

Supplemental Table 1. Adapter and primer sequences used in this study

Primer name	Primer sequence (5' to 3')
Forked_Type1	AATAGGGCTCGAGCGGCAGCTATTAATAGTACT
Forked_Com	GTACTATTAATAGCATCTTCGTTTCGTCGAT
AP2	AATAGGGCTCGAGCGGC
<i>Rtsp-1</i> _ppt	ATCTAATCTTCAAGTGGGAGATTGTCCG
D501	aatgatacggcgaccaccgagatctacac <u>TATAGCCTTATCCCACTTCCGCGGGCGCAACA</u>
D502	aatgatacggcgaccaccgagatctacac <u>ATAGAGGCTATCCCACTTCCGCGGGCGCAACA</u>
D503	aatgatacggcgaccaccgagatctacac <u>CCTATCCTTATCCCACTTCCGCGGGCGCAACA</u>
D504	aatgatacggcgaccaccgagatctacac <u>GGCTCTGATATCCCACTTCCGCGGGCGCAACA</u>
D505	aatgatacggcgaccaccgagatctacac <u>AGGCGAAGTATCCCACTTCCGCGGGCGCAACA</u>
D506	aatgatacggcgaccaccgagatctacac <u>TAATCTTATATCCCACTTCCGCGGGCGCAACA</u>
D507	aatgatacggcgaccaccgagatctacac <u>CAGGACGTTATCCCACTTCCGCGGGCGCAACA</u>
D508	aatgatacggcgaccaccgagatctacac <u>GTA CTGACTATCCCACTTCCGCGGGCGCAACA</u>
D509	aatgatacggcgaccaccgagatctacac <u>TAGATCGCTATCCCACTTCCGCGGGCGCAACA</u>
D510	aatgatacggcgaccaccgagatctacac <u>CTCTCTATTATCCCACTTCCGCGGGCGCAACA</u>
D701	caagcagaagacggcatacagagat <u>CGAGTAATGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D702	caagcagaagacggcatacagagat <u>TCTCCGAGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D703	caagcagaagacggcatacagagat <u>AATGAGCGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D704	caagcagaagacggcatacagagat <u>GGAATCTCGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D705	caagcagaagacggcatacagagat <u>TTCTGAATGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D706	caagcagaagacggcatacagagat <u>ACGAATTCGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D707	caagcagaagacggcatacagagat <u>AGCTTCAGGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D708	caagcagaagacggcatacagagat <u>GCGCATTAGGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D709	caagcagaagacggcatacagagat <u>CATAGCCGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D710	caagcagaagacggcatacagagat <u>TTCGCGGAGGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D711	caagcagaagacggcatacagagat <u>GCGCGAGAGGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
D712	caagcagaagacggcatacagagat <u>CTATCGCTGGGCTCGAGCGGCAGCTATTAATAGTACT</u>
Positive_control_F	CTAAAGACAGCTGACCGTGTAGTC
Positive_control_R	TACTGAGAAACCAACCCATCCTC
<i>Rtsp-1</i> _LTR_D1	CTCCTTGTTAGTTAGAGAGTGGTTG
MiSeq_C1260	GCTCCGGTGTGGAGGAGAA
MiSeq_C134	CAGGTGGCATATTTTGCTCC

Underlined sequences represent barcode sequences.

Lower-case letters in D501–D510 and D701–D712 indicate P5 and P7 sequences, respectively.

Supplemental Table 2. The information of primer combinations and the number of reads in each sample

Cultivar/strain	Primer (P5)	Primer (P7)	No. of reads	Cultivar/strain	Primer (P5)	Primer (P7)	No. of reads
PSL_1	D501	D701	238,064	PI68	D505	D705	165,479
90IDN-47_1	D501	D702	226,600	PI69	D505	D706	151,598
PI1	D501	D703	212,457	PI71	D505	D707	148,731
PI2	D501	D704	229,576	PI72	D505	D708	123,313
PI5	D501	D705	195,276	PI73	D505	D709	114,233
PI7	D501	D706	237,063	PI74	D505	D710	138,183
PI8	D501	D707	257,671	PI76	D505	D711	127,808
PI9	D501	D708	197,683	PI77	D505	D712	128,497
PI11	D501	D709	174,310	PI79	D506	D701	141,783
PI12	D501	D710	185,259	PI80	D506	D702	152,814
PI13	D501	D711	190,618	PI82	D506	D703	121,206
PI14	D501	D712	218,276	PI84	D506	D704	164,999
PI15	D502	D701	168,387	PI85	D506	D705	168,777
PI17	D502	D702	176,299	PI86	D506	D706	135,781
PI18	D502	D703	239,500	PI87	D506	D707	157,138
PI20	D502	D704	225,316	PI88	D506	D708	218,168
PI22	D502	D705	228,215	PI89	D506	D709	189,224
PI23	D502	D706	218,067	PI91	D506	D710	168,218
PI24	D502	D707	207,092	PI92	D506	D711	133,059
PI25	D502	D708	182,518	PI94	D506	D712	124,947
PI26	D502	D709	180,429	PI95	D507	D701	170,964
PI27	D502	D710	158,437	PI96	D507	D702	119,757
PI29	D502	D711	158,285	PI97	D507	D703	158,211
PI30	D502	D712	147,210	PI98	D507	D704	184,843
PI31	D503	D701	121,908	PI99	D507	D705	126,890
PI32	D503	D702	140,411	PI100	D507	D706	107,261
PI33	D503	D703	211,697	PI101	D507	D707	113,460
PI34	D503	D704	148,569	PI102	D507	D708	118,768
PI36	D503	D705	201,291	PI103	D507	D709	104,860
PI37	D503	D706	185,541	PI104	D507	D710	126,564
PI38	D503	D707	185,225	PI105	D507	D711	117,598
PI39	D503	D708	153,394	PI106	D507	D712	103,502
PI41	D503	D709	186,715	PI107	D508	D701	160,023
PI43	D503	D710	149,488	PI108	D508	D702	133,796
PI45	D503	D711	126,393	PI109	D508	D703	108,676
PI46	D503	D712	132,339	PI110	D508	D704	114,458
PI47	D504	D701	242,624	PI111	D508	D705	153,238
PI49	D504	D702	187,250	PI112	D508	D706	136,558
PI50	D504	D703	165,582	PI113	D508	D707	104,959
PI51	D504	D704	196,465	PI114	D508	D708	145,806
PI52	D504	D705	181,130	PI115	D508	D709	117,505
PI54	D504	D707	163,935	PI116	D508	D710	122,826
PI55	D504	D708	140,724	PI117	D508	D711	120,515
PI56	D504	D709	141,051	PI118	D508	D712	111,280
PI57	D504	D710	123,064	PI119	D509	D701	122,629
PI59	D504	D711	128,800	PI120	D509	D702	143,255
PI60	D504	D712	145,246	PI121	D509	D703	132,041
PI61	D505	D701	136,148	PI122	D509	D704	137,956
PI62	D505	D702	127,131	PI123	D510	D705	129,864
PI63	D505	D703	164,228	PSL_2	D510	D706	239,430
PI64	D505	D704	135,554	90IDN-47_2	D510	D707	251,504

Supplemental Table 3. The information of marker sequences in linkage maps

Marker name	Sequence information
Cl100s	GCTAAAACCGAAGGCGCCAACAGAAATGCAACGATCACACTGTGAAAAC
Cl102s	GTGCATAGTCAAGATTGAATATTCAATGAATTTATGGAAATTTGGAAAGG
Cl105s	GTCTTGAGGTACATCAAGCCTGGACAAGGGTTGTTTTATTAGGCTTCTTC
Cl106s	GTCTGGAGGATAAGATTGGGAAACTTGAAGCGGCTGAGGCAAATGACA
Cl108s	GTCCAAATGAACCACAGCGTGCATACAATCACAGTCTAACCTTGGCGC
Cl109s	GTCAAGTCTATGCTCCACCAAGTTTTCTTGAGATAATGATGAAAGAGCT
Cl111s	GTATATGCTACGGAATGGACATACTATTGTTTGGTTCTCGACAGCAGAAG
Cl112s	GTATAGTATAACCATAGTTTCATCCACCCACCATGTCTGAACAAGTTTCA
Cl113s	GTAACAATTGAGCGCGGCAATCCTCTGCATTCTCAACAAGATGCTTTGC
Cl114s	GTAACAACATTCTCATAGGTTGTAGGAATAATATTGTTTTTGAGAGCAA
Cl115s	GGTTTCACAGAGCAGCGAACCTCCTCCTCTACAGTGGAAAGGATAAC
Cl117s	GGTGCTTGACAGTGAATCAAGTGGCAATGCTACAAATGCTAGCCACACTC
Cl118s	GGCCGAACGGTATTATAATGAGATGAAGCCCAATGGTTTCTTTGAATT
Cl120s	GGATTCGCCATCCCTGCTTGGCAAGCAGGGCAACATTAATAATCGCGTAA
Cl121ds	ACTCCTTTAGACCTTAGTGTGAGGCATTTCCACCCAAAACCTTGGTTCC
Cl123s	GGAGTGTGATCAACTATGAGCAATCTAGACTACTTTAGCCATTTCTGAT
Cl124s	GGACCAAGACATTAGACTTCAAACCTGTTAAAGTCATCATTCAATCCTTGC
Cl125s	GGAAGAATCCCTGAATCGGGCAGAGCTGAGTCTATACTAGTCTAAATTAG
Cl126s	GGAACAACAATGAACAAATATAATTTGCTATGCAAAATAAAATAAAGTT
Cl127s	ACCTCTTGAATGAAACCATCCATTTCTGTGAATGGCATGGTGTTTGTG
Cl128s	ACAGTTACCTTTTAAAGTTGTGACCAAAGGGTCCATAGGTGGCCTTGTA
Cl129s	GCTTGGTGGCCGACGCGACGTGTAACCGGGGAAAGACCAATTCAAGCCGT
Cl130s	GCGGCAACCATCCATGCATCTGAAACCAACTTTGGAATTGGAATCCAAAG
Cl133s	GCCCTTTAAGCATTCAAAAATTAATGCACATTCAAAATTTCTAAGACTTT
Cl135s	GCAATGCGTCTTTGAACCCGGACATGCGTCTTTTTGGACCAAGATTCCG
Cl136s	GATGGCTCCCACGGTCGGGCGAAGTAAAGGAAGTTTACATATGAGAAACC
Cl137ds	GATATGATGTTCTGCAGTGCATATACACTTTTGAGCTAAAGAAAATGAG
Cl138s	GATATGGTGGGACATCTATGTGACTTTGGTGTGCAAAGCTCTTAGGAGA
Cl139s	GATATCATAGATTTTTCTCAAATCTTTGATAATGCTTGCATTTAATCTT
Cl13s	AAAAAGAGATAACACAGTATACCAACTGCATATTTCTCTTGTGGACGGAG
Cl141s	GAGAGCAAGGCCAAGACGGATTGGATGAGTGGAAGCAAGTTCTGTGCTAG
Cl142s	GACCTGTCCATGGGCAACAGGCTAAGGGGAGAGCTCTTTGCGTGACGTACG
Cl143ds	GACCCGACTCATGGTGAGACGGTCTCACACAAGTTTTTGCCTTTATAAAG
Cl145s	GAAGTGAGCATAACCAACAAGCAATGATGAATCTTGAATTTACCTTATTA
Cl147s	GAACTAGTAGTTTATAAACATTAAGCTTTGAATTTATGAACACATAACA
Cl148s	GAAATTAAGGCAAGCAAACATTAATTTGCGTACATACTTACAGACTTT
Cl14ds	AAAAAACTAATTGTATGTTTATACAATTTGAAAACAAAGAGTAAAAAAT
Cl150s	GAAATGAGGATGTTCTAGGAATATTCCCTTTCTGGAGTTATATATTGCCA
Cl151s	GAAATCTGTATGGCTTCCAACCGTTCCTACTAATGCGCAAAACATGGTTC
Cl152s	CAAATACAATCGACGTCTTAACGCTATGCTTCCATCATTTACGTACAT
Cl153s	GAAACTACCTAGCTTTCAAAGTTTCAAAAACCTTCAAAAATTGTAAGCAT
Cl15s	TTTTTGTGCTGCTTCATCCAGCCCACCTTCGACGGTTTTGGGCCACTGAT
Cl160s	CTCGGCACCTTAACAAATCTTCAAAGTATTCATTTTTCTCGCAACAACCT
Cl161s	CTATCAGAGTTGATTTGAGGTGGGACTTAAAGTGTGGAGGTGTATGCAC
Cl166s	CTCTGAACTAACTTTATAAATTGTTATTTGCTGTCCAGAGTTGGCATAAG
Cl167s	CTCTGGATTCAAATTTGACTTCATCATTAGCACGATCCAAATTCGCACTG
Cl168s	CTCCTGTGGCAAGCAGTGACATAGCACCATCAGAGGCAGTGCCTCTGGAA
Cl169ds	TCCCTGACAAGTGATGTGAGTTTATATCTGTTGGCATGAAAAGAAAACAA
Cl170s	CTCCAAGCCACTCACAACAGGCCTATTAATGAGTGGTAATAGAGATT
Cl173s	CTACATAGCACCAGAAGTCTTCTCAGCAATTTGGGAATGCTCGTATA
Cl174s	CTAATTCACCCTTGATGGTCTTTTTGAGTTATACTTTTACACATCAAGTG
Cl176s	CGTTGTACCCTATGTTTTCCATGATAAAAATAATTTTACTATTTAAAAGTT
Cl179s	CGAAGTGAGGGACAATTTGCCAAACGCAATTACCAACAGGCTCCTAGCC
Cl181s	GAGTCGGCGCTCACTCCACATCCTCCGAGCCTCGACGAGGTTTATG
Cl182s	CCGACTACGTTGTCGAGTCAAGCTCACTGTTGATTATATAGAGTAAA
Cl183s	CCCCGCACTGCAAAAAGTTCCGCCCCGAGATTGTGGACATTACCCCAAAGC
Cl185ds	CCCGACGAACCTTAGCAAGAAAGGGGGCAAAGAACCCAAAGTGATATATCC
Cl189ds	CCAAAGAACCTAAATCAAAGATTGAACTTAATATTTTTTAAAACACGAT
Cl191s	CATTTTAGAATCAAATCAATCCAACCCAATAACACACTCAACATTAATT
Cl192ds	CATTCACACTATAGAAAACACTTTTAAACGTCGGTTTTTTAGCACTTTTA

Supplemental Table 3. (continued)

Marker name	Sequence information
Cl194s	CATGTAGCTATTAGGTACGTGGTATATAGGTTTTGACTAAGTGGGATAGA
Cl195s	CATGATTTGGGTGACAAGAAGTTGAAAAATTGCTTTTTATATTTGCATA
Cl198s	CATCTCAAAGGGTAAGGTGGGGTGTAGTTTCTGAAAAAGTTACTCTGT
Cl199s	CATACTACGGCCTACAGGTGCAGCTGCTACCACATTTTCAGTAAACGCTC
Cl19s	TTTGGGTCTTCTTATAGTGCATCTGTTAAATGTTGTTCCAGAACATAA
Cl1s	CATGCCAAGCTTTAGATACTGCCACCGCAAGGAAAGTGTACTGGTTGTT
Cl202ds	CAGATTAAGCCATTTATTTACTTCTTTTCAGCCCCATTTCTCTCTCTT
Cl203s	CAGAGTACCTTGAGATTCTTGCCAAAGTAAAGGTCATAGCTTTTGACAAG
Cl204s	CAAATCCCTAACACTAACAATCACACCCATTTTCCGCAGTTGCTGACTA
Cl205s	CAAGTATGGTGGGGAGAGTCCATCAGCAGCAAGAGTAATTTCAAATAA
Cl207ds	CAAACGGCGCATATATCATCGGATTGAGTTGGTCAGTGCTTTTGTTGTCG
Cl208s	CAAAAAGGCACTAGCTTTGCTAAAAATAATTCATCTCTACTAAGAAAAAG
Cl211s	ATTTAATCATATGAATATTC AATAGAAAAATAATGCTTTTGCGAGATTCCA
Cl216ds	ATTCCAACAAAAATAAAAAAGAAAACAAAAACTAGTGAATAGTGTATGAA
Cl217s	ATTATGACCAAACTGATCTGAGACAATGGCCAAATAGCACATCTTAATG
Cl219s	ATTATATATGCAGCTTTTTTCTTTTATTGTA AAAATCTAAAAATCCATAG
Cl21s	TTTGAATGTTACAAA ACTGGGGA ACTGATTGATTACAGTTTCAATTATTG
Cl220s	ATTAAGGTGTTAAGAAGTGTATGGTCATATTA AAAAAGTAAATTAATTTTA
Cl221s	ATTAAGGGTCAAATAGACCTTCAA ACTATACTAAATGTGCAATTAGGCC
Cl222s	ATTAACAGAGTCATCATCACTTGT TTTGTGGCTGTGGATGTGGATGAGTAC
Cl223s	ACCCCAAGCCTTCTACGCAGAAACAGTCTAATTTACTTCTGTAATTCATT
Cl224s	ATGGGCACATGCTCTAAGGACTTGATGTTTCTGGTACGTGTCCTTAATTG
Cl229s	ATCACCTCCCTTG TACCAATACTCCTTTGCCCTTATTTCCAGTGTGCTC
Cl230s	ATATTAAGCGGAGATTCTCTCTAATAAATGTACGGAGTAGTACTTATTA
Cl231ds	ATGTCTTTAAGGGCTGTCCAGGTCTGCCACGACCTATTCTCTATAGCCGGC
Cl232s	ATATATTCTTCTTTTTAAGGGATGAATTAATTTGAACCAAACTGCATGT
Cl233ds	TCCTATTGCTCCGCTCCGTCACCAGA ACTATCTCGGAGCACGTTCCAC
Cl234ds	ATATAACCCCTAAAAAATGGATCAGCTCAACAAAATATATATGGGGATCA
Cl237s	ATACCTAATTTCTGTTTCGATGTCGTCTGCACCTTACGGACATGGAGTAT
Cl238s	GTAACGAAATTCGTCCCAAGTTTCATGCCTGGCAATAGAGTATCTGTAGG
Cl23s	TGCCCAGGTTTCCGGACGAGGAAAAGGGCGATCACACGGGTAATGTCTGG
Cl240s	ATAACAACACCCCATTGCTTTCAAATTTCTTTAAAAATATTCTTTGTTTT
Cl241s	ATAAACACGGTATAATGAACATGAATTAACACTTAACATAATACACATA
Cl242ds	TAATCGACTTGAGGGCTATCTTCCACCAAGTCTAGGCTCTGTTCTTCAA
Cl244s	AGTTCAACGGAGTGTGACAGTGAGTCAGTGACTCAGTGGACTCGAGCCCG
Cl245s	AATGTTCTTAATTA AATTGACAGGATCAAGGGTCCAGATTGAGTGCAGAA
Cl246s	AGTATTTCCATGGAAAATGCTCGCACTGGCAGCTCAGTTATTTCTAGGC
Cl248s	AGGATAACCGTAAATGCAAAA CTGATAATTTTGAGGATGTCGGAATCTGT
Cl252s	AGAAGTACTCTACTGATAAAATAGATGAAGATTTCTTTTAGAAAATCTG
Cl253s	AGAACTAGTTTGCATATATAGTTACTCAATGATTCATACA ACTTTAAATT
Cl254s	AGAAAGACTGCTTAAATTAGAGCAAAGATCAGTAAGAATATATATGAACT
Cl255s	ATTTTAACTTCGAATGCACACAAATGTCGTATAGACAATGCGGCACAAC
Cl256s	ACCACTACAAAAGCTAGCATAAGAGGTATTATATTTCAAAGAGGCAACATA
Cl258s	ACTAAAACATGTCTCCTCATTACACTCATTCTTCGTACCTATGGACTT
Cl262s	ACATATATTTCAATCAGCAGGTATATATGATATGAGGGTAATTAATGAA
Cl263s	ACAATCCACTTTTAGTCCCTTCTTATTAGATCATCCTCATTTGGTTCTAG
Cl264ds	ACAAGTACGTACTTGCAAAAAACATGGGAAATGGGGAAGGCAATTTCCCTA
Cl265ds	ACA ACTTTTAAGCCAGCTTAGAGTCTCCCTCATACCACAGCTTCCACCA
Cl266s	ACAAATCCACCAATCAACTAATTAGTAATGCTATTATATTTCTCAGTCG
Cl276s	AAGCAAAGCTCCAGAGGAAGAGAGAGAGAGATGGCCACCGCAAGCACC
Cl278s	AAGATGTTGAAAGTAGTTTGGTAGAAACATCTCACATGTTATTTCAAACAA
Cl280s	AACTCAGCATGCTGCTACGTGGCTGGGAAATATGGGGGTCACATTCCATG
Cl281s	AACTATATATTTGGTTTAAAGTCCTAAAGCTTCCATTTATGCTACTGTAC
Cl283s	AACCCAATCACAAGATTGTTAAGATAATGGATCCAACACTCTTAGTGAAG
Cl285s	AAATGGAGGAGAATGCTTATGACCCAGAAGATTGCTCAACTTCCCCATG
Cl286s	AAAGTGAATACAGTAGAGAAAATAAAAAAATAACAGAGATTCCCTAAAGTC
Cl287s	AAAAAGCCATACTTGGGAGAGTTGGGTCATTGAGGAAAGCACATCAATAG
Cl28ds	CATTATACTTATTTTAGTTTATTTTCAATGTCTGGACTCTGGATCTTGAT
Cl292s	TTCTTCATTGGTGGAGAAAGCAAAATGCGAGGCCAGGCCTTCTTCAATC
Cl295ds	TTATCGTCTTTTTCATTGCATAAATTTCTCATAAATAAGTGAGTACGCGG

Supplemental Table 3. (continued)

Marker name	Sequence information
Cl296s	TTATGCTCAAAGATTGCTTCTGCATACGGATTATAAAAGCTAAAACCTGT
Cl297s	TGAGGATGAAGGTGAATTATACTTCTTTCCTATCAACTCAAAGGTGGTGT
Cl299s	TCTGGTTTCTATGATTCTTGAAGATGTTTTCTTCTTTTCTTGATTGTATA
Cl29s	TTCCCTCACTTTTAATCTCTTGATTATATGCAGGTAACATAAACCATGGGTT
Cl300s	TCCCTAAGCTTATATAGCCTTCAATCCTTCATTAAGGTTGATTTACGAAG
Cl301s	TCCAATAACCAGAAACACAAAACAGAGTAATTCAAACAAATAAAATCAAC
Cl305s	GTGTAAGGCCACAATTGGGCTTACAGTGAGCAGCGGAGTGGAGATAGGA
Cl306s	GGTTGAGTCTTTGTGAAAACCTCAAGCAACATAATGCCATAACTATACAT
Cl307s	GGTTATTGTGTTCTTAATTTCCGGTCTGTTATTAGGCGAATTGAATATC
Cl308s	GGTAGCTTGATGAATTTAACTTGAAGAATTTATGTGATGACTCCATATG
Cl309s	GGCAACGGTGCCATATTTGACAAAACTTTAATTCTTTAAAGATGATAAC
Cl30s	TTCCAGACTATACGAGCTGTTGTTTTCTTGCCACTCACAACTCTAGGA
Cl311s	GCCACAATGAGTTTCAATTTGGGCTCTGTTTATAGTGACAATTGCAGATA
Cl312s	GATTCTTCAATGGAACCCTAGTTCTCTCTCTCGGAACCAAGAAACGCT
Cl313s	GATGTAACCCGATCTTCTACTTCTCTGATCATAGTGCAGACACCCCTG
Cl316s	GAAGTGAACAAGAATCTAATCTTGTTCAAAGTGTAGATTGTTGTAATG
Cl317s	GAAATTACTCAAAAAAAAAAGGTCCAAATTGAGATATTGCACAAGGCC
Cl319ds	CTCAATTGCTCGCTCAAAATACCAGAGGATACCAATCTCCATAAAGCCCA
Cl31s	TTATTTGGAAGTATGGGTACTATATAAGTAAAAGCAGTTTGTATCATATA
Cl321s	CTAGGCTCTATAGCGTTATTGATCCATAAACTGTGTAAGATTATGAGCCT
Cl323s	CGTGGGCACCAAATTAAGAATCAAATTTCAATCTGTTTTGTTTTTCAA
Cl325s	CCTCTACACCAATGCAATAACTAGAGTCGAAGTCCCCTGTAGCTCAAT
Cl327s	CATTTGAATCGCGATCCGGCCCGACCCGACCCGCTCATGGTGAGACGGT
Cl328s	CATTGTGGGCACTGTAGGGTGGGGGCTTGGGATCTCTTTGAGGAATGCTG
Cl329s	CATTATCTTCTTTTCAATCTGGGAGGGAGTTGAAAGCCGCAAAACATGA
Cl32s	TTATGTTTATATTATGCTCAACAACACCTAAACGCCACATTTTCACAA
Cl330s	CAGCCAGCCAACAAAAGAGAGGAAAAGGAGACGATAGAGAAAAATAGATA
Cl331s	CAACATGCAATTTCTCATGTAGCTCCACTGATTTCTGGATTTTCACT
Cl332s	ATTCTAATAGGTGGTCACAAGATTGAACCCGCTGGTATGGGCATTGAAT
Cl333s	ATTAGAACTTGACCGCGCGCGGAAAATTATGGCGTGATTTGCAAATGA
Cl334s	ATATTTCAACTCCATCTTGAGAGCTTTTCTTAACTGGTAAAAAGTGGC
Cl336s	AATTGATTGCTCGGGAGGCTCATATCCATAGTCTTCTGTCAAAGATGAGG
Cl340s	GTTTATACATGCAAGAAATGAAATTGTATATATTTTTAAGAGTTTATTAC
Cl342s	GTGGCGGCAAGCGTGGGAGCAGTGGAGGCCTGAAAGACCAAGGCTTCGC
Cl343s	GATAGATGATGCATTAATCATAGTACAATTTTTTGTCAAGATGACCACAA
Cl345s	GAGAGTTTTCCCAACCAAAATGGGAAAAGTATCAGATATCATATTGTTCC
Cl347s	CATATTTGATCAGTATTACTCCCATGTTAATTTTTATATGTGCTTTA
Cl349s	CAATCATTCTAGTTTTTGGGAGGCTCAATGCACCACTCTTCCAGCTATAC
Cl34s	TTAGGGATAGCTGTTGGAGGCAAAATATGCCACCTGACCATCCGCTTAAT
Cl350s	ATTCATTGTGTAATAGTCGCTGGTATTGACGCCATCATTAGGCCTGGGTG
Cl352s	ATAATTTTGGTGCTAGCTATCTTTCTTTTTTTTTTTTTTTTAAATTAAC
Cl353s	ACCCTTATATGTCATCACCTTGAAGCGTTCCAAGCAACGCAAGCCTGTCA
Cl355s	AAAAATGTATTAGGGCTTTGCCTTAGTTTTGCTTATATATTTGGGTGGAA
Cl358s	TATGTTATATATATGTTTTGTCTTGGTGGATGAGGCACGCATGCTTATGA
Cl359s	ATATGAACCTTATCAATAGTCGATCTATCGTCACTCTTGAGTCTCAAGCTT
Cl35ds	ATAGGGACATGCTTAATATGCACATATCATAATGCCTAATATGTCACAGA
Cl361s	TTAGAGCAACCCATCAGTAAAAAACTTCCCTGAGTTTTTTTTTTGTTAGCA
Cl362s	GTTAACCCATATTTTCGGCCACATTGTGAAAATAGTACAATTTTTTTTTTA
Cl363ds	GGCTGGTGGCTCAGAGATCACAGCCAACCCGCGGGGACGAATAAAAACT
Cl365s	GAATCCCAATGAAAGTCATGTGTTACTTGAAAAGGCACTTTTATATT
Cl366s	CTATTTTTTAAATTTACAAGAAAATATGTTGTCGCTATTGAAAAGTGAG
Cl367s	CATTATACTTATTTTAGTTTATACTTATATATAATGTAACAGTGCCTCGC
Cl375s	GAATTAATTTATAGTCTATTTAGGTAGACTATATCTTTATATTTATCTT
Cl376s	CATTCAATATACAAAATATACCTCCTCTGAATACAATGTATATTTTAA
Cl377s	ATATATAGTGGAGTATAAGACTCATCATAATCATAATCATAAATAGAAAT
Cl378s	ATAATGTGGTGCACATGAGTTCTAGTGTAATTGTTGGTGAGGACTATACT
Cl379s	AGGTGGACCTCGGTTTATGTTATAATTTGAAAAAAAAAAAAATACTACGTG
Cl380ds	TTGATGCTAATGGCCACCCTCTCAGAGTGACAAAGATACTGAGGAGCTG
Cl382s	TTCTTCAATTTCTGTATAGGTAATTAATAATACGTATTATTCACAATTC
Cl383s	TCTAGAACTATACCACTGTTGTTATATTTTTATATATTAATTTATCGACT

Supplemental Table 3. (continued)

Marker name	Sequence information
Cl384s	ATATGTATAGTCATACCAACTTTTTTTAAAGTGAGCAAACCTGTTTAATAT
Cl386s	TGTTGCATAAAGTGGGGGGGGGGGCATGTACAAGTTTGAGGGTAAACACTT
Cl387s	TATATAAAGTAAGTTGACCCCGCTATATTTTTATGTTTTTTTTTAAAAAA
Cl392s	AATGACTTCTGGAAAATAATTTCTGGAAAATGAGTCATTTTCCGGAAAAAT
Cl39s	TGTTCAAGTGAGTCTACCTCTCCTTATGGGTTTGATGAACAAATTTAGA
Cl3s	CCAAACGTTCAATCCCCTCATCACTCACCCCTCAAGCATCCATGATACA
Cl40s	TGTTACATTAGAAAAGTAAAATTAGAAAATAAAAATTTGGGAATTCATAGAG
Cl41s	TGTTACACAAGAGAGATGCAAAAGTTTTAAGAAACTCACAACATTTCTAGT
Cl42s	TGTTAAGCGTTCATTAATGTTTCGTTAACGTTTCGTGGACACGTTTCATGAAT
Cl46s	TGGACCGCGGTCCACAATGCATTGTGGATCGCGATCCCCAAAACGACGTC
Cl49s	TGAGCAAGCTAATTCACATAATCGTGAATGTAGCGACAAAAACAACTTTGA
Cl4ds	AAACCAAATGCTGTTTTCAGATTAGACAATCTTCTAGCCCTAAAACCTCTGC
Cl52s	TGAAGATGCTCGGCTGATGAGGTCAGCTTTCCCGGACAATGGTGCACAAA
Cl53s	TGAACTAATTACTTAAAATGCATTGATGAAGAGAGATAGGGGACATGGAA
Cl54s	TAAAAACACTAGTCTTGTTTTGTTGTTGCAGATGAACATGATTTCTTGAA
Cl56ds	TCTTGTTGATGACAAAATCAAGTACTCGTAATTTGAGAAGTTCCAAAAC
Cl58s	TCTCAGCCGTGCGAAAAAGATTCTCCGCCCGTCAGGAAGAGGAAAAGTGGAA
Cl63s	TCCTCCAACATAAAGGAAGACATACAATTTTTGGGTGGACCACCCCTGT
Cl64s	TCCATCACTTGTATATATAATCTTTTTTTGGAATGAAATGGTGGAAAT
Cl69s	TCAACCACTGGGTGTTTCGGAGTTCACCATAATTGTTGAAATGCGCGG
Cl6s	AAACACGCATTGCTCGAAAAGTACGTAGTTAACTTTACTAGTTGGGAGAAA
Cl70s	TATTTGCTCCTGAAGATCAATCTCATATATTTGCAGGCTATATGTAATCA
Cl73ds	TATGCATCACAAGATTGTGTTCAAGACTGCAAAACAATTTTATATACCTTT
Cl75s	TATGATTCAAAAATGGTAGCCAATGGAGGGATTTGTACCAGGATGAATT
Cl76s	TATATCACTCTGATCTTTTGCATTTTCAGGCAGAGAAAATGGAGCTCC
Cl77ds	TATATAAACATAAATGTGCACTAATCTAATCGCTTTTAGTTAAATGGAGC
Cl79s	TATAAATCATAGATAGAAAAATTGTGGTGTATGTGGAAGCCGTATTTCGTA
Cl81s	TAGCTATCATAAAAGAGTATAAAGTCATTGTTATTGTTTGGTTGACAGGT
Cl82s	TAGATGTATTTCGAGTTGCATCAATTAGTCCTTAGAGTTCATGAAAATGT
Cl83s	TAGATGATAAGTCTGTTGAAACTCCTTTTTCTTCTCCATTCAACAATGCA
Cl87ds	GAATGAACACTTGACGTTTTAGCGTTTACAACGTAAAGTTCCAACATAAG
Cl89s	GTTTTTTTCTTGGGGGTTCCCTCACCTGCTACTAGTTCAAATAAGTACAGT
Cl93s	GTTTCCTTAATCTGCGAGACAATTTAAGCAATAACATAAAGATATCCAC
Cl94s	GTTTCATATATTTCTTTGACAAAAGTGCTTTCACAAATCACATCCGTTT
Cl95s	ATTTCATAAATTGGAGAGAATTACAATCCATCGAATAAAATCCCAGAATT
Cl98s	ATTGGTATCAGAATAAGGGTGGTTAAATCTTTAGAGAAAATGGTGTGG
Cl9s	AAAACCTCCTAAAAGTGAACAGTATACCTGAAAATAAAGGTTGCATAATG
pattern383s	AATAAATAATAAAAGCACACAATAAGTTACCAATTAATTAATCAACTAAT
pattern386s	ATGACTTTTATTAAGATTACACACAATTTTATAATTATTACAAGTATTC
pattern395s	CTCCTCAATAGTAAAATTGTTTAATCTACAAGATGCTCTCATTGCAACT
pattern396s	ACAGAGTGTATATAATTAATTGGAAAAGTGCATGGATAATGGATTGATT
pattern397s	ATTTTTAGTTTGGCCTGATTTAGGAAACACACATTTATATTATATACTAA
pattern398s	ATGCTTCTATTTAAATATTTTATCCAAACAATCTTAACTATTTTAAAA
pattern411s	ATAATTTTAAAATATTTTTTCAAACCTTTTAAATATTTTTTAAATAATCCA

The description of 's' and 'ds' represents simplex and double-simplex markers, respectively.

Supplemental Table 4. Summary of marker information per linkage group

Linkage groups	No. of markers	Length of linkage groups (cM)	Average distance between markers (cM)	Linkage groups	No. of markers	Length of linkage groups (cM)	Average distance between markers (cM)
P01	8	91.7	11.5	I03	3	1.9	0.6
P02	4	6.8	1.7	I04	3	9.7	3.2
P03	3	2.1	0.7	I05	2	21.7	10.9
P04_1	3	15.9	5.3	I06	2	1.1	0.6
P04_2	3	15.3	5.1	I07	2	13.6	6.8
P05	3	24.2	8.1	I08*	2	0.0	0.0
P06	2	1.1	0.6	I09	3	1.1	0.4
P07	3	22.5	7.5	I10	2	11.2	5.6
P08	2	0.1	0.1	I11	3	7.5	2.5
P09	3	1.1	0.4	I12	2	5.4	2.7
P10	2	7.9	4.0	I13	4	46.4	11.6
P11	2	10.0	5.0	I14	3	1.5	0.5
P12	2	14.0	7.0	I15	2	14.0	7.0
P13	6	47.3	7.9	I16*	2	0.0	0.0
P14	4	46.0	11.5	I17	2	21.3	10.7
P15	2	3.2	1.6	I18	3	25.1	8.4
P16	3	4.2	1.4	I19	2	7.7	3.9
P17	4	48.6	12.2	I20	3	23.1	7.7
P18	3	30.8	10.3	I21	3	21.4	7.1
P19	4	19.1	4.8	I22	2	10.1	5.1
P20	4	50.7	12.7	I23	5	32.4	6.5
P21	4	52.5	13.1	I24	4	25.1	6.3
P22	2	3.2	1.6	I25	2	14.0	7.0
P23	3	32.2	10.7	I26	2	29.8	14.9
P24	2	10.1	5.1	I27	5	62.1	12.4
P25	2	28.0	14.0	I28	2	2.1	1.1
P26	3	15.9	5.3	I29	4	16.2	4.1
P27	2	33.6	16.8	I30	4	24.8	6.2
P28	2	2.7	1.4	I31	3	20.8	6.9
P29	2	1.0	0.5	I32	2	10.1	5.1
P30	2	3.2	1.6	I33	2	21.3	10.7
P31	2	26.2	13.1	I34	2	19.8	9.9
P32	2	1.0	0.5	I35	2	5.4	2.7
P33	2	8.9	4.5	I36	2	11.4	5.7
P34	2	6.7	3.4	I37	4	18.2	4.6
P35	5	86.9	17.4	I38	3	28.8	9.6
P36	2	2.1	1.1	I39*	2	0.0	0.0
P37	2	31.7	15.9	I40	3	44.3	14.8
P38	2	19.8	9.9	I41	2	4.3	2.2
P39*	2	0.0	0.0	I42	2	19.8	9.9
P40	2	22.9	11.5	I43	2	14.0	7.0
P41	2	28.0	14.0	I44	2	2.1	1.1
P42	2	10.6	5.3	I45	2	4.3	2.2
P43	2	31.7	15.9	I46	2	3.9	2.0
I01	2	12.9	6.5	I47	2	35.7	17.9
I02	3	6.9	2.3				

*Although the linkage groups with this length contain more than two independent markers, the recombination were not observed in our F₁ mapping populations. Thus, the markers in these linkage groups were considered to be closely linked.