

**Table S4.** Cleaved amplified polymorphic sequence (CAPS) markers developed from the common introgression regions in two near-isogenic lines.

Marker ID	Position		Gene ID	SNP	Primer sequence (5'-3')	Enzyme	Size (bp)
	Chr.	bp		(D/R) <sup>a</sup>			(D/R) <sup>a</sup>
CIR6-M1	6	24514564	Cla97C06G122150	C/T	F:AGGGAGATTGTGAAGTAGAGAGCTT R:GGAATTTTCATATTTTCTTCCGAACT	<i>MseI</i>	345, 88/295, 50, 88
CIR6-M2	6	24590478	Cla97C06G122230	G/A	F:AGTGAACACAGGTGAGAATGCTAAT R:CATTTCATCTTGAAGTTCATTTTCC	<i>FokI</i>	184, 30/214
CIR6-M3	6	24620757	Cla97C06G122260	T/C	F:CTGAACCTTATCAATAGCTTTCCAA R:CTTGAGAATGCTGAGATTATCCATT	<i>Hpy188III</i>	140, 123/263
CIR6-M4	6	24687928	Cla97C06G122350	A/G	F:CTGAAGTCTTTAGGCACTGGACTAC R:TTAAACAAATGTCTTTGATGTCAGG	<i>MseI</i>	55, 162, 3/217, 3
CIR6-M5	6	24751036	Cla97C06G122390	T/C	F:ACAGTGACTGCTATATCCTTCCAAC R:CTAGATGGGAATCTCAAGGTATTCA	<i>RsaI</i>	87, 143/230
CIR6-M6	6	24810309	Cla97C06G122460	T/C	F:TCAGAACTGTAATGAACGAACCTAA R:TCGAAAGAATTTATGAGAACAGAGG	<i>DdeI</i>	22, 37, 123, 88/22, 37, 211
CIR6-M7	6	24838861	Cla97C06G122510	A/G	F:AGAACTCAACTTCATCATCTCCAAC R:TGAACGTAGATATTATGGGTTCGAT	<i>TaqI</i>	48, 103, 95, 23/48, 198, 23
CIR6-M8	6	24851621	Cla97C06G122540	G/A	F:GATCAATATCGAACCACAGTAATC R:GAGCAAATCATGTTCTCAATCTTTT	<i>AluI</i>	89, 140/229
CIR9-M1	9	1647313	Cla97C09G163980	G/A	F:CCTTCACAGTCTTCAAAGTAACACA R:CTCTTCGGTAATGATTTTGAGGATA	<i>HhaI</i>	96, 181/277
CIR9-M2	9	1771791	Cla97C09G164160	C/A	F:AAACCCAATACAATTTTTCATCAGA R:ATAACTGGAGTGTGAAGGCAATTAG	<i>MnII</i>	108, 46, 45/154, 45
CIR9-M3	9	1863987	Cla97C09G164320	T/G	F:CTAGTTTCTGCCTGTTTCAGAGATT R:TGATAGCAATCCTAAGATTTTCTCTG	<i>MluCI</i>	102, 43, 36, 61, 38/145, 36, 61, 38
CIR9-M4	9	1865138	Cla97C09G164320	T/C	F:GTGAAATATTGAGGCTTAGGAGTGA R:GTAACAGGATAACCAGATGTTGGAG	<i>MluCI</i>	143, 88/231
CIR9-M5	9	1919043	Cla97C09G164360	T/G	F:GCGACTCAAAAAGATGGAGATAATA R:CTTACCACCACTTACACATTCATCA	<i>ApoI</i>	87, 186/273
CIR9-M6	9	2135592	Cla97C09G164610	G/T	F:GTGCAGCTGTGCTATACTATTCTGA R:CATTCCCATACAGATCTCACTTTCT	<i>BclI</i>	160, 82/242
CIR9-M7	9	2263785	Cla97C09G164820	G/A	F:GCTGACATGATATCTGGTGATGTAG R:GTGATAACCTTGTCTCATCTTGGTAT	<i>AccI</i>	175, 97/272
CIR9-M8	9	3363590	Cla97C09G166230	G/A	F:TGATATGTCATCTTCAAAACAACCA R:GAAGAAACAAAGAATTGCCAGATAG	<i>DdeI</i>	164, 212/285
CIR9-M9	9	3714121	Cla97C09G166750	C/A	F:CAACAATTTTGTAGAAACCAATGGAG R:TTTGGCTAAGAGGAAGGTTTACTT	<i>AccI</i>	142, 103/245
CIR9-M10	9	3759192	Cla97C09G166820	T/G	F:CCATTCTTCCCTCTTTTAAACCT R:CCTTAGTGTAAGAAATCAACGGAATC	<i>TaqI</i>	63, 206/63, 60, 146
CIR9-M11	9	3834373	Cla97C09G166910	T/C	F:GATCATGGTTCATTTCTCATCTAC R:TTATTATCACGGAGAAAAGTTCTGG	<i>HinfI</i>	189/78, 111
CIR9-M12	9	3876768	Cla97C09G166950	T/C	F:TGCGTAGCTACCAAAATTACTAAATG R:ATTTGTTGCACCAAGGATAAGAAT	<i>HincII</i>	285/150, 135
CIR9-M13	9	3905300	Cla97C09G166980	C/T	F:TGAAATTCAACCTGAAGTAAAAGAA R:AGAGTAAAAATTGCTGTAGGTGCTG	<i>TaqI</i>	117, 89, 58/206, 58
CIR10-M1	10	29440068	Cla97C10G199470	G/T	F:AGAGGACTGCAAGTTACAAGCTGTT R:GAAGTTTCCTCTGACAGCTGATTTC	<i>HinfI</i>	350/131, 219
CIR10-M2	10	29447001	Cla97C10G199480	T/C	F:AGTTGATGAATTTGTAGCAGGTGGT R:TACCCAAATCCTGGACTACTGTCTC	<i>HaeIII</i>	350/148, 202
CIR10-M3	10	29476855	Cla97C10G199500	G/A	F:CTCATTGCATGGTAATCTTCATTTGGT R:GGGATTAAGCTGTACAAACATGACC	<i>Hpy188I</i>	61, 137, 170/61, 307
CIR10-M4	10	29548144	Cla97C10G199570	A/T	F:TAGAGACGGATCATGAGCAATGTAA R:AAGATCAACCTCAACAAAAGTCACC	<i>MboII</i>	72, 64, 55, 147/71, 64, 202
CIR10-M5	10	29676339	Cla97C10G199740	T/C	F:CGGAACCTCTATAATTTCAACGCAAA R:CATGGAAAGATGTGAGCAATGGTATT	<i>AccI</i>	262/72, 190

<sup>a</sup>D, donor parent (DRD); R, recurrent parents (SBA and 45NC)