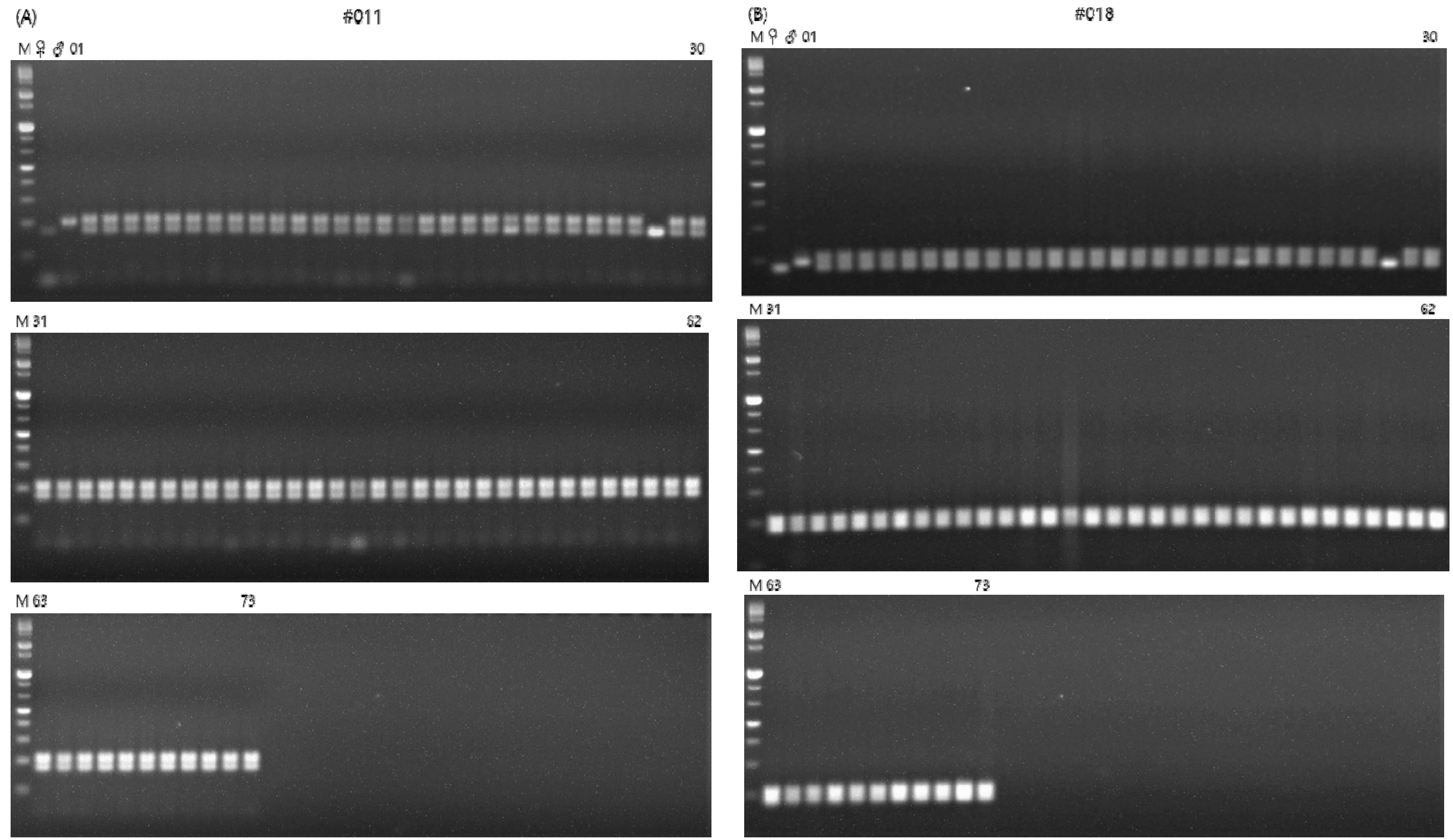

Supplementary Fig. 1. The electrophoresis gel results of no segregated lines in mapping progenies with single polymorphic SSR primer 11 and 18.

Supplementary Table 1. Statestic information of selected 260 SSR primers of *Prunus persica*

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_2-84395-84404-CT-5	1	Scaffold_2	84395	84404	CT	5	10	0	9	10	10	4.856267428	460
Scaffold_2-559815-559854-TC-20	2	Scaffold_2	559815	559854	TC	20	40	62	.	40	-22	12.70170592	490
Scaffold_2-981342-981371-TCTGTC-5	3	Scaffold_2	981342	981371	TCTGTC	5	30	48	36	48	-18	9	480
Scaffold_2-5583894-5583915-TC-11	4	Scaffold_2	5583894	5583915	TC	11	22	11	9	23	11	7.274384281	472
Scaffold_2-7523131-7523168-AT-19	5	Scaffold_2	7523131	7523168	AT	19	38	28	28	38	10	5.773502692	488
Scaffold_2-8051705-8051760-CT-28	6	Scaffold_2	8051705	8051760	CT	28	56	41	41	54	15	8.124038405	506
Scaffold_2-8351975-8352020-TC-23	7	Scaffold_2	8351975	8352020	TC	23	46	32	26	46	14	10.11599394	496
Scaffold_2-8447798-8447815-GA-9	8	Scaffold_2	8447798	8447815	GA	9	18	5	18	18	13	6.5	468
Scaffold_2-8546854-8546913-CT-30	9	Scaffold_2	8546854	8546913	CT	30	60	40	40	58	20	11	510
Scaffold_2-9172638-9172669-AT-16	10	Scaffold_2	9172638	9172669	AT	16	32	14	.	32	18	10.39230485	482
Scaffold_2-9174261-9174304-CT-22	11	Scaffold_2	9174261	9174304	CT	22	44	18	18	44	26	15.011107	494
Scaffold_2-9541896-9541945-CT-25	12	Scaffold_2	9541896	9541945	CT	25	50	40	46	50	10	4.725815626	500
Scaffold_2-10181866-10181927-AG-31	13	Scaffold_2	10181866	10181927	AG	31	62	34	56	58	28	12.58305739	512
Scaffold_2-10897973-10898008-CT-18	14	Scaffold_2	10897973	10898008	CT	18	36	22	22	36	14	8.082903769	486
Scaffold_2-10950204-10950231-CT-14	15	Scaffold_2	10950204	10950231	CT	14	28	16	16	28	12	6.92820323	478
Scaffold_2-11359345-11359374-CT-15	16	Scaffold_2	11359345	11359374	CT	15	30	17	16	30	13	7.804912983	480
Scaffold_2-11405128-11405159-GA-16	17	Scaffold_2	11405128	11405159	GA	16	32	20	20	32	12	6.92820323	482
Scaffold_2-11991327-11991390-GA-32	18	Scaffold_2	11991327	11991390	GA	32	64	50	50	60	14	7.118052168	514
Scaffold_2-12272933-12272980-CT-24	19	Scaffold_2	12272933	12272980	CT	24	48	30	30	48	18	10.39230485	498
Scaffold_2-12376105-12376152-GA-24	20	Scaffold_2	12376105	12376152	GA	24	48	30	30	46	18	9.848857802	498
Scaffold_2-12530656-12530683-AT-14	21	Scaffold_2	12530656	12530683	AT	14	28	14	14	28	14	8.082903769	478
Scaffold_2-12535624-12535679-CT-28	22	Scaffold_2	12535624	12535679	CT	28	56	38	38	54	18	9.848857802	506
Scaffold_2-13092546-13092575-AT-15	23	Scaffold_2	13092546	13092575	AT	15	30	14	14	30	16	9.237604307	480
Scaffold_2-13462879-13462916-CT-19	24	Scaffold_2	13462879	13462916	CT	19	38	27	26	27	11	5.686240703	488
Scaffold_2-13862329-13862378-AG-25	25	Scaffold_2	13862329	13862378	AG	25	50	40	50	50	10	5	500
Scaffold_2-14321890-14321945-CT-28	26	Scaffold_2	14321890	14321945	CT	28	56	34	55	54	22	10.53169819	506
Scaffold_2-14358662-14358691-AT-15	27	Scaffold_2	14358662	14358691	AT	15	30	20	30	30	10	5	480
Scaffold_2-14599028-14599061-TC-17	28	Scaffold_2	14599028	14599061	TC	17	34	16	34	34	18	9	484
Scaffold_2-15112426-15112463-AT-19	29	Scaffold_2	15112426	15112463	AT	19	38	18	.	38	20	11.54700538	488
Scaffold_2-17555714-17555783-AG-35	30	Scaffold_2	17555714	17555783	AG	35	70	58	58	66	12	6	520
Scaffold_4-5176661-5176726-GA-33	31	Scaffold_4	5176661	5176726	GA	33	66	95	.	66	-29	16.74315781	516
Scaffold_4-8548058-8548113-GA-28	32	Scaffold_4	8548058	8548113	GA	28	56	43	72	42	13	14.03269991	506
Scaffold_4-8937028-8937065-TA-19	33	Scaffold_4	8937028	8937065	TA	19	38	24	25	38	14	7.804912983	488
Scaffold_4-10737061-10737106-TC-23	34	Scaffold_4	10737061	10737106	TC	23	46	34	46	46	12	6	496
Scaffold_4-11682579-11682612-TA-17	35	Scaffold_4	11682579	11682612	TA	17	34	22	22	36	12	7.549834435	484
Scaffold_4-11736785-11736820-TC-18	36	Scaffold_4	11736785	11736820	TC	18	36	21	.	36	15	8.660254038	486
Scaffold_4-11815384-11815411-AG-14	37	Scaffold_4	11815384	11815411	AG	14	28	19	28	28	9	4.5	478
Scaffold_4-12019773-12019814-GA-21	38	Scaffold_4	12019773	12019814	GA	21	42	22	.	42	20	11.54700538	492

Supplementary Table 1. Continued

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_4-14262664-14262711-AAAAAGAA-6	39	Scaffold_4	14262664	14262711	AAAAAGAA	6	48	35	.	48	13	7.505553499	498
Scaffold_4-15209186-15209223-GA-19	40	Scaffold_4	15209186	15209223	GA	19	38	25	24	38	13	7.804912983	488
Scaffold_4-15212003-15212048-CT-23	41	Scaffold_4	15212003	15212048	CT	23	46	32	32	46	14	8.082903769	496
Scaffold_4-15640461-15640490-TA-15	42	Scaffold_4	15640461	15640490	TA	15	30	16	16	30	14	8.082903769	480
Scaffold_4-16942015-16942070-TG-28	43	Scaffold_4	16942015	16942070	TG	28	56	44	56	56	12	6	506
Scaffold_4-17153746-17153811-TC-33	44	Scaffold_4	17153746	17153811	TC	33	66	54	.	62	12	6.110100927	516
Scaffold_4-18086330-18086347-TA-9	45	Scaffold_4	18086330	18086347	TA	9	18	0	18	18	18	9	468
Scaffold_4-18961784-18961835-GA-26	46	Scaffold_4	18961784	18961835	GA	26	52	35	48	48	17	7.410578025	502
Scaffold_4-19395556-19395591-TC-18	47	Scaffold_4	19395556	19395591	TC	18	36	16	16	36	20	11.54700538	486
Scaffold_4-20345940-20345989-AG-25	48	Scaffold_4	20345940	20345989	AG	25	50	61	.	50	-11	6.350852961	500
Scaffold_4-20420437-20420460-TA-12	49	Scaffold_4	20420437	20420460	TA	12	24	36	24	24	-12	6	474
Scaffold_4-20623730-20623767-CT-19	50	Scaffold_4	20623730	20623767	CT	19	38	26	38	38	12	6	488
Scaffold_4-21304708-21304759-GA-26	51	Scaffold_4	21304708	21304759	GA	26	52	38	.	40	14	7.571877794	502
Scaffold_4-21695285-21695326-CT-21	52	Scaffold_4	21695285	21695326	CT	21	42	23	40	.	19	10.44030651	492
Scaffold_4-22014631-22014660-TA-15	53	Scaffold_4	22014631	22014660	TA	15	30	20	30	30	10	5	480
Scaffold_4-22066284-22066339-GA-28	54	Scaffold_4	22066284	22066339	GA	28	56	45	53	51	11	4.645786622	506
Scaffold_4-22086347-22086388-AG-21	55	Scaffold_4	22086347	22086388	AG	21	42	31	.	42	11	6.350852961	492
Scaffold_4-22113282-22113325-CT-22	56	Scaffold_4	22113282	22113325	CT	22	44	30	42	42	14	6.403124237	494
Scaffold_4-22321215-22321256-CT-21	57	Scaffold_4	22321215	22321256	CT	21	42	33	32	.	9	5.507570547	492
Scaffold_4-22576590-22576627-AG-19	58	Scaffold_4	22576590	22576627	AG	19	38	54	38	38	-16	8	488
Scaffold_4-23184684-23184710-AAG-9	59	Scaffold_4	23184684	23184710	AAG	9	27	18	19	18	9	4.358898944	477
Scaffold_4-24909540-24909571-TA-16	60	Scaffold_4	24909540	24909571	TA	16	32	22	31	35	10	5.597618541	482
Scaffold_6-753836-753867-AT-16	61	Scaffold_6	753836	753867	AT	16	32	12	13	.	20	11.26942767	482
Scaffold_9-406192-406218-GAA-9	62	Scaffold_9	406192	406218	GAA	9	27	18	27	27	9	4.5	477
Scaffold_9-1031311-1031370-TC-30	63	Scaffold_9	1031311	1031370	TC	30	60	48	57	56	12	5.123475383	510
Scaffold_9-1411986-1412015-AG-15	64	Scaffold_9	1411986	1412015	AG	15	30	20	30	30	10	5	480
Scaffold_9-3739614-3739643-GAA-10	65	Scaffold_9	3739614	3739643	GAA	10	30	50	57	30	-20	13.86542462	480
Scaffold_10-154371-154418-CCT-16	66	Scaffold_10	154371	154418	CCT	16	48	30	.	48	18	10.39230485	498
Scaffold_10-394735-394798-AG-32	67	Scaffold_10	394735	394798	AG	32	64	42	.	63	22	12.42309677	514
Scaffold_10-659070-659079-AT-5	68	Scaffold_10	659070	659079	AT	5	10	24	10	10	-14	7	460
Scaffold_10-694698-694719-AG-11	69	Scaffold_10	694698	694719	AG	11	22	34	22	22	-12	6	472
Scaffold_10-3060940-3060989-AG-25	70	Scaffold_10	3060940	3060989	AG	25	50	26	26	50	24	13.85640646	500
Scaffold_10-3800990-3801027-GA-19	71	Scaffold_10	3800990	3801027	GA	19	38	28	28	38	10	5.773502692	488
Scaffold_10-3832613-3832650-AG-19	72	Scaffold_10	3832613	3832650	AG	19	38	24	38	.	14	8.082903769	488
Scaffold_10-9471653-9471698-CT-23	73	Scaffold_10	9471653	9471698	CT	23	46	33	45	46	13	6.350852961	496
Scaffold_10-9481109-9481122-GT-7	74	Scaffold_10	9481109	9481122	GT	7	14	32	.	14	-18	10.39230485	464
Scaffold_10-9518247-9518288-TC-21	75	Scaffold_10	9518247	9518288	TC	21	42	25	15	42	17	13.34166406	492
Scaffold_10-9518290-9518299-CT-5	76	Scaffold_10	9518290	9518299	CT	5	10	0	10	10	10	5	460

Supplementary Table 1. Continued

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_10-10305861-10305870-TC-5	77	Scaffold_10	10305861	10305870	TC	5	10	20	10	10	-10	5	460
Scaffold_10-11365070-11365138-TCT-23	78	Scaffold_10	11365070	11365138	TCT	23	69	58	.	69	11	6.350852961	519
Scaffold_10-11491973-11492022-GA-25	79	Scaffold_10	11491973	11492022	GA	25	50	35	50	50	15	7.5	500
Scaffold_10-22059573-22059612-TA-20	80	Scaffold_10	22059573	22059612	TA	20	40	28	.	40	12	6.92820323	490
Scaffold_10-22941627-22941644-AT-9	81	Scaffold_10	22941627	22941644	AT	9	18	8	8	18	10	5.773502692	468
Scaffold_10-23456010-23456039-TC-15	82	Scaffold_10	23456010	23456039	TC	15	30	13	28	28	17	7.889866919	480
Scaffold_10-23756985-23757010-TA-13	83	Scaffold_10	23756985	23757010	TA	13	26	16	16	19	10	4.716990566	476
Scaffold_10-24240748-24240783-TC-18	84	Scaffold_10	24240748	24240783	TC	18	36	54	54	36	-18	10.39230485	486
Scaffold_10-25958500-25958561-TC-31	85	Scaffold_10	25958500	25958561	TC	31	62	48	49	39	14	9.469248474	512
Scaffold_10-25974388-25974417-AT-15	86	Scaffold_10	25974388	25974417	AT	15	30	21	20	19	9	5.066228051	480
Scaffold_10-26113222-26113259-TC-19	87	Scaffold_10	26113222	26113259	TC	19	38	18	34	18	20	10.51982256	488
Scaffold_10-26171809-26171841-CCT-11	88	Scaffold_10	26171809	26171841	CCT	11	33	45	.	39	-12	6	483
Scaffold_10-26614625-26614694-CT-35	89	Scaffold_10	26614625	26614694	CT	35	70	52	.	51	18	10.69267662	520
Scaffold_10-27003780-27003821-CT-21	90	Scaffold_10	27003780	27003821	CT	21	42	30	32	31	12	5.560275773	492
Scaffold_10-27031675-27031702-CT-14	91	Scaffold_10	27031675	27031702	CT	14	28	44	28	.	-16	9.237604307	478
Scaffold_10-27955280-27955323-AG-22	92	Scaffold_10	27955280	27955323	AG	22	44	31	31	44	13	7.505553499	494
Scaffold_15-776342-776365-TA-12	93	Scaffold_15	776342	776365	TA	12	24	14	28	26	10	6.218252702	474
Scaffold_15-881735-881778-CT-22	94	Scaffold_15	881735	881778	CT	22	44	33	41	.	11	5.686240703	494
Scaffold_15-2485964-2485975-CT-6	95	Scaffold_15	2485964	2485975	CT	6	12	32	12	12	-20	10	462
Scaffold_15-2806809-2806842-AG-17	96	Scaffold_15	2806809	2806842	AG	17	34	13	13	34	21	12.12435565	484
Scaffold_15-2950736-2950785-AG-25	97	Scaffold_15	2950736	2950785	AG	25	50	38	38	50	12	6.92820323	500
Scaffold_15-3442035-3442066-CT-16	98	Scaffold_15	3442035	3442066	CT	16	32	20	32	32	12	6	482
Scaffold_15-5104899-5104922-CTT-8	99	Scaffold_15	5104899	5104922	CTT	8	24	14	23	24	10	4.856267428	474
Scaffold_15-6655646-6655685-GA-20	100	Scaffold_15	6655646	6655685	GA	20	40	26	40	40	14	7	490
Scaffold_15-6873053-6873092-CT-20	101	Scaffold_15	6873053	6873092	CT	20	40	56	36	.	-16	10.58300524	490
Scaffold_15-6929396-6929407-AT-6	102	Scaffold_15	6929396	6929407	AT	6	12	34	12	12	-22	11	462
Scaffold_15-7441145-7441168-CA-12	103	Scaffold_15	7441145	7441168	CA	12	24	4	.	24	20	11.54700538	474
Scaffold_15-7515529-7515576-TC-24	104	Scaffold_15	7515529	7515576	TC	24	48	32	.	48	16	9.237604307	498
Scaffold_15-9461623-9461670-AG-24	105	Scaffold_15	9461623	9461670	AG	24	48	35	.	48	13	7.505553499	498
Scaffold_15-9640130-9640163-CT-17	106	Scaffold_15	9640130	9640163	CT	17	34	20	20	30	14	7.118052168	484
Scaffold_15-10023387-10023418-CT-16	107	Scaffold_15	10023387	10023418	CT	16	32	42	32	32	-10	5	482
Scaffold_15-12327662-12327677-AG-8	108	Scaffold_15	12327662	12327677	AG	8	16	6	6	7	10	4.856267428	466
Scaffold_15-12718309-12718368-AG-30	109	Scaffold_15	12718309	12718368	AG	30	60	48	60	.	12	6.92820323	510
Scaffold_15-13012569-13012604-GA-18	110	Scaffold_15	13012569	13012604	GA	18	36	52	36	.	-16	9.237604307	486
Scaffold_15-13542465-13542504-TC-20	111	Scaffold_15	13542465	13542504	TC	20	40	16	40	40	24	12	490
Scaffold_15-14750956-14751005-TC-25	112	Scaffold_15	14750956	14751005	TC	25	50	60	46	40	-10	8.406346809	500
Scaffold_15-16020116-16020135-TA-10	113	Scaffold_15	16020116	16020135	TA	10	20	11	10	10	9	4.856267428	470
Scaffold_15-16072052-16072085-AT-17	114	Scaffold_15	16072052	16072085	AT	17	34	18	18	34	16	9.237604307	484

Supplementary Table 1. Continued

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_15-16116159-16116192-TC-17	115	Scaffold_15	16116159	16116192	TC	17	34	21	21	20	13	6.683312552	484
Scaffold_15-16224555-16224588-CT-17	116	Scaffold_15	16224555	16224588	CT	17	34	21	20	21	13	6.683312552	484
Scaffold_15-16241591-16241620-AT-15	117	Scaffold_15	16241591	16241620	AT	15	30	18	16	18	12	6.403124237	480
Scaffold_15-16729756-16729773-CT-9	118	Scaffold_15	16729756	16729773	CT	9	18	9	7	3	9	6.34428877	468
Scaffold_15-18574966-18574983-AT-9	119	Scaffold_15	18574966	18574983	AT	9	18	32	18	18	-14	7	468
Scaffold_15-19385429-19385458-AACTCA-5	120	Scaffold_15	19385429	19385458	AACTCA	5	30	18	30	30	12	6	480
Scaffold_15-20158053-20158078-AT-13	121	Scaffold_15	20158053	20158078	AT	13	26	13	41	30	13	11.56143013	476
Scaffold_15-20694725-20694762-CT-19	122	Scaffold_15	20694725	20694762	CT	19	38	26	.	22	12	8.326663998	488
Scaffold_15-21027530-21027539-TC-5	123	Scaffold_15	21027530	21027539	TC	5	10	0	10	.	10	5.773502692	460
Scaffold_15-21846417-21846444-CT-14	124	Scaffold_15	21846417	21846444	CT	14	28	44	28	28	-16	8	478
Scaffold_15-22718598-22718649-CT-26	125	Scaffold_15	22718598	22718649	CT	26	52	42	48	48	10	4.123105626	502
Scaffold_15-23243081-23243112-GA-16	126	Scaffold_15	23243081	23243112	GA	16	32	23	32	32	9	4.5	482
Scaffold_15-23686855-23686884-TA-15	127	Scaffold_15	23686855	23686884	TA	15	30	21	20	20	9	4.856267428	480
Scaffold_15-24101551-24101594-AT-22	128	Scaffold_15	24101551	24101594	AT	22	44	32	30	24	12	8.386497084	494
Scaffold_15-24438536-24438569-TA-17	129	Scaffold_15	24438536	24438569	TA	17	34	21	15	34	13	9.556847458	484
Scaffold_15-24439014-24439047-TA-17	130	Scaffold_15	24439014	24439047	TA	17	34	25	.	16	9	9	484
Scaffold_15-24660933-24660946-GA-7	131	Scaffold_15	24660933	24660946	GA	7	14	3	9	.	11	5.507570547	464
Scaffold_15-24764331-24764372-AG-21	132	Scaffold_15	24764331	24764372	AG	21	42	30	35	.	12	6.027713773	492
Scaffold_15-25076106-25076147-CT-21	133	Scaffold_15	25076106	25076147	CT	21	42	27	35	60	15	14.07124728	492
Scaffold_15-25262278-25262317-GA-20	134	Scaffold_15	25262278	25262317	GA	20	40	28	32	32	12	5.033222957	490
Scaffold_15-35958679-35958774-GA-48	135	Scaffold_15	35958679	35958774	GA	48	96	68	.	71	28	15.37313674	546
Scaffold_15-38927254-38927289-AT-18	136	Scaffold_15	38927254	38927289	AT	18	36	14	14	36	22	12.70170592	486
Scaffold_15-41116796-41116831-CT-18	137	Scaffold_15	41116796	41116831	CT	18	36	16	46	16	20	15	486
Scaffold_15-41160698-41160743-AG-23	138	Scaffold_15	41160698	41160743	AG	23	46	26	26	74	20	22.71563338	496
Scaffold_15-42234817-42234852-TC-18	139	Scaffold_15	42234817	42234852	TC	18	36	26	26	28	10	4.760952286	486
Scaffold_15-42526796-42526823-CT-14	140	Scaffold_15	42526796	42526823	CT	14	28	17	16	16	11	5.852349955	478
Scaffold_15-42654471-42654518-GA-24	141	Scaffold_15	42654471	42654518	GA	24	48	39	41	.	9	4.725815626	498
Scaffold_15-43543310-43543351-TC-21	142	Scaffold_15	43543310	43543351	TC	21	42	27	42	.	15	8.660254038	492
Scaffold_15-44494892-44494919-AT-14	143	Scaffold_15	44494892	44494919	AT	14	28	18	22	22	10	4.123105626	478
Scaffold_15-44530874-44530903-TC-15	144	Scaffold_15	44530874	44530903	TC	15	30	20	30	28	10	4.760952286	480
Scaffold_15-44599079-44599118-GA-20	145	Scaffold_15	44599079	44599118	GA	20	40	31	40	.	9	5.196152423	490
Scaffold_22-909444-909461-AG-9	146	Scaffold_22	909444	909461	AG	9	18	30	30	18	-12	6.92820323	468
Scaffold_22-1449793-1449812-CT-10	147	Scaffold_22	1449793	1449812	CT	10	20	34	32	20	-14	7.549834435	470
Scaffold_22-3570365-3570406-CT-21	148	Scaffold_22	3570365	3570406	CT	21	42	27	26	27	15	7.681145748	492
Scaffold_22-4194306-4194327-TC-11	149	Scaffold_22	4194306	4194327	TC	11	22	3	.	22	19	10.96965511	472
Scaffold_22-4664217-4664252-CT-18	150	Scaffold_22	4664217	4664252	CT	18	36	50	24	24	-14	12.36931688	486
Scaffold_22-4774584-4774621-GA-19	151	Scaffold_22	4774584	4774621	GA	19	38	27	27	47	11	9.673847907	488
Scaffold_22-5241965-5242000-AT-18	152	Scaffold_22	5241965	5242000	AT	18	36	20	20	22	16	7.724420151	486

Supplementary Table 1. Continued

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_22-5325337-5325346-AT-5	153	Scaffold_22	5325337	5325346	AT	5	10	0	0	10	10	5.773502692	460
Scaffold_22-5344259-5344294-TGAGTG-6	154	Scaffold_22	5344259	5344294	TGAGTG	6	36	24	24	36	12	6.92820323	486
Scaffold_22-6020723-6020778-CT-28	155	Scaffold_22	6020723	6020778	CT	28	56	32	52	53	24	10.9658561	506
Scaffold_22-6476608-6476645-AG-19	156	Scaffold_22	6476608	6476645	AG	19	38	22	38	.	16	9.237604307	488
Scaffold_22-7153372-7153417-GA-23	157	Scaffold_22	7153372	7153417	GA	23	46	62	46	.	-16	9.237604307	496
Scaffold_22-8004533-8004558-TA-13	158	Scaffold_22	8004533	8004558	TA	13	26	14	15	14	12	5.852349955	476
Scaffold_22-8204192-8204207-AG-8	159	Scaffold_22	8204192	8204207	AG	8	16	28	15	15	-12	6.350852961	466
Scaffold_22-8875942-8875979-AT-19	160	Scaffold_22	8875942	8875979	AT	19	38	29	28	28	9	4.856267428	488
Scaffold_22-11136829-11136880-CT-26	161	Scaffold_22	11136829	11136880	CT	26	52	28	28	52	24	13.85640646	502
Scaffold_22-11423785-11423808-TA-12	162	Scaffold_22	11423785	11423808	TA	12	24	13	24	24	11	5.5	474
Scaffold_22-15538195-15538252-TC-29	163	Scaffold_22	15538195	15538252	TC	29	58	33	58	.	25	14.43375673	508
Scaffold_22-19827360-19827433-GA-37	164	Scaffold_22	19827360	19827433	GA	37	74	62	62	73	12	6.652067348	524
Scaffold_22-25500183-25500240-TC-29	165	Scaffold_22	25500183	25500240	TC	29	58	48	44	44	10	6.608075867	508
Scaffold_22-25842602-25842641-GA-20	166	Scaffold_22	25842602	25842641	GA	20	40	30	40	.	10	5.773502692	490
Scaffold_22-26806512-26806537-TA-13	167	Scaffold_22	26806512	26806537	TA	13	26	17	17	22	9	4.358898944	476
Scaffold_22-27017932-27017971-AG-20	168	Scaffold_22	27017932	27017971	AG	20	40	31	30	31	9	4.69041576	490
Scaffold_22-27038745-27038780-TC-18	169	Scaffold_22	27038745	27038780	TC	18	36	18	26	.	18	9.018499506	486
Scaffold_22-27100775-27100812-GA-19	170	Scaffold_22	27100775	27100812	GA	19	38	28	29	29	10	4.69041576	488
Scaffold_22-27173699-27173728-GA-15	171	Scaffold_22	27173699	27173728	GA	15	30	21	20	30	9	5.5	480
Scaffold_22-27175057-27175094-GA-19	172	Scaffold_22	27175057	27175094	GA	19	38	29	28	38	9	5.5	488
Scaffold_22-28816756-28816805-TC-25	173	Scaffold_22	28816756	28816805	TC	25	50	37	32	.	13	9.291573243	500
Scaffold_23-96131-96174-GA-22	174	Scaffold_23	96131	96174	GA	22	44	28	.	42	16	8.717797887	494
Scaffold_23-101379-101413-TTGAGAG-5	175	Scaffold_23	101379	101413	TTGAGAG	5	35	21	.	35	14	8.082903769	485
Scaffold_23-200513-200554-GAG-14	176	Scaffold_23	200513	200554	GAG	14	42	15	28	42	27	12.97112177	492
Scaffold_23-286838-286870-GAG-11	177	Scaffold_23	286838	286870	GAG	11	33	24	24	33	9	5.196152423	483
Scaffold_23-406319-406350-CT-16	178	Scaffold_23	406319	406350	CT	16	32	42	32	32	-10	5	482
Scaffold_23-482009-482041-GAA-11	179	Scaffold_23	482009	482041	GAA	11	33	15	24	33	18	8.61684397	483
Scaffold_23-627379-627426-TC-24	180	Scaffold_23	627379	627426	TC	24	48	26	47	48	22	10.84358489	498
Scaffold_23-641417-641455-TCC-13	181	Scaffold_23	641417	641455	TCC	13	39	27	37	39	12	5.744562647	489
Scaffold_23-810365-810374-TG-5	182	Scaffold_23	810365	810374	TG	5	10	22	.	10	-12	6.92820323	460
Scaffold_23-933912-933925-TC-7	183	Scaffold_23	933912	933925	TC	7	14	27	15	15	-13	6.184658438	464
Scaffold_23-952863-952880-AG-9	184	Scaffold_23	952863	952880	AG	9	18	9	9	18	9	5.196152423	468
Scaffold_23-1115985-1116024-GACAAGGT-5	185	Scaffold_23	1115985	1116024	GACAAGGT	5	40	24	40	40	16	8	490
Scaffold_23-1122981-1123030-CT-25	186	Scaffold_23	1122981	1123030	CT	25	50	36	.	50	14	8.082903769	500
Scaffold_23-1163383-1163412-CT-15	187	Scaffold_23	1163383	1163412	CT	15	30	42	28	28	-12	6.733003292	480
Scaffold_23-1328807-1328816-TA-5	188	Scaffold_23	1328807	1328816	TA	5	10	31	31	10	-21	12.12435565	460
Scaffold_23-1393534-1393561-AC-14	189	Scaffold_23	1393534	1393561	AC	14	28	8	.	28	20	11.54700538	478
Scaffold_23-1693691-1693732-GA-21	190	Scaffold_23	1693691	1693732	GA	21	42	33	32	42	9	5.5	492

Supplementary Table 1. Continued

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_23-1873678-1873695-CT-9	191	Scaffold_23	1873678	1873695	CT	9	18	27	18	18	-9	4.5	468
Scaffold_23-1905435-1905470-TA-18	192	Scaffold_23	1905435	1905470	TA	18	36	26	28	36	10	5.259911279	486
Scaffold_23-1929515-1929564-GA-25	193	Scaffold_23	1929515	1929564	GA	25	50	33	47	50	17	8.124038405	500
Scaffold_23-2059453-2059510-CT-29	194	Scaffold_23	2059453	2059510	CT	29	58	42	54	56	16	7.187952884	508
Scaffold_23-2538883-2538896-CT-7	195	Scaffold_23	2538883	2538896	CT	7	14	1	14	13	13	6.350852961	464
Scaffold_23-3537390-3537461-TC-36	196	Scaffold_23	3537390	3537461	TC	36	72	52	58	68	20	9.146948489	522
Scaffold_23-3594886-3594927-CT-21	197	Scaffold_23	3594886	3594927	CT	21	42	33	42	42	9	4.5	492
Scaffold_23-3627955-3628006-AG-26	198	Scaffold_23	3627955	3628006	AG	26	52	30	30	52	22	12.70170592	502
Scaffold_23-3904644-3904739-CT-48	199	Scaffold_23	3904644	3904739	CT	48	96	77	.	80	19	10.21436896	546
Scaffold_23-4508427-4508466-TC-20	200	Scaffold_23	4508427	4508466	TC	20	40	30	31	40	10	5.5	490
Scaffold_23-5286238-5286285-CT-24	201	Scaffold_23	5286238	5286285	CT	24	48	30	48	48	18	9	498
Scaffold_23-5693911-5693940-AT-15	202	Scaffold_23	5693911	5693940	AT	15	30	18	20	30	12	6.403124237	480
Scaffold_23-5696336-5696375-CT-20	203	Scaffold_23	5696336	5696375	CT	20	40	30	.	40	10	5.773502692	490
Scaffold_23-6325640-6325683-CT-22	204	Scaffold_23	6325640	6325683	CT	22	44	24	25	43	20	10.98483804	494
Scaffold_23-6492817-6492856-GGAT-10	205	Scaffold_23	6492817	6492856	GGAT	10	40	25	.	40	15	8.660254038	490
Scaffold_23-6565068-6565097-TA-15	206	Scaffold_23	6565068	6565097	TA	15	30	19	29	30	11	5.354126135	480
Scaffold_23-7820065-7820102-TC-19	207	Scaffold_23	7820065	7820102	TC	19	38	23	38	22	15	8.958236434	488
Scaffold_23-11413260-11413311-AG-26	208	Scaffold_23	11413260	11413311	AG	26	52	41	.	52	11	6.350852961	502
Scaffold_23-13574562-13574571-TC-5	209	Scaffold_23	13574562	13574571	TC	5	10	26	.	10	-16	9.237604307	460
Scaffold_23-22927760-22927769-TC-5	210	Scaffold_23	22927760	22927769	TC	5	10	26	26	11	-16	8.958236434	460
Scaffold_23-23361614-23361677-GA-32	211	Scaffold_23	23361614	23361677	GA	32	64	52	52	53	12	5.852349955	514
Scaffold_24-95563-95604-ATACATG-6	212	Scaffold_24	95563	95604	ATACATG	6	42	32	40	42	10	4.760952286	492
Scaffold_24-108347-108368-CA-11	213	Scaffold_24	108347	108368	CA	11	22	13	.	22	9	5.196152423	472
Scaffold_24-420058-420101-GA-22	214	Scaffold_24	420058	420101	GA	22	44	31	30	.	13	7.810249676	494
Scaffold_24-1228333-1228362-AT-15	215	Scaffold_24	1228333	1228362	AT	15	30	18	18	28	12	6.403124237	480
Scaffold_24-1300387-1300402-CT-8	216	Scaffold_24	1300387	1300402	CT	8	16	7	16	16	9	4.5	466
Scaffold_24-1330871-1330900-GA-15	217	Scaffold_24	1330871	1330900	GA	15	30	46	.	32	-16	8.717797887	480
Scaffold_24-1353952-1353963-AT-6	218	Scaffold_24	1353952	1353963	AT	6	12	22	12	12	-10	5	462
Scaffold_24-1756230-1756247-CTC-6	219	Scaffold_24	1756230	1756247	CTC	6	18	32	24	18	-14	6.633249581	468
Scaffold_24-2766911-2766940-TC-15	220	Scaffold_24	2766911	2766940	TC	15	30	45	29	45	-15	8.958236434	480
Scaffold_24-3323351-3323376-CT-13	221	Scaffold_24	3323351	3323376	CT	13	26	17	.	26	9	5.196152423	476
Scaffold_24-4372209-4372278-GA-35	222	Scaffold_24	4372209	4372278	GA	35	70	59	.	57	11	7	520
Scaffold_24-5578669-5578756-AG-44	223	Scaffold_24	5578669	5578756	AG	44	88	74	80	82	14	5.773502692	538
Scaffold_24-7139636-7139679-CT-22	224	Scaffold_24	7139636	7139679	CT	22	44	22	.	44	22	12.70170592	494
Scaffold_24-8945327-8945396-AG-35	225	Scaffold_24	8945327	8945396	AG	35	70	56	58	67	14	6.800735254	520
Scaffold_24-9528738-9528775-CT-19	226	Scaffold_24	9528738	9528775	CT	19	38	26	38	38	12	6	488
Scaffold_24-10240886-10240907-AG-11	227	Scaffold_24	10240886	10240907	AG	11	22	32	22	22	-10	5	472
Scaffold_24-14764107-14764136-AG-15	228	Scaffold_24	14764107	14764136	AG	15	30	16	30	30	14	7	480

Supplementary Table 1. Continued

#SSRid	#Primer	Scaffold ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Referemce)	KH	CH	YM	Diff bp of parents (MHvsKH)	Standard Deviation	MH_Seq_Length
Scaffold_24-17599472-17599497-GA-13	229	Scaffold_24	17599472	17599497	GA	13	26	16	13	.	10	6.806859286	476
Scaffold_24-18099174-18099239-GA-33	230	Scaffold_24	18099174	18099239	GA	33	66	43	51	43	23	10.84358489	516
Scaffold_24-19315015-19315032-AT-9	231	Scaffold_24	19315015	19315032	AT	9	18	9	9	10	9	4.358898944	468
Scaffold_25-844846-844879-AT-17	232	Scaffold_25	844846	844879	AT	17	34	20	21	34	14	7.804912983	484
Scaffold_25-854352-854391-TC-20	233	Scaffold_25	854352	854391	TC	20	40	26	27	40	14	7.804912983	490
Scaffold_25-929866-929893-GT-14	234	Scaffold_25	929866	929893	GT	14	28	18	28	28	10	5	478
Scaffold_25-1119658-1119709-GA-26	235	Scaffold_25	1119658	1119709	GA	26	52	40	.	52	12	6.92820323	502
Scaffold_25-1257283-1257324-TC-21	236	Scaffold_25	1257283	1257324	TC	21	42	30	28	42	12	7.549834435	492
Scaffold_25-1595968-1595999-TA-16	237	Scaffold_25	1595968	1595999	TA	16	32	21	32	32	11	5.5	482
Scaffold_25-2593258-2593325-AG-34	238	Scaffold_25	2593258	2593325	AG	34	68	39	68	66	29	14.19800455	518
Scaffold_25-2664281-2664334-TC-27	239	Scaffold_25	2664281	2664334	TC	27	54	32	54	54	22	11	504
Scaffold_25-3330429-3330440-AG-6	240	Scaffold_25	3330429	3330440	AG	6	12	23	12	12	-11	5.5	462
Scaffold_25-4344147-4344174-AG-14	241	Scaffold_25	4344147	4344174	AG	14	28	48	48	28	-20	11.54700538	478
Scaffold_25-4714986-4714995-CT-5	242	Scaffold_25	4714986	4714995	CT	5	10	30	30	10	-20	11.54700538	460
Scaffold_25-6290438-6290495-GA-29	243	Scaffold_25	6290438	6290495	GA	29	58	42	45	58	16	8.460693431	508
Scaffold_25-6534603-6534644-AGGAAG-7	244	Scaffold_25	6534603	6534644	AGGAAG	7	42	31	30	30	11	5.852349955	492
Scaffold_25-6778492-6778507-GA-8	245	Scaffold_25	6778492	6778507	GA	8	16	3	10	10	13	5.315072906	466
Scaffold_25-7183480-7183513-GA-17	246	Scaffold_25	7183480	7183513	GA	17	34	24	34	34	10	5	484
Scaffold_25-7674465-7674498-CT-17	247	Scaffold_25	7674465	7674498	CT	17	34	24	34	34	10	5	484
Scaffold_25-7802871-7802898-GA-14	248	Scaffold_25	7802871	7802898	GA	14	28	15	28	28	13	6.5	478
Scaffold_25-7831800-7831809-CT-5	249	Scaffold_25	7831800	7831809	CT	5	10	0	10	10	10	5	460
Scaffold_25-8324406-8324493-AG-44	250	Scaffold_25	8324406	8324493	AG	44	88	71	78	81	17	7.047458171	538
Scaffold_25-8527853-8527904-CT-26	251	Scaffold_25	8527853	8527904	CT	26	52	39	52	50	13	6.238322424	502
Scaffold_25-9980615-9980654-TC-20	252	Scaffold_25	9980615	9980654	TC	20	40	28	38	38	12	5.416025603	490
Scaffold_25-11356470-11356499-TA-15	253	Scaffold_25	11356470	11356499	TA	15	30	16	30	16	14	8.082903769	480
Scaffold_25-12380097-12380156-GA-30	254	Scaffold_25	12380097	12380156	GA	30	60	36	37	36	24	11.84271928	510
Scaffold_25-18275860-18275879-GA-10	255	Scaffold_25	18275860	18275879	GA	10	20	46	20	.	-26	15.011107	470
Scaffold_25-18952969-18952990-TA-11	256	Scaffold_25	18952969	18952990	TA	11	22	3	3	22	19	10.96965511	472
Scaffold_25-18998296-18998379-AG-42	257	Scaffold_25	18998296	18998379	AG	42	84	70	.	83	14	7.810249676	534
Scaffold_25-19757313-19757340-AG-14	258	Scaffold_25	19757313	19757340	AG	14	28	48	48	28	-20	11.54700538	478
Scaffold_25-22258458-22258477-AT-10	259	Scaffold_25	22258458	22258477	AT	10	20	48	46	46	-28	13.3666251	470
Scaffold_25-22426498-22426511-GA-7	260	Scaffold_25	22426498	22426511	GA	7	14	1	14	14	13	6.5	464

Supplementary Table 2. Anchoring genetic SSR markers of *Prunus persica*

SSR_marker_name	Chr#	cM	Seq ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Reference)	KH	CH	YM	Diff bp of parents (MH vs KH)	Standard Deviation _forur	Seq Length	Position	Primer Begin	Primer End	Product size	Left Primer	Left Primer TM	Right Primer	Right Primer TM
SSR_SC_015_2807	Chr1	4.015	Scaffold_15	2806809	2806842	AG	17	34	13	13	34	21	12.12435565	484	226	129	323	196	TACGATTACAGCCACTCACG	57.377	GCTGGATTTTGGTAGGTAGCTC	59.29
SSR_SC_015_7516	Chr1	16.021	Scaffold_15	7515529	7515576	TC	24	48	32	.	48	16	9.237604307	498	226	161	319	160	AATGCATGCTGCGATTCC	60.757	GGGAGAAGGAGAATTGGGTA	58.04
SSR_SC_015_12328	Chr1	38.283	Scaffold_15	12327662	12327677	AG	8	16	6	6	7	10	4.856267428	466	226	177	335	160	GCAGACCAATCGAACAAACC	60.504	TCTGTAACTGCCACTTCTCCC	59.343
SSR_SC_015_13013	Chr1	40.26	Scaffold_15	13012569	13012604	GA	18	36	52	36	.	-16	9.237604307	486	226	181	359	180	AGCGTTGCTTTGAAGCCC	61.468	GTCTCTTTCTGTCAGCTTCCC	58.119
SSR_SC_015_19385	Chr1	40.93	Scaffold_15	19385429	19385458	AACTCA	5	30	18	30	30	12	6	480	226	144	328	186	ACAGTTTCCTGTGACGACTCTC	58.45	CTTGAGAAGTCGATTGTGGG	58.286
SSR_SC_015_13542	Chr1	43.269	Scaffold_15	13542465	13542504	TC	20	40	16	40	40	24	12	490	226	178	349	173	ACATTGGGGGTTCAGGTATC	58.569	GCTGTAGCCAATCGATGAGT	57.921
SSR_SC_015_14751	Chr1	50.738	Scaffold_15	14750956	14751005	TC	25	50	60	46	40	-10	8.406346809	500	226	155	339	186	CTGCTCCTGGACGTGTTAAA	58.923	GACATCTGGTGAAGCAGAGC	58.541
SSR_SC_015_16730	Chr1	50.738	Scaffold_15	16729756	16729773	CT	9	18	9	7	3	9	6.34428877	468	226	163	352	191	CCCACCATTTAGGTCCATTACC	61.499	GAGTACACATCCACCTCTTGGT	58.038
SSR_SC_015_16116	Chr1	57.066	Scaffold_15	16116159	16116192	TC	17	34	21	21	20	13	6.683312552	484	226	114	305	193	ACCCAAACTAGTACGCAGAGAC	57.572	CCACAGTGTATTGTTGGAACCC	61.432
SSR_SC_015_23243	Chr1	67.579	Scaffold_15	23243081	23243112	GA	16	32	23	32	32	9	4.5	482	226	139	334	197	GGCCTTCCACTTCTTCTCAT	58.324	AAAAACCCAGCCCCTCTC	59.065
SSR_SC_015_24438	Chr1	74.277	Scaffold_15	24438536	24438569	TA	17	34	21	15	34	13	9.556847458	484	226	114	312	200	AGGCCCTCTGTCCTAAAAGA	58.002	GTTTGCTCCACACTAGTCCC	57.225
SSR_SC_015_24439	Chr1	77.856	Scaffold_15	24439014	24439047	TA	17	34	25	.	16	9	9	484	226	159	317	160	ACTGGTAAGTACTGGACTGGAGC	58.867	CAGACTCTACAGAGAAACGTCTGG	59.625
SSR_SC_015_24764	Chr1	82.739	Scaffold_15	24764331	24764372	AG	21	42	30	35	.	12	6.027713773	492	226	179	376	199	GTGAGGTATACCCAGCCTCACT	59.529	GGGAAGAAGGGAAAACACTG	58.618
SSR_SC_015_21028	Chr1	86.609	Scaffold_15	21027530	21027539	TC	5	10	0	10	.	10	5.773502692	460	226	135	324	191	ACCCTCTCTATGCCCTTCTAAC	57.942	GCAGAATCTGAGAACCCAAC	57.288
SSR_SC_015_25262	Chr1	88.102	Scaffold_15	25262278	25262317	GA	20	40	28	32	32	12	5.033222957	490	226	143	337	196	GACAGGAGGAGGAGAGAAACA	58.453	CATGTTAGTTGGTGCCTGC	57.687
SSR_SC_015_41117	Chr1	119.196	Scaffold_15	41116796	41116831	CT	18	36	16	46	16	20	15	486	226	141	328	189	GCTACGTTATACCGGATCAAGC	60.016	GGTGAGAGAGAGTGACTGAGAGA	57.849
SSR_SC_015_43543	Chr1	125.291	Scaffold_15	43543310	43543351	TC	21	42	27	42	.	15	8.660254038	492	226	171	321	152	CAGTTGATGACCCAGAGGAG	58.216	CACAGTCACATGCTCATACCAG	59.239
SSR_SC_015_42527	Chr1	125.575	Scaffold_15	42526796	42526823	CT	14	28	17	16	16	11	5.852349955	478	226	162	321	161	GTAGTGTCATGGCCCAACTA	56.055	AGCATCAACAGAGCTTGACC	58.028
SSR_SC_015_44599	Chr1	148.499	Scaffold_15	44599079	44599118	GA	20	40	31	40	.	9	5.196152423	490	226	176	337	163	ACTTGTATGGAAGCTGGTGC	57.824	CCACACTTCTCACTACCTAACCC	59.088
SSR_SC_023_96	Chr2	0	Scaffold_23	96131	96174	GA	22	44	28	.	42	16	8.717797887	494	226	148	346	200	GACCGGGATCTTGACAATC	57.833	AGGTATTCTAACCCCAACCCTC	59.615
SSR_SC_023_482	Chr2	0	Scaffold_23	482009	482041	GAA	11	33	15	24	33	18	8.61684397	483	226	173	352	181	TTATGAAGGTGAGGCCACTG	58.722	AGAGCCCTCTACTCTTCTCCC	58.187
SSR_SC_023_1123	Chr2	5.596	Scaffold_23	1122981	1123030	CT	25	50	36	.	50	14	8.082903769	500	226	163	336	175	CCAAAGACCATCAGTGTACCTC	58.576	ACTGGAGCTTCATAGACCGAC	58.417
SSR_SC_023_1694	Chr2	14.172	Scaffold_23	1693691	1693732	GA	21	42	33	32	42	9	5.5	492	226	135	312	179	GCTTTGCCAATTTCCGGT	60.983	GCCATGTTATCACTCCTGCT	57.765
SSR_SC_023_1930	Chr2	19.768	Scaffold_23	1929515	1929564	GA	25	50	33	47	50	17	8.124038405	500	226	170	330	162	TGCACAGACACCAAAGTCAG	58.401	GCTTCATCTTCATGCACGCT	61.501
SSR_SC_023_2059	Chr2	24.056	Scaffold_23	2059453	2059510	CT	29	58	42	54	56	16	7.187952884	508	226	166	362	198	ACACTGACCCCTTTGCAGT	58.127	CAGAAAAGCTTGTGGGGAC	58.272
SSR_SC_023_3537	Chr2	33.858	Scaffold_23	3537390	3537461	TC	36	72	52	58	68	20	9.146948489	522	226	155	344	191	GGCTTTCTAAGCAGATGCAG	57.877	GGTGGGTGTTTTAGTGACTGAG	58.625
SSR_SC_023_3628	Chr2	33.858	Scaffold_23	3627955	3628006	AG	26	52	30	30	52	22	12.70170592	502	226	158	355	199	CCAACTTGCTCCTTGCAG	58.051	AGTCTGTCCTGCTTTGCTTG	58.243
SSR_SC_023_5286	Chr2	40.925	Scaffold_23	5286238	5286285	CT	24	48	30	48	48	18	9	498	226	180	357	179	CACTTCCAAAGCCAAACCAC	60.529	CACTCTTAGGGGTCTCTGATAGC	58.572
SSR_SC_023_6493	Chr2	52.279	Scaffold_23	6492817	6492856	GGAT	10	40	25	.	40	15	8.660254038	490	226	176	325	151	GGAGGAGGTACCAGCGTTA	57.753	CCATGCCATGTATCAACCAG	59.799
SSR_SC_023_11413	Chr2	73.547	Scaffold_23	11413260	11413311	AG	26	52	41	.	52	11	6.350852961	502	226	163	356	195	ACACAGCCAATCTCACTTCG	58.882	CAGTAGCGTCTTGGTTTCTCTC	58.278
SSR_SC_023_13575	Chr2	80.98	Scaffold_23	13574562	13574571	TC	5	10	26	.	10	-16	9.237604307	460	226	170	346	178	GACTCTGGAACCATCTGTCATC	58.594	CGGCTCAATATGTCAACCTG	59.148
SSR_SC_009_3740	Chr2	101.111	Scaffold_9	3739614	3739643	GAA	10	30	50	57	30	-20	13.86542462	480	226	126	306	182	CTGGTTACCGGCTATTTCG	58.254	CTACCAGAGAGATGAGAGACAGC	57.44
SSR_SC_004_8937	Chr4	0	Scaffold_4	8937028	8937065	TA	19	38	24	25	38	14	7.804912983	488	226	161	330	171	ATGCGTGCCTATCCTGAG	57.27	TGTTGGTGGCCTTATAGCTG	58.796
SSR_SC_004_11737	Chr4	8.51	Scaffold_4	11736785	11736820	TC	18	36	21	.	36	15	8.660254038	486	226	131	312	183	CTTGAGATCAGAACTACGGAGC	58.227	CGCTGTAGACGGTTTTGTACTC	58.975
SSR_SC_004_11815	Chr4	13.987	Scaffold_4	11815384	11815411	AG	14	28	19	28	28	9	4.5	478	226	166	317	153	GCGAAAGTGAAGTCATGGTG	59.293	CTCACAGTACCCGCCTTCTTAT	59.674
SSR_SC_004_12019	Chr4	20.435	Scaffold_4	12019773	12019814	GA	21	42	22	.	42	20	11.54700538	492	226	175	329	156	CAGAGAAGAGGGAGAAGGAGAC	58.69	TCGTCGACAGAACCCATT	
SSR_SC_004_12020	Chr4	20.435	Scaffold_4	12019773	12019814	GA	21	42	22	.	42	20	11.54700538	492	226	175	329	156	CAGAGAAGAGGGAGAAGGAGAC	58.69	TCGTCGACAGAACCCATT	57.474
SSR_SC_004_15209	Chr4	32.097	Scaffold_4	15209186	15209223	GA	19	38	25	24	38	13	7.804912983	488	226	152	326	176	GATTTGGTTGGAGACTTGGG	59.381	CTCTCTCTCCCCTCCCTATAAA	58.003
SSR_SC_004_16942	Chr4	45.59	Scaffold_4	16942015	16942070	TG	28	56	44	56	56	12	6	506	226	133	328	197	CACACCCAATTCAGCACC	58.389	CGTCTTGCTCAAAAGTGTCG	59.634
SSR_SC_004_18962	Chr4	63.885	Scaffold_4	18961784	18961835	GA	26	52	35	48	48	17	7.410578025	502	226	173	322	151	CCAGACTCATTTGATGCCAC	59.09	CTCTGCAGTTTCCAGCATGAC	60.991
SSR_SC_004_22321	Chr4	90.479	Scaffold_4	22321215	22321256	CT	21	42	33	32	.	9	5.507570547	492	226	160	354	196	GGTGGACCTACTGGAGATTTTC	58.967	CGCTTAGCTACTTCCTAGAGCA	58.285
SSR_SC_004_21695	Chr4	110.245	Scaffold_4	21695285	21695326	CT	21	42	23	40	.	19	10.44030651	492	226	179	368	191	CTCTTTGGCTATGACACAGGTC	58.865	AGAAGAGCTCCTGATATCACCC	58.831
SSR_SC_004_22577	Chr4	117.505	Scaffold_4	22576590	22576627	AG	19	38	54	38	38	-16	8	488	226	177	361	186	GCTTAGACGAGGCATTCTGA	58.201	ACTCCCCCATAGCATTCTTC	58.067

Supplementary Table 2. Continued

SSR_marker_name	Chr#	cM	Seq ID	TR_Start	TR_End	Consensus	Ave. Copy Number	MH (Reference)	KH	CH	YM	Diff bp of parents (MH vs KH)	Standard Deviation _forur	Seq Length	Position	Primer Begin	Primer End	Product size	Left Primer	Left Primer TM	Right Primer	Right Primer TM
SSR_SC_010_395	Chr5	0	Scaffold_10	394735	394798	AG	32	64	42	.	63	22	12.42309677	514	226	164	341	179	AGGAGTTGGCCATCTAAAGC	58.411	CTCTAGCTTTCTTCCTCCTTCG	58.934
SSR_SC_002_5584	Chr5	15.295	Scaffold_2	5583894	5583915	TC	11	22	11	9	23	11	7.274384281	472	226	118	316	200	GGTTGGCCTAAGTCTCTGCT	58.551	GAAACCCAAAACCCACAG	56.281
SSR_SC_002_8052	Chr5	18	Scaffold_2	8051705	8051760	CT	28	56	41	41	54	15	8.124038405	506	226	167	337	172	GTATACTCTCTGCGACCCTAACC	58.382	CTCACTGAAACCCTTGTTGG	58.187
SSR_SC_010_3833	Chr5	22.319	Scaffold_10	3832613	3832650	AG	19	38	24	38	.	14	8.082903769	488	226	173	344	173	CTGATAATCTGCAGAGGAGGTG	58.958	AGTTCTGAGTCCAACCCACA	58.113
SSR_SC_002_8547	Chr5	26.135	Scaffold_2	8546854	8546913	CT	30	60	40	40	58	20	11	510	226	166	347	183	GACTGGAACAAGGGAAAAGC	58.766	ATCCCTACCATTTAGCCCTG	58.02
SSR_SC_002_9173	Chr5	33.933	Scaffold_2	9172638	9172669	AT	16	32	14	.	32	18	10.39230485	482	226	121	317	198	GCTGGACCAATTTCTCTCCT	58.324	GGCGACTTTTGTCATGTGTC	59.143
SSR_SC_010_9518	Chr5	52.48	Scaffold_10	9518290	9518299	CT	5	10	0	10	10	10	5	460	226	142	298	158	ACGTCCCAGTACGTCTCTTTCT	59.32	ACCTCAAAAGCCAGTGGG	58.641
SSR_SC_010_10306	Chr5	55.527	Scaffold_10	10305861	10305870	TC	5	10	20	10	10	-10	5	460	226	157	355	200	CTCACTTTTGGGAACCCTG	58.115	CTCCACTGCTGACTTCCATT	57.87
SSR_SC_002_14322	Chr5	66.114	Scaffold_2	14321890	14321945	CT	28	56	34	55	54	22	10.53169819	506	226	176	371	197	ACAGAAAGCTGTGTCCTACACC	58.388	GTGACTTCCCTGAGAAGAGGTT	58.857
SSR_SC_002_14599	Chr5	66.114	Scaffold_2	14599028	14599061	TC	17	34	16	34	34	18	9	484	226	145	340	197	TTCCTCAGAGTCAATCCAGC	57.94	GTCTCTCAGGTACTTCCATGTG	56.351
SSR_SC_010_23456	Chr5	78.814	Scaffold_10	23456010	23456039	TC	15	30	13	28	28	17	7.889866919	480	226	121	319	200	TACATATCCATCCCACCCAC	57.932	ACCAAGCAAGCACCTTTGAC	60.299
SSR_SC_010_26172	Chr5	96.684	Scaffold_10	26171809	26171841	CCT	11	33	45	.	39	-12	6	483	226	131	329	200	ATCCTGATGTGCTGGTTGTC	58.512	CGGGTCGCGTTTCTTTAGTA	60.257
SSR_SC_010_27004	Chr5	101.186	Scaffold_10	27003780	27003821	CT	21	42	30	32	31	12	5.560275773	492	226	174	336	164	GGCATTGCTTGAAGTCTGTC	58.444	ACAAACACTCAGACTAGGCCC	58.322
SSR_SC_010_27955	Chr5	110.716	Scaffold_10	27955280	27955323	AG	22	44	31	31	44	13	7.505553499	494	226	175	337	164	CAATACCCTTCACCACAACC	57.768	GAGTTGATATTGCAGGCCC	58.102
SSR_SC_022_1450	Chr6	2.113	Scaffold_22	1449793	1449812	CT	10	20	34	32	20	-14	7.549834435	470	226	104	302	200	CCCTACTATGGCCAGCTTTT	58.353	CTACTTCTGGCACTGTGTGG	56.872
SSR_SC_022_4194	Chr6	8.984	Scaffold_22	4194306	4194327	TC	11	22	3	.	22	19	10.96965511	472	226	155	339	186	CCCCTACAACTGGAGATTCA	57.582	GATCTTCACTTGTCCCCCAC	59.359
SSR_SC_022_4664	Chr6	11.939	Scaffold_22	4664217	4664252	CT	18	36	50	24	24	-14	12.36931688	486	226	159	307	150	CGAAAGCCGACGAGAATAG	58.611	GGAGAGCTTTAGAAGCACACAG	58.42
SSR_SC_022_6021	Chr6	23.579	Scaffold_22	6020723	6020778	CT	28	56	32	52	53	24	10.9658561	506	226	181	339	160	GCAAAGCACCCTCTCTTTCT	58.672	CCGTGGATGTCTTTTGTACC	57.923
SSR_SC_022_6477	Chr6	25.315	Scaffold_22	6476608	6476645	AG	19	38	22	38	.	16	9.237604307	488	226	149	329	182	TTGGGTTGTGTTTGGACC	57.65	CATGCCAAATACCCCACTAC	57.821
SSR_SC_022_7153	Chr6	30.215	Scaffold_22	7153372	7153417	GA	23	46	62	46	.	-16	9.237604307	496	226	176	345	171	CACCCTTACAAACTTCCCCT	58.029	GTGCCTCCTCTTCCACAACTAT	59.643
SSR_SC_022_15538	Chr6	50.124	Scaffold_22	15538195	15538252	TC	29	58	33	58	.	25	14.43375673	508	226	136	334	200	CCCCACTCACCTCACTCA	57.99	GAAGCGTAGGAGAGAAGGAGAT	58.263
SSR_SC_022_19827	Chr6	64.179	Scaffold_22	19827360	19827433	GA	37	74	62	62	73	12	6.652067348	524	226	178	370	194	CCACAATCACGCACAAGA	57.572	TAGACCAAGTTTTGGGCCTC	59.17
SSR_SC_022_27039	Chr6	98.929	Scaffold_22	27038745	27038780	TC	18	36	18	26	.	18	9.018499506	486	226	160	337	179	CTCTTGTTACGCCGCATC	57.937	GAAATCACTTGAGGGCTACG	57.422
SSR_SC_022_27101	Chr6	100.318	Scaffold_22	27100775	27100812	GA	19	38	28	29	29	10	4.69041576	488	226	140	333	195	GCTCTGTGGGTAAGACCAAGA	59.343	AGACGACTTGTTAAGCGGTG	58.036
SSR_SC_022_28817	Chr6	104.606	Scaffold_22	28816756	28816805	TC	25	50	37	32	.	13	9.291573243	500	226	156	352	198	AACAGAGCCTAAGAAACGCC	58.604	AACTCAGCTGGTGATTCTGC	58.028
SSR_SC_022_27018	Chr6	114.566	Scaffold_22	27017932	27017971	AG	20	40	31	30	31	9	4.69041576	490	226	135	331	198	CTCTTGTGGCTCTTGTGGTT	57.93	CGAGTAGGGACCACTGTTACAT	58.135
SSR_SC_024_420	Chr7	4.288	Scaffold_24	420058	420101	GA	22	44	31	30	.	13	7.810249676	494	226	147	345	200	CTGCCTGCCCTTTTGTTT	58.847	CACATCCCATAATCCACCTC	57.646
SSR_SC_024_96	Chr7	9.98	Scaffold_24	95563	95604	ATACATG	6	42	32	40	42	10	4.760952286	492	226	151	315	166	GTGGTGGCCATCTATCTACG	58.048	GAAGAATGGGTCCTTCTCAC	56.136
SSR_SC_024_1756	Chr7	18.959	Scaffold_24	1756230	1756247	CTC	6	18	32	24	18	-14	6.633249581	468	226	167	358	193	GGAAATAAGGAACGCACCC	59.377	TAGTTCCAGTGGTACCAGGC	57.671
SSR_SC_024_2767	Chr7	24.595	Scaffold_24	2766911	2766940	TC	15	30	45	29	45	-15	8.958236434	480	226	103	301	200	AGGGATGAGTTTGCCACA	57.474	CCCCGCCAAACTTTCATT	60.832
SSR_SC_024_7140	Chr7	42.904	Scaffold_24	7139636	7139679	CT	22	44	22	.	44	22	12.70170592	494	226	178	376	200	GTTGTAAAGGGGCTTTAGCTGG	61.292	ACAGCTAGGCTAGGACAACAGAC	59.137
SSR_SC_024_8945	Chr7	51.317	Scaffold_24	8945327	8945396	AG	35	70	56	58	67	14	6.800735254	520	226	164	362	200	CTTGATTTTCCCCCACTCAC	59.381	GCCTTATCCTTTTGCTCCTC	58.019
SSR_SC_024_9529	Chr7	54.135	Scaffold_24	9528738	9528775	CT	19	38	26	38	38	12	6	488	226	167	344	179	AGGGTTCACAGAACTCATGC	57.708	GATTGAGACCCTTGAGAGAGAC	57.027
SSR_SC_024_10241	Chr7	58.423	Scaffold_24	10240886	10240907	AG	11	22	32	22	22	-10	5	472	226	142	312	172	AGACCTCAAACATATCCGCC	59.009	GTCTCCTCCAAACATTAGCTGC	60.27
SSR_SC_024_17599	Chr7	90.793	Scaffold_24	17599472	17599497	GA	13	26	16	13	.	10	6.806859286	476	226	150	310	162	AGTAATACATGGGCCCAACC	58.647	CTGTTATTCACCTCACCTCACC	58.576
SSR_SC_025_1120	Chr8	2.799	Scaffold_25	1119658	1119709	GA	26	52	40	.	52	12	6.92820323	502	226	167	364	199	CGGTCAACTAGGGGTTGAAT	58.909	GGCCGGGCATATACAAAT	58.255
SSR_SC_025_2593	Chr8	11.173	Scaffold_25	2593258	2593325	AG	34	68	39	68	66	29	14.19800455	518	226	179	369	192	AAGTATGCAAGCCGATGC	57.374	GTGTTGGTGAGTTGGTGACA	57.89
SSR_SC_025_2664	Chr8	19.009	Scaffold_25	2664281	2664334	TC	27	54	32	54	54	22	11	504	226	180	344	166	AGGACACCAATTTTGGGGAG	61.103	GAGTGGGAAGAGGAACATAGC	57.866
SSR_SC_025_4344	Chr8	37.289	Scaffold_25	4344147	4344174	AG	14	28	48	48	28	-20	11.54700538	478	226	142	312	172	GCCACCATGAAACAGACACT	58.568	GCAATGGGGAGCAAATCA	60.573
SSR_SC_025_8324	Chr8	88.357	Scaffold_25	8324406	8324493	AG	44	88	71	78	81	17	7.047458171	538	226	169	360	193	GGCTAGGGTTTTGATGGTG	58.005	AGTGGCCTTTCCATCTCTCT	57.925
SSR_SC_025_9981	Chr8	99.438	Scaffold_25	9980615	9980654	TC	20	40	28	38	38	12	5.416025603	490	226	126	318	194	AAGCTAACCTACTTGTCGTCCC	58.85	GAGTTGGCCTTCAACTCTTC	56.536
SSR_SC_025_22258	Chr8	108.552	Scaffold_25	22258458	22258477	AT	10	20	48	46	46	-28	13.3666251	470	226	152	349	199	CTATCTAGAAAGGATCCCCG	55.509	CTCCTAGAGGAAGGATCAAGC	57.241
SSR_SC_025_18953	Chr8	127.547	Scaffold_25	18952969	18952990	TA	11	22	3	3	22	19	10.96965511	472	226	171	332	163	GCACATGCTCGTACAGACATAC	58.338	CTAGAGGCGGCCTTCATAACT	59.885

Supplementary Table 3. The PCR amplicon survuey of Mihong (MH) and Yumi (YM) of *Purunus persica*

Locus name	MH	YM	Polymorphism	Locus name	MH	YM	Polymorphism	Locus name	MH	YM	Polymorphism	Locus name	MH	YM	Polymorphism
SSR_SC_002_84	1	1		SSR_SC_010_154	na	na		SSR_SC_015_24661	2	2		SSR_SC_023_3537	1	1	
SSR_SC_002_560	3	3		SSR_SC_010_395	1	1		SSR_SC_015_24764	2	2		SSR_SC_023_3595	1	1	
SSR_SC_002_981	2	2		SSR_SC_010_659	na	na		SSR_SC_015_25076	2	2		SSR_SC_023_3628	1	1	
SSR_SC_002_5584	1	2	polymorphic	SSR_SC_010_695	1	1		SSR_SC_015_25262	2	2		SSR_SC_023_3905	1	1	
SSR_SC_002_7523	1	2	polymorphic	SSR_SC_010_3061	2	1	polymorphic	SSR_SC_015_35959	1	1		SSR_SC_023_4508	1	1	
SSR_SC_002_8052	1	2	polymorphic	SSR_SC_010_3801	1	1		SSR_SC_015_38927	na	1		SSR_SC_023_5286	1	1	
SSR_SC_002_8352	1	2	polymorphic	SSR_SC_010_3833	2	1	polymorphic	SSR_SC_015_41117	2	2		SSR_SC_023_5694	na	1	
SSR_SC_002_8448	1	2	polymorphic	SSR_SC_010_9472	1	1		SSR_SC_015_41161	1	1		SSR_SC_023_5696	1	1	
SSR_SC_002_8547	1	2	polymorphic	SSR_SC_010_9481	1	1		SSR_SC_015_42235	2	2		SSR_SC_023_6326	1	1	
SSR_SC_002_9173	1	1		SSR_SC_010_9518	na	na		SSR_SC_015_42527	2	2		SSR_SC_023_6493	1	1	
SSR_SC_002_9174	1	1		SSR_SC_010_9518	1	1		SSR_SC_015_42654	na	1		SSR_SC_023_6565	1	1	
SSR_SC_002_9542	na	na		SSR_SC_010_10306	1	1		SSR_SC_015_43543	1	1		SSR_SC_023_7820	2	1	polymorphic
SSR_SC_002_10182	1	1		SSR_SC_010_11365	na	na		SSR_SC_015_44495	2	2		SSR_SC_023_11413	2	1	polymorphic
SSR_SC_002_10898	1	1		SSR_SC_010_11492	1	1		SSR_SC_015_44531	1	1		SSR_SC_023_13575	2	1	polymorphic
SSR_SC_002_10950	1	1		SSR_SC_010_22060	1	1		SSR_SC_015_44599	1	1		SSR_SC_023_22928	2	1	polymorphic
SSR_SC_002_11359	1	1		SSR_SC_010_22942	2	2		SSR_SC_022_909	2	2		SSR_SC_023_23362	2	1	polymorphic
SSR_SC_002_11405	1	1		SSR_SC_010_23456	1	1		SSR_SC_022_1450	2	2		SSR_SC_024_96	2	2	
SSR_SC_002_11991	1	1		SSR_SC_010_23757	1	1		SSR_SC_022_3570	2	2		SSR_SC_024_108	1	2	polymorphic
SSR_SC_002_12273	1	1		SSR_SC_010_24241	2	2		SSR_SC_022_4194	2	2		SSR_SC_024_420	2	1	polymorphic
SSR_SC_002_12376	1	1		SSR_SC_010_25959	3	3		SSR_SC_022_4664	3	3		SSR_SC_024_1228	na	na	
SSR_SC_002_12531	1	1		SSR_SC_010_25974	1	1		SSR_SC_022_4775	2	2		SSR_SC_024_1300	1	1	
SSR_SC_002_12536	1	1		SSR_SC_010_26113	1	1		SSR_SC_022_5242	1	1		SSR_SC_024_1331	1	2	polymorphic
SSR_SC_002_13093	1	1		SSR_SC_010_26172	1	1		SSR_SC_022_5325	1	1		SSR_SC_024_1354	1	2	polymorphic
SSR_SC_002_13463	1	1		SSR_SC_010_26615	na	na		SSR_SC_022_5344	1	1		SSR_SC_024_1756	2	2	
SSR_SC_002_13862	2	1	polymorphic	SSR_SC_010_27004	2	2		SSR_SC_022_6021	1	1		SSR_SC_024_2767	2	2	
SSR_SC_002_14322	1	1	size diff.	SSR_SC_010_27032	2	2		SSR_SC_022_6477	na	na		SSR_SC_024_3323	3	3	
SSR_SC_002_14359	na	na		SSR_SC_010_27955	2	2		SSR_SC_022_7153	2	2		SSR_SC_024_4372	1	1	
SSR_SC_002_14599	1	2	polymorphic	SSR_SC_015_776	2	na		SSR_SC_022_8005	2	1	polymorphic	SSR_SC_024_5579	2	2	
SSR_SC_002_15112	1	1		SSR_SC_015_882	na	na		SSR_SC_022_8204	2	1	polymorphic	SSR_SC_024_7140	1	1	
SSR_SC_002_17556	1	1		SSR_SC_015_2486	1	2	polymorphic	SSR_SC_022_8876	1	1		SSR_SC_024_8945	1	1	
SSR_SC_004_5177	1	1		SSR_SC_015_2807	1	2	polymorphic	SSR_SC_022_11137	2	2		SSR_SC_024_9529	1	1	
SSR_SC_004_8548	1	1		SSR_SC_015_2951	2	2		SSR_SC_022_11424	1	1		SSR_SC_024_10241	1	1	
SSR_SC_004_8937	1	1		SSR_SC_015_3442	1	1		SSR_SC_022_15538	2	2		SSR_SC_024_14764	1	1	
SSR_SC_004_10737	1	1		SSR_SC_015_5105	na	1		SSR_SC_022_19827	1	1		SSR_SC_024_17599	2	2	
SSR_SC_004_11683	1	1	size diff.	SSR_SC_015_6656	na	3		SSR_SC_022_25500	2	1	polymorphic	SSR_SC_024_18099	3	3	
SSR_SC_004_11737	1	2	polymorphic	SSR_SC_015_6873	1	1		SSR_SC_022_25843	1	1		SSR_SC_024_19315	1	1	
SSR_SC_004_11815	1	1		SSR_SC_015_6929	1	1		SSR_SC_022_26807	1	1		SSR_SC_025_845	1	1	
SSR_SC_004_12020	1	2	polymorphic	SSR_SC_015_7441	na	na		SSR_SC_022_27018	1	1		SSR_SC_025_854	1	1	
SSR_SC_004_14263	1	2	polymorphic	SSR_SC_015_7516	1	1		SSR_SC_022_27039	2	2		SSR_SC_025_930	1	1	

Supplementary Table 3. Continued

Locus name	MH	YM	Polymorphism	Locus name	MH	YM	Polymorphism	Locus name	MH	YM	Polymorphism	Locus name	MH	YM	Polymorphism
SSR_SC_004_15209	1	2	polymorphic	SSR_SC_015_9462	1	1		SSR_SC_022_27101	2	2		SSR_SC_025_1120	1	1	
SSR_SC_004_15212	1	2	polymorphic	SSR_SC_015_9640	1	1		SSR_SC_022_27174	1	2	polymorphic	SSR_SC_025_1257	1	1	
SSR_SC_004_15640	1	2	polymorphic	SSR_SC_015_10023	1	1		SSR_SC_022_27175	1	2	polymorphic	SSR_SC_025_1596	1	1	
SSR_SC_004_16942	1	2	polymorphic	SSR_SC_015_12328	2	2		SSR_SC_022_28817	3	3		SSR_SC_025_2593	1	1	
SSR_SC_004_17154	2	2		SSR_SC_015_12718	1	1		SSR_SC_023_96	1	1		SSR_SC_025_2664	1	1	
SSR_SC_004_18086	1	1		SSR_SC_015_13013	2	2		SSR_SC_023_101	1	1		SSR_SC_025_3330	1	1	
SSR_SC_004_18962	1	1		SSR_SC_015_13542	2	2		SSR_SC_023_201	1	1		SSR_SC_025_4344	1	1	
SSR_SC_004_19396	1	1		SSR_SC_015_14751	2	2		SSR_SC_023_287	1	1		SSR_SC_025_4715	1	1	
SSR_SC_004_20346	1	1		SSR_SC_015_16020	2	2		SSR_SC_023_406	1	1		SSR_SC_025_6290	2	2	
SSR_SC_004_20420	na	na		SSR_SC_015_16072	2	2		SSR_SC_023_482	1	1		SSR_SC_025_6535	2	2	
SSR_SC_004_20624	1	na		SSR_SC_015_16116	2	2		SSR_SC_023_627	2	2		SSR_SC_025_6778	3	3	
SSR_SC_004_21305	na	na		SSR_SC_015_16225	2	2		SSR_SC_023_641	1	1		SSR_SC_025_7183	1	1	
SSR_SC_004_21695	2	2		SSR_SC_015_16242	1	1		SSR_SC_023_810	1	1		SSR_SC_025_7674	1	1	
SSR_SC_004_22015	2	2		SSR_SC_015_16730	2	2		SSR_SC_023_934	1	1		SSR_SC_025_7803	2	2	
SSR_SC_004_22066	2	2		SSR_SC_015_18575	na	na		SSR_SC_023_953	1	1		SSR_SC_025_7832	1	1	
SSR_SC_004_22086	1	1		SSR_SC_015_19385	1	1		SSR_SC_023_1116	1	1		SSR_SC_025_8324	1	1	
SSR_SC_004_22113	1	1		SSR_SC_015_20158	2	2		SSR_SC_023_1123	1	1		SSR_SC_025_8528	1	1	
SSR_SC_004_22321	2	2		SSR_SC_015_20695	2	2		SSR_SC_023_1163	1	1		SSR_SC_025_9981	1	1	
SSR_SC_004_22577	1	1		SSR_SC_015_21028	2	2		SSR_SC_023_1329	1	1		SSR_SC_025_11356	na	na	
SSR_SC_004_23185	1	1		SSR_SC_015_21846	3	3		SSR_SC_023_1394	1	1		SSR_SC_025_12380	2	1	polymorphic
SSR_SC_004_24910	na	na		SSR_SC_015_22719	1	1		SSR_SC_023_1694	1	1		SSR_SC_025_18276	2	1	polymorphic
SSR_SC_006_754	1	1		SSR_SC_015_23243	1	1		SSR_SC_023_1874	1	1		SSR_SC_025_18953	2	1	polymorphic
SSR_SC_009_406	1	na		SSR_SC_015_23687	2	na		SSR_SC_023_1905	1	1		SSR_SC_025_18998	2	2	
SSR_SC_009_1031	1	1		SSR_SC_015_24102	1	1		SSR_SC_023_1930	1	1		SSR_SC_025_19757	2	1	polymorphic
SSR_SC_009_1412	1	1		SSR_SC_015_24438	1	1		SSR_SC_023_2059	1	1		SSR_SC_025_22258	2	2	
SSR_SC_009_3740	2	2		SSR_SC_015_24439	2	2		SSR_SC_023_2539	1	1		SSR_SC_025_22426	2	1	polymorphic

1, one band; 2, two band; na, not amplified