

**Figure S1.** Collinerity analysis of *PpyAP2/ERF* TFs. a Red lines indicate the *PpyERFS* duplicated genes while the gray lines show the whole genome duplication events. Red bars indicate each chromosome number. b Duplicated gene pairs of *PpERFs* TFs while the red highlighted duplicated gene pairs belong to *PpyCBFs* subfamily.

Table S1. Sequence identity Matrix of all isolated PpyCBF TFs:

Seq->	Pbr013924	Pbr032764	Pbr003714	Pbr003734	Pbr030749	Pbr021780	Pbr037203	Pbr037204	Pbr037205	Pbr021781	Pbr037202	Pbr030748	Pbr003716	Pbr003732	Pbr016792
Given name	PpyCBF3	PpyCBF5	PpyCBF4	PpyCBF15	PpyCBF12	PpyCBF9	PpyCBF10	PpyCBF11	PpyCBF8	PpyCBF1	PpyCBF7	PpyCBF2	PpyCBF13	PpyCBF14	PpyCBF6
Chr. Pos.	Chr7	Chr1	Scaf. 117.0.1	Scaf. 117.0.1	Chr6	Chr4	Scaf.752.0	Scaf.752.0	Scaf.752.0	Chr4	Scaf.752.0	Chr6	Scaf. 117.0.1	Scaf. 117.0.1	Chr14
PpyCBF3	1	0.799	0.557	0.556	0.396	0.365	0.365	0.407	0.49	0.529	0.498	0.558	0.557	0.557	0.458
PpyCBF5		1	0.559	0.557	0.387	0.354	0.354	0.393	0.487	0.525	0.495	0.563	0.563	0.563	0.447
PpyCBF4			1	0.994	0.621	0.573	0.573	0.618	0.774	0.837	0.79	0.936	0.942	0.942	0.475
PpyCBF15				1	0.616	0.57	0.57	0.615	0.77	0.832	0.785	0.931	0.936	0.936	0.471
PpyCBF12					1	0.271	0.271	0.316	0.492	0.534	0.503	0.597	0.594	0.594	0.297
РруСВF9					Incomplete seq	1	1	0.921	0.647	0.701	0.66	0.579	0.579	0.579	0.363
PpyCBF10							1	0.921	0.647	0.701	0.66	0.579	0.579	0.579	0.363
PpyCBF11								1	0.689	0.747	0.704	0.624	0.624	0.624	0.393
PpyCBF8									1	0.922	0.949	0.772	0.772	0.772	0.426
PpyCBF1										1	0.941	0.834	0.834	0.834	0.454
PpyCBF7											1	0.788	0.788	0.788	0.436
PpyCBF2								Same	Clade			1	0.984	0.984	0.47
PpyCBF13													1	1	0.469
PpyCBF14														1	0.469
PpyCBF6															1

Table S2. Total number of stress related cis-elements in promoters of PpyCBF TFs:

TFs	Cold	Salt	Drought	Oxidative	Light	Iron toxicity	Pathogen	Heat	ABA	GA	Auxin
PpyCBF3	9	11	8	3	15	1	5	0	1	6	3
PpyCBF1	8	11	8	1	16	4	3	1	5	3	2
PpyCBF2	8	13	6	3	18	1	7	2	7	6	2
PpyCBF4	6	11	8	1	12	4	3	2	7	4	2
PpyCBF5	13	15	11	1	12	1	8	0	1	2	2
PpyCBF6	7	13	9	2	15	1	5	3	7	3	1

Table S3. Promoter analysis of *PpyCORs*:

TFs family	Functions	cis-element	Sequences	PpyCOR47	PpyCOR15A	PpyRD29A	PpyKIN
ABF/AREB	ABA responsive	ABRE	CATGC	5	5	3	4
AP2/EREBP	Cold, drought, NaCl	CRT/DRE	CCGAC	6	0	0	0
			CGAC	10	6	7	3
AP2/RAV	Photoperiodism	В3	CAACA	2	8	6	6
bHLH	Iron toxicity	IRO2	CACGTG	3	3	0	2
bZIP	ABA, NaCl, drought,	G-box1	CACGTG	3	3	0	2
bZIP	Salt, Pathogen	GT-1-like	GAAAAA 2		3	4	8
		box					
ERF	Defense responses	GCC box	AGCCG	1	2	3	0
GATA	Light response	GATA box	GATA	10	17	15	14
MADS	Plant development	MIKC	CC[A/T]5	1	1	2	1
MYB like	Light response	I BOX	AAACCA	3	2	2	4
MYB/SANT	Gibberellin response	GARC	AACAAA	2	2	6	0
<b>MYC-like</b>	Cold stress	ICE1-like	CATTTG	4	3	1	0
bHLH							
NAC	Cold, drought, NaCl,	NAC	CATGT	3	5	3	8
TCP/PCF1	Oxidative stress	Site 2	TGGGC	6	5	2	2
WRKY	WRKY Bacterial blight		ACGCTG	2	1	0	1
		PRE4	TGCGCT	1	0	2	0

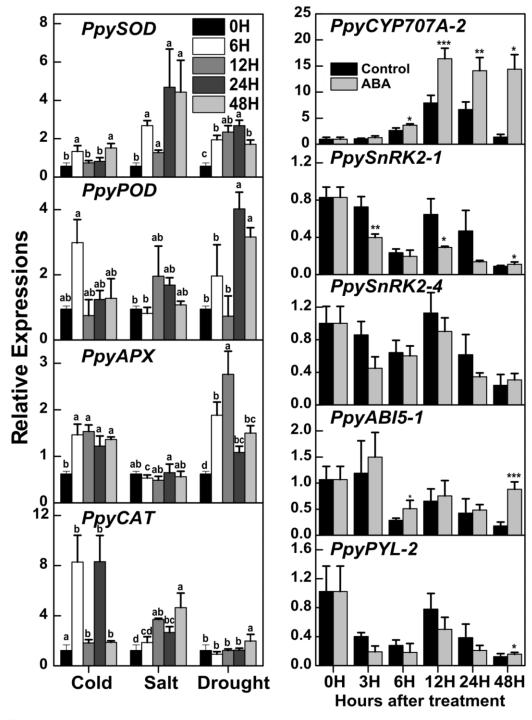


Figure S2. Expression analysis of antioxidant and ABA-responsive genes in pear explants and pear calli during abiotic stresses and ABA treatment. Both relative expressions were normalized to PpyActin expression level. Error bars indicate standard errors from three biological replicates (\*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001) while means with different letters had significant differences (P < 0.05).

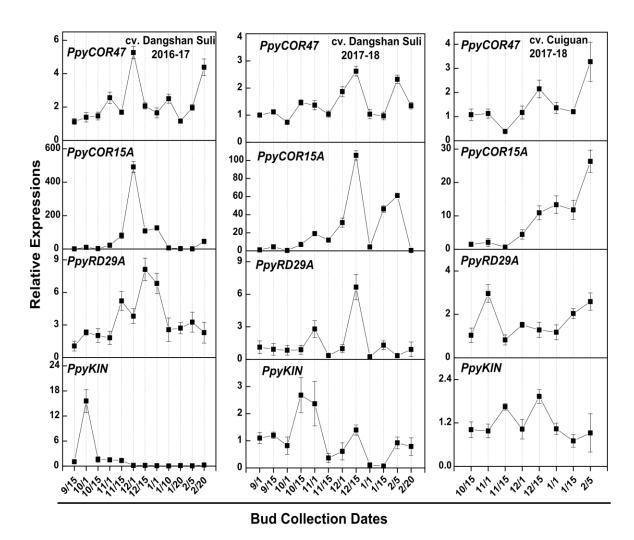
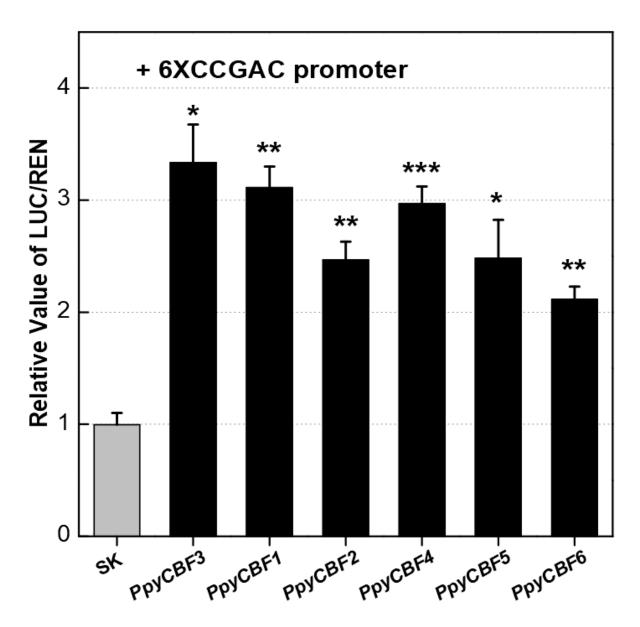


Figure S3. Relative expressions of *PpyCORs* during bud endodormancy in *Pyrus pyrifolia* cv 'Dangshan Suli' and 'Cuiguan' during two successive years 2016-2017 and 2017-2018. Buds were collected from 9/15 to 2/25 with about 15 days interval. The data were normalized to *PpyActin* expression level and the mean expression value was premeditated from 4 independent replicates. The standard deviation was shown by vertical bars.

**Figure S4.** Phenotypic analysis of *PpyCBF2* and *PpyCBF3* overexpressing arabidopsis and WTs during abiotic stresses and recovery periods. a Phenotype of overexpressed and WTs arabidopsis during control, LT, drought and salt stresses. Black lines indicate the root lengths before stresses while below these lines are increase in root lengths during abiotic stress conditions. **b.** After abiotic stress, explants were transformed into normal conditions without abiotic stress conditions to check their recovery.



**Figure S5. Transcriptional activity of** *PpyCBFs* **with 6XCRT binding sites.** The ratio of LUC/REN of the empty vector (SK) plus promoter was used as calibrator (set as 1). Three independent experiments were done to verify the results. Error bars showed SEs with at least four biological replicates while asterisks showed significant differences of genes SK with empty SK (\*P < 0.05, \*\*P < 0.01, \*\*\*P < 0.001).