Table S1 Founder distribution patterns used for triplets in simulation. The variance class of pairs of markers in the order X-Y, Y-Z, X-Z is given by Class.

	Low			Medium			High		
	X	Y	Z	X	Y	Z	X	Y	Z
A	1	1	1	1	1	1	1	1	1
B	1	1	1	1	0	1	0	1	0
C	0	0	0	1	0	1	1	1	1
D	0	0	0	0	1	0	1	0	1
Class	1	1	1	3	3	2	4	4	2

Table S2 Marker sequences aligned to the 3B pseudomolecule. One sheet is included for each of the four cases considered during alignment: either zero (suffix .s0) or one (suffix .s1) substitutions allowed per 100 bp, and either the given allele in the marker sequence or an alternate sequence substituting the second allelic base at the SNP location (suffix AltAllele). Table S2 is available for download as an Excel file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.167577/-/DC1

In each sheet, columns are:

Marker: the original marker sequence name; if the alternative allelic base is used then the marker name is suffixed with _S

Sense: if 0 then the marker aligns sense to the target; if 16 then the marker aligns reverse complemented to the target.

TargetLoci: Phyisical position at which alignment starts for the marker sequence

MarkerLen: marker sequence length

MarkerSequence: marker sequence

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Files S1-S3

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.167577/-/DC1

File S1 Simulation script in R

File S2 Genotypes for wheat parents and RILs from a four-parent MAGIC

File S3 R script to perform the uncertainty analysis of the included Chr 3B data