

Figure S1

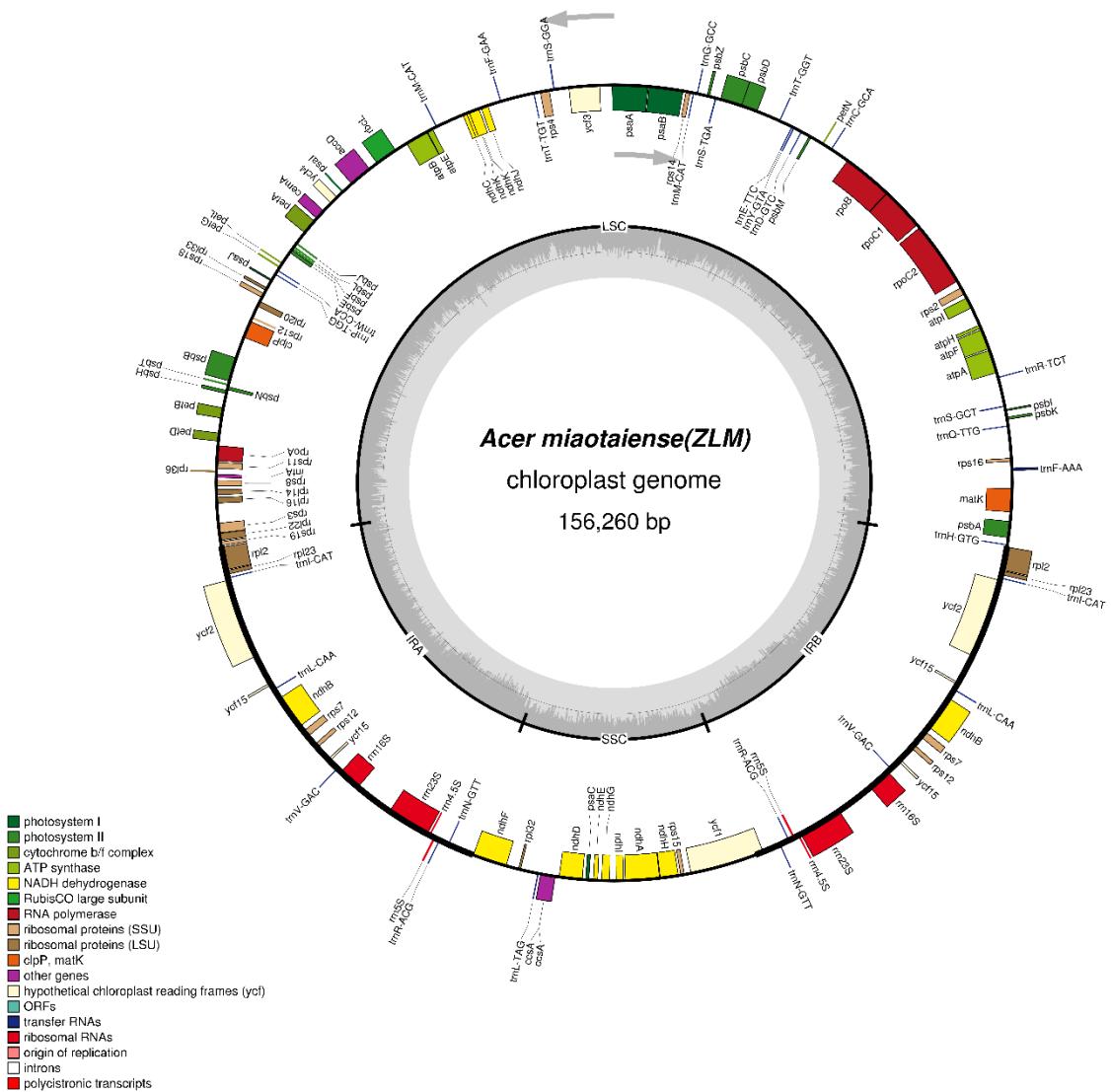


Figure S2

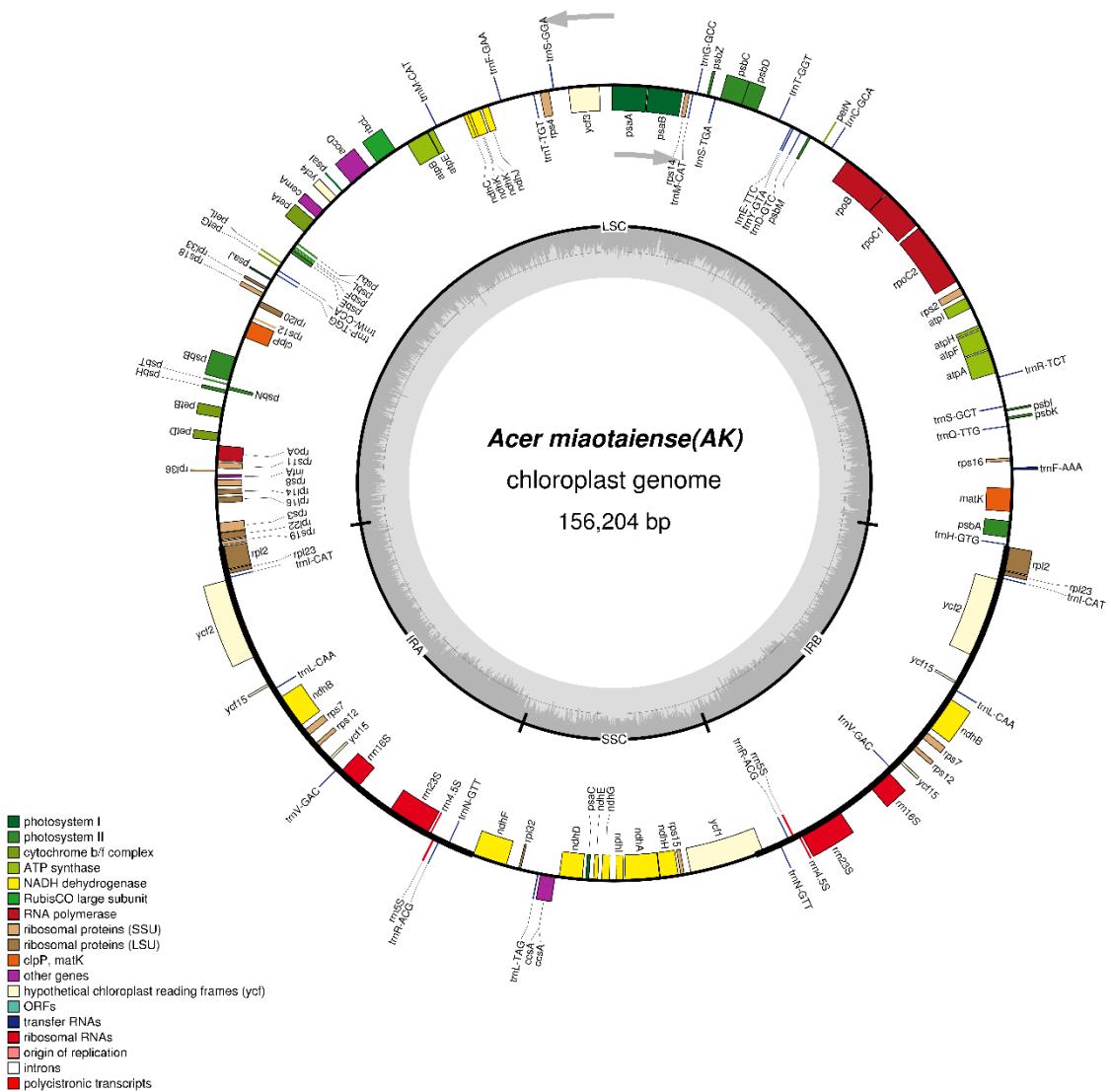


Figure S3

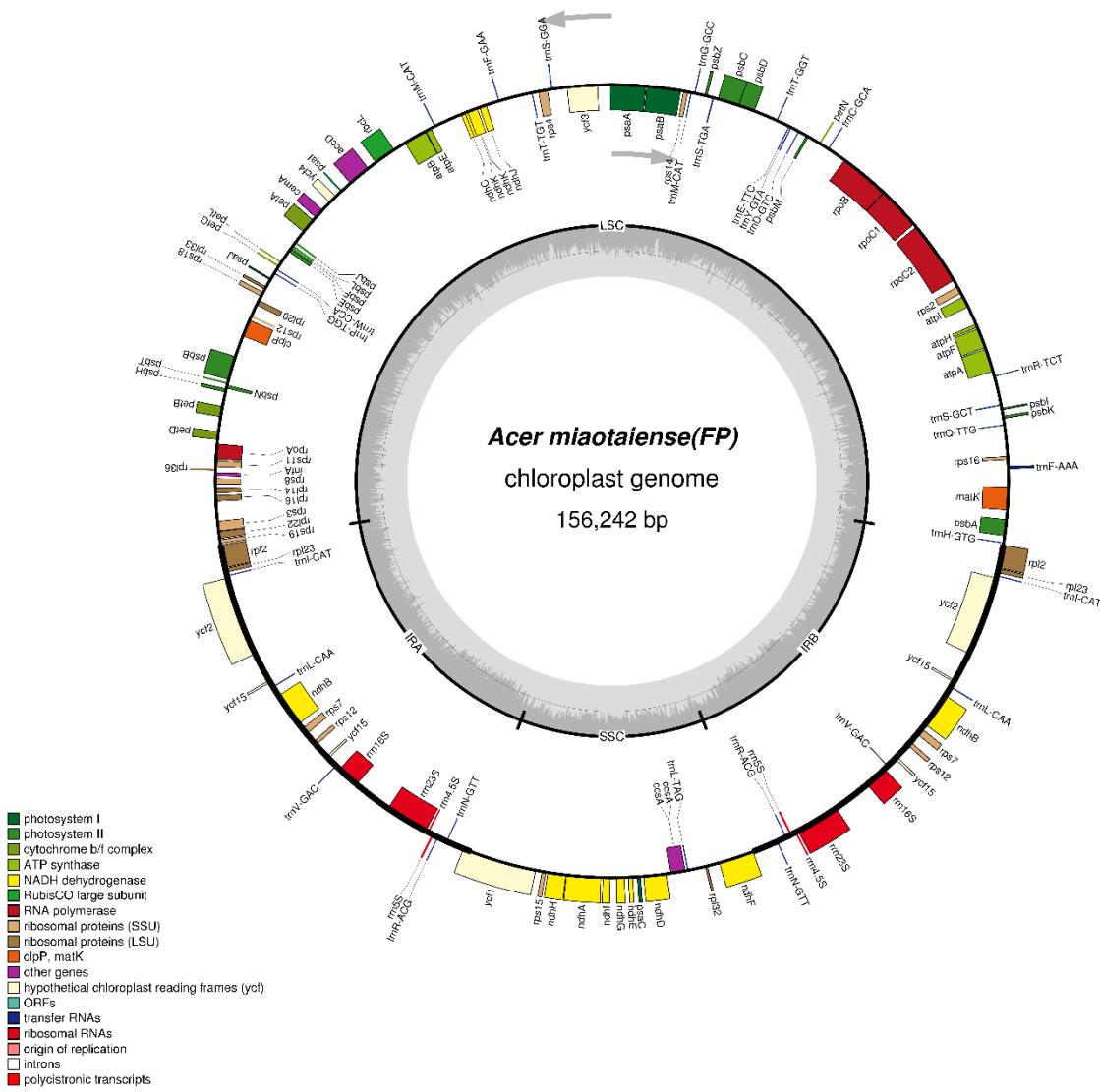


Figure S4

A	atpB NS	ATAACTTCCATTCAAGCCGTTTATGTACCTGCGGACGATT	1000
	atpB DB	ATAACTTCCATTCAAGCCGTTTATGTACCTGCGGACGATT	1000
	atpB FP	ATAACTTCCATTCAAGCCGTTTATGTACCTGCGGACGATT	1000
	atpB YP	ATAACTTCCATTCAAGCCGTTTATGTACCTGCGGACGATT	1000
	atpB ZL	ATAACTTCCATTCAAGCCGTTTATGTACCTGCGGACGATT	1000
	atpB ref	ATAACTTCCATTCAAGCCGTTTATGTACCTGCGGACGATT	1000
	Consensus	ataacttccattcaagccgttatgtacctgc gacgatt	
B	rf_1_atpB NS	ITSIQAVYVPADDLTDPAATTFAHLDATTVLSRGLAAKG	360
	rf_1_atpB DB	ITSIQAVYVPADDLTDPAATTFAHLDATTVLSRGLAAKG	360
	rf_1_atpB FP	ITSIQAVYVPADDLTDPAATTFAHLDATTVLSRGLAAKG	360
	rf_1_atpB YP	ITSIQAVYVPADDLTDPAATTFAHLDATTVLSRGLAAKG	360
	rf_1_atpB ZL	ITSIQAVYVPADDLTDPAATTFAHLDATTVLSRGLAAKG	360
	rf_1_atpB ref	ITSIQAVYVPADDLTDPAATTFAHLDATTVLSRGLAAKG	360
	Consensus	itsiqavyvpaddltdpapattfahldattvlsrglaakg	

Figure S5

Table S1. Sequencing quality of *Acer miaotaiense* from five regions.

Samples	BRD-ID	Read Number	Base Number	GC Content	≥Q30
YPG	R01	19,350,980	5,805,294,000	36.78%	89.76%
ZLM	R02	18,853,398	5,656,019,400	36.36%	90.74%
AK	R03	18,094,930	5,428,479,000	36.88%	93.04%
DBC	R04	20,218,759	6,065,627,700	37.20%	93.24%
FP	R05	18,919,122	5,675,736,600	36.63%	91.59%
Average	-	19,087,438	5,726,231,340	36.77%	91.67%

Table S2. Detailed information of the detected SNPs in the chloroplast genome at five geographical locations. .

SNP	Location	position	gene	SNP	species	position	gene																
t	NS	73744	matK	g	DB	73734	matK	g	FP	73711	matK	g	YP	73730	matK	t	ZL	73734	matK	g	ref	3532	matK
g	NS	86091	atpI	t	DB	86077	atpI	t	FP	86054	atpI	t	YP	86073	atpI	t	ZL	86093	atpI	t	ref	15873	atpI
t	NS	117326	rps4	a	DB	117312	rps4	a	FP	117289	rps4	a	YP	117308	rps4	a	ZL	117328	rps4	a	ref	47082	rps4
c	NS	125832	atpB	c	DB	125870	atpB	c	FP	125847	atpB	c	YP	125866	atpB	t	ZL	125885	atpB	c	ref	55640	atpB
t	NS	140451	rpl20	g	DB	140488	rpl20	g	FP	140465	rpl20	g	YP	140484	rpl20	t	ZL	140504	rpl20	g	ref	70621	rpl20