

Appendix A

Table S1 List of plant material analyzed

No.	Species name	Scientific name	Collected region
1	Cara cara	<i>C. sinensis</i>	HZAU
2	Newhall	<i>C. sinensis</i>	HZAU
3	Tempo	<i>C. sinensis</i>	HZAU
4	Jincheng	<i>C. sinensis</i>	HZAU
5	Xin-hui	<i>C. sinensis</i>	HZAU
6	Mashuiju	<i>C. reticulata</i>	HZAU
7	Hongju	<i>C. reticulata</i>	HZAU
8	Xinshengxi	<i>C. reticulata</i>	HZAU
9	Kukhan mandarin	<i>C. reticulata</i>	HZAU
10	Nafeng	<i>C. reticulata</i>	HZAU
11	Qingpi	<i>C. reticulata</i>	HZAU
12	Shatangiu	<i>C. reticulata</i>	HZAU
13	Zhushaju	<i>C. reticulata</i>	HZAU.
14	Eureka Lemon	<i>C. limon</i>	HZAU
15	Wild Lemon	<i>C. limon</i>	HZAU
16	Chinese lime	<i>C. limonia</i>	HZAU
17	Rough Lemon	<i>C. jambhiri</i>	HZAU
18	Mexican Lime	<i>C. aurantiifolia</i>	HZAU
19	HB pummelo	<i>C. grandis</i>	HZAU
20	Jinshi pummelo	<i>C. grandis</i>	HZAU
21	Fenghuang pummelo	<i>C. grandis</i>	HZAU
22	Wendan pummelo	<i>C. grandis</i>	Citrus institution of Guangxi Zhuang
23	Hongxin pummelo	<i>C. grandis</i>	Citrus institution of Guangxi Zhuang
24	Guanxi pummelo	<i>C. grandis</i>	Citrus institution of Guangxi Zhuang
25	Wanbai pummelo	<i>C. grandis</i>	Yichang city of Hubei province
26	Huoyansh pummelo	<i>C. grandis</i>	Yichang city of Hubei province.
27	Wild Kumquat (XHS01)	<i>Fortunella sp</i>	Longyan in Fujian province
28	Wild Kumquat (XHS03)	<i>Fortunella sp</i>	Longyan in Fujian province
29	Wild Kumquat (GZ01)	<i>Fortunella sp</i>	Longyan in Fujian province
30	Wild Kumquat (ZL01)	<i>Fortunella sp</i>	Longyan in Fujian province
31	Wild Kumquat (RYS01)	<i>Fortunella sp</i>	Sanming in Fujian province
32	Wild Kumquat (MP04)	<i>Fortunella sp</i>	Sanming in Fujian province
33	Wild Kumquat (MP10)	<i>Fortunella sp</i>	Sanming in Fujian province
34	Wild Kumquat (BZ10)	<i>Fortunella sp</i>	Nanping in Fujian province
35	Trifoliata 1	<i>Poncirus trifoliata</i>	HZAU
36	Trifoliata 2	<i>Poncirus trifoliata</i>	HZAU
37	Trifoliata 3	<i>Poncirus trifoliata</i>	HZAU

38	Trifoliata 4	<i>Poncirus trifoliata</i>	HZAU
39	Trifoliata 5	<i>Poncirus trifoliata</i>	HZAU
40	Trifoliata wild1	<i>Poncirus trifoliata</i>	HZAU
41	Trifoliata wild2	<i>Poncirus trifoliata</i>	HZAU
42	Trifoliata wild3	<i>Poncirus trifoliata</i>	HZAU

Table S2 Characteristics of 61 novel SSR markers developed from *P. trifoliata* ESTs

Locus ID	Primer Sequences (5'-3')	Repeat motif	Tem	Product Size/bp	Description of top blast hits	Gene bank/sequence ID
PteSR010	F: GAGTACTGTCACTCAAAGA R: CTGAAATGTATCGAAGGATAG	(AGAACA) ⁴	50	212-212	11s globulin subunit beta	gi188469468
PteSR040	F: GAGGTGAAATGAGGTTGAT R: TAAATTCACCTCACCAATC	(GAGGAT) ⁵	51	193-199	dnaj heat shock n-terminal protein	gi188446258
PteSR046	F: CGTCCGAAATCCCTCCTTC R: ATTCTCTCGGAAAGCTCCATT	(CAA) ⁸	52	225-241	protein	gi188440842
PteSR048	F: ACTCTACTCTCGAATCTCC R: GCAAGTGATTAGAAACATTC	(AT) ¹¹	50	162-176	bell homeotic	gi188438688
PteSR094	F: CAGTAGCGGCCCTTIG R: GCGATTTATTTGAATAGAGA	(CTT) ⁹	52	126-135	cu zn-superoxide	gi188401095
PteSR100	F: TTTGACAGAATCAAATCTC R: CCTTCATGATTTCTTAAA	(TTA) ⁷	51	236-256	protein phosphatase 2	gi188393160
PteSR164	F: CTTTGAACCTCCTTGTAACAC R: TTCTGAAATGGATAGAAAA	(AAAG) ⁶	50	228-242	sigma factor	gi188325367
PteSR168	F: GCGATTTGGAATCCAGAAAA R: TATTTTGTGGTGGAGGGAG	(CAG) ⁹	54	275-345	transcriptional corepressor leunig	gi188324237
PteSR185	F: CCATCACAGAGACCCAT R: CTTTCTCTCCCTTTTCTT	(GCT) ⁷	53	263-269	uncharacterized protein	gi188305443
PteSR193	F: AAGAAAAATGCGGTCTGTTGG R: TGATACACAAGAACGCCGAG	(AG) ⁸	54	253-340	constans-like protein	gi188300527
PteSR218	F: ATTCGTACAAGATCAAGAAA R: GAGACGGTGTAGATTATGAC	(CAA) ⁷	50	127-136	protein	gi188282623
PteSR254	F: GTTCCAAAAGAGAAATCAAA R: TATGAGAGCTCTGTAAAAGG	(GAA) ⁷	51	185-197	plasma membrane intrinsic protein	gi188251830
PteSR264	F: CATTTTGTTCATTTTCTCTC R: CCATCTGGGTATTGTAGATA	(CAAAAC) ⁶	50	263-332	protein binding protein	gi188238729
PteSR294	F: AATAACAAAAGAACTCGTCAA R: GCAAATGAATCTGCAT	(TCA) ⁷	50	135-144	acid invertase	gi55291231
PteSR299	F: TTAGAAAACATTTCCATGAC R: GTGAAGCATCACAAAGACTAT	(AT) ²²	51	203-232	secretory peroxidase	gi55290865
PteSR300	F: GTCAGAAAGACTCCCTTACTT R: ATATATGGAAGCACATCAAC	(TCT) ¹⁰	50	200-346	surfeit locus protein 2	gi55290654
PteSR301	F: AAATGCACAAGAACCCTTAC R: TTCAGTTGATTTTGTACTTT	(AT) ¹⁵	51	182-198	mads box	gi55290500
PteSR337	F: CTTTCTTTATAGCCACATTT R: GTATGTCTAGTATCCCGTCA	(TA) ¹⁰	50	130-170	annexin	gi57876826
PteSR338	F: TTCAACTCCAATCTCTCTA R: AAGGATTGATAAACAACACTGTG	(GCCTCA) ⁴	50	120-132	uncharacterized protein	gi57876659

PteSR353	F: R:	CCACATATTTATTATCTCCG CAGGTCACCTGCAGATTTAT	(AAAAGA)4	53	236-242	zinc finger	gi57870494
PteSR366	F: R:	TTTCATCCTATTCAAGACAC CAAAAATCTTCTTTGAGTA	(CAACAC)4	50	230-230	ubp1-associated protein 2a	gi57573208
PteSR377	F: R:	CCGTTTGTCTTAATAATACTC GAATTTGAGATCTTCAGACA	(CT)12	50	118-140	acetyl co-enzyme	gi57571736
PteSR389	F: R:	CACCCATTACCTTCAATC AATGGGAAGGAATAGTATGT	(CACCAT)6	52	164-165	l-galactono- -lactone dehydrogenase	gi57569653
PteSR396	F: R:	CTAAAACAGACAGGAGAATG GAAGGAAGATTTAGAAAAGG	(AGA)7	51	167-173	methyl binding domain protein	gi34430920
PteSR407	F: R:	TTTGATTCCTATCAGAAGAT TGCAGTTCCAAGTTAGTATT	(ATAAA)4	50	213-214	glycosyltransferase	gi31671622
PteSR439	F: R:	ACAAGAAAACAATCAGAAG GGGATAGAGTGAAGAAGAT	(CT)15	51	100-119	transketolase	Contig499
PteSR445	F: R:	ACAATATCAACAAGAACGAC GTTGGATGAAGCTGTTG	(GA)9	50	258-270	structural constituent of cell	Contig623
PteSR450	F: R:	ACACACAACCTCTGTTCTGA CAAAAACCTCAACAGAAAATC	(TC)8	53	275-276	galactosyltransferase family protein	Contig688
PteSR481	F: R:	CACGTAAATCTTCGAGATAC ATTGGAAAATGAAAATGTTA	(TG)8	54	191-288	potassium channel tetramerisation	Contig1248
PteSR484	F: R:	TCCAGTTGAAGGAAAACGACC GACACTACCGACGAAACGTGA	(TAAT)5	55	270-294	epidermal patterning factor-like protein	Contig1316
PteSR493	F: R:	TAGAGAACGCGCCAGCAG AAGATCTTGGTGGCCAGAGA	(CCAGAA)5	55	229-312	dna binding	Contig1534
PteSR509	F: R:	TTGTTAGAGGAGACAGACAG GACAATTTCTCTCTGAAC	(GAA)11	50	268-271	ring u-box domain-containing protein	Contig1834
PteSR510	F: R:	ATCACTCAAAGGAGAGAAGT TTTTCTTCCATAIGATTA	(CTGGAG)4	54	132-138	ctc-interacting domain 11 protein	Contig1886
PteSR523	F: R:	AATTGATTTTCCAAGAAAGAC CAATCTTCA TCAGAACTCTC	(TCCAAT)4	51	214-214	dehydration responsive element	Contig2055
PteSR525	F: R:	TTTGGTTCATTTTTCTACTC CTTCCAAATAGTAACGGTAA	(CTTCAA)4	50	279-279	cle26 protein	Contig2088
PteSR527	F: R:	TTACGAAAGGTAATGAACAAT TTAGCAAAACAATAAATACCC	(AAAA)4	50	171-182	nac domain protein nac2	Contig2109
PteSR559	F: R:	TTGAAATTCGAGATAAAAAG TATTGCTGTTGTTGTTATG	(CAACGG)4	50	265-265	myb family transcription factor	Contig2618
PteSR550	F: R:	CACATCCCTATTCCTCTGC TCCCTACTCCAGTGTCTCCG	(GTTGA)6	51	249-185	gtp binding protein gb2	Contig2476
PteSR562	F: R:	TAAATCAAAAATGTTACGGAT AGATTGCAGATTACCAAATTA	(ACTC)5	51	181-181	purple acid phosphatase-like protein	Contig2631
PteSR563	F: R:	CGTCCGAGCAAAAACAGAAG CCTTTAGCCATGTTGAGGGA	(AAGA)8	52	208-240	glutathione s-transferase	Contig2634

Table S3 Results of microsatellite search

Item	Number/Size
Total number of sequences examined	25388
Total size of examined sequences/bp	22799411
Total number of identified SSRs	976
Number of SSR containing sequences	887
Number of sequences containing more than 1 SSR	79
Number of SSRs present in compound formation	50