## Supplementary Data

Supplementary data listed below are available at www.dnaresearch.oxfordjournals.org.

Table S1 Statistics of the assembled scaffolds only by short-read sequences
Table S2 Summary of BAC clones
Table S3 Linkages of both ends of scaffolds
Table S4 Genes of 80,521 predicted by Augustus.
Table S5 Gene prediction by Augustus 2.7 with *A. thaliana* training set
Table S6 Numbers of predicted tRNAs
Table S7 Blast search of RSA_r1.0 with RadishBase
Table S8 Comparison of repetitive sequences in three Brassicaceae species
Table S9 Classification of predicted gene into Clusters of Orthologous Groups of proteins (KOG)
Table S10 Numbers of SNPs between sequences of RSA_r1.0 and reads of Sayatori
Table S11 List of SNP DNA markers
Table S12 List of RGB PCR-RFLP markers
Table S13 List of RGC PCR-RFLP markers.
Table S14 Integrated linkage map
Table S15 A summary of genetic map
Table S16 Assignment of scaffolds to integrated linkage map
Table S17 Number of SNPs between different lines of radish
Table S18 Number of common amplicons containing SNPs between different lines of radish
Fig. S1 Distribution of the number of distinct kmers in each multiplicity (kmer = 17).
Fig. S2 A linkage map of *R. sativus*.

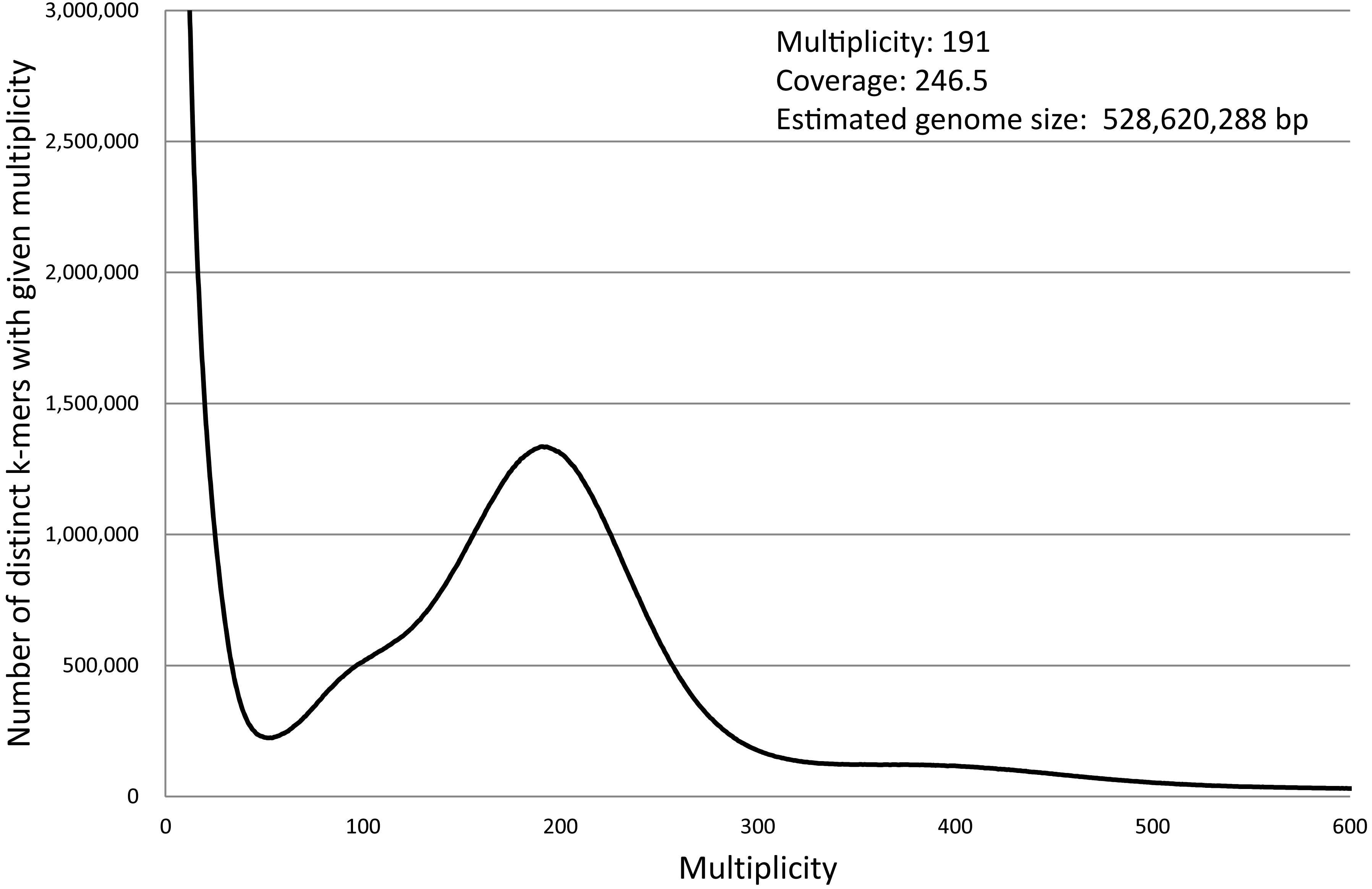

Fig. S1 Distribution of the number of distinct kmers in each multiplicity (kmer = 17).

Fig. S2 A linkage map of R. sativus.
Nine linkage groups are labelled as R1–R9 according to Li et al. (2011). Scale of genetic distance (in cM) are shown on the left side of the figure. Marker names are shown on the right side of each linkage group.