A Plot: 1 Event 1 Chr 1A Type: A/B_−/A_−/A Marker 107 cfn0966629   AAA:203 AHA:1 A−A:0 BBB:41 BHB:148 B−B:12

B Plot: 2 SIMULATION Event 2 Chr 1A Type: A/B_−/A_−/A Marker 107 cfn0966629   AAA:194 AHA:3 A−A:0 BBB:42 BHB:164 B−B:0

C Plot: 5 Event 3 Chr 2B Type: A/B_A/−_−/A Marker 2319 cfn0613668   AAA:196 AHA:5 A−A:1 BBB:52 BHB:149 B−B:2

D Plot: 6 SIMULATION Event 4 Chr 2B Type: A/B_A/−_−/A Marker 2319 cfn0613668   AAA:195 AHA:0 A−A:0 BBB:43 BHB:155 B−B:0

E Plot: 7 Event 4 Chr 6A Type: A/B_A/−_A/− Marker 7516 cfn0832458   AAA:167 AHA:2 A−A:1 BBB:10 BHB:213 B−B:6

F Plot: 8 SIMULATION Event 5 Chr 6A Type: A/B_A/−_A/− Marker 7516 cfn0832458   AAA:188 AHA:1 A−A:0 BBB:40 BHB:161 B−B:0

G Plot: 9 Event 5 Chr 4B Type: A/B_B/−_−/B Marker 4661 cfn2431308   AAA:41 AHA:163 A−A:4 BBB:195 BHB:0 B−B:1

H Plot: 10 SIMULATION Event 6 Chr 4B Type: A/B_B/−_−/B Marker 4661 cfn2431308   AAA:55 AHA:124 A−A:0 BBB:218 BHB:2 B−B:0

I Plot: 11 Event 6 Chr 4A Type: A/B_B/−_B/− Marker 3860 cfn0742796   AAA:49 AHA:159 A−A:3 BBB:193 BHB:1 B−B:0

J Plot: 12 SIMULATION Event 7 Chr 4A Type: A/B_B/−_B/− Marker 3860 cfn0742796   AAA:69 AHA:137 A−A:0 BBB:187 BHB:3 B−B:0

Supplementary Figure S2. Examples of allele frequency profiles for each type of three-locus events found in wheat

Data are from the wheat RIL population WHEAT. The type of event is indicated in the header of each panel. Each type is encoded using the same conventions as for 1:2 CNVs (e.g., A/B_-/A_-/A for panel A) and is as follows: the encoding uses a string of 3 groups of 3 characters each, separated by an underscore. The first group is always "A/B" and indicates the reference locus, located at the position where the candidate marker was initially mapped. The two other groups indicate the two other copies of the regions 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, and of the second parent. Panels A, C, E, G, I show experimental data. Panels B, D, F, H, J show simulation results reproducing the CNV situation inferred from A, C, E, G, and I respectively (see text). The allele of parent 1 is called "A", the allele of parent 2 is called "B", heterozygotes are called "H", and missing data are called "-". Each curve shows the frequency of the allele "A" along the genome (X-axis indicates cumulated genetic positions), when considering different subsets of individuals of the population as follows: pink dots and curve for individuals (denoted "AHA") genotyped "H" at the candidate marker and "A" on both non-candidate flanking markers indicating the allelic context of the region, and similarly cyan for "BHB" individuals, red for "AAA" individuals, dark blue for "BBB" individuals. Curves generated by the software for classes based on missing data (light grey for "A-A" individuals, and black for "B-B" individuals) were hidden here for better clarity of the profiles. Hatched rectangles indicate the estimated confidence intervals on the position of the detected loci involved in the event. They are black for the reference locus (see text), and red or green for the two secondary loci. Dots represent values of individual markers and associated curves show the result of the smoothing procedure used to detect the peaks. Lastly, the black dashed line indicates the frequency of "A" allele based on all individuals of the population. The name of the candidate (non-Mendelian) marker considered is given in the header of each panel, as well as numbers of individuals counted for each three-locus genotype class.