Additional File 7: Statistics of consensus map by chromosome.

Map features were calculated for the whole dataset and various subsets obtained by removing selected groups of loci while maintaining the locus order of the consensus map.

	1H	2H	3H	4H	5H	6H	7H	Genome
Number of loci								
All	423	522	470	278	379	362	501	2,935
DArT	301	362	361	148	270	270	373	2,085
'bPb' DArT	212	276	255	91	213	219	280	1,546
Others	122	160	109	130	109	92	128	850
Number of bins[a]								
All	225	298	246	162	241	191	266	1,629
DArT	154	206	190	82	169	140	189	1,130
'bPb' DArT	130	178	158	58	143	127	165	959
Others	81	108	73	92	82	66	92	594
Average/median inter-bin distance (cM)[a]								
All	0.7/0.3	0.6/0.3	0.8/0.3	0.9/0.4	0.8/0.5	0.8/0.3	0.6/0.3	0.7/0.3
DArT	1.0/0.4	0.8/0.3	1.0/0.3	1.8/1.0	1.2/0.6	1.1/0.4	0.9/0.3	1.0/0.4
'bPb' DArT	1.2/0.4	0.9/0.4	1.7/0.3	2.4/1.3	1.4/0.7	1.2/0.4	1.0/0.3	1.2/0.4
Others	1.9/1.3	1.5/1.0	2.5/2.0	1.5/1.0	2.4/1.9	2.1/1.4	1.8/1.1	1.9/1.3
Map length (cM)								
All	151.9	166.7	184.6	148.6	194.2	147.1	165.4	1,159
DArT	151.1	164.9	184.6	148.6	193.2	147.1	165.0	1,155
'bPb' DArT	148.1	161.6	183.6	137.4	193.2	147.1	165.0	1,136
Others	151.9	163.3	180.0	132.3	193.5	137.5	164.4	1,123

[a] Segregation signatures were concatenated across populations and co-segregating loci were collapsed into bins (unique loci) based on a minimum of 50 overlapping genotype calls (see *Methods* section entitled "Construction of component maps").