Figure S1

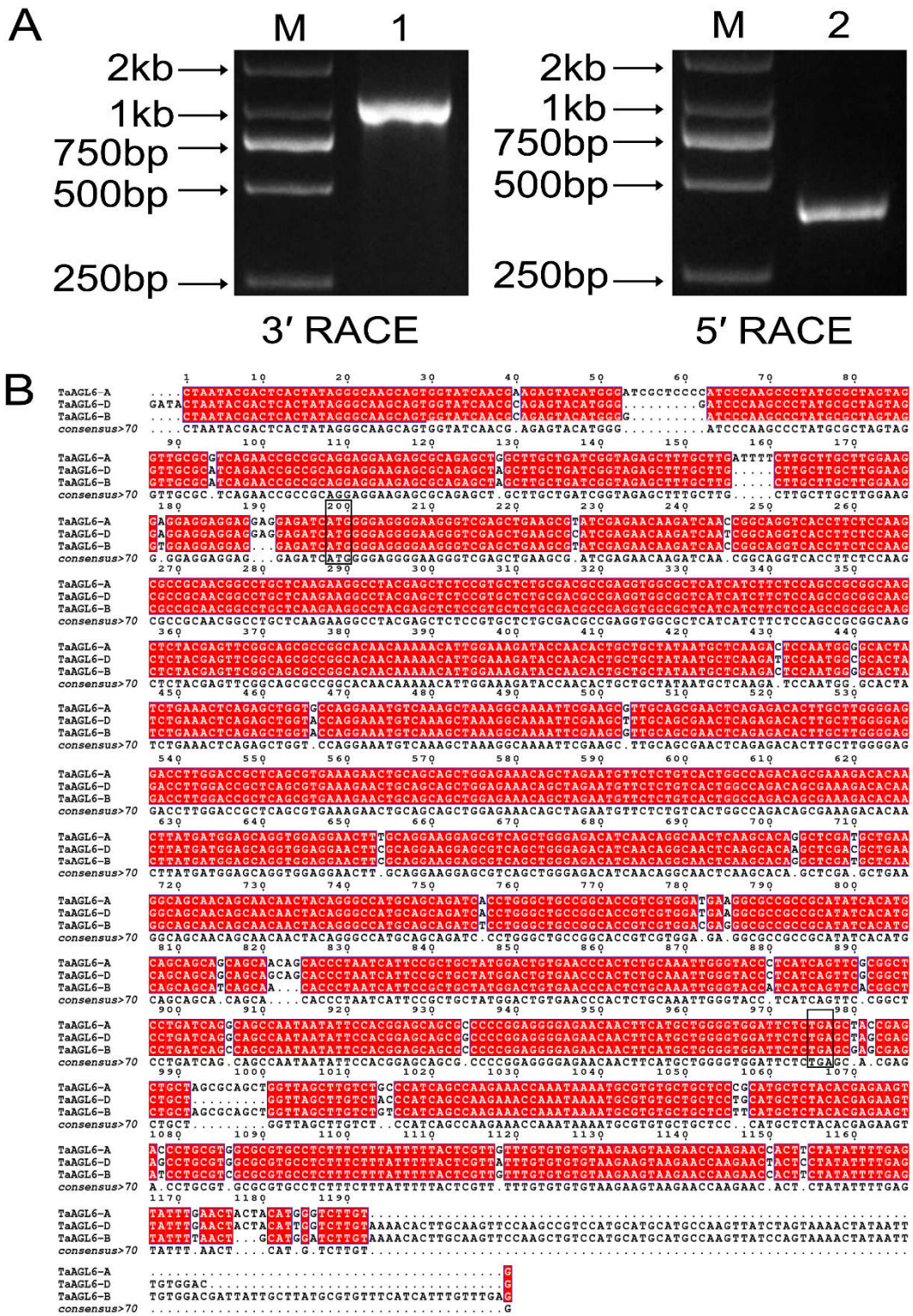
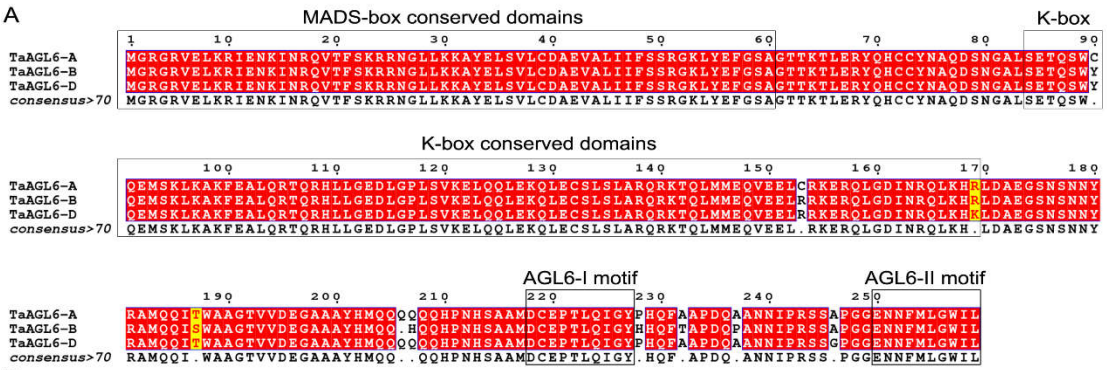


Fig. S1 Full cDNAs of *TaAGL6* genes.

(A) Results of RACE. (B) Alignment of *TaAGL6* full cDNAs. Rectangular boxes indicate the start and stop codons, respectively.

Figure S2

A



B

Variant	PROVEAN score	Prediction(cutoff=-2.5)
C90Y	6.431	Neutral
C153R	7.056	Neutral
Q206H	-0.219	Neutral
Q207del	0.379	Neutral
P228H	1.914	Neutral
A232T	-0.297	Neutral
A237P	-0.575	Neutral

C

Variant	PROVEAN score	Prediction(cutoff=-2.5)
C90Y	6.431	Neutral
C153R	7.056	Neutral
A246G	-0.842	Neutral

Fig. S2 Protein sequence and the effect of SNPs.

(A) Multiple allignment of TaAGL6 proteins. Rectangular boxes indicated MADS-box, K domains, AGL6 motifs I and II, respectively. (B and C) The effect of SNPs to the protein functions. Default threshold is -2.5, that is: The variant with a score equal to or below -2.5 is considered "deleterious," the variants with a score above -2.5 are considered "neutral."

Figure S3

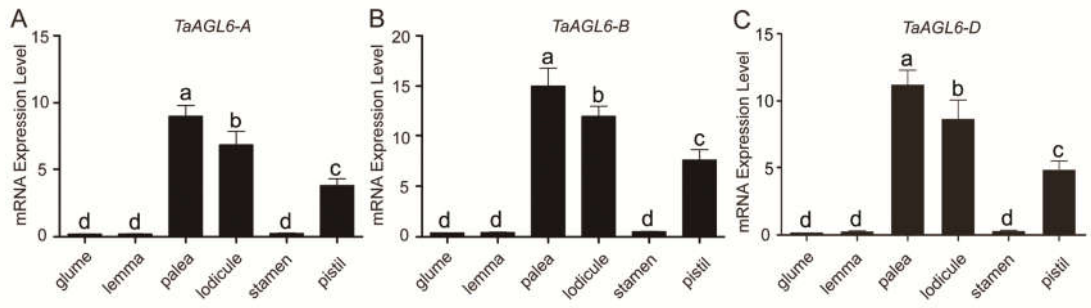


Fig. S3 The expression of *TaAGL6-A* (A), *TaAGL6-B* (B) and *TaAGL6-D* (C) in different floral organs.

Mean and SD values were obtained from three replications. Different letters indicate a significant difference ($P < 0.05$ by Student's *t* test).

Figure S4

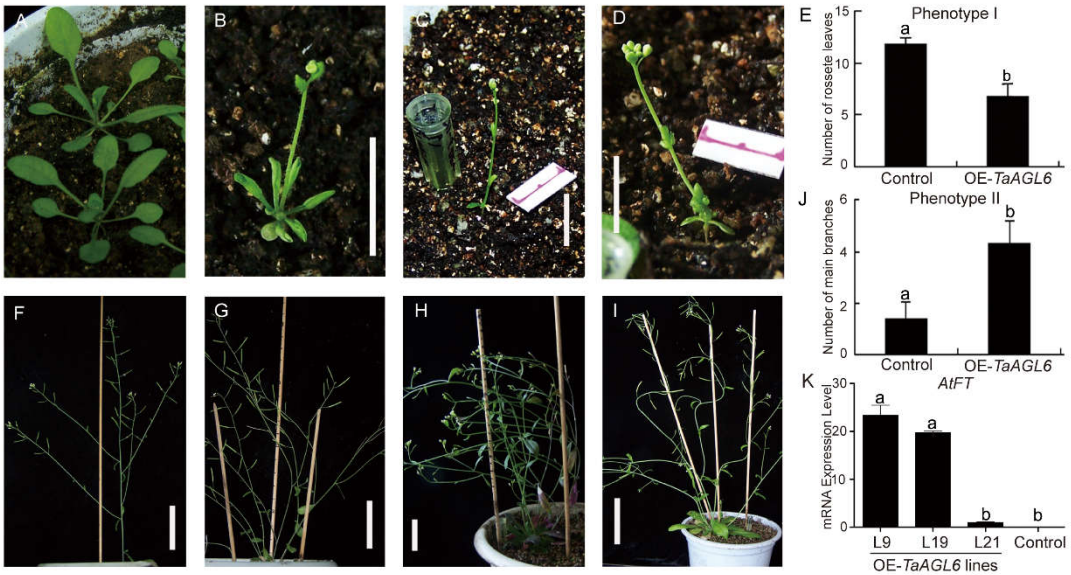


Fig.S4 Phenotypes of transgenic *Arabidopsis* over-expressing *TaAGL6* genes

(A-D) Four-week plants of wild type (A) and transgenic *Arabidopsis* overexpressing *TaAGL6-A* (B), *TaAGL6-B* (C), and *TaAGL6-D* (D) to show the early flowering phenotype of transgenic lines. (E) The number of rosette leaves in the control and in transgenic line overexpression *TaAGL6-B* at flowering time. (F-I) Wild type (F), transgenic *Arabidopsis* overexpressing *TaAGL6-A* (G), *TaAGL6-B* (H), and *TaAGL6-D* (I) to show the multi-shoot phenotypes. (J) The number of main stems in the control and transgenic *Arabidopsis* overexpressing *TaAGL6-B*. (K) The expression level of *AtFT* in different transgenic lines. Bars = 1cm in A to D, F to I. In E and J, mean and SD values were obtained from 30 replications (n=30), and letters a and b indicated the significant difference between the control and transgenic plants according to Student's *t*-test (P<0.05). Mean and SD values in K were obtained from three replications, and different letters in K indicated a significant difference ($P < 0.05$ by Student's *t* test).

Figure S5

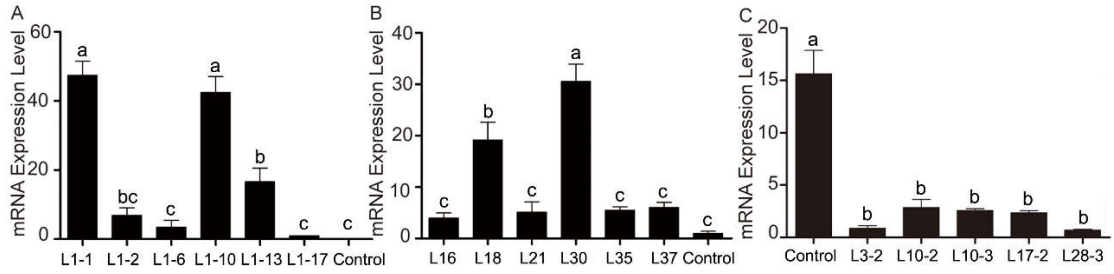


Fig. S5 The expression of *TaAGL6* genes in transgenic *Arabidopsis* (A), transgenic wheat (B) overexpressing *TaAGL6-B*, and *TaAGL6* RNAi wheat (C).

Mean and SD values were obtained from three replications, and different letters indicated significant differences ($P < 0.05$ by Student's *t* test).

Figure S6

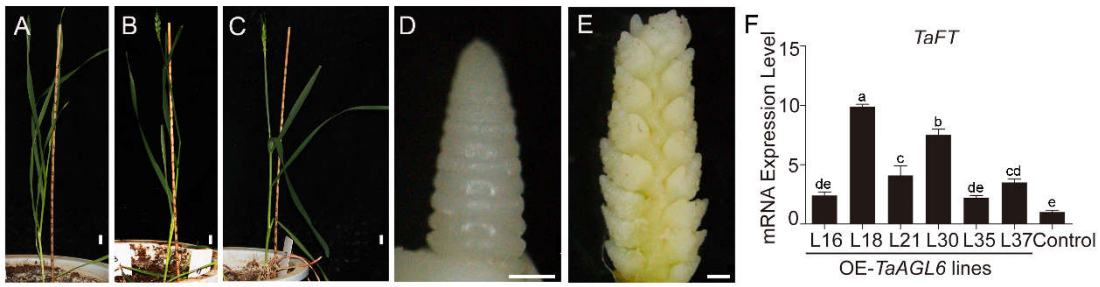


Fig. S6 Phenotype of transgenic wheat over-expressing *TaAGL6-B*.

(A-C) One plant of control (A) and transgenic Line 11 (B) and Line 18 (C) photographed at the same time. (D and E) One inflorescence of control (D) and one inforescence of transgenic plants (E) collected at the same time. (F) The expression of *TaFT* in different transgenic lines at vegetative stage. Bars = 1cm in A-C, 50μm in D and E. Mean and SD values in F were obtained from three replications, and different letters in F indicated a significant difference ($P < 0.05$ by Student's *t* test).

Figure S7

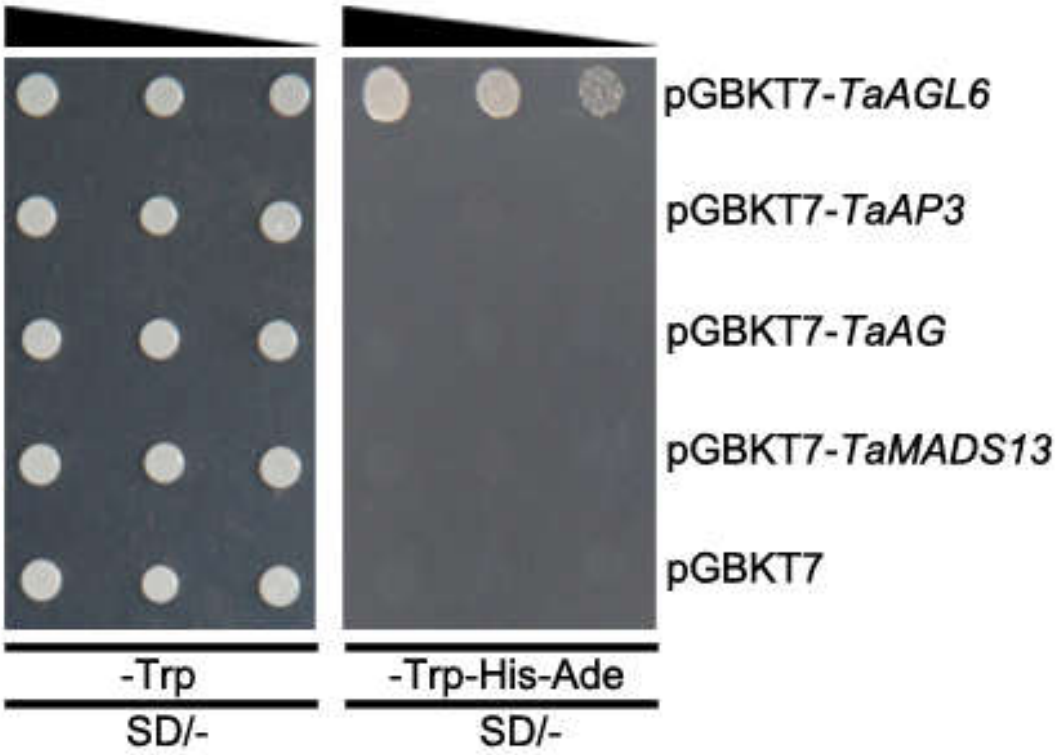


Fig. S7 Self-activation assays of TaAGL6, TaAP3, TaAG, and TaMADS13.

Figure S8

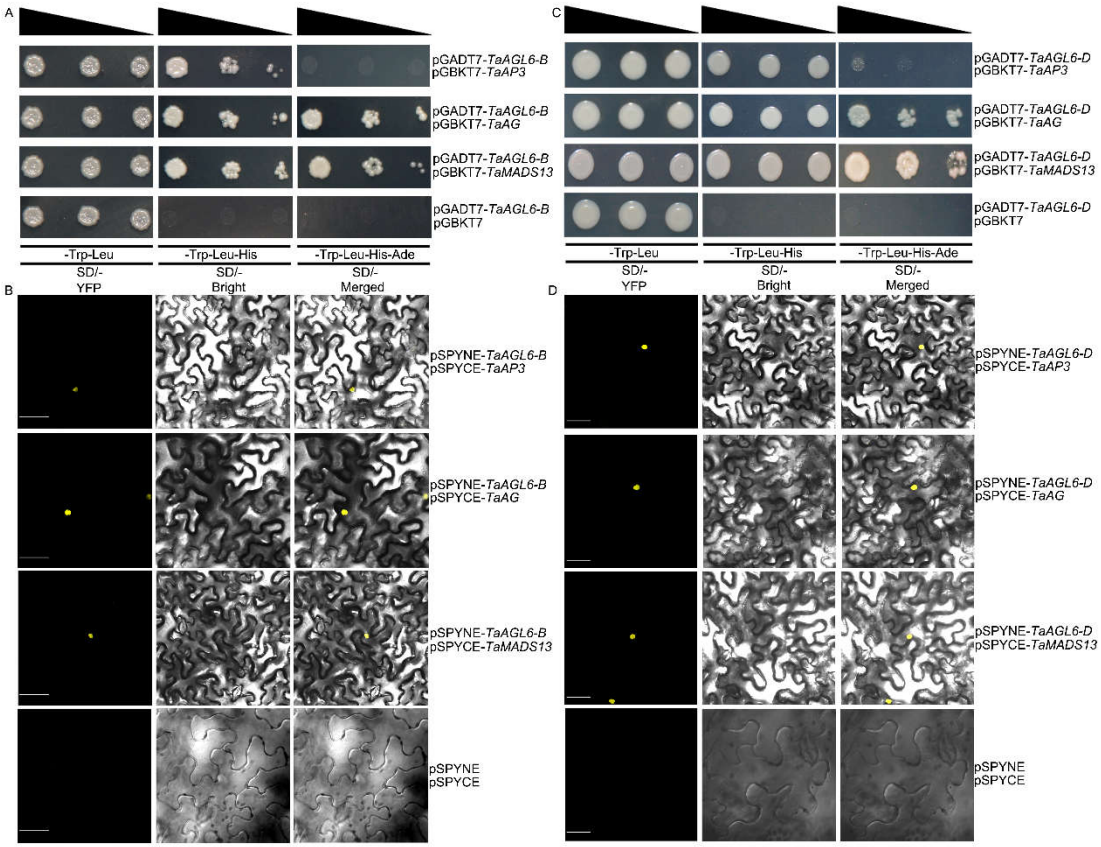


Fig. S8 Interactions between TaAGL6-B/TaAGL6-D and TaAP3, TaAG, TaMADS13. (A and B) Interactions between TaAGL6-B and TaAP3, TaAG, TaMADS13 in yeast cells (A), and tobacco leaf cells (B). (C and D) Interactions between TaAGL6-D and TaAP3, TaAG, TaMADS13 in yeast cells (C), and tobacco leaf cells (D). In B and D, left, YFP; middle, Bright; right, Merged.

Figure S9

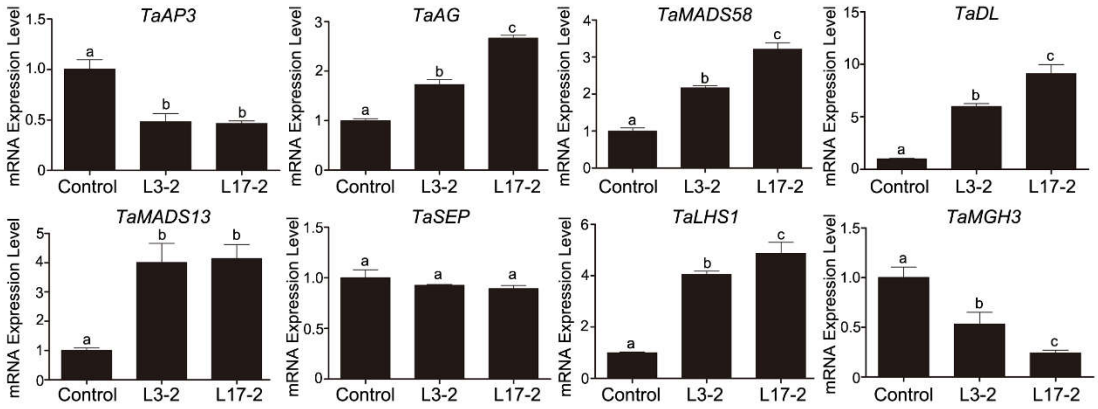


Fig. S9 The expression of wheat floral genes and *TaMGH3* in wild type and *TaAGL6* RNAi stamens.

Mean and SD values in were obtained from three replications, and different letters indicated significant differences ($P < 0.05$ by Student's *t* test).

Figure S10

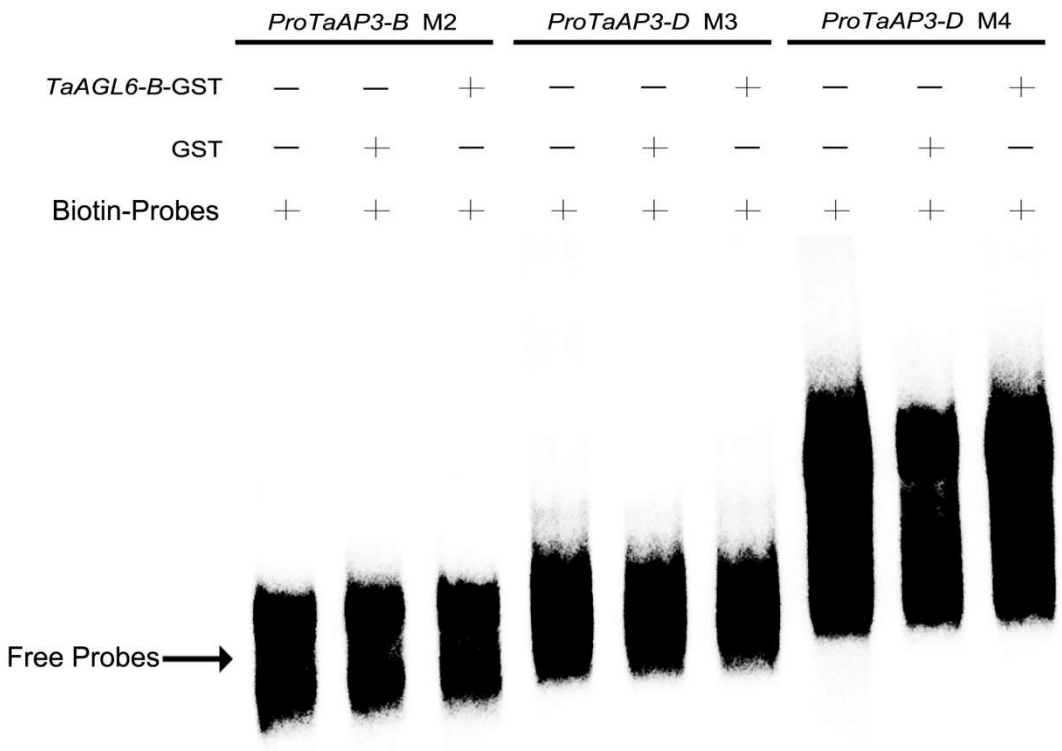


Fig. S10 Results of EMSA to show that AGL6 proteins could not bind to CArG motifs 2-4.

Figure S11

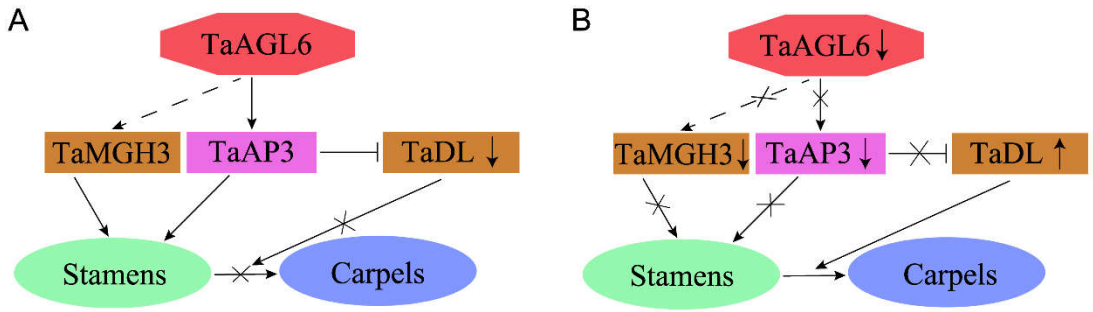


Fig. S11 Proposed model to illustrate the function and mechanism of TaAGL6 in stamen development

(A) In wild type wheat, TaAGL6 transcription factors directly and indirectly regulate the expression of *TaAP3* and *TaMGH3*, respectively. *TaAP3* and *TaMGH3* function in stamen development. Meanwhile, *TaAP3* represses the expression of *TaDL* in stamens. As a result, stamens develop normally. (B) In *TaAGL6* RNAi plants, the expression of *TaAGL6* genes is down-regulated. Consequently, the expression of *TaAP3* and *TaMGH3* is down-regulated, while *TaDL* is ectopically expressed in stamens. As a result, the stamens develop abnormally, and display the potential to transform into carpels.

Table S1. Primers used in this research.

Name	Sequence（5’-3’）
3GSP	ATGGGGAGGGGAAGGGTCGAG
5GSP	ATCTTTCCAATGTTTTTGTTGTGCC
TaAGL6ADLF	TAGTAGGTTGCGCGTCAGAA
TaAGL6ADLR	CCTCCTTCCAAGCAAGCAAGAAAAT
TaAGL6BDLF	GAAGGCAGCAACAGCAACAA
TaAGL6BDLR	GGAATGATTAGGGTGTTGCTGA
TaAGL6DDLF	GTACCCTCATCAGTTCGCGG
TaAGL6DDLR	ACAAGCTAACCAGCAGCTCGCT
TaAGL6DLF	CTTGCTTGGGGAGGACCTTGGA
TaAGL6DLR	CATCATAAGTTGTGTCTTTCGCTGT
TaAGL6RNAiPF	GGTGGTAAGCTTGCGGCCGCTGAAGGCAGCAACAGCAACAACTA
TaAGL6RNAiPR	GGTGGTGAATTCGGATCCATGGACAGCTTGGAACTTGCA
T7 promoter sequence	TAATACGACTCACTATAGGG
TaAGL6T7-F	TAATACGACTCACTATAGGGCTGAAGGCAGCAACAGCAACAACTA
TaAGL6T7-R	TAATACGACTCACTATAGGGATGGACAGCTTGGAACTTGCAA
TaActinPF	TATGCCAGCGGTCGAACAAC
TaActinPR	GGAACAGCACCTCAGGGCAC
TaAGL6OF	GGTGGTCCATGGGGAGGGGAAGGGTCGAG
TaAGL6OR	GGTGGTCACGTGTCAGAGAATCCACCCCAGCAT
1301PF	GTGATATCTCCACTGACGTAAGGG
1301PR	GATAATCATCGCAAGACCGGCA
pBSKR	GACAGCAGCAGTTTCATCAATCA
AtGAPCPF	TCAGACTCGAGAAAGCTGCTACC
AtGAPCPR	GATCAAGTCGACCACACGGGAA
TaAGL6PF	ATGGGGAGGGGAAGGGTC

TaAGL6PR	TCAGAGAATCCACCCCAGCAT
TaAP3PF	ATGGGGCGGGGGAAGAT
TaAP3PR	TTAGCCGAGGCGCAGGTC
TaAGPF	ATGCAGATACTCAACGAGCAGCT
TaAGPR	TCACCTTCCAACTGAGTT
TaMADS13PF	ATGGGGAGGGGAAGGATTG
TaMADS13PR	CTAGAACTGATGAGCCACATCGC
TaAP3DLF	AGGAGGCATACAAGAATCTGCA
TaAP3DLR	GCTAGTAGGAGCGATCGAAGTGA
TaAGDLF	TACTCCAACAACAGCGTGAAAGC
TaAGDLR	GTATCGCCTATTAGAGTCCTGTTGG
TaMADS58DLF	ATCAAGCGCATCGAGAACAC
TaMADS58DLR	ATGGTTGCTTTCACGCTGTT
TaDLDLF	AACCTCTCCTTTCTCAGCCC
TaDLDLR	GGGCTTCACAACAAAGGGAG
TaMADS13DLF	TCAGAACCAAGATTGCGGAGGA
TaMADS13DLR	CTAGAACTGATGAGCCACATCGC
TaSEPDLF	AAGAAGGCCTACGAGCTCTC
TaSEPDLR	GGTACTCATTGCGGCTGTTT
TaLHS1DLF	CTCAAGCATATCAGGTCAAAAAAGAATCAA
TaLHS1DLR	TCAGAAGCCACGTGATCTCTGTT
TaMGH3DLF	CCTACATCCAGCGCATTGTC
TaMGH3DLR	ACGAACAGGAAGTAGAGGCC
TaAP3BCARG1PROBEF	AAAAGATCTTTTCGTTCCAGAAGAA
TaAP3BCARG1PROBER	GGTAGCCAAAAAATTCTAAATACCA
TaAP3BCARG2PROBEF	TGCCCGTTCTATTCT
TaAP3BCARG2PROBER	ATCATTGCTTCGCTGCTTT
TaAP3DCARG1PROBEF	GAACGCTAGCTAAGCCATAGG
TaAP3DCARG1PROBER	CTGTCCACTTCCAAAAGAGGT

TaAP3DCARG2PROBEF	CCTTCTTCCTCCTCCTA
TaAP3DCARG2PROBER	TGGATAGAAGGGGCATTGTCT
TaAGL6-BGSTF	CCTGGGATCCCCGGAATTCATGGGGAGGGGAAGGGTC
TaAGL6-BGSTR	GTCACGATGCGGCCGCTCGAGTCACCTGTGCTTGAGTTGCCTGTT
TaAP3F	AAGCTTGAATTCGAGCTC
	GACTAATTAAAGCAGACTAATTAAAGCAGACTAATTAAAGCA
	GTCGACCTCGAGGCATGT
TaAP3R	ACATGCCTCGAGGTCGAC
	TGCTTTAATTAGTCTGCTTTAATTAGTCTGCTTTAATTAGTC
	GAGCTCGAATTCAAGCTT
Mut TaAP3F	AAGCTTGAATTCGAGCTC
	GACTCGTTCGCGCAGACTCGTTCGCGCAGACTCGTTCGCGCA
	GTCGACCTCGAGGCATGT
Mut TaAP3R	ACATGCCTCGAGGTCGAC
	TGCGCGAACGAGTCTGCGCGAACGAGTCTGCGCGAACGAGTC
	GAGCTCGAATTCAAGCTT
TaAGL6-BOE6HAF	GTCGACGGTATCGAT AAGCTT ATGGGGAGGGGAAGGGTCGAG
TaAGL6-BOE6HAR	AGAACTAGTGGATCC CCCGGG GAGAATCCACCCCAGCAT
TaAP31302GFPF	CATGGTAGATCTG ACTAGT ATGGGGCGGGGGAAGAT
TaAP31302GFPR	GCCCTTGCTCACCAT CCTAGG GCCGAGGCGCAGGTC
TaAG 1302GFPF	CATGGTAGATCTG ACTAGT ATGCAGATACTCAACGAGCAGCT
TaAG 1302GFPR	GCCCTTGCTCACCAT CCTAGG CCTTCCAACTGAGTT
TaMADS13GFPF	CATGGTAGATCTG ACTAGT ATGGGGAGGGGAAGGATTG
TaMADS13GFPR	GCCCTTGCTCACCAT CCTAGG GAACTGATGAGCCACATCGC
TaAGL6-B 62SKF	CGCTCTAGAACTAGT GGATCC ATGGGGAGGGGAAGGGTCGAG
TaAGL6-B 62SKR	GTCGACGGTATCGAT AAGCTT TCAGAGAATCCACCCCAGCAT
TaAP3B-0800LUCF	GGCCCCCCCTCGAG GTCGACAAAAGATCTTTTCGTTCCAGAAGAA
TaAP3B-0800LUCR	GCTCTAGAACTAGT GGATCC GGGGCGGCCGTGGTTTTGA