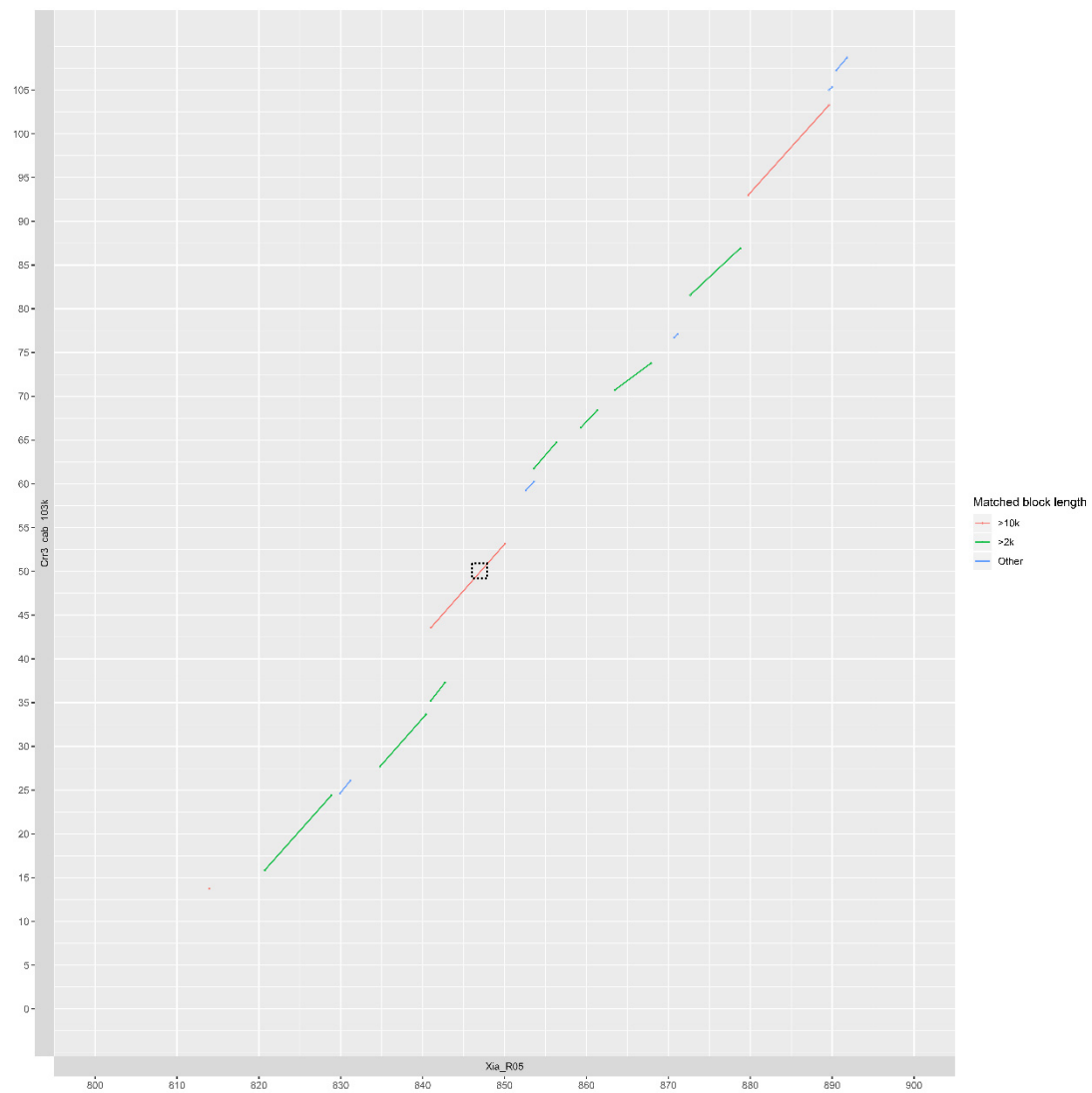
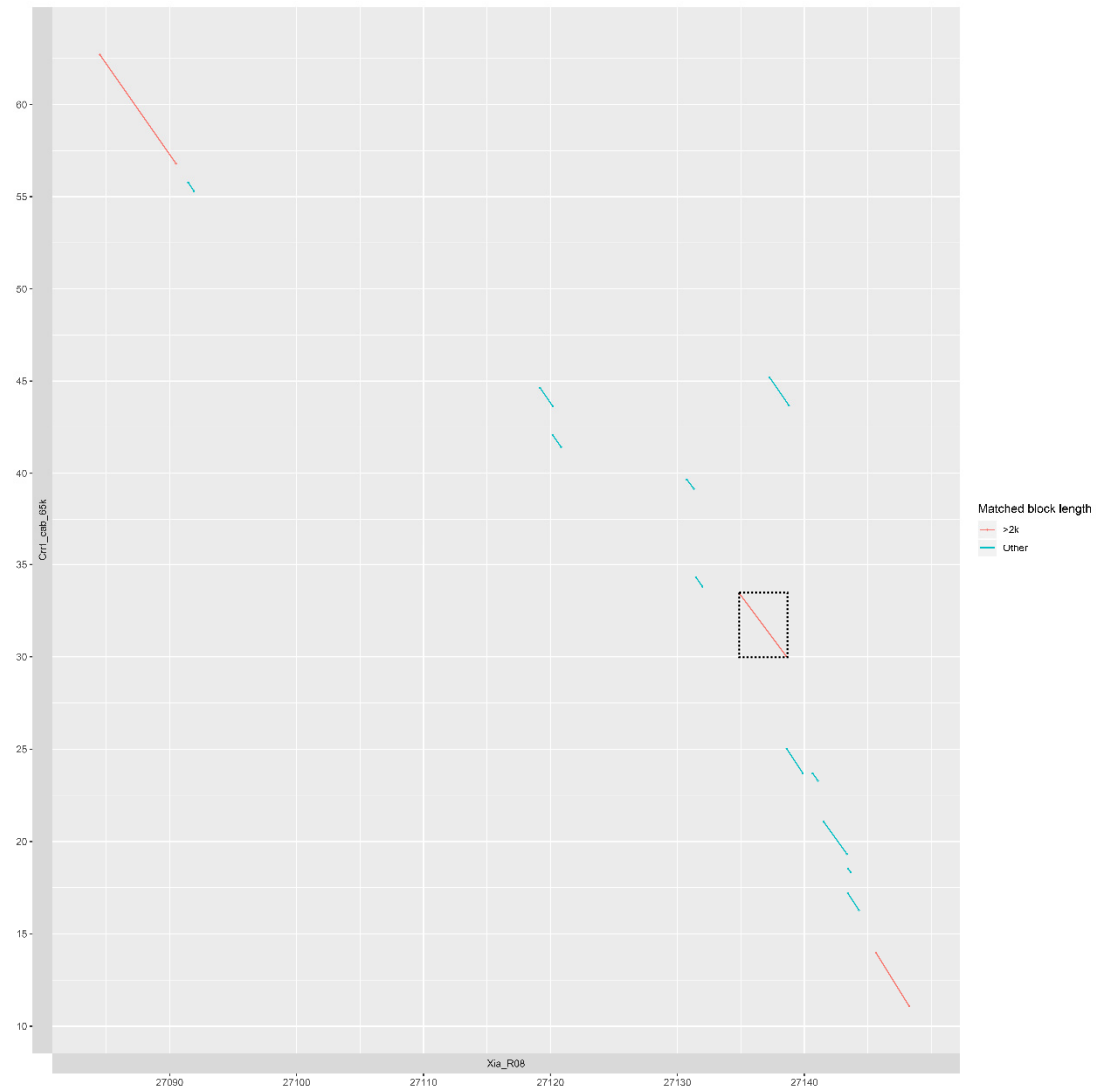


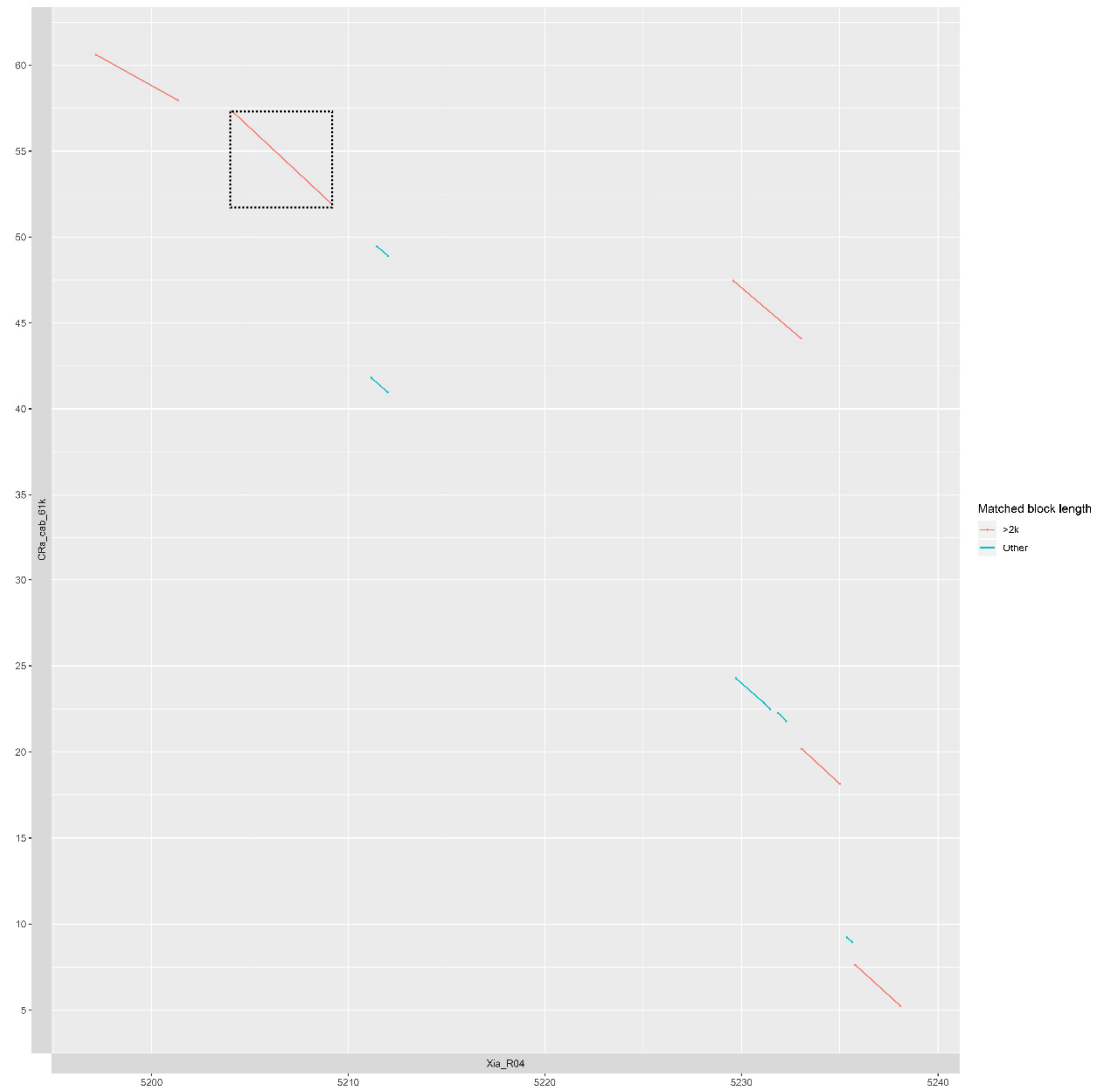
Supplementary Figure S1. Collinearity between the clubroot resistance genes and flanking region of *B. rapa* and the radish 'XYB36-2' genome. The syntenic regions of *Crr3*, *Crr1*, and *CRa* of *B. rapa* was located on chromosome R05, R08 and R04 of radish (Dotted box). X-axis means chromosome (R01 – R09) and the length (Mb). Y-axis means the flanking sequences of *Crr3* (103kb), *Crr1* (65kb), and *CRa* (61kb) from Chinese cabbage.



Supplementary Figure S2. Collinearity between the *Crr3* gene and flanking region of *B. rapa* and the radish chromosome R05 (798486 bp – 891819 bp, Table 2). X-axis means chromosome length (kb) of “XYB36-2” radish genome. Y-axis means the flanking sequences of *Crr3* (103kb) from Chinese cabbage. Dotted box indicated the location of *Crr3* QTL marker (BrSTS-61).



Supplementary Figure S3. Collinearity between the *Crr1* gene and flanking region of *B. rapa* and the radish chromosome R08 (27084498 bp – 27148246 bp, Table 2). X-axis means chromosome length (kb) of “XYB36-2” radish genome. Y-axis means the flanking sequences of *Crr1* (65kb) from Chinese cabbage. Dotted box indicated the location of *Crr1* homologous gene (*Rsa10003637*) with 91.69% sequence identity (Table 2).



Supplementary Figure S4. Collinearity between the *CRa* gene and flanking region of *B. rapa* and the radish chromosome R04 (5197160 bp – 5238084 bp, Table 2). X-axis means chromosome length (kb) of “XYB36-2” radish genome. Y-axis means the flanking sequences of *CRa* (61kb) from Chinese cabbage. Dotted box indicated the location of *CRa* homologous gene (*Rsa10025571*) with 85.93% sequence identity (Table 2).