Supplementary Figure S3. Examples of allele frequency profiles showing different situations where no CNV was identified by the software

Data are from the Maize doubled-haploid population GABI. Panel A shows a typical allelic profile when the candidate marker is not duplicated, so there are no peaks other than those in the reference locus. Panels B and C clearly indicate that there is a second locus involved, but the peak signature does not correspond to any case classified in the software. Panel D (respectively E) clearly indicate that there are two (respectively three) loci in addition to the reference locus, but the peak signature does not correspond to any classified case in the software. 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, dark blue for "BBB" individuals, red for "AAA" individuals, grey for "A-A" individuals, and black for "B-B" individuals. 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.