

Supplementary data

Figure S1-3

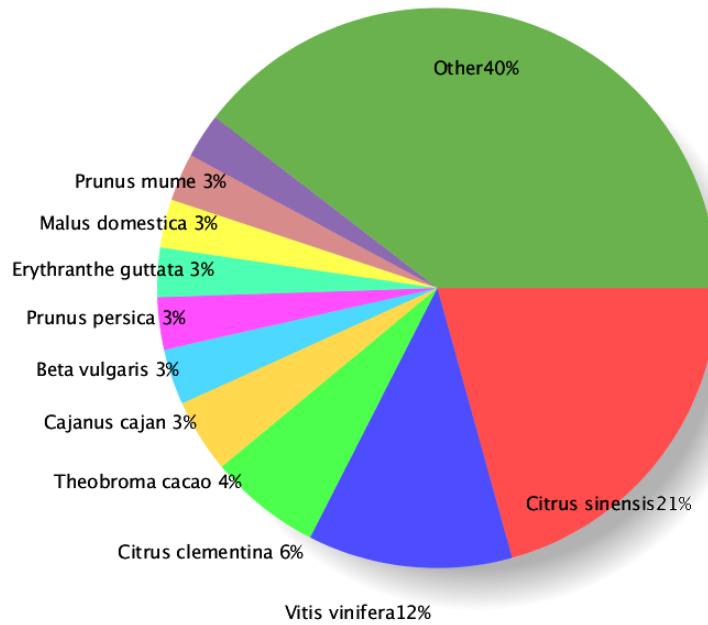


Figure S1. Species distribution of the top BLAST hits in the NR database.

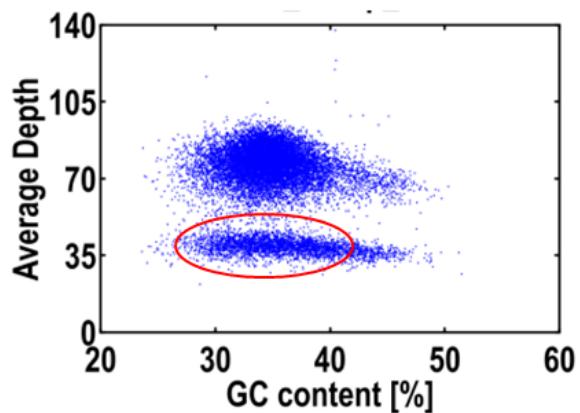


Figure S2. GC content and average sequencing depth of the *Acer truncatum* genome data.

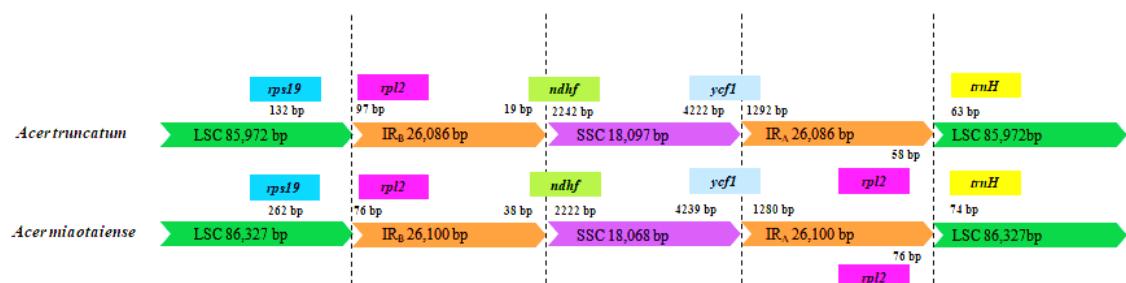


Figure S3. Comparison of the LSC, SSC and IR regions in chloroplast genomes of *Acer truncatum* and *Acer miaotaiense*.

Table S1-3**Table S1.** Statistics of *Acer truncatum* sequencing data.

Library	Raw reads	Raw base (bp)	Clean base (bp)	Depth (X)	Q30 (%)
300bp	207,271,108	62,181,332,400	61,902,168,600	116	94.81

Table S2. Statistics of gene functional annotation.

Annotation database	Annotated number
COG	11,834
GO	28,508
KEGG	7,552
KOG	47,213
Pfam	41,800
Swiss-Prot	46,398
TrEMBL	77,574
Nr	77,211
Nt	48,893
All	87,308

Table S3. The SSR types detected in the *Acer truncatum* sequences.

Searching item	Number	Percentage (%)
Total number of sequences examined	145,640	–
Total size of examined sequences (bp)	380,814,193	–
Total number of identified SSRs	392,961	100.00
Number of SSRs containing sequences	103,829	26.42
Number of sequences containing more than 1 SSR	75,320	19.17
Number of SSRs present in compound formation	76,281	19.41
Mono-nucleotide	251,731	64.06
Di-nucleotide	97,797	24.89
Tri-nucleotide	30,161	7.68
Tetra-nucleotide	9,265	2.36
Penta-nucleotide	2,418	0.62
Hexa-nucleotide	1,589	0.40