Supporting Information

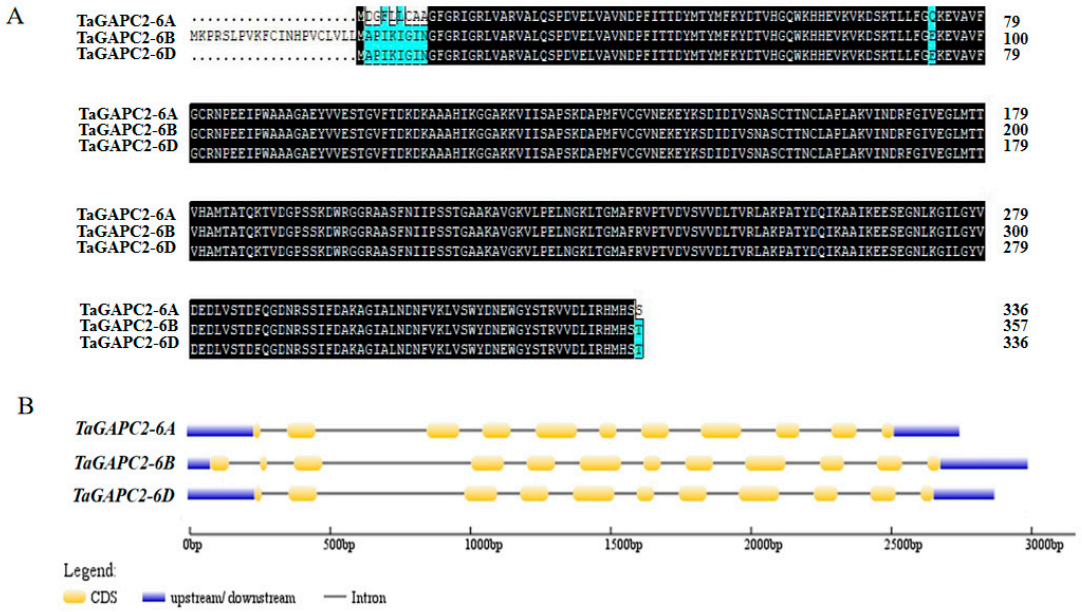

Figure S1. Sequence analysis. (A) Alignment of the Amino acid sequence of TaGAPC2. The identical and 75% amino acid sequence similarity are separately indicated by mazarine and green color. (B) Exons, introns, upstream/downstream are indicated by yellow boxes, black horizontal lines and blue boxes, respectively.

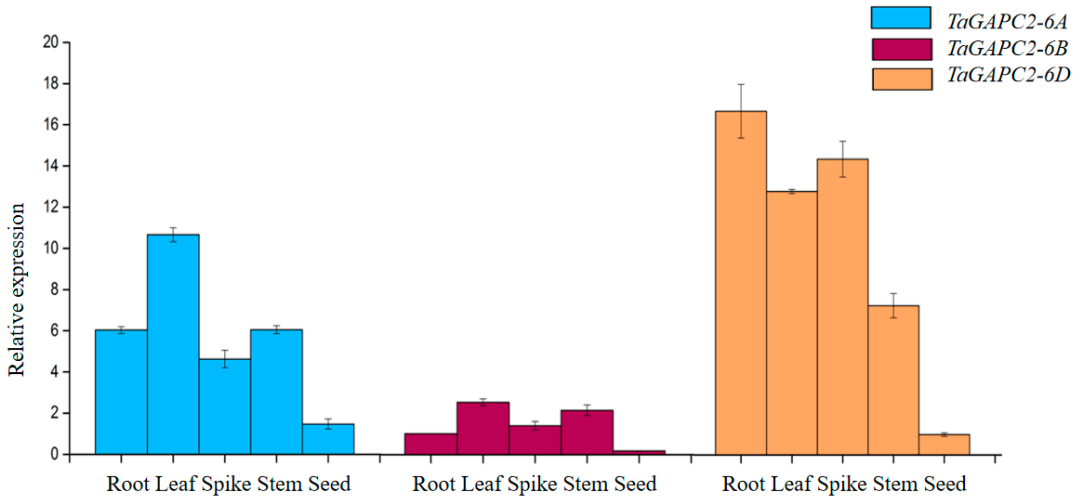

Figure S2. Organ expression assay of TaGAPC2 in different wheat organs. The indicated values are the average of three independent experiments. The standard deviation (SD) is indicated at each point.

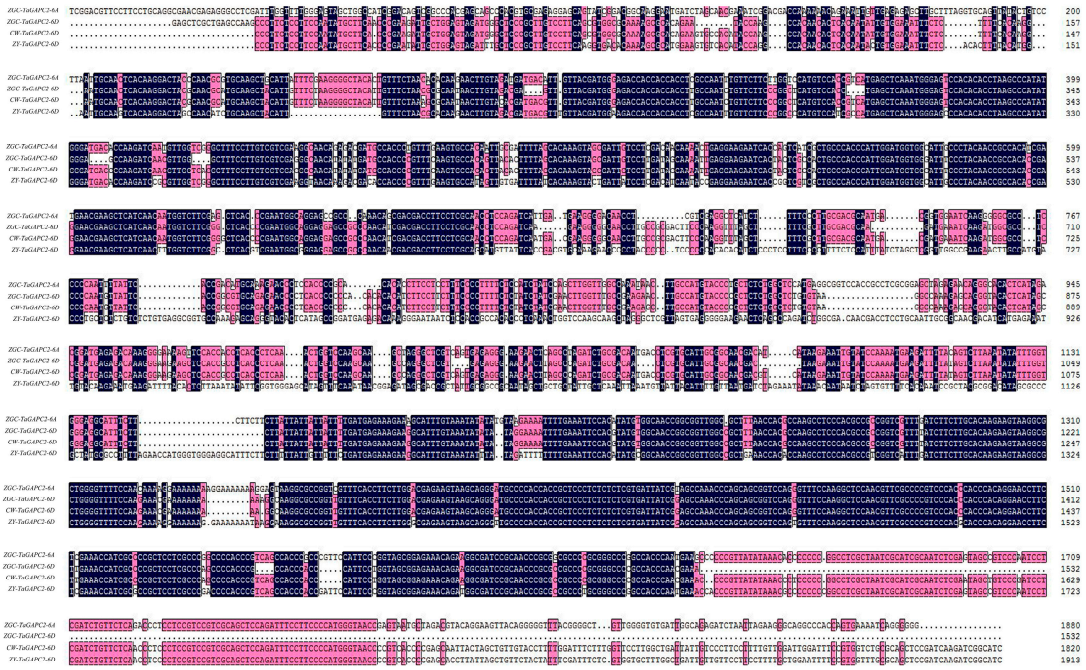

Figure S3. Promoter sequence alignment of *TaGAPC2* in wheat. *ZGC-TaGAPC2-6A*: The *TaGAPC2-6A* promoter in *Chinese spring* wheat; *ZGC-TaGAPC2-6D*: The *TaGAPC2-6D* promoter in *Chinese spring* wheat; *CW-TaGAPC2-6D*: The *TaGAPC2-6D* promoter in *Chang Wu* wheat; *ZY-TaGAPC2-6D*: The *TaGAPC2-6D* promoter in *Zheng Yin* wheat. The identical and 75% amino acid sequence similarity are separately indicated by mazarine and pink color.

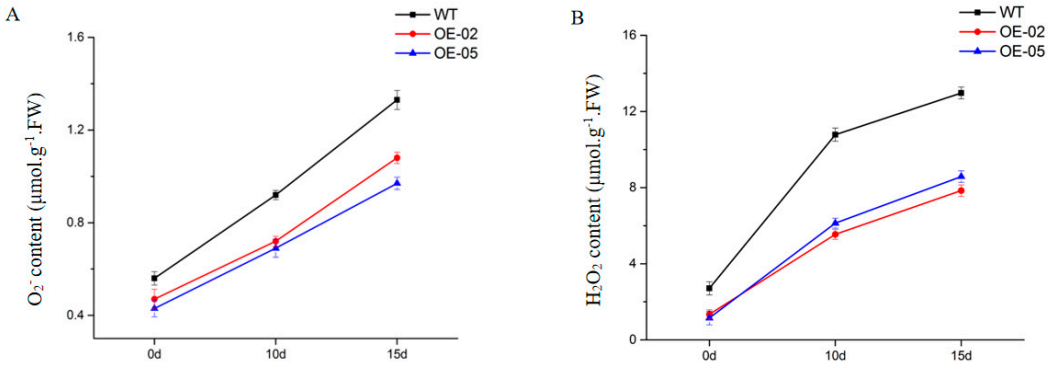

Figure S4. The contents of O_2^- (A) and H_2O_2 (B) in WT and transgenic plants after drought stress.The datas are representative of three independent experiment.

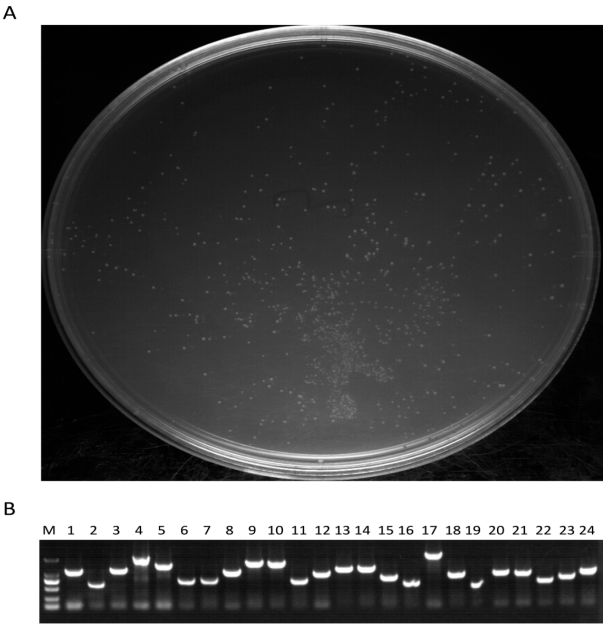

Figure S5. Quality of cDNA library (Yeast). (A) Measurement result of the library titer. (B) Detecting of the insert fragments.

Table S1. Putative cis-acting elements in the TaGAPC2 promoters.

Gene Element	ABRE	CBFHV	DRE/CRT	GARE	LTRE	MYB	MYC	W-box
TaGAPC2-6A Promoter	3	2	3	1	2	10	4	7
TaGAPC2-6D Promoter	3	4	2	1	3	10	8	10

Table S2. Basic local alignment search tool (BLAST) results for potential candidate interacting proteins with TaGAPC2-6D in cDNA wheat library.

Number	Name	GenBank
1	Plastid glutamine synthetase 2	ACT22496.1
2	Chromatin structure-remodeling complex protein BSH	EMS62932.1
3	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	AHI44627.1
4	Hypothetical protein TRIUR3-14212	EMS50462
5	Phospholipase Dδ	AK334478.1
6	Photosystem II 47 kDa protein	NP_114283.1
7	26S protease regulatory subunit 7	OAY64297.1
8	Hexokinase-2	AAX84838.1
9	Cytochrome b6-f complex iron-sulfur subunit	Q7X9A6.1
10	Glutamate receptor	EMT00479.1

Table 3. All primers used in this experiment.

Primers for qRT-PCR (The underline showed the restriction enzyme sites. F, forward; R, reverse)		
Name	Sequences(5′ -3′)	Experiments
TaGAPC2–6A F/R	AATCGCATCGCAATCTCG/GCAGCGCAAAGCAAAAAT	qRT-PCR
TaGAPC2–6B F/R	AAGTTTTGTATCAATCACCCTGT/ATGTAGGTCATGTAGTCGGTGG	qRT-PCR
TaGAPC2–6D F/R	AATCGCATCGCAATCTCG/TGGTGATGAAGGGGTCGT	qRT-PCR
Primers for generating DNA vector		
Name	Sequences(5′ -3′)	Experiments
PR-6A F	CTGCAGGTCGACGGATCCCCCGGGCCTTCTCCTTCCAATATGCTT	TaGAPC2-6Apromoter: transient expression
PR-6A R	GGTGGACTCCTCTTAGAATTCGGGAAGGAAATCTGGAGCT	TaGAPC2-6A promoter: transient expression
PR-6D F	CTGCAGGTCGACGGATCCCCCGGGCTTCCAATATGCTTCACCCCG	TaGAPC2-6D promoter:transient expression
PR-6D R	GGTGGACTCCTCTTAGAATTCCAGGAAACGAACCCACGGAA	TaGAPC2-6Dpromoter:transient expression
Ta1302-F	GGACTCTTGACCATGATGGCTCCGATCAAGATCG	PCAMBIA1302, overexpression
Ta1302-R	TCAGATCTACCATGGCCTTGGTGCTGTGCATGTGA	PCAMBIA1302, overexpression
Pr1	GGGGGACTCTTGACCATG	Detection of transgenic Arabidopsis
Pr2	TTACTAGTCAGATCTACCATGGC	Detection of transgenic Arabidopsis
Pr3	AGTTCATCCATGCCATGTGT	Detection of transgenic Arabidopsis