

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 |
| PpyCBF9 | --- | --- | --- | --- | 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 | B3 | CAACA | 2 | 8 | 6 | 6 |
| bHLH | Iron toxicity | IRO2 | CACGTG | 3 | 3 | 0 | 2 |
| bZIP | $\mathrm{ABA}, \mathrm{NaCl}$, drought, | G-box1 | CACGTG | 3 | 3 | 0 | 2 |
| bZIP | Salt, Pathogen | GT-1-like box | GAAAAA | 2 | 3 | 4 | 8 |
| 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 |
| MYC-like bHLH | Cold stress | ICE1-like | CATTTG | 4 | 3 | 1 | 0 |
| NAC | Cold, drought, NaCl , | NAC | CATGT | 3 | 5 | 3 | 8 |
| TCP/PCF1 | Oxidative stress | Site 2 | TGGGC | 6 | 5 | 2 | 2 |
| WRKY | Bacterial blight | PRE2 | 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 $(P<0.05)$.


Bud Collection Dates
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).

