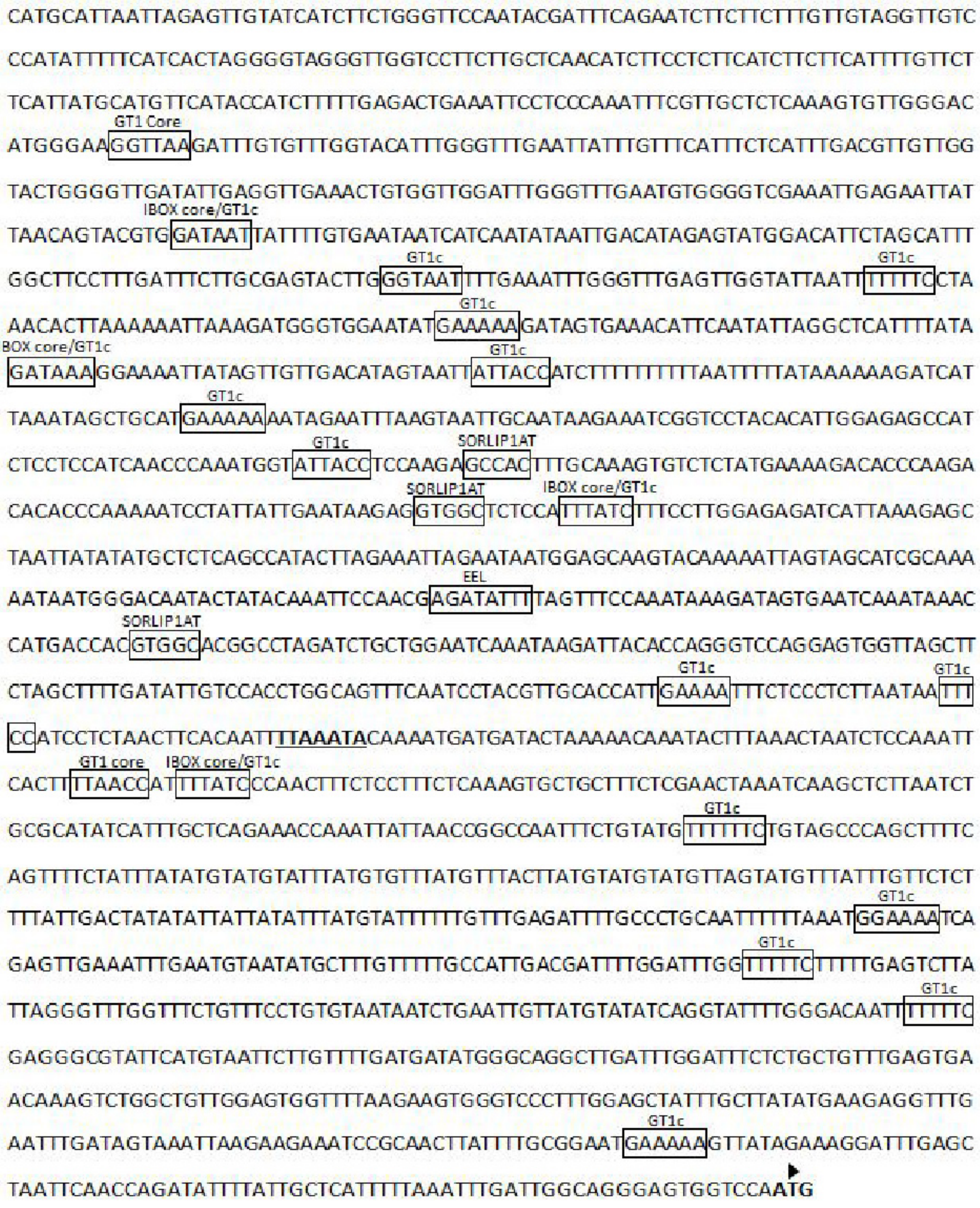

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TAATTCAACCAGATATTTTATTGCTCATTTTTAAATTTGATTGGCAGGGAGTGGTCCA**ATG**

Fig. 1 Suppl. The *BvPRR7* promoter. Two kilobase genomic sequence upstream of the translation start site of *BvPRR7* was selected from the scaffold sequence of the beet genome (RefBeet 1.2) (Dohm *et al.* 2014). The TATA box sequence is indicated in *bold letters* as predicted according to the transcription start site prediction program TSSP (http://www.softberry.com/berry.phtml). The functional description of identified domains/motifs: GT-1 consensus: recognizes GT-1 proteins which have tri-helix DNA-binding domains; EEL (Evening Element-Like): transcriton factors bind to these motifs to integrate cold- and clock- associated genes, for example, as found in cold induction of *COL1* and *COR27* in *Arabidopsis* (Mikkelsen *et al.* 2009); GT-CORE: a consensus binding site in many light-regulated genes; TATA Box: a binding site for RNA polymerase signifying the start of transcription; I-Box: activates a heterologous promoter in phytochrome-, cryptochrome-, and plastid signal-dependent manners (Martínez-Hernández *et al.* 2002); SORLIP: listed as one of the over represented sequences found in light induced promoters especially in *Arabidopsis*, also in light-induced cotyledon and root specific genes (Jiao *et al.* 2005).

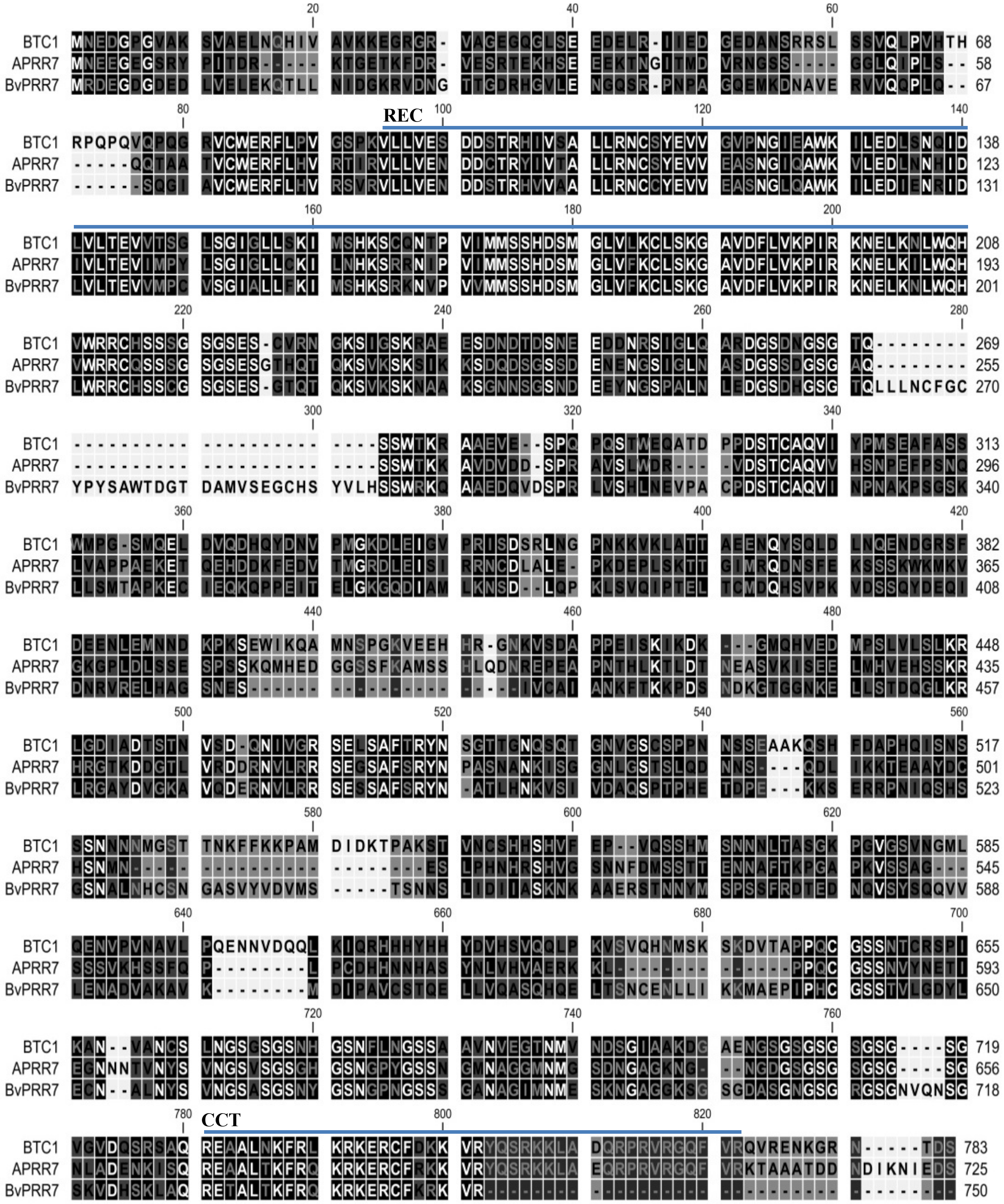

Fig. 2 Suppl. The pairwise sequence alignment between BTC1, BvPRR7, and APRR7. The alignment was generated using *ClusterW2* (http://www.ebi.ac.uk/Tools/msa/clustalw2/) and *CLC Main Workbench v. 5.5* (*CLC Bio*, Aarbus Denmark). The annotation of protein domains was identified using *Pfam 26.0* (http://pfam.xfam.org/) and marked as horizontal line in the alignment.

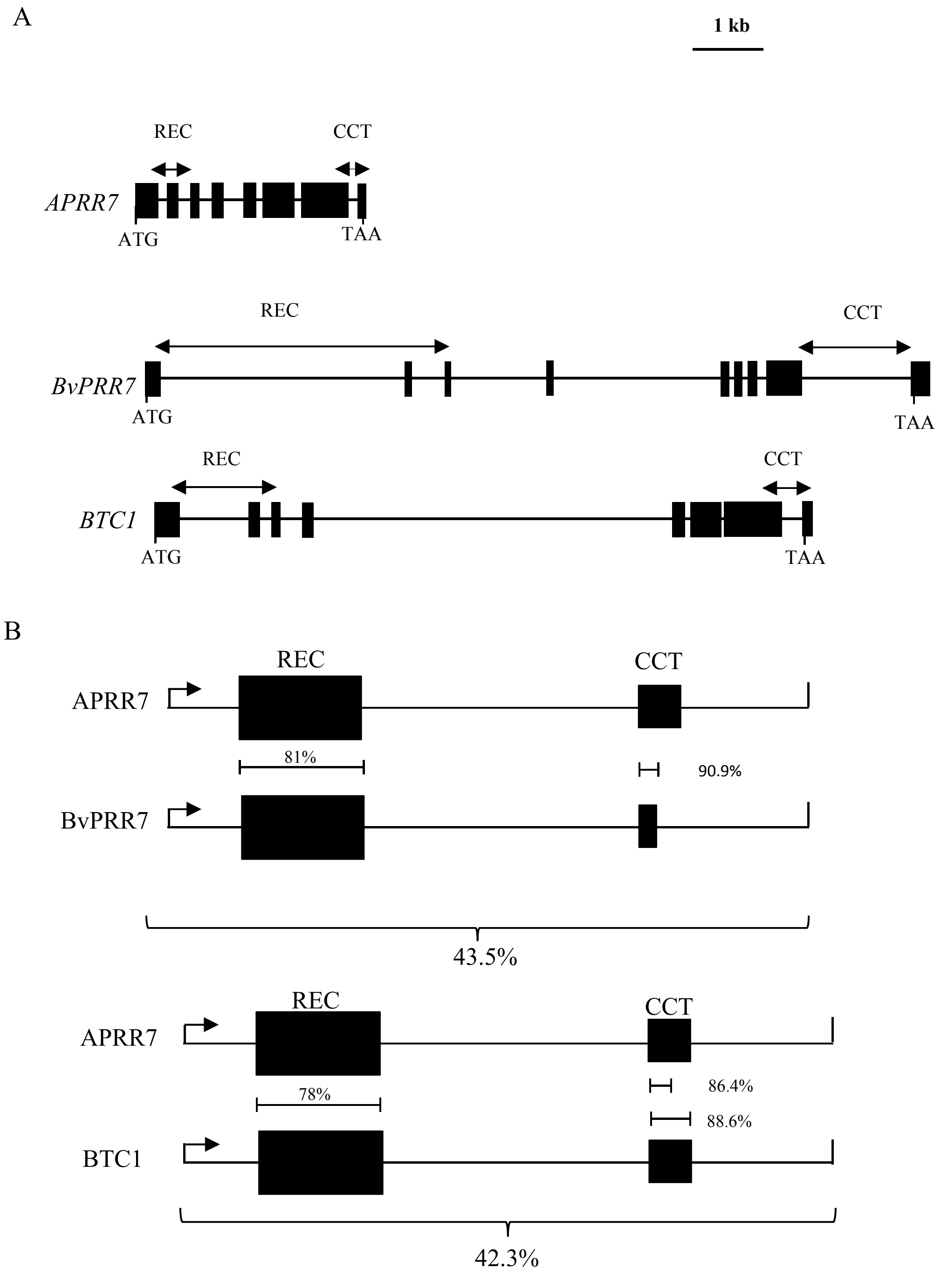

Fig. 3 Suppl. The exon-intron structure and domain organization of *BvPRR7*, *BTC1*, and the *Arabidopsis* homolog *APRR7* (accession numbers HQ709096, HQ709099, and AB046954, respectively). *A* - Exons and introns are represented as *black rectangles* and *horizontal lines*, respectively. START and STOP codons are indicated by ATG and TAA, respectively. REC - receiver domain; CCT - CONSTANS, CO-like, and TOC1 domain. *B* - Protein domain and the whole amino acid identity comparison between the PRR7 homologs in beet and *Arabidopsis*. The amino acid identity comparison of each domain is also given (a position considered for analysis is represented by a *horizontal line bridge*). The positions of the start and stop are indicated by *arrows* and *vertical lines*, respectively.

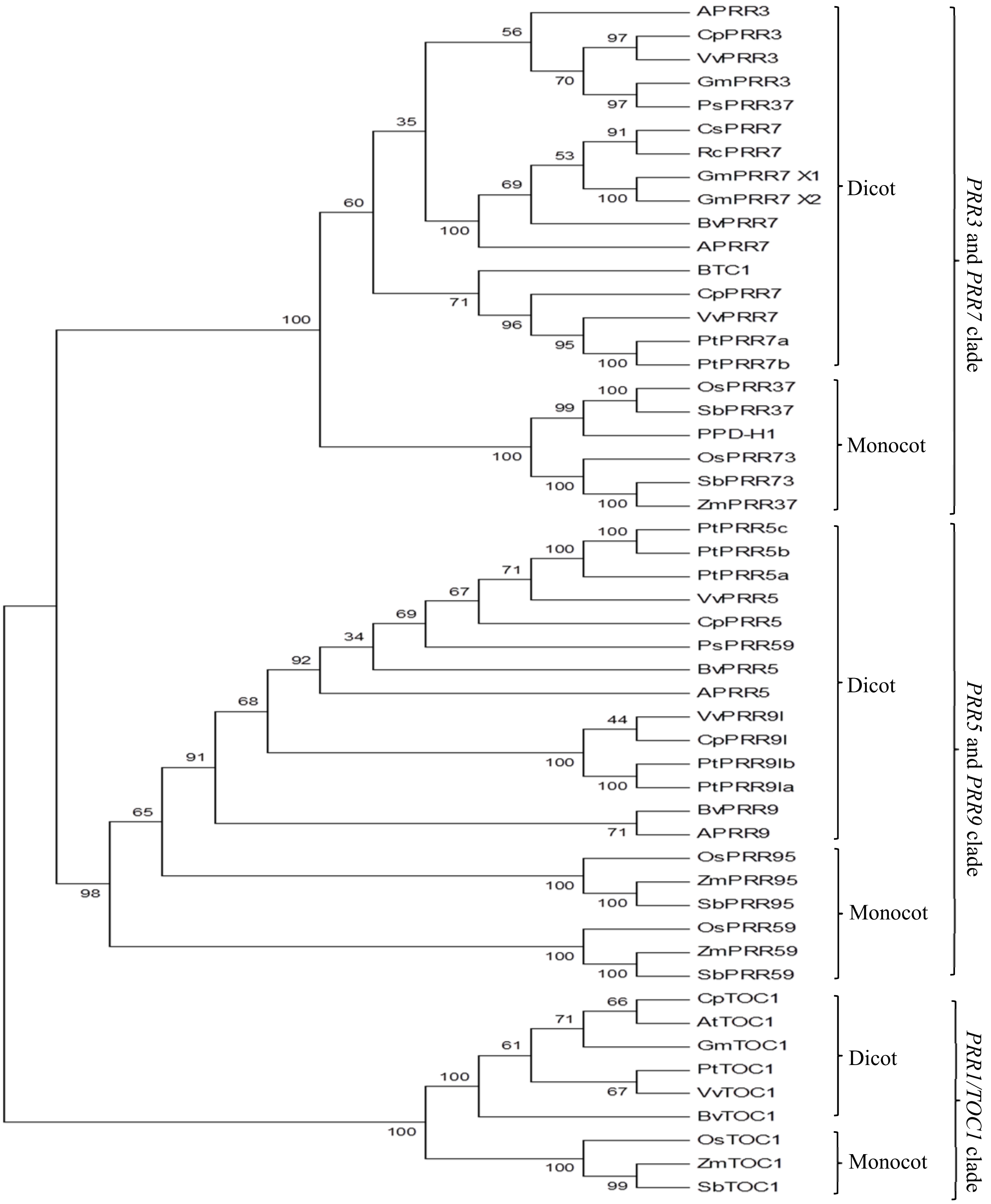

Fig. 4 Suppl. The phylogenetic diversification and relationship of *PRR* genes. Homologs of *Arabidopsis PRR* genes in beet were identified using the *Arabidopsis PRR* genes as query in *TBLASTN* against the beet genome draft 0.9 (Dohm *et al*. 2012). The multiple sequence alignment was done using *Cluster Omega* (http://www.ebi.ac.uk/Tools/msa/clustalo/).The tree reconstruction was done with *MEGA 6* (Tamura *et al*. 2011) using the JTT+G+I (considering a non-uniformity of evolutionary rates) protein model. Bootstrap values were calculated for 500 replications. Cp - *Carica papaya*, Vv - *Vitis vinifera*, *Ppd-H1* - *PRR7* homolg from barley, Bv - *Beta vulgaris*, A - *Arabidopsis thaliana*, showing the normal nomenclaure for *APRR* genes), Gm - *Glycine max*, Cs - *Citrus sinensis*, Rc - *Ricinus communis*, Pt - *Populus tremula*, Os - *Orysa sativa*, Sb - *Sorghum bicolor*, Zm - *Zea mays*, Gm - *Glycine max*, Ps - *Pisium sativum*, *BTC1* - *Bolting Time Control 1* from *Beta vulgaris*. Bootstrap values [%] are shown at the nodes. The tree separated into three clades namely *PRR3* and *7*, *PRR9* and *5*, and *TOC1*, respectively.

Table 1 Suppl. Annual and biennial beet samples for expression analysis of *BvPRR7*. Plants were sown on 29/09/2011.

Time point	BBCH scale	BBCH description	Date of sampling	Sample
T1	12	2 leaves unfolded	13/10/2011	two weeks after sowing (seedlings)
T2	16-20	9 and more leaves unfolded	30/10/.2011	1 d before cold treatment (vegetative stage)
T3	16-20	9 leaves unfolded	01/11/2011	24 h of cold treatment
T4	16-20	9 leaves unfolded	151/2/2011	45 d after beginning of cold treatment
T5	16-20	9 leaves unfolded	25/01/2012	90 d after beginning of cold treatment
T6	16-20	9 leaves unfolded	26/01/2012	1 d after cold treatment
T7	>20	leaves start to cover the soil	08/02/2012	21 d after cold treatment
T8	51-52	elongation of stem	01/03/2012	bolting stage
T9	65	full flowering (50 % opened)	22/03/2013	flowering stage

Table 2 Suppl. Primer combinations used in expression and functional analyses of *BvPRR7*.

Gene	Primers	Primer sequences 5´→ 3´	Purpose	Reference
BvPRR7	B620-B621	GAGTGGTCCAATGAGGGATGCTGTGTTGATCCATACAGGTC	vector construction	this study
	B629-B630	TGAAAGAAATGTACTCAGACGGGTCAGTTTCATGAGGAGT	vector construction	this study
	B622-B623	GCTCTCCTATCTCACCTTCCCGACACACTTGTCTACTC	vector construction	this study
	B631-B632	TGGTTTTAAGAAGTGGGTCCCCTATCCCCTGTTGTTCCA	vector construction	this study
	B655-B656	TTGAGAGGGTAGTGCAGCGCTGCCATTGTACTCTTC	vector construction	this study
	B701-B702	TGGAGAGTAAAAATGGAGCAGGAGAGAATCGGTGTCAAGGCTGG	RT-qPCR	Pin *et al*. 2012
BvGAPDH	B582-B583	GCTTTGAACGACCACTTCGCACGCCGAGAGCAACTTGAAC	RT-qPCR	Pin *et al*. 2012
AtCCA1	B705-B706	CCAGATAAGAAGTCACGCTCAGAAGTCTAGCGCTTGACCCATAGCT	RT-qPCR	Farre and Kay 2007
AtIPP2	B715-B716	GTATGAGTTGCTTCTCCAGCAAAGGAGGATGGCTGCAACAAGTGT	RT-qPCR	Farre and Kay 2007

References (other than in the main paper)

Jiao, Y., Ma, L., Strickland, E., Deng, X.W.: Conservation and divergence of light-regulated genome expression patterns during seedling development in rice and *Arabidopsis*. - Plant Cell **17**: 3239-3256, 2005.

Martinez-Hernandez, A., Lopez-Ochoa, L., Arguello-Astorga, G., Herrera-Estrella, L.: Functional properties and regulatory complexity of a minimal RBCS light-responsive unit activated by phytochrome, cryptochrome, and plastid signals. - Plant Physiol **128**: 1223-1233, 2002.

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