

Table S1. Genome coverage of substituted segments in the DHMAS-K343 CSSLs.

S. No.	Chromosome no.	Chromosomal length observed (cM)	Effective Coverage length (cM)	Coverage rate (%)
1	1	2.2506	0.56	24.88
2	2	12.3537	3.27	26.47
3	3	1.1087	0.55	50.00
5	5	31.3509	16.47	52.53
6	6	10.1317	4.56	45.00
7	7	3.4257	0.56	16.37
8	8	3.4257	1.74	50.14
9	9	25.0756	12.09	48.12
11	11	3.1475	1.57	49.88
12	12	7.4695	3.73	49.90
Average				41.33

Table S2. Genome Coverage of Substituted segments in RML22-K343 CSSLs.

S. No.	Chromosome no.	Chromosomal length (cM)	Effective Coverage length (cM)	Coverage rate (%)
1	1	2.2506	0.56	24.88
2	2	12.3537	7.28	58.94
4	4	2.2659	1.11	48.67
5	5	31.3509	4.71	15.02
6	6	10.1317	0.57	5.62
7	7	3.4257	0.53	15.49
8	8	3.4257	1.96	56.48
9	9	25.0756	5.89	23.49
12	12	7.4695	3.76	50.40
Average			2.92	33.22