popName	GABI	IBM	WHEAT
mappingPanelType	DH	IRIL	RIL
parents	P1-P2	P1-P2	P1-P2
nbSelfingGenerationsRils	6	6	6
nbIntermatingGenerations	4	4	4
nuGamma	3	3	3
maxPercentGenot	90	90	90
quantThresHetMend	70	70	95
quantThresMissMend	70	70	95
minMafMend	0.15	0.05	0
analyzeMarkersWithoutHetero	TRUE	TRUE	TRUE
quantThresHetCand	93	93	93
quantThresMissCand	95	95	95
minNbMrkPerTarget	2	2	2
maxGenDistToFusePeaks	10	10	10
winSizeToFitPeakShape	40	40	40
minSlopePeak	-0.05	-0.05	-0.05
toleranceFreq	0.05	0.05	0.05
minR2peak	0.7	0.7	0.7
simulateProfiles	TRUE	TRUE	TRUE
plotCNVstrong	TRUE	TRUE	TRUE
plotCNVweak	TRUE	TRUE	TRUE
plotUnclassified	TRUE	TRUE	TRUE
plotSingleLocus	FALSE	FALSE	FALSE
Markers_Before_Filtering	13160	20913	83721
Individuals_Before_Filtering	625	239	406
Markers_Remaining_After_Filtering	12061	20824	83598
Individuals_Remaining_After_Filtering	625	239	406
Max_Num_Indiv_H_for_Mend	0	3	16
Max_Num_Indiv_M_for_Mend	2	3	9
Min_Num_Indiv_H_for_Cand	6	9	15
Min_Num_Indiv_M_for_Cand	86	9	9
Candidate_Markers	746	938	10754
Mendelian_Markers	10872	16420	72844
Non-Mendelian_Non-Candidate_Markers	443	3466	0
A/B	52	122	667
A/B|Ah	44	0	1176
A/B|Am	179	271	99
A/B|Bh	44	0	784
A/B|Bm	170	122	81
A/B_A/-	16	3	12
A/B_A/-|Hm	1	10	0
A/B_A/-|HmHb	7	30	68
A/B_-/A	21	0	3
A/B_-/A|Hm	0	0	0
A/B_-/A|HmHb	12	30	59
A/B_B/-	20	0	17
A/B_B/-|Hm	0	0	0
A/B_B/-|HmHa	14	23	80
A/B_-/B	19	14	15
A/B_-/B|Hm	0	8	0
A/B_-/B|HmHa	9	32	71
A/B_-/A_-/A	0	0	5
A/B_A/-_A/-	0	0	1
A/B_-/B_-/B	3	1	0
A/B_B/-_B/-	0	0	9
A/B_-/A_A/-	0	0	0
A/B_A/-_-/A	1	0	16

A/B_-/A_-/B	0	0	
A/B_-/B_-/A	1	0	
A/B_-/A_B/-	0	0	
A/B_B/-_-/A	0	0	
A/B_A/-_-/B	0	0	
A/B_-/B_A/-	0	0	
A/B_A/-_B/-	0	0	
A/B_B/-_A/-	0	0	
A/B_-/B_B/-	0	0	
A/B_B/-_-/B	0	0	19
No_profile	2	260	6163
Unknown	131	12	1409

Table S1. Detailed statistics of the three populations GABI, IBM, and WHEAT

Data as provided in the file with suffix "_CNV_Stats" generated by the software. From top to bottom, the four sections (separated by horizontal lines) are: (1) characteristics of the populations analyzed, (2) parameters for data filtering and CNV detection. All lines of these two sections are the arguments of the function CNVdetect (descriptions of each parameter are available by typing "? CNVdetect" in R after installing and loading the package CMVmap), (3) numbers of markers and individuals before and after data filtering, and number of candidates considered by the software for CNV detection, based on their anomalously high number of heterozygote or missing data calls. Thresholds for theses numbers are given as Max_Num_Indiv_H_for_Cand and Max_Num_Indiv_M_for_Cand, respectively. Markers having more than Max_Num_Indiv_H_for_Mend heterozygote calls or more than Max_Num_Indiv_M_for_Mend missing data calls were automatically removed from the analysis to improve quality of the profiles, and (4) number of events detected for each possible category. Each category is encoded as a string of 1 to 3 groups of 3 characters each, separated by an underscore. The first group is always encoded "A/B" and indicates the reference locus, located at the position where the candidate marker was initially mapped. Further groups indicate other copies of the region targeted by the candidate marker. For all groups (loci), the letters just before and just after the slash represent respectively the haplotypes of the first parent (alleles denoted "A"), and of the second parent (alleles denoted "B").