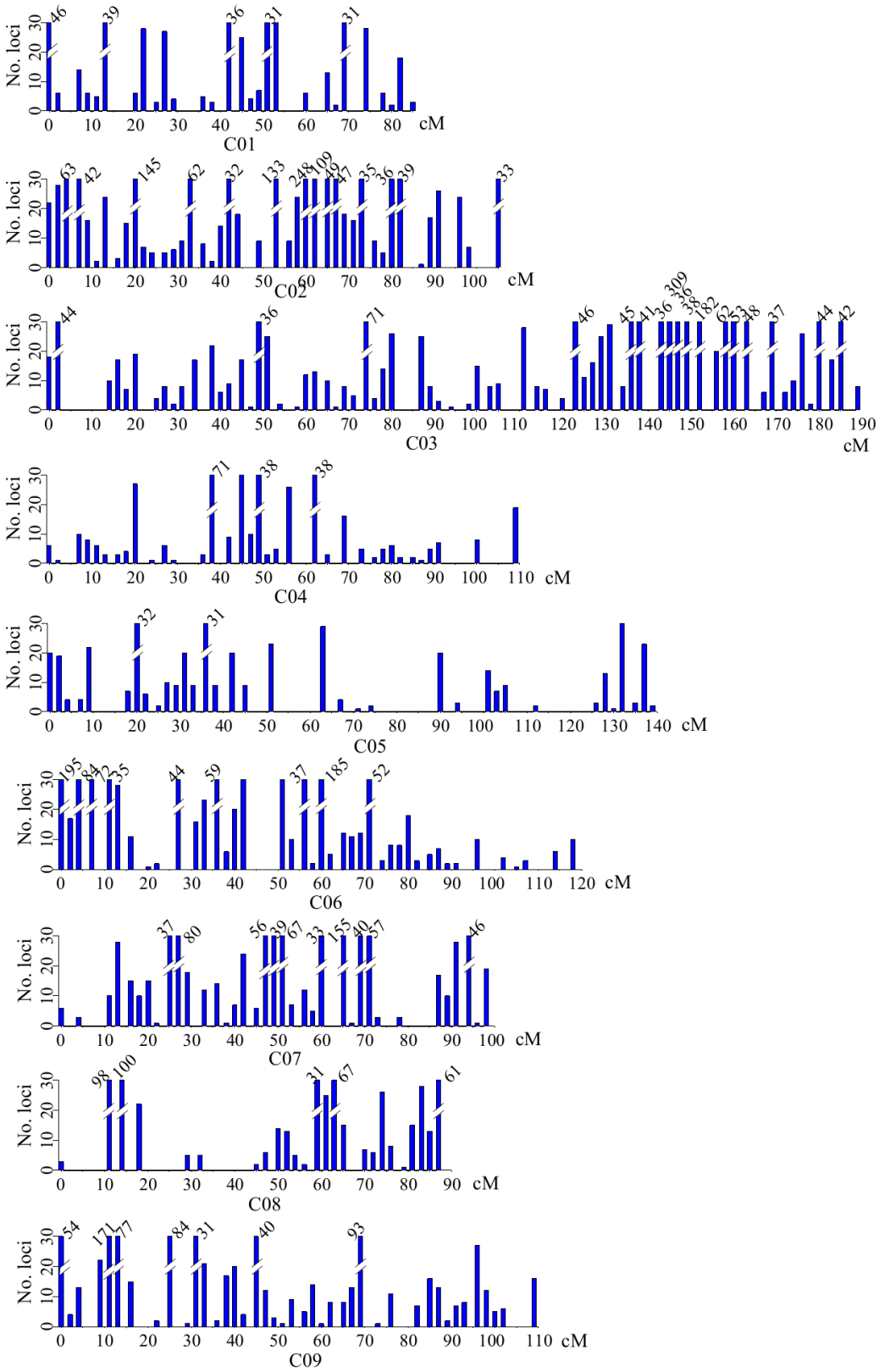


Figure S4. The PAV genetic map constructed with 45 DH individuals with about 2.0 million of sequence reads.

The X axis indicates the genetic distance (cM), and the height of bars represents the number of makers in each bin. The height of bars is limited under 30 in order to discriminate lower value. The values more than 30 are signed above the bars with corresponding numbers.

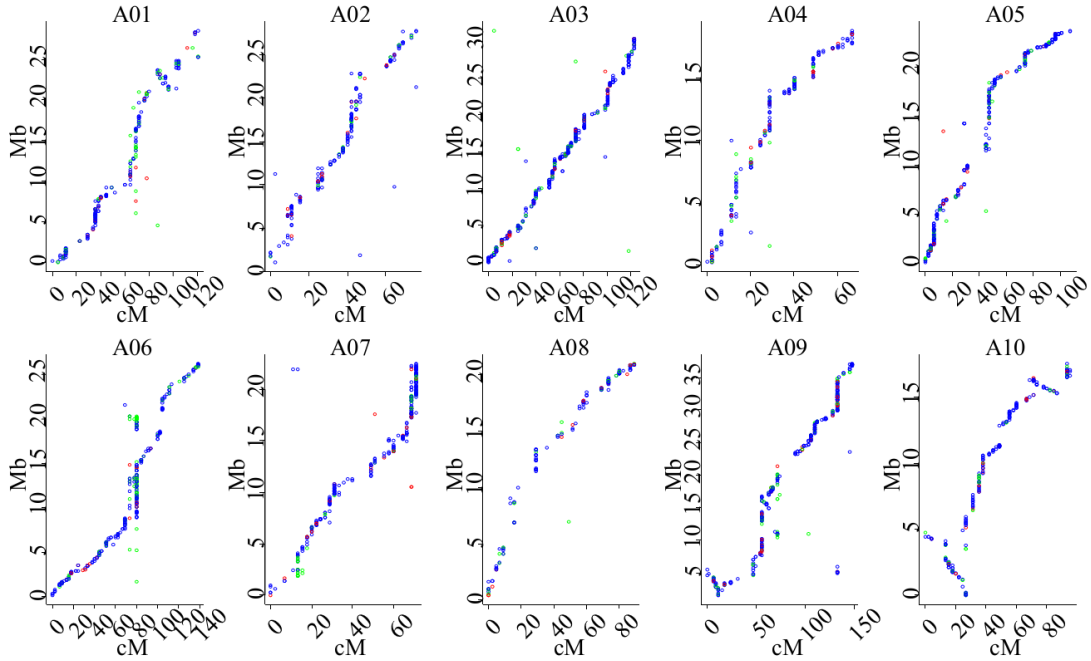


Figure S5. Collinearity between the A genomes of *B. rapa* and *B. napus* revealed by the PAV linkage groups.

The X axis represents the genetic distance in each linkage group of *B. napus*, and the Y axis represents the physical distance of corresponding *B. rapa* chromosome. If a locus is mapped to multiple paralogous positions in the *B. rapa* genome (green points), only the location with the best hit is selected here (E value <=1e-10). The red points represent loci with only one end of the PE read having a unique position in the *B. rapa* genome. The blue points represent loci with both ends of the PE read having a unique position in the *B. rapa* genome.

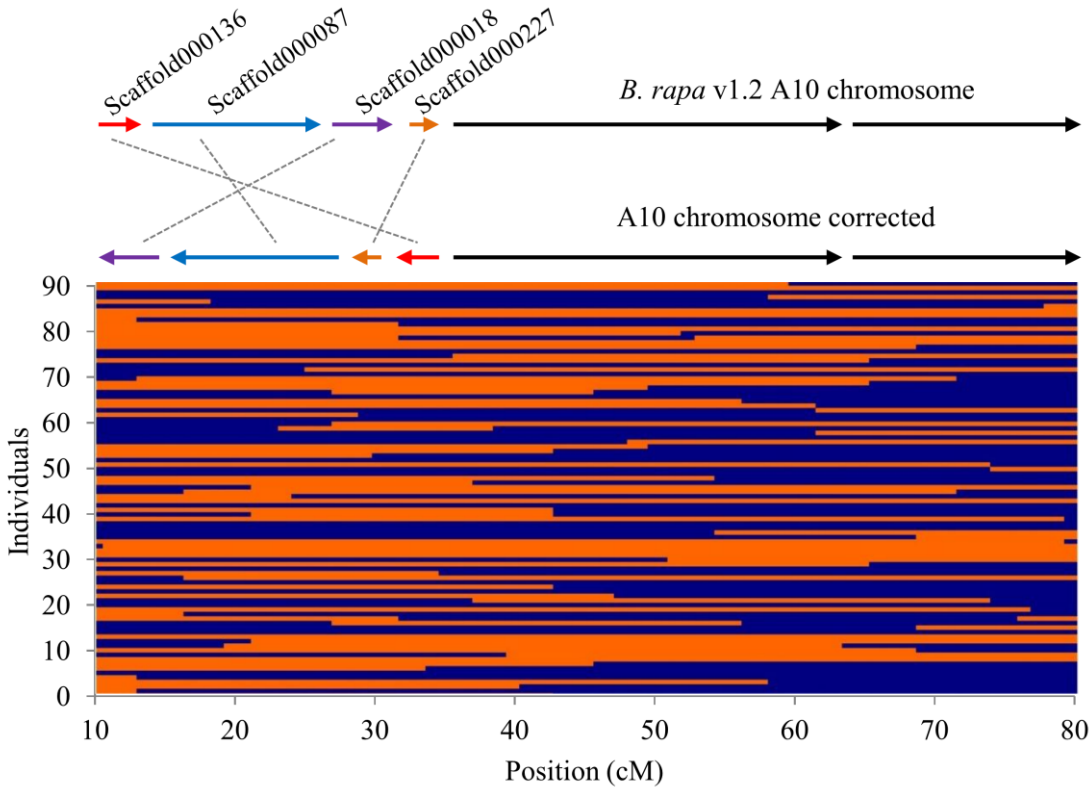


Figure S6. The four instances of mis-ordered sequence scaffolds on the *B. rapa* A10 chromosome.