

Supplementary Table S1. List of primers used for qRT-PCR analysis

Gene name	Forward primer (5'-3')	Reverse primer (5'-3')
<i>OsCBP60a</i>	AGTGCATTGGATCCTTGTCC	GAAGCCTTTCAATGCAGCTC
<i>OsCBP60bcd-1</i>	AAGGTGTTGGCACTGTAGGG	GAGGATCTCGAACCACAAGC
<i>OsCBP60bcd-2</i>	ATATGATGGCAAGGCACTCC	TATCGTCCTGCCTGATTTCC
<i>OsCBP60bcd-3</i>	GGTTTGCGAGTCTCTTCAGG	ACACATGTCTTCGCATGCTC
<i>OsCBP60g-1/OsSARDL</i>	TGAAGAGGGTTTTGGAGGTG	TGGAAGTGCAGCTTGTATCG
<i>OsCBP60g-2</i>	AGGAAAACGTTGCAATGACC	ATTGTTGGCGTGGTAAGGAG
<i>OsCBP60g-3</i>	CAAGCGTATGATGCTCTGGA	CACCGTAGATCTGAGCCACA
<i>OsCBP60g-4</i>	ATGACGCTCAGTGATGATGC	CTGGTCCGATCATGTTGTTG
<i>OsCBP60g-5</i>	AGTTCATGGGCATGTTCTC	TGCTTTTCAAATCCCTCCAC
<i>OsCBP60g-6</i>	TGGCAAACCAAGACAAATCA	GTCACCGAGGCTGCTATCTC
<i>OsCBP60g-7</i>	GGGTGAGCTGGACTGAAGAG	TCCCATCTTTGCAGATTTCC
<i>OsCBP60g-8</i>	CAAGAGGCTTGTGGAGAAGG	ATGCAATGTAACTGCCACCA
<i>OsSARDL-1</i>	GATGGTGAAGCAGATGCAG	GACGTCGACGAGGATGATC
<i>OsSARDL-2</i>	ATTGGTCAGCCAAGCATACC	TCAGCAGTTGAGGTTGTTGC
<i>OsSARDL-3</i>	GAGGCCAGATGATGAGGTG	ATTGCCTGAGGCTGTCTTG
<i>OsPRIa</i>	ATGGCACCTTCCAAGGTCAG	TGCAGGTTGACGTAGTCCTG
<i>Rice ACTIN</i>	GAGTATGATGAGTCGGGTCCAG	ACACCAACAATCCCAAACAGAG

Supplementary Table S2. Prediction of CBDs in OsCBP60s

Gene name	Interaction Prediction Score (using CaMELS)	Binding Site Score (using CaMELS)
<i>OsCBP60bcd-1</i>	79.4	1.85
<i>OsCBP60bcd-2</i>	22.84	1.85
<i>OsCBP60bcd-3</i>	18.63	1.85
<i>OsCBP60a</i>	7.53	1.53
<i>OsSARDL-1</i>	4.3	1.53
<i>OsSARDL-2</i>	8.62	1.89
<i>OsSARDL-3</i>	3.22	1.46
<i>OsCBP60g-1/OsSARDL</i>	1.62	1.47
<i>OsCBP60g-2</i>	1.45	1.65
<i>OsCBP60g-3</i>	2.46	1.58
<i>OsCBP60g-4</i>	1.3	1.46
<i>OsCBP60g-5</i>	3.82	1.37
<i>OsCBP60g-6</i>	13.72	1.47
<i>OsCBP60g-7</i>	4.49	1.59
<i>OsCBP60g-8</i>	2.17	1.51

Supplementary Table S3. Analysis of transcription factor binding sites (TFBSs) in putative promoter sequences of *OsCBP60s* and *AtCBP60s*. The 1000 bp and 2000 bp upstream sequences of rice and Arabidopsis *CBP60* genes were retrieved from Phytozome and TAIR, respectively. The CAMATA, TGACG and W-box binding sequences were identified using Plant PAN 3 software. The BES1 and BZR1 TFBSs were identified manually.

Gene name	BES1		BZR1		TGACG		CAMTA		WRKY	
	1kb	2kb	1kb	2kb	1kb	2kb	1kb	2kb	1kb	2kb
<i>OsCBP60a</i>	08	13	00	00	07	07	00	00	06	08
<i>OsCBP60bcd-1</i>	04	11	00	00	00	00	00	02	00	01
<i>OsCBP60bcd-2</i>	09	11	00	00	02	03	03	04	03	03
<i>OsCBP60bcd-3</i>	04	11	00	00	06	06	05	05	06	06
<i>OsCBP60g-1/OsSARDL</i>	02	08	00	01	05	08	03	06	00	00
<i>OsCBP60g-2</i>	01	07	01	02	00	02	04	04	15	23
<i>OsCBP60g-3</i>	02	07	01	01	06	13	12	12	13	35
<i>OsCBP60g-4</i>	07	12	00	01	02	02	04	06	23	26
<i>OsCBP60g-5</i>	04	08	00	00	02	07	00	00	08	13
<i>OsCBP60g-6</i>	02	06	00	00	00	05	00	05	15	23
<i>OsCBP60g-7</i>	03	07	00	00	00	00	04	04	09	09
<i>OsCBP60g-8</i>	00	03	00	01	02	02	02	04	04	08
<i>OsSARDL-1</i>	05	14	01	01	04	04	00	09	11	20
<i>OsSARDL-2</i>	05	07	00	01	00	00	00	00	08	18
<i>OsSARDL-3</i>	03	10	00	00	00	02	00	00	05	10
<i>AtCBP60a</i>	03	06	00	00	06	06	01	01	10	23
<i>AtCBP60b</i>	04	06	00	00	00	00	00	00	01	11
<i>AtCBP60c</i>	03	06	00	00	00	00	06	06	19	20
<i>AtCBP60d</i>	07	08	00	00	02	02	01	01	06	18
<i>AtCBP60e</i>	07	12	00	00	00	00	06	06	13	45
<i>AtCBP60f</i>	05	10	00	00	05	09	00	00	21	33
<i>AtCBP60g</i>	03	05	00	00	08	13	03	03	32	46
<i>SARD1</i>	04	05	00	00	40	42	01	14	23	32