Global selection on sucrose synthase haplotypes during a century of wheat breeding

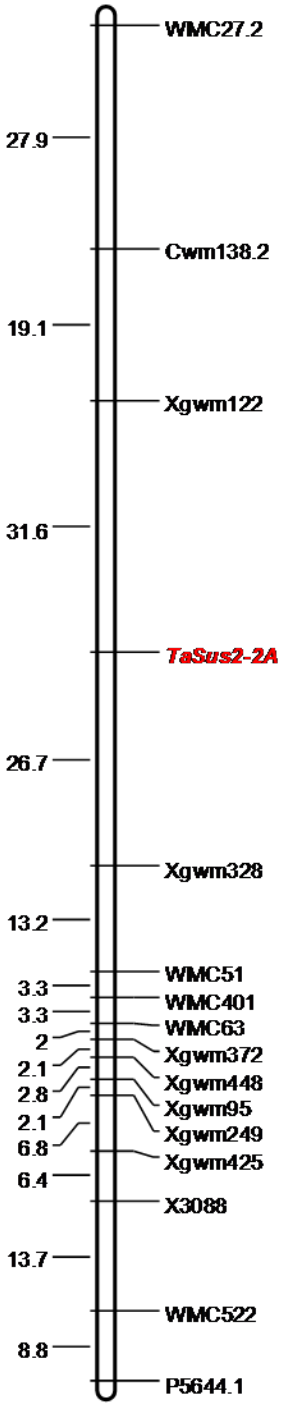


Figure S1 *TaSus2-2A* was mapped on 2AS flanked by SSR markers X*gwm*122 and X*gwm* 328 in DH population derived from Hanxuan 10 × Lumai 14.

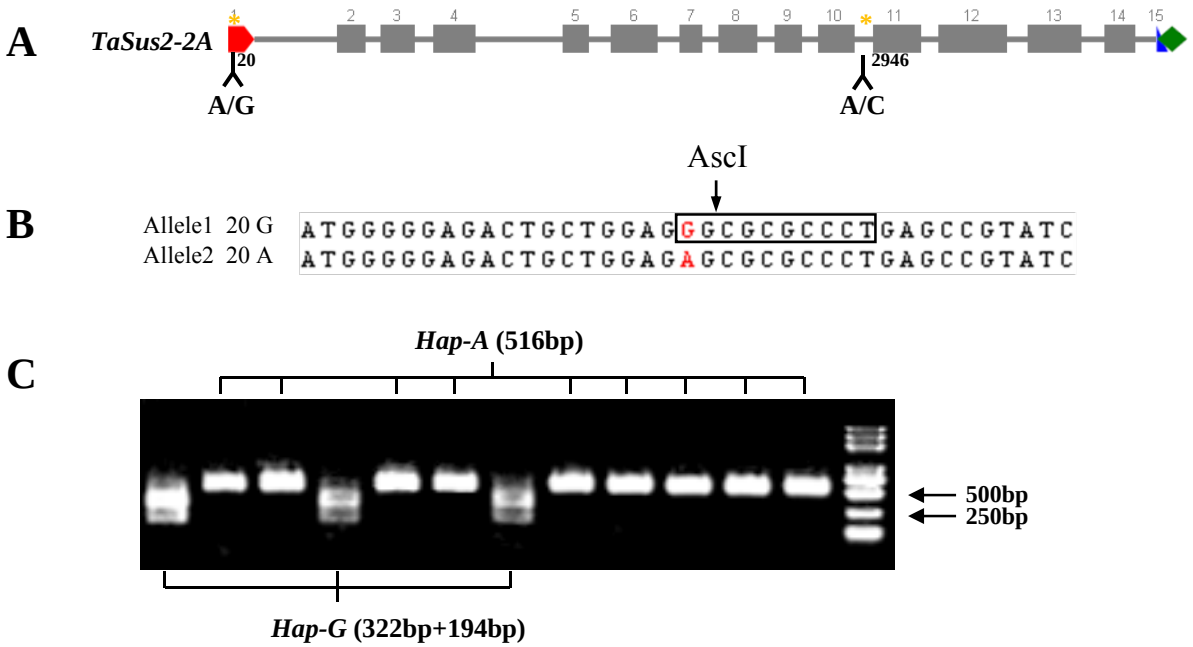
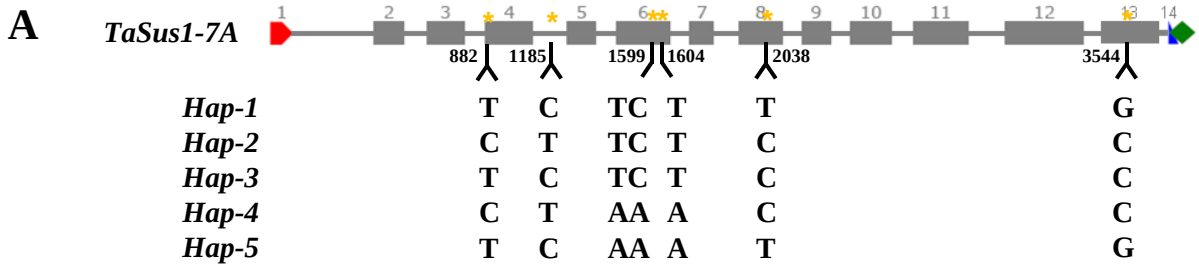
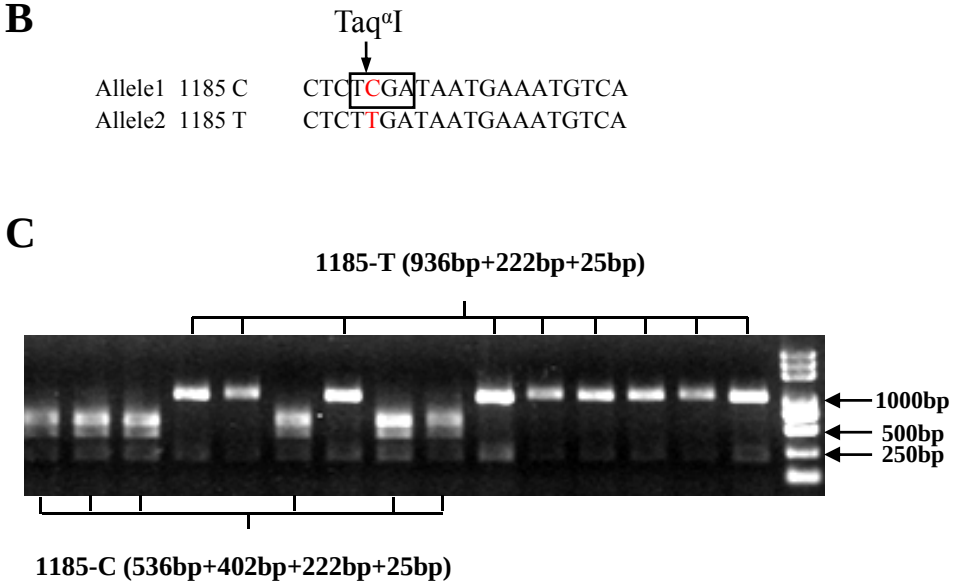
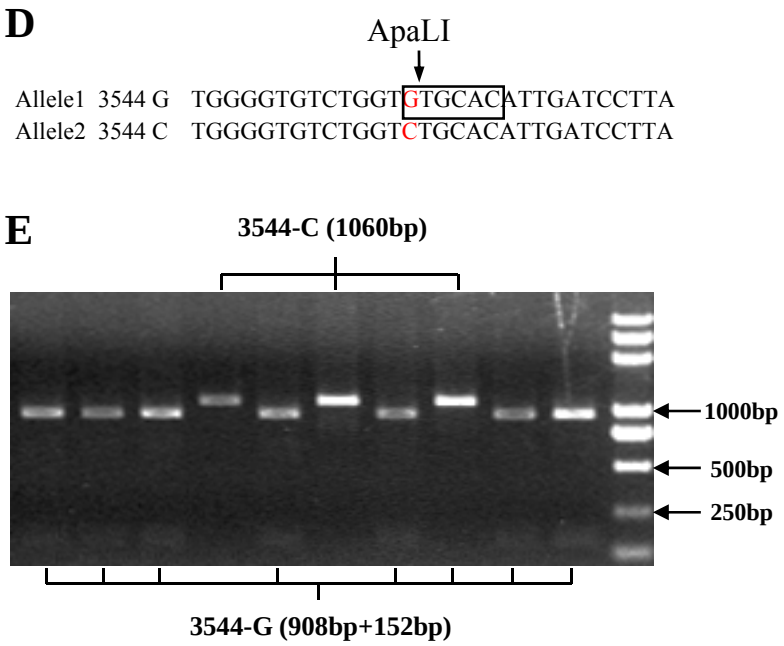


Figure S2 Polymorphisms and marker development at *TaSus2-2A*. (A) Coding region of *TaSus2-2A*, the rectangles represented exons (the red one represented the first exon) and the lines represented introns. Two SNPs at 20 and 2946 bp were labeled below. (B) The polymorphism site at 20 bp between different haplotypes. The rectangle and the arrow represented the recognition and digestion site of restriction endonuclease AscI. (C) PCR products amplified by different haplotypes after digestion.


A
TaSus1-7A
1
2
3
4
5
6
7
8
9
10
11
12
13
14
882
1185
1599
1604
2038
3544
Hap-1 T C TC T T G
Hap-2 C T TC T C C
Hap-3 T C TC T C C
Hap-4 C T AA A C C
Hap-5 T C AA A T G


B
TaqαI
Allele1 1185 C CTCTCGATAATGAAATGTCA
Allele2 1185 T CTCTTGATAATGAAATGTCA
C
1185-T (936bp+222bp+25bp)
1000bp
500bp
250bp
1185-C (536bp+402bp+222bp+25bp)


D
ApaLI
Allele1 3544 G TGGGGTGTCTGGTGTGCACATTGATCCTTA
Allele2 3544 C TGGGGTGTCTGGTCTGCACATTGATCCTTA
E
3544-C (1060bp)
1000bp
500bp
250bp
3544-G (908bp+152bp)

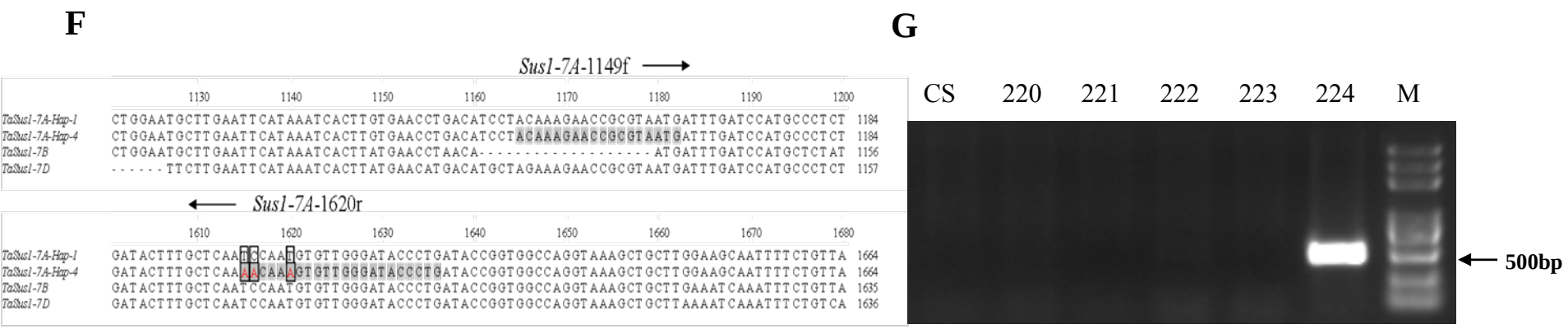


Figure S3 Polymorphisms and marker developments at *TaSus1-7A*. (A) Coding region of *TaSus1-7A*. Seven SNPs at 822, 1185, 1599, 1600, 1604, 2038 and 3544 bp were labeled below, which formed five haplotypes. (B) The polymorphism site at 1185 bp between different haplotypes. The rectangle and the arrow represented the recognition and digestion site of restriction endonuclease Taq$^{\alpha}$I. (C) PCR products amplified by primer pair *Sus1-7A*-539f and *Sus1-7A*-1720r between different haplotypes after digestion at 1185 bp. (D) The polymorphism site at 3544 bp between different haplotypes. The rectangle and the arrow represented the recognition and digestion site of restriction endonuclease ApaLI. (E) PCR products amplified by primer pair *Sus1-7A*-2636f and *Sus1-7A*-3696r between different haplotypes after digestion at 3544 bp. (F) Sequences alignment (part) among *TaSus1-7A-Hap-1*, *TaSus1-7A-Hap-4*, *TaSus1-7B* and *TaSus1-7D*. Genome-specific primer *Sus1-7A*-1620r was development based on the polymorphism sites at *TaSus1-7A-Hap-4*. (G) PCR product amplified by primer pair *Sus1-7A-1149f* and *Sus1-7A-1620r*. Only DNA from *Hap-4* (224) or *Hap-5* could be amplified.

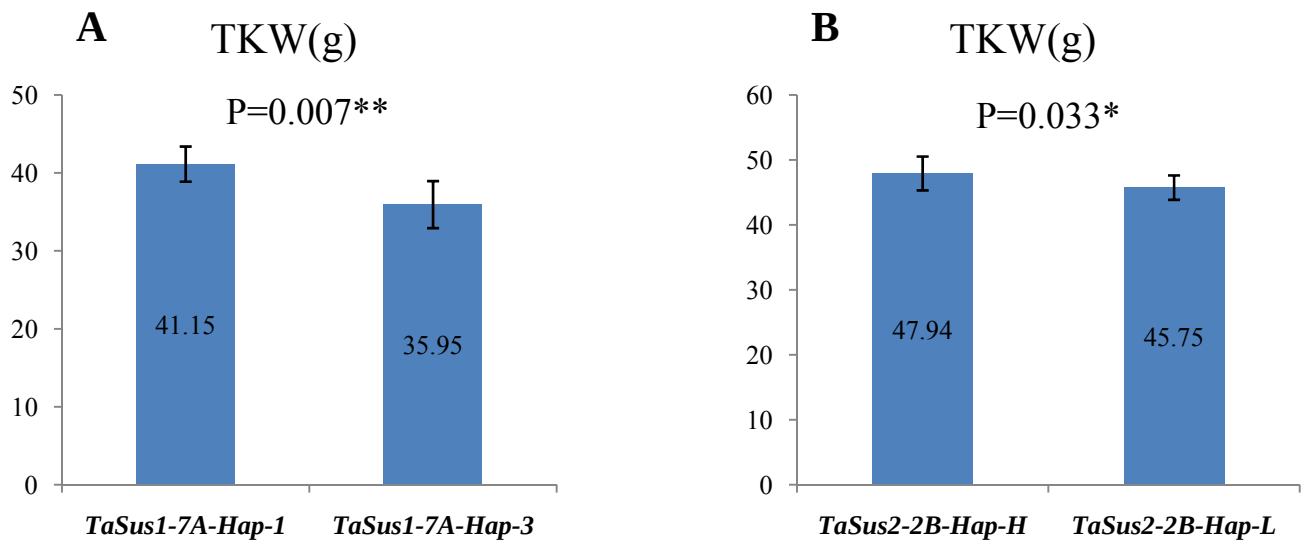


Figure S4 Difference of TKW in two NIL lines in 2012 yield trial plot. (A) NILs derived from BC_3F_6 of Youzitou / Zhengmai 366*4. The mean TKW of *TaSus1-7A-Hap-1* (41.15g) is significantly higher than that of *TaSus1-7A-Hap-3* (35.95g). (B) NILs derived from BC_3F_2 of Shijiazhuang8 / Shi4185*4. The mean TKW of *TaSus2-2B-Hap-H* (47.94g) is significantly higher than that of *TaSus2-2B-Hap-L* (45.75g).

Table S5 F_{ST} between different populations and the corresponding P value at *TaSus1-7A*

Pairwise difference between populations (F_{ST})

	DI	TE	LA	MV
DI	0			
TE	0.542	0		
LA	0.946	0.462	0	
MV	0.907	0.319	0.050	0

F_{ST} P value

	DI	TE	LA	MV
DI				
TE	0.000*			
LA	0.000*	0.000*		
MV	0.000*	0.000*	0.009*	

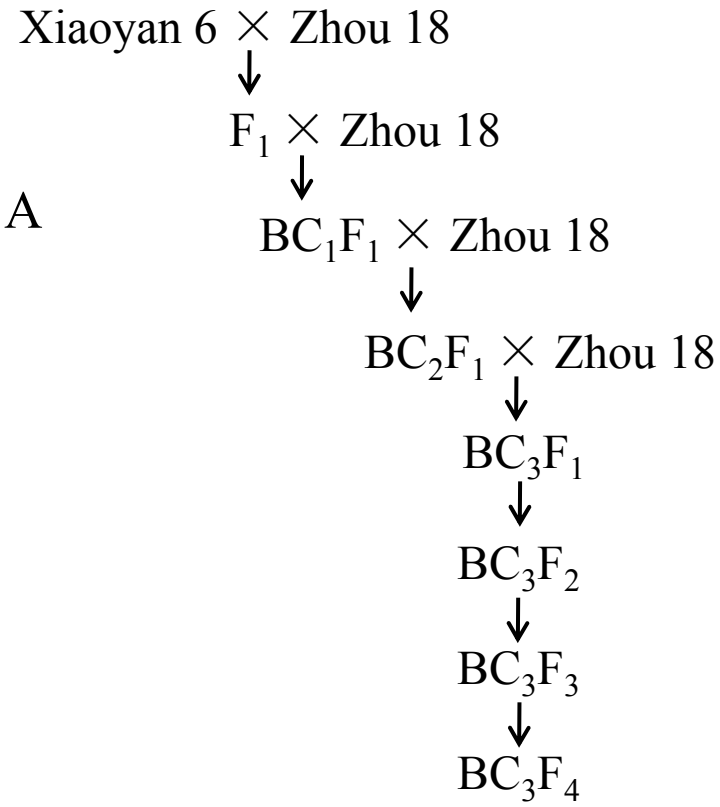
	DS	DM	LA	MV
DS	0			
DM	-0.096	0		
LA	0.899	0.516	0	
MV	0.772	0.368	0.050	0

	DS	DM	LA	MV
DS				
DM	0.459			
LA	0.009*	0.000*		
MV	0.000*	0.000*	0.009*	

DI diploid accessions, TE tetraploid accessions, LA landraces in MCC, MV Chinese modern varieties in MCC, DS *T. dicoccoides*, DM other tetraploid accessions (Supplementary Table S2). *P < 0.05

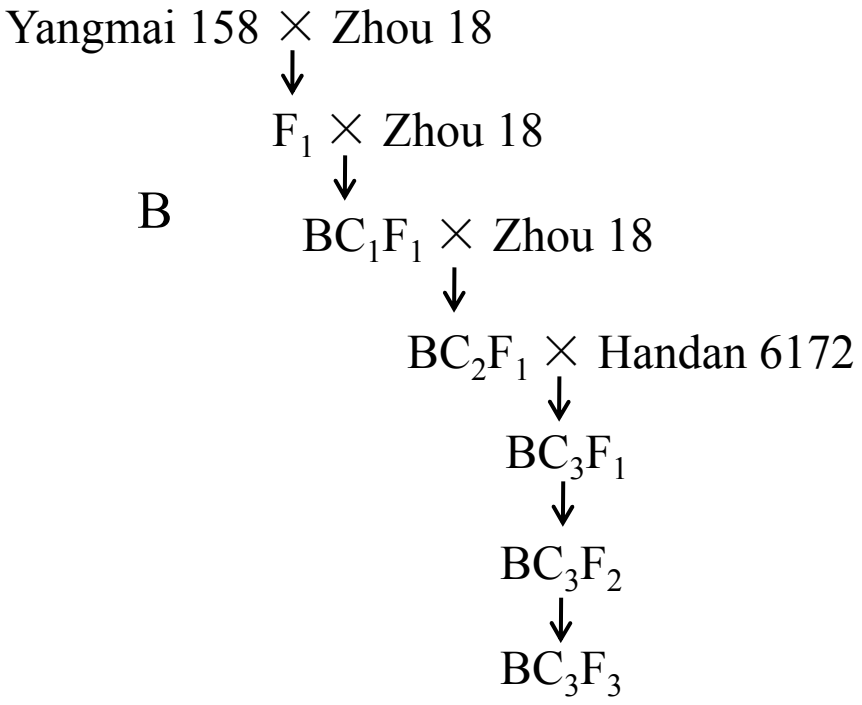
Table S6h Accessions of hexaploid wheats used in this study (NILs)

A



BC_3F_4 population of Xiaoyan 6 / Zou 18*4

B



F3 population of

Yangmai 158 / Zhou 18*3 // Handan 6172

Other three NILs (BC_3F_3 population of Isengrain / Yanzhan 4110*4, BC_3F_6 of Youzitou / Zhengmai 366*4, BC_3F_2 of Shijiazhuang8 / Shi4185*4) followed as A