Supplemental Table 1. The 125 DNA markers used for selecting CSSLs

chr.	Marker name	IRGSP1.0 position	Forward primer	Reverse primer	Method	Enzyme
1	aa01000007	35,239	ACTGAGTGAGTGACTTGTGGC	GTCCCATTCTCCGCTGCATATT	CAPS	*Xsp* I
1	RM8068	1,660,242	AAACCTCTCGCTGTAATTAG	TGAACATTTATTGATATGGTAAA	SSR	
1	RM6451	4,797,266	TATGACATTGACCGTGGGC	TCTCCCCATGTTTGATCCTC	SSR	
1	ac01000670	8,036,400	GCTATATTTGTCACGTGAAATCAAGC	GAATGTAATATGTACTGGTGCAACCGTCTA	dCAPS	*Xsp* I
1	aa01005640	10,971,527	TTTTCCTAGTGCACAAGTGATTGTCATGCT	TGCATGATAAACTTAGAATATAGGAACCCA	dCAPS	*Xsp* I
1	aa01006150	15,231,386	GTTTCACCCTCACGCCTAGC	GCCGGTTGCGCATGTTAC	CAPS	BglI
1	aa01006249	16,727,125	GGGCGCAAGAAGGATGGG	TAGTGGCCTTCTCAGGGACC	CAPS	EcoRV
1	aa01006770	19,890,642	GATGTGCATTTGAACTTTAATTCAATTCAT	GTATTGTAAAGTTTTATGGTCCCCACGCGA	dCAPS	EcoRV
1	aa01006903	22,112,410	GGTAGGAGAAATACCGCCACC	TCCAGCACTTGTCTGAGGTT	CAPS	AflIII
1	RM7202	26,203,636	AACGTGGAGGCTCCTTTTTC	TTGCTATTAGTTGGTGGGGC	SSR	
1	RM246	27,336,246	GAGCTCCATCAGCCATTCAG	CTGAGTGCTGCTGCGACT	SSR	
1	RM8085	34,863,114	TGCGTTTCGATTTCTTTTTA	GGAAAGTTGTGTTCTTTGGC	SSR	
1	RM5448	37,398,380	GGGGCCCTTAGAGTTTTTAC	CTGCTACAGGACAAAACCAG	SSR	
1	RM3523	39,824,122	CGCTCTCTCGTCGATCTTAGC	CGAGGATATGGAGCGCAAGAG	SSR	
1	RM8136	42,927,329	ATGTAAGCTAGGTAGAGCTG	GCGTACGTACGTAAGTAATA	SSR	
2	aa02000022	576,767	GAAGTCTCCAGCACTGAGGC	GAGACTTCACAGCAGCCACC	CAPS	*Pst* I
2	RM5345	4,206,392	CAGATACCCTCGCAAAAAGG	CGGACCCCAAAGAAAGAAAG	SSR	
2	aa02000715	6,104,069	GACTACCGCACATGTATAGGAGTC	GATTAAGTGACGCACGCGGG	CAPS	BccI
2	aa02000772	9,597,460	ACACATTAAATAAGATGCCCACG	TTTTGGTGCTACGACGATTGC	dCAPS	HpyCH4IV
2	RM1313	11,262,999	TGTGTCTGAAAACCAAGGGG	CGTCCAAGCTGTTCGTTCTC	SSR	
2	ab02000375	18,766,399	GGCATGTAGTACAACTGCCCT	ACGATACCTCAAGTGCGATGG	CAPS	NdeI
2	RM3762	22,462,497	GACGGGTCAGCTACCGTAAG	TCCCCCCTCTAAAACCCTAG	SSR	
2	RM5651	23,574,244	AAGAGAACATTTGGAATCCT	TAACCTGTGCCTTGTTTG	SSR	
2	aa02002928	25,592,080	CCTTCTGTTCCCGGCCGATA	GGAACCTGCACTGGCGAT	CAPS	BccI
2	RM1342	28,165,372	AGAAACCAAAGATGGGAGGG	CTAGCCAGCTCTCCCTTTTG	SSR	
2	RM530	30,538,116	GCACTGACCACGACTGTTTG	ACCGTAACCCGGATCTATCC	SSR	
2	RM5472	30,643,103	CACTCAAGACCAGACCTGTACG	CGGCACGTCATTGTAGTGAC	SSR	
2	aa02003577	32,133,628	ATCACCCACCACATTCGCTG	CGATAGCGTAACATAGGCCGT	CAPS	*Hpa* II
2	RM3542	35,144,500	CTCCATGGAAAGCTAGCCAG	AATCACCCTTTCAGTGCCTC	SSR	
3	aa03000001	198,008	CTGAGTCAGCCAGTTGGACC	CCACATAGACAGCCACGTACG	CAPS	*Dra* I
3	aa03000455	2,196,417	GGGAGGAGGAGTAGATCGGG	TCGGTAACACCAACTGGGAC	CAPS	*Pst* I
3	RM3864	5,860,933	AGTCAACCTTGGGGGTAAGG	AGATACTGCCCGTGTCATCC	SSR	
3	RM3461	8,350,161	AAAGTCTCCCTGTTGTAGCC	CATGAACGTAAAGCAAACG	SSR	
3	aa03000871	14,283,311	TGCCGATACCTAGATACCTCCC	GAACATGCGAAGGCCTGAAAG	CAPS	DdeI
3	aa03002153	19,543,200	AACTCACCTCGTGACTCG	GCCAGCCAATCAGTCATCCT	CAPS	PciI
3	RM3513	25,114,637	TACTCCTATCCTGCCATGGC	TGTAGTAGACGAGAGGCCGG	SSR	
3	RM6329	28,811,876	CCCTGGATGAAAAGCACAAG	GAAGTTGTAGATGCCCCATC	SSR	
3	Hd6_FNP	32,363,542	ACCTGGCAGCATGTTATGAC	CTACAGATCCACAGAACAGG	CAPS	*Hin* dIII
3	RM1038	33,660,437	TGGTTCGATTCGGATTTC	AAGCTATTCACAAGCAGCTC	SSR	
3	Hd16_FNP[a]	33,852,154			PCR-CTPP	
3	RM2187	35,617,014	GTCATTTGAAGTAAATCCGT	GGTCTACTTGCGAAATAAGT	SSR	
4	aa04000040	1,075,655	AAACCTAACCTAGGCCCTGGATTACGGGCG	CATTCTTTCAGTTACCTTCAGAAGAGCAGC	dCAPS	*Hha* I
4	aa04003724	8,271,354	GCCTATGGTCTAGTAGCCACC	CCGTGAAGCTGAGATCATGGT	CAPS	AciI
4	RM1359	20,032,598	AACGAATTCTATTTTGCGTC	TTCTTCTCATTTCAATTCGC	SSR	
4	RM3524	22,893,828	CGGAGCTGGTCTAGCCATC	GTCTCCGTCTTCCTCACTCG	SSR	
4	RM1388	25,220,380	TTCAATGAGGCAAAGGTAAG	ATTGTAGCTTGGACTAGGGG	SSR	
4	ab04001194	26,796,353	CGACCTCTAGGGACGTGACT	GCGAGATCGATTCTAGGGCC	CAPS	AflIII
4	RM5503	30,363,699	GGGAAGAAGATAGGAGATGG	CTCTGGGTACACTTCACGAG	SSR	
4	RM349	32,684,626	TTGCCATTCGCGTGGAGGCG	GTCCATCATCCCTATGGTCG	SSR	
4	RM1272	35,296,066	TCTATGGATCTGCATGCTGG	CTGCCCTGTCCTTTTAATCG	SSR	
5	RM1248	94,011	ACAAGCAGCTAATGGTTGGG	GTGATTTTGGCTCAGGTCAG	SSR	
5	ac05000101	7,480,964	CGGTGGCATGATTTATATCCATTATCTAAT	AAATTTTATAGTGCCGTAGCGTTAGCATCG	dCAPS	TaqI
5	ab05000119	9,316,830	CGTATAGGCCAAAGAAGCAGGT	TCGTCCTCCTCGATAGCACAAA	CAPS	Hpy188I
5	ac05000153	14,774,503	TGCTTGGTGCTATAGTCTGC	CTATCGCCAGACACGTGGAG	CAPS	*Mbo* I
5	RM430	18,753,970	AAACAACGACGTCCCTGATC	GTGCCTCCGTGGTTATGAAC	SSR	
5	RM5592	22,115,574	GTAACGCTTATTAACGATAA	ATATTCTAGAACGAGGGTAG	SSR	
5	RM3476	23,906,612	GATTCTCGTCGTAATCAAGA	ATCCACGGTTAAGATAAATG	SSR	
5	aa05000868	26,835,497	CCATGGAGGGTGATGAACGG	CCACCATTTGTCCGACCACC	CAPS	*Bsp* 1286I
5	aa05001022	28,904,853	GCGAGGATGAGCTTTCTCTTGA	GCACAACAGAGTAGCACTTCC	dCAPS	Hpy188III
6	aa06000004	397,429	TGGTATCCTGAACAATTTAAACAATGAATG	CAAAATCTAAACTTTGCGTTGAACTAAACC	dCAPS	*Xsp* I
6	RM1369	1,563,657	CAATTGGCCCAAGGTCGT	GCGGATTCAAGATCATGTTGGT	SSR	
6	Hd17_FNP	2,234,192	ATGGCTTGTCCCTGTCACCACTCCTT	CCCATATGTTGGGCTGATG	dCAPS	BstXI
6	ab06000075	5,344,224	TGTACCGAGTACCCACACGA	AATTGCGACTCTGCGAGGAG	CAPS	*Sma* I
6	RM2615	5,960,082	CAGAGTGCTTTAGACAATCA	AAATTGGTAAGAGATTCTGC	SSR	
6	RM5585	7,606,869	TCAGAGGTGGCAGCTTATTTTATACC	ATGTAAATGGTCACACACACACACAC	SSR	
6	RM2523	8,920,014	CCGTAGGTCTTCAAGTGATA	GCAAAACCGAACTAAAATTA	SSR	
6	ac06000592	11,844,371	GCCAACGATGCATCAGTGATAC	TCTAAAGGCTAAAGTCCTGGCG	CAPS	HpyCH4IV
6	ab06001118	17,240,935	AGAGCGACGACATCAACACC	AGACGTGCCGGATCTAGACA	CAPS	BsmAI
6	RM1340	23,344,226	TCCAAACTAGTGGGAACGC	CTCAACGCCATGAACCTC	SSR	
6	aa06000951	25,865,811	CCAACCGACACTCAATTTCA	CAGTTGCCGGTGAGAAGACT	CAPS	*Xsp* I
6	RM1370	28,533,532	AAACGAGAACCAACCGACAC	GGAGGGAGGAATGGGTACAC	SSR	
6	RM5753	30,967,924	AACATGCTCAACTTCTGGGC	GCTAGGTACGATCCAGCTGC	SSR	
7	aa07000004	1,017,334	GGGTAGCCTAATCATCTGAGACCA	GCTCGCTTTGTTTAGCTTCTCC	CAPS	*Dra* I
7	RM8010	4,166,570	GAGCCACTGCTATATAAAGC	ACCAAAATCCAAACTTTGTA	SSR	
7	RM8006	7,686,234	TGCCGGTTCTTAATTTTATC	AATGGTCCACATTACTCCAC	SSR	
7	ab07000446	8,883,010	CAGAACGAGCAGTGGAGAGG	TCTCTCGCTGCTCCATTGTG	CAPS	*Xsp* I
7	RM8036	14,637,706	AGCAGAGCAATTTAACTAAG	GCCTATCATAATATCCATCA	SSR	
7	RM1279	21,615,000	GGGTATAAAATGCGTGGCAC	ATGGATGGTACGAGGACGAG	SSR	
7	aa07005234	24,146,716	AGTCGCTGATATGTGGGGCTCA	CACTCGACTCATGGGCTAGAGTCCT	dCAPS	Hpy188III
7	RM1364	26,775,051	AAGAAATTCAAAACACATGA	AAAACATCTACTTTGATCCA	SSR	
7	RM1306	28,947,976	TGCCAATTACCTTCCCGTAC	TGCTCCGTATTGCTGCTATG	SSR	
8	RM3819	3,016,139	ACCTCACCTGTGGATCTTGG	CAATCCCCTTCTCTCCTTCC	SSR	
8	RM5556	4,589,534	ATCTCCCTCCCTCTCCTCAC	TCCACACCTTCACAGTTGAC	SSR	
8	aa08001325[b]	7,383,135	TGAAATCAGTTACTACCCAG	AGAGGAGAGGAAGAGTCAACAGA	CAPS	*Dra* I
8	aa08001560	8,839,169	CATGTGGTAGCTGTGCGGAC	CCATCCTCACTGCCAAGCTG	CAPS	DdeI
8	RM2910	16,945,565	CAGCTGCTCATATTCATATA	ATAAGGTACTTCATCCGTTA	SSR	
8	RM7049	20,815,151	AACCTAGATCTAATCCGTGG	CATCTCTGAGTTGAGCAAAC	SSR	
8	RM5485	24,072,950	CTTCCACAAGCTTGGCTAGG	AATGCCATCCCCTACTCATG	SSR	
8	RM3155	27,905,344	AATCCACATTTGGCTTCTC	CGTGTAACTGTTTCGCTTG	SSR	
9	aa09000002	1,742,371	GTGCAGTGGATGTACGCCTT	CTCGAGGCTAGCTTTGGACC	CAPS	TaqI

9	RM2855	3,839,880	GGAGCTTAGAATCTCACCTA	CGCATTTTCCTATACATACA	SSR	
9	aa09000030	8,073,443	TTAAAAGAAAGGCTGATGGGAGCTTA	CCGGACTAAAGGTGTCCTCA	dCAPS	DdeI
9	aa09000038	9,071,039	GTGGGGTGCCATCAATTCCAGCTTA	GGCTCGAAGAATCGACTCAA	dCAPS	DdeI
9	ac09000231	11,753,935	GCACCAGAATGCAACTGCTCATCACTT	TCACTGCCTTTCATTAGCCACA	dCAPS	DdeI
9	ac09000278	16,115,195	CGTCCTACTGCTAGCTGCTG	CGACGACTCGTACACACCAA	CAPS	TaqI
9	RM160	19,788,768	AGCTAGCAGCTATAGCTTAGCTGGAGATCG	TCTCATCGCCATGCGAGGCCTC	SSR	
9	RM215	21,189,620	CAAAATGGAGCAGCAAGAGC	TGAGCACCTCCTTCTCTGTAG	SSR	
9	RM2144	22,210,016	ACATTATGAAACGGAGGAAG	GAAATGATGCATCAGCATTA	SSR	
10	RM5271	1,936,630	CGGTGTAGATTGTAGGTACA	GTAGTTTAGTTATTGCGCAC	SSR	
10	aa10001353	6,801,371	CGCCACCCGCATAAGAAA	AGTTGGGACCTCGAGTGAGT	CAPS	ApoI
10	aa10001449	9,388,361	GCGATTCCTTAGACATTGCC	GTCTCAGCTCCCTTCCGC	CAPS	BsrDI
10	RM4455	11,737,240	CTCTCAAAGAACTAGGACTC	GAGAAGGTATGATAACCAAT	SSR	
10	RM1083	14,677,003	CCTTGATTGCAGCATCCG	TTGAGCCTTTTACGAGACGG	SSR	
10	RM6704	18,005,569	CACACATTGCATTACGAGGG	CAGGGGCAGCTTGAATACTG	SSR	
10	RM5352	21,192,137	GGAACTAAACATGGTGCAAG	ACCAGATCACATGAAGAGGA	SSR	
10	aa10003607	22,389,675	GGTTTGCAAGCGCTTGATCA	GGCCACAATAACGTCTGAAGGA	CAPS	*Eco* RI
11	RM1761	306,167	ACGCTTAAAGAACATTTGAT	GCGATTAACTTTTAACCATT	SSR	
11	aa11000089	2,717,750	GCCACTGCCTCTATGGATTG	TCCTGCAACAGTTTTTCATCAGTGAA	dCAPS	*Eco* RI
11	aa11000115	3,282,952	CTTACAATTGGACCCAGCAGG	GACTTGTCTCGTAGCATCGGT	CAPS	*Bsp* 1286I
11	RM3625	6,669,050	CTTGCAATTCAATTGCTTAC	GGTGGCCTAGTGAAACTAAA	SSR	
11	aa11002722	9,053,289	TTGAGTATGATTCGACTTCAGAAAATATGG	CAGTAGATGCTTAGAGAATTGTCAACAGCG	dCAPS	*Hha* I
11	aa11003294	15,388,528	CTGCCATGTCACTGGGACCTGATTCTGCTGCA	ATCACAGATCAAACATGGGTAAAATGCGAAATGTC	dCAPS	*Pst* I
11	RM1341	20,143,256	GAACTGGGTGACGAGATCCTG	ACCACCAGCAGCGTTTCTC	SSR	
11	aa11006712	24,455,971	CCTCACGGTGCAGGTCATG	CTTCGTCACCGCGTGATGTC	CAPS	MnlI
12	RM1880	748,006	ACCACTAAATAAGCACATAC	GGCATCATACATTAAAATAC	SSR	
12	RM3747	2,305,433	AGCAATGCACTCCCTTGATC	TGTCTTCCTCCTTGGTTTGG	SSR	
12	RM3455	4,920,662	TGAATCCACACTCGCAGATC	GCCAGTCCACGATTGGTC	SSR	
12	RM2529	7,567,768	CATTAAAATCAGTGGGACTG	AGGCATTTCCTGATATGATC	SSR	
12	RM101	8,829,342	GTGAATGGTCAAGTGACTTAGGTGGC	ACACAACATGTTCCCTCCCATGC	SSR	
12	aa12004460	12,185,846	GGCCAAGCTCCTAGGTGAAG	CCTGGAGCTGGAGTCCATTG	CAPS	Hpy188III
12	aa12004617	15,775,760	GTGTTTGCGATCCCGTGTTC	GGACTTGCACTGATGACATGAC	CAPS	AcuI
12	RM2972	19,167,185	GAGCCAATATGTTGTCTTGA	GTTCAGATCATGATGCCTAC	SSR	
12	RM1986	21,246,578	TAACGGAGGGAGTAGTTTTC	GAACCTACATATCGAGAGCA	SSR	
12	aa12005161	24,239,197	GCTGGAGTGACGTGTACACTAC	TTAGCAGTTTTGAAGTGTGACGTAATCATG	dCAPS	Hpy188III
12	RM2196	27,384,347	ACTGAGAACTTTAATCATCG	GAACAACTTTGAAGAGAAAC	SSR	

[a]: The primers of *Hd16*_FNP were Fin; CGACATTTTACAGGGGAACAATTAGATCCG, Fou; TGGAAAGAAGCATCATCTGGTCAGCATG, Rin; TACGACCTAAGTGGGCATGGACGCTCGT, Rou; ACCTGATACCCTTGCCAAGGTAATCTCCCT.

[b]: This marker showed Built5 position.

Supplemental Table 2A. The genotype of CSSLs cultivated in 2015

Chr.	Marker[a]	Physical location (bp)[b]	CSSL1-1	CSSL1-2	CSSL1-3	CSSL1-4	CSSL1-5	CSSL2-1	CSSL2-2	CSSL2-3	CSSL3-1	CSSL3-2	CSSL3-3	CSSL3-4	CSSL4-1	CSSL4-2	CSSL4-3	CSSL4-4	CSSL5-1	CSSL5-2	CSSL5-3	CSSL5-4	CSSL5-5	CSSL6-1	CSSL6-2	CSSL6-3	CSSL6-4	CSSL6-5	CSSL6-6	CSSL7-1	CSSL7-2	CSSL7-3	CSSL7-4	CSSL8-1	CSSL8-2	CSSL8-3	CSSL9-1	CSSL9-2	CSSL9-3	CSSL9-4	CSSL10-1	CSSL10-2	CSSL10-3	CSSL11-1	CSSL11-2	CSSL11-3	CSSL11-4	CSSL12-1	CSSL12-2	CSSL12-3	CSSL12-4
	aa01000007	35,239	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1
	aa01000048	600,441	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	1	1	1
	RM8068	1,660,242	2	2	1	1	1	1	1	1	1	3	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	3	1	1	1	1	1	1	1	1
	aa01004844	3,615,363	2	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	RM6451	4,797,266	3	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01005142	4,838,836	3	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	ac01000670	8,036,400	1	2	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01005640	10,971,527	1	2	2	3	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01006075	12,337,906	1	1	2	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006089	12,999,615	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006150	15,231,386	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006181	?	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006249	16,727,125	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006340	18,110,213	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006478	18,589,881	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006756	19,013,746	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3
	aa01006765	19,420,219	1	1	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3
	aa01006770	19,890,642	1	1	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3
	aa01006817	20,876,398	1	1	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01006855	21,376,950	1	1	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01006903	22,112,410	1	1	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01006939	22,360,188	1	1	2	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01006944	22,879,044	1	1	3	2	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
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	aa07006550	24,703,983
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	aa07007512	28,292,991
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	aa07007516	?
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	aa08006226	21,138,054
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	aa09000038	9,071,039
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	RM160	19,788,768
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	RM215	21,189,620
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	aa09000165	22,403,093
	ab09001160	22,854,691
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	RM5271	1,936,630
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	aa11000002	?
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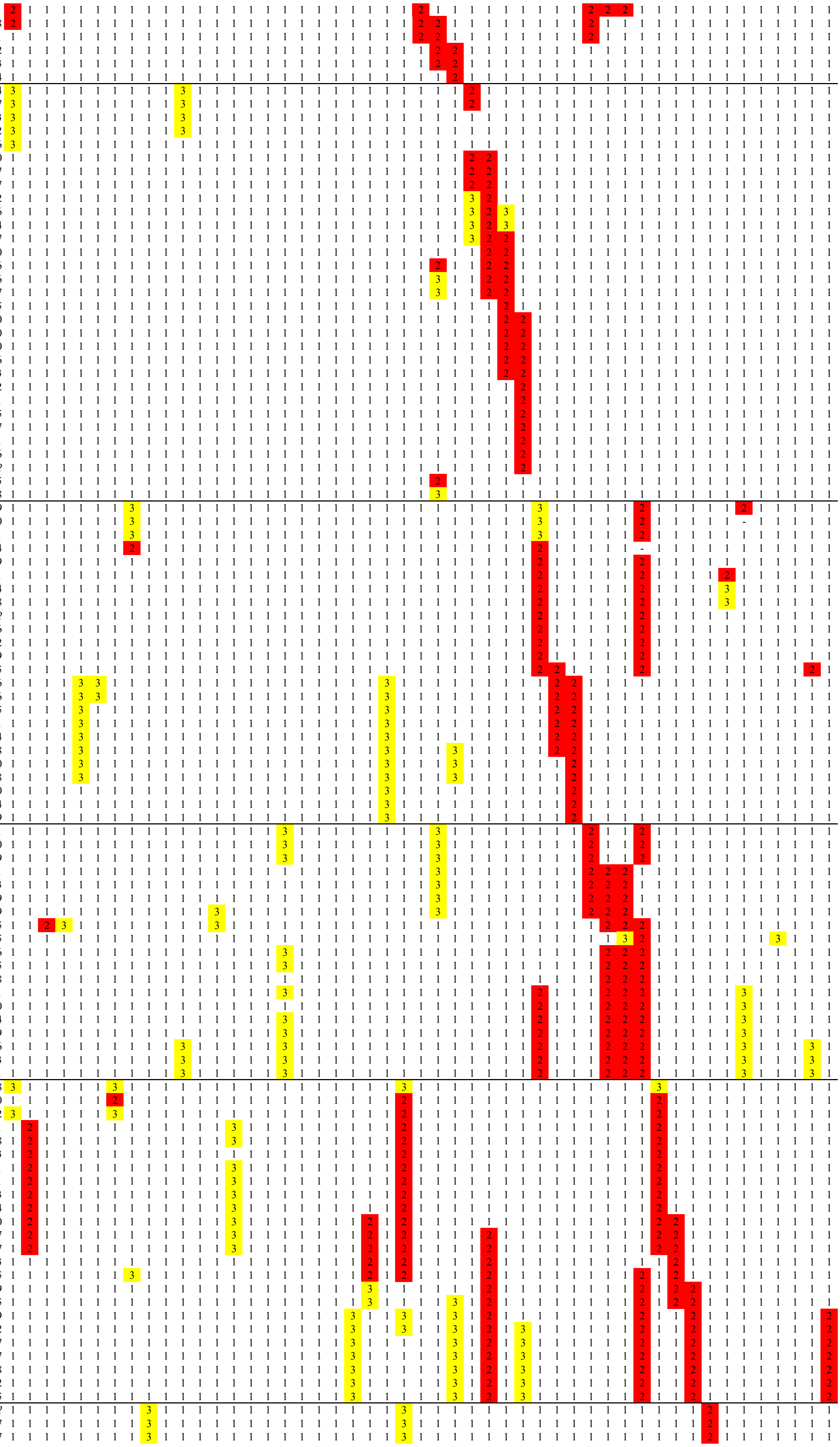

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	aa11002995	?	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	3	2	3	1	1	1	1
	aa11003079	13,047,944	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	3	2	3	1	1	1	1
11	aa11003243	13,928,335	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	3	2	3	1	1	1	1
	aa11003281	14,998,289	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	3	2	3	1	1	1	1
	aa11003294	15,388,528	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	3	2	3	1	1	1	1
	aa11003403	16,958,635	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	2	3	1	1	3	1
	aa11003517	17,576,163	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	2	1	1	1	1	1	1	1	2	3	1	1	3	1
	aa11004053	18,048,063	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	2	1	1	1	1	1	2	3	1	1	3	1
	aa11004155	20,346,745	1	1	1	1	1	1	1	1	1	1	2	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	2	3	1	1	3	1
	aa11004494	21,059,521	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	2	3	1	1	3	1
	aa11004500	21,472,745	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	1	-	-	1	2	1	1	1	1	1	1	1	2	2	1	1	-	1
	aa11004506	21,888,015	1	1	1	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	2	1	1	3	1
	aa11004535	22,207,750	1	1	3	3	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	2	1	1	3	1
	aa11004652	22,936,415	1	1	3	3	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
	aa11005083	23,613,989	1	1	3	3	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
	aa11005455	23,912,038	1	1	3	3	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
	aa11006712	24,455,971	1	1	3	3	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
	aa11007380	26,199,319	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
	aa11007953	?	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1
	ab11002174	29,014,394	1	3	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1
	RM1880	748,006	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1
	RM3747	2,305,433	1	3	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2
	aa12000060	2,443,806	1	3	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2
	aa12000100	2,838,271	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2
	aa12001361	4,433,324	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2
	RM3455	4,920,662	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	2	2	1	2
	aa12002375	6,213,351	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	2
	aa12002973	6,760,146	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	2
	RM2529	7,567,768	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	2
	aa12004213	7,987,137	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	2
	RM101	8,829,342	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004348	9,100,911	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004405	9,772,678	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004429	10,799,287	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004439	11,771,970	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004460	12,185,846	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004471	12,937,191	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004480	13,579,319	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
12	aa12004494	14,328,206	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004528	14,881,061	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004589	15,344,038	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	3	1	2	2	2
	aa12004617	15,775,760	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	3	1	2	2	2
	aa12004637	16,697,390	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	2	1
	aa12004649	17,482,934	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	2	1
	RM2972	19,167,185	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1
	aa12004709	19,864,859	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1
	aa12004730	20,258,554	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1
	RM1986	21,246,578	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004743	21,484,803	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	3	1	1	2	2	2
	aa12004757	22,097,355	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	3	2	2
	aa12004766	22,520,720	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	3	2	2
	aa12005161	24,239,197	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	2	2
	aa12005164	24,387,429	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	aa12005168	24,556,276	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	aa12005291	26,067,625	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	RM2197	27,384,347	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	aa12007098	27,502,348	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2

a: The genotype of markers represented 1 for Koshihikari homozygous, 2 for Yamadanishiki homozygous and 3 for heterozygous.

b: Physical positions showed IRGSP1.0 positions.

Supplemental Table 2B. The genotype of CSSLs cultivated in 2016

Chr.	Marker[a]	Physical Location (bp)[b]	CSSL1-1	CSSL1-2	CSSL1-3	CSSL1-4	CSSL1-5	CSSL2-1	CSSL2-2	CSSL2-3	CSSL3-1	CSSL3-2	CSSL3-3	CSSL3-4	CSSL4-1	CSSL4-2	CSSL4-3	CSSL4-4	CSSL5-1	CSSL5-2	CSSL5-3	CSSL5-4	CSSL5-5	CSSL6-1	CSSL6-2	CSSL6-3	CSSL6-4	CSSL6-5	CSSL6-6	CSSL7-1	CSSL7-2	CSSL7-3	CSSL7-4	CSSL8-1	CSSL8-2	CSSL8-3	CSSL9-1	CSSL9-2	CSSL9-3	CSSL9-4	CSSL10-1	CSSL10-2	CSSL10-3	CSSL11-1	CSSL11-2	CSSL11-3	CSSL11-4	CSSL12-1	CSSL12-2	CSSL12-3	CSSL12-4
	aa01000007	35,239	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1
	aa01000048	600,441	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	1	1	1
	aa01004844	3,615,363	2	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01005142	4,838,836	2	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	ac01000670	8,036,400	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01005640	10,971,527	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa01006075	12,337,906	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006089	12,999,615	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006150	15,231,386	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006181	?	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006249	16,727,125	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006340	18,110,213	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
	aa01006478	18,589,881	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2
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	ab03000111	8,200,582	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1
	ac03000229	9,294,457	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1
	aa03000871	14,283,311	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1
	ac03000493	17,359,999	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1
3	aa03002121	18,876,501	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002290	22,448,146	1	1	1	1	1	1	1	1	2	-	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1
	aa03002346	24,263,268	1	1	1	1	1	1	1	1	3	2	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1
	RM3513	25,114,637	1	1	1	1	1	1	1	1	3	2	2	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002379	27,419,086	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002391	27,955,288	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002463	29,085,775	1	1	1	1	1	1	1	2	1	1	1	2	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002610	33,549,681	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002659	34,097,328	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002705	34,611,745	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002737	35,128,028	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002747	35,738,359	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa03002773	36,353,850	1	1	1	1	1	1	1	1	1	1	1	2	1	2	1	1	1	1	1	-	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa04000002	110,027	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	-	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1

	aa04000030	773,152	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I
	aa04000040	1,075,655	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I
	aa04000098	2,471,266	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I
	ac04000042	?	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I
	aa04001503	3,823,164	I	3	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I
	aa04002724	4,765,704	I	3	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04002984	?	I	3	I	I	I	I	I	I	I	I	I	3	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04003046	6,483,280	I	3	I	I	I	I	I	I	I	I	I	3	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04003107	6,900,036	I	3	I	I	I	I	I	I	I	I	I	3	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04003679	7,794,199	I	3	I	I	I	I	I	I	I	I	I	3	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04003724	8,271,354	I	3	I	I	I	I	I	I	I	I	I	3	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04004570	?	I	3	I	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I
4	aa04004785	15,506,877	I	3	I	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I
	ac04000676	16,740,388	I	3	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	3	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I
	aa04007763	20,528,759	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04007919	21,072,150	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ac04001045	21,526,703	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab04001157	23,126,372	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ac04001066	25,164,916	I	2	I	I	I	I	I	I	I	I	I	I	I	3	2	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab04001194	26,796,353	I	2	I	I	I	I	I	I	I	I	I	I	I	3	2	I	I	2	3	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I
	aa04008763	31,406,658	I	I	I	I	I	I	I	2	I	I	I	I	I	3	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab04001335	31,520,401	I	I	I	I	I	I	I	2	I	I	I	I	I	3	2	2	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04009515	32,809,201	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa04009569	33,225,262	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I
	aa04009829	34,992,381	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	2	I	2	I	I	I	I
	aa04009883	35,435,056	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I
	aa05000026	164,299	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	3
	ac05000011	463,712	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	2	I	I	I	2	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	2	I	3
	aa05000263	3,890,358	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	2	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa05000309	?	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa05000340	5,338,054	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I
	ac05000104	7,863,267	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	3	2	I	I	I	I	I	I	I	I	I	I	I
	ab05000119	9,316,830	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	3	2	I	I	I	I	I	I	I	I	I	I	I
	ab05000124	11,338,410	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	3	2	I	I	I	I	I	I	I	I	I	I	I
	ab05000128	12,399,321	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	3	2	I	I	I	I	I	I	I	I	I	I	I
	ab05000132	13,020,923	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	3	2	I	I	I	I	I	I	I	I	I	I	I
	ac05000144	13,695,604	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	-	2	I	I	I	I	I	I	I	I	I	I	I
5	ac05000151	14,541,042	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	2	3	2	I	I	I	I	I	I	I	I	I	I	I
	ac05000227	18,197,017	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	ac05000233	18,850,836	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	aa05000835	20,182,442	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	-	I	I	I	I	I	I
	aa05000842	21,605,013	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I
	ab05000280	22,805,256	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I
	ac05000298	23,216,295	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I
	ac05000302	23,876,975	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I
	ac05000304	24,166,413	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa05000868	26,835,497	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3
	ac05000341	28,218,584	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa05001022	28,904,853	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa06000004	397,429	I	I	I	I	3	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	2	I	I	I	I	I	I	I	I	I
	aa06000024	776,092	I	I	I	I	3	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	2	I	I	I	I	I	I	I	I	I
	aa06000247	2,118,780	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	2	I	2	I	I	I	I	I	I	I	I	I
	ac06000103	6,088,952	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	ac06000385	8,659,334	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	ac06000397	9,138,291	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab06000799	10,382,180	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I
	ac06000518	10,746,979	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I
	ac06000592	11,844,371	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I
6	ac06000665	18,886,290	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ac06000764	21,700,126	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	2	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa06000938	24,322,701	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	I	I	I	I	I	I
	aa06000951	25,865,811	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	2	2	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	3	3	I	I	I	I
	aa06001097	26,875,901	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	I	I	I	I	I	I
	aa06001119	27,389,348	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa06001139	27,875,211	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa06001158	29,671,063	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	RM5753	30,967,924	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07000004	1,017,334	3	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07000201	1,565,547	3	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07000566	2,072,143	3	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07000615	2,651,062	3	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07001067	3,654,626	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07001130	4,244,077	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07001807	4,767,907	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07001816	5,205,982	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07001842	7,181,306	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab07000442	8,424,447	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab07000446	8,883,010	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ac07000428	15,644,976	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
7	aa07001859	16,222,057	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07001934	19,241,445	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07004070	22,748,400	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07005205	23,712,500	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07005234	24,146,716	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07006550	24,703,983	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007162	26,640,932	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007461	27,050,785	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007493	27,485,237	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007512	28,292,991	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007516	?	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007522	29,064,675	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa07007554	29,361,828	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa08000005	700,999	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	I	I	I	I
	aa08000031	1,282,290	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	aa08000727	1,798,321	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	aa08000774	2,229,664	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	-	I	I	I	I	I	I	I	I	I	I	I
	ab08000087	3,951,991	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	I	I	I	2	I	I	I	I	I	I
	aa08000792	5,082,368	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	aa08001334	8,024,296	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	aa08001338	8,443,462	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
8	aa08001560	8,839,169	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	I	I	I	I	I	2	I	I	I	I	I	I	I	I	I	I	I
	RM2910	16,945,565	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	2	I	I	I	I	I	I	I	I	I	2	I
	aa08005473	19,454,816	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ab08000759	20,024,976	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	ac08000862	20,572,325	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa08006226	21,138,054	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I
	aa08006250	21,733,028	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I	3	I	I	I	I	I	2	2	I	I	I	I	I	I	I	I	I	I	I	I	I	I	I

	ab08000934	24,839,818	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa08006353	27,221,650	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	ac08000993	28,216,759	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
	aa09000002	1,742,371	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2	1	1	1	1	1	1	1	1	1	1	1
	aa09000018	5,462,009	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	2	1	1	1	1	1	1	1	1	1	1	1
	aa09000027	7,397,241	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1
	aa09000030	8,073,443	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1
	aa09000038	9,071,039	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1
	aa09000044	9,442,989	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1	1
	ac09000231	11,753,935	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1
9	ac09000278	16,115,195	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	3	1	1	1
	ab09001084	18,095,906	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1
	ab09001088	18,450,455	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1
	ab09001133	20,890,011	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1
	aa09000103	21,629,154	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	2	2	2	1	1	1	1	1	1	1	1	1	1	1
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	aa12004528	14,881,061	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004589	15,344,038	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	3	1	2	2	2
	aa12004617	15,775,760	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	3	1	2	2	2
	aa12004637	16,697,390	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	2	1
	aa12004649	17,482,934	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	2	1
	aa12004709	19,864,859	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1
	aa12004730	20,258,554	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1
	aa12004743	21,484,803	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	2
	aa12004757	22,097,355	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	3	2	2
	aa12004766	22,520,720	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	3	1	1	1	1	1	1	1	1	1	2	2	2
	aa12005161	24,239,197	1	1	1	1	1	1	1	1	1	1	3	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	2	2
	aa12005164	24,387,429	1	1	1	1	1	1	1	1	1	1	3	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	aa12005168	24,556,276	1	1	1	1	1	1	1	1	1	1	3	2	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	aa12005291	26,067,625	1	1	1	1	1	1	1	1	1	1	3	3	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2
	aa12007098	27,502,348	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	2	1	1	1	1	1	1	1	1	1	1	1	2

a: The genotype of markers represented 1 for Koshihikari homozygous, 2 for Yamadanishiki homozygous and 3 for heterozygous.

[b]: Physical positions showed IRGSP1.0 positions.