**File S2. List of Supplementary Materials**

File S1. Full methods and results for development of the A-2551TN maternal haplotype map.

Table S1. Accession numbers corresponding to Sequence Reads Archive (SRA) and assembly data of the four Rosaceae species used for comparative analysis of repeat composition with the ‘Hillquist’ blackberry (*R. argutus*) genome assembly. *Potentilla micrantha* datasets were retrieved from the GigaScience GigaDB repository.

Table S2. Summary of sequencing data from PacBio, Hi-C, and 10X platforms.

Table S3. Summary statistics for the seven chromosome-length scaffolds corresponding to the ‘Hillquist’ blackberry (*R. argutus*)base chromosomes.

Table S4. Depth of genotyping-by-sequencing read coverage in the parents and F1 progeny of the A-2551TN x APF-259TN mapping population and percent of reads aligning to unique positions in the ‘Hillquist’ blackberry (*R. argutus*) and black raspberry (*R. occidentalis*) reference genomes.

Table S5. Distribution of single-dose allele markers across the A-2551TN maternal haplotype map.

Table S6. Marker positions in the A-2551TN maternal haplotype map, physical positions on the 'Hillquist' blackberry (*R. argutus*) genome assembly, and genotype scores in the parents and progeny.

Table S7. Number and classification of full-length long terminal repeat retrotransposons (LTR-REs) identified in the genomes of five Rosaceae species.

Table S8. Predicted proteins in the *R. argutus* genome assembly along with physical positions and matches obtained from blastp analyses with nr, Araport11, RefSeq, SwissProt and TrEMBL databases as subjects.

Table S9. Summary of functional annotation of ‘Hillquist’ gene predictions including transcripts with matches to InterPro domains, Gene Ontology (GO) terms, KEGG pathway and KEGG orthologs.

Table S10. *R. argutus* blackberry homologs of *Arabidopsis* flowering time genes listed in FLOR-ID database.

Figure S1. Pedigree of the A-2551TN x APF-259TN mapping population.

Figure S2. Flowchart of the structural gene annotation.

Figure S3. GenomeScope *k-mer* analysis with 10x Genomics Illumina paired-end reads.

Figure S4. Whole-genome alignment plot between the ‘Hillquist’ blackberry (*R. argutus*) genome assembly and the chromosome-scale assembly of *R. chingii.*

Figure S5. The 30 linkage groups of the A-2551TN maternal haplotype map. Marker positions are expressed in cM.

Figure S6. The amount of sequence repeat-masked by repeats grouped by their length.

Figure S7. Distribution of the number of multiple alternative isoforms per protein-coding locus. There are 36,836 genes without alternative isoforms.

Figure S8. BUSCO annotation assessment of the ‘Hillquist’ blackberry (*R. argutus*) genome assembly.