## **Supplementary materials**

**Table S1.** Relationships between IDs of *P. sativum*, *M. truncatula* and *A. thaliana BELL* genes based on phylogenetic tree reconstruction (Figure 1).

MtV5 ID	MtV4 ID	Pisum sativum v1	Arabidopsis thaliana	Our names
MtrunA17_Chr1g0151681	Medtr1g016490	Psat6g019760	ATH1	BELL1-7
MtrunA17_Chr1g0155681	Medtr1g023050	Psat6g007960	BLH3/BLH10	-
MtrunA17_Chr1g0177751	Medtr1g057790	Psat0s189g0080	BLH1	BELL1-3
MtrunA17_Chr2g0327021	Medtr2g095050	Psat5g279880	BLH8	-
MtrunA17_Chr3g0141931	Medtr3g112290	Psat5g015400	BLH11	BELL1-5
MtrunA17_Chr3g0141941	Medtr3g112300	Psat5g015360	BLH3/BLH10	-
MtrunA17_Chr4g0008591	Medtr4g019450	Psat7g241960	BLH9	-
MtrunA17_Chr4g0025521	Medtr4g051532	Psat7g205080	BLH5	-
MtrunA17_Chr4g0028701	NA	Psat7g192320	BLH8	-
MtrunA17_Chr5g0403251	Medtr5g018860	Psat2g162960	BLH2/BLH4	BELL1-1
MtrunA17_Chr7g0240371	Medtr7g065050	Psat3g133160	BLH9	BELL1-6
MtrunA17_Chr7g0267481	Medtr7g106320	Psat3g028480	BLH1	-
MtrunA17_Chr8g0373801	Medtr8g078480	Psat4g090560	BLH2/BLH4	BELL1-2
MtrunA17_Chr8g0387321	Medtr8g098815	Psat7g031320	BEL1	BELL1-4

**Table S2.** IDs of *L. japonicus BELL* genes detected in ChIP-Seq analysis [18] as possible targets of NIN transcription factor and relevant Fold Enrichment Score.

Lotus japonicus (v 2.5) ID	Lotus japonicus (v 3.0) ID e	Fold enrichment	Ortholog in M. truncatula	Ortholog in M. truncatula	Ortholog in P. sativum
chr4.CM0165.220.r2.d	Lj4g3v0911380.1	26.78	(ID from v5) MtrunA17_Chr8g0373801	(ID from v4) Medtr8g078480, MtBELL1-2	Psat4g090560
chr1.CM0029.400.r2.m	Lj1g3v4752480.1	23.95	MtrunA17_Chr7g0267481	Medtr7g106320	Psat3g028480
chr4.CM0004.760.r2.d	Lj4g3v2976870.1, Lj4g3v2976880.1	18.97	MtrunA17_Chr8g0387321	Medtr8g098815, MtBELL1-4	Psat7g031320
LjT35B07.30.r2.d	Lj0g3v0034399.1, Lj0g3v0250849.1	10.4	MtrunA17_Chr1g0177751	Medtr1g057790, MtBELL1-3	Psat0s189g0080
chr2.CM0323.330.r2.m	Lj2g3v1828460.1	6.21	MtrunA17_Chr5g0403251	Medtr5g018860	Psat2g162960
chr3.CM0649.190.r2.m	Lj3g3v3082350.1	3.17	MtrunA17_Chr2g0327021	Medtr2g095050	Psat5g279880



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**Figure S1.** A. Expression level of *M. truncatula BELL* genes based on re-analysis of RNA-Seq data from PRJNA552042 project [27] using *M. truncatula* genome v.5 as a reference. Bars represent means of counts per million values (CPM) based on 4-6 replicates. B. Heatmap of the *M. truncatula BELL* gene expression values as log2fold changes at 24 and 48 h and 3, 4, 5, and 7 days after inoculation.



**Figure S2.** Expression of *PsBELL* genes normalized to the reference *Ubiquitin* gene. The data of three independent biological experiments were analyzed. For one biological experiment three technical replicates were obtained at each developmental stage. Bars represent the mean of raw expression values (2 <sup>-deltaCt</sup>) normalized to the maximum value between all genes  $\pm$  SEM. Different letters indicate statistically significant differences between groups as analyzed by One-way analysis of variance (One-way ANOVA), followed by Tukey's post hoc test.



**Figure S3.** Graphic illustration of data for *P. sativum BELL* gene expression in the roots and nodules (cv. Cameor) based on RNA-Seq analysis [43] using *P. sativum* genome sequence v1 as reference. Roots: F - 8 days after sowing; B - start of flowering. Nodules: G - 18 days after sowing, i.e. 10 days after inoculation; A - 7–8 nodes, 5–6 opened leaves; B - start of flowering. Columns represent means of Transcripts Per Kilobase Million values (TPM).



**Figure S4.** Expression level of *M. truncatula BELL* genes in the nodules and roots based on reanalysis of RNA-Seq data [16]. Bars represent means of TPM values for 3 replicates. MtrunA17\_Chr8g0373801 (*MtBELL1-2*), MtrunA17\_Chr1g0177751 (*MtBELL1-3*), and MtrunA17\_Chr8g0387321 (*MtBELL1-4*).



**Figure S5.** Expression level of *M. truncatula BELL* genes in the different nodule zones. Zone I (ZI) - bacteria free meristematic region; zone II (ZIIp) — the proximal part of the infection zone; zone II (ZIId) — the distal part of the infection zone; zone III (ZIII) — symbiosomes, which consist of differentiated bacteroids; the interzone (IZ) - a few cell layers wide between ZII and ZIII.

 Table S3. List of primers used in this study.

DT DCD	
KI-PCR primers:	
PsBELL1-1_F	TCAACAGCAGCAACAACAACAAAC
PsBELL1-1_R	AGAGGGAGGGCTAGGGAGTAACAT
PsBELL1-2_F	CTCACGGCGCCTCTCCTG
PsBELL1-2_R	TGAAATATGCTGCTGCTGCTACTG
PsBELL1-3_F	GGTTCTGTTGGTGGTGGTGAT GG
PsBELL1-3_R	TTGGCCCGTGATTGCGTC TT
PsBELL1-4_F	TTTCTCCATCCGTATCCAAG
PsBELL1-4_R	ACCAATTTGATACCTGGC
PsBELL1-5_F	GGAGACCCATTCGAGGCTTACC
PsBELL1-5_R	GCTGCTGGATTGGAGTCTTCTGAT
PsBELL1-6_F	ACTTTCTCCACCCTTATCCTACTG
PsBELL1-6_R	TTCTCGGCAATGTTGTTATCAC
PsBELL1-7_F	TTCGCTAAGTCTTGCAACATCTCC
PsBELL1-7_R	TATTTCCTTGCCCTCTAACACCAG
Primers for CDS cloning	in pDONR221 or pEntry-TOPO vectors
PsDELLA1_BP_F	AAAGCAGGCTTCATGAAGAGAGAGATCGTCAAGAAACC
PsDELLA1_BP_R	AAGCTGGGTGTCACTTTGACTCACTGAGTGGAA
PsKNOX9_BP_F	AAAGCAGGCTTCATGGCTTTTCACGACCATCT
PsKNOX9_BP_R	AAGCTGGGTGTCACATGAAGCTCTGATT
PsBELL1-2_BP_F	CACCATGGGGATAGCAACAACT
<i>PsBELL1-2_</i> BP_R	TTAAATGCCTCCAAAGTCTGTAAG