SUPPLEMENTAL INFORMATION

Supplemental Table S1. *MtCLE* identification.

Identified *MtCLE* genes with their corresponding names in the general nomenclature and number of the bacterial artificial clone or of the expressed sequence tag. General nomenclature according to Cock and McCormick (2001) and Oelkers et al. (2008), who numbered each CLE member independently of the species origin and prefixed the numbers with "*CLE*".

M. truncatula nomenclature	General nomenclature	BAC clone, EST number
MtCLE1	CLE74	AW586793, BQ139113
MtCLE2	CLE67	AC137080.13, AC135319.28, AC147499.5, BI311733
MtCLE3	CLE69	BQ157494
MtCLE4	CLE71	AW329414
MtCLE5	CLE70	BM812815, BE999212
MtCLE6	CLE64	BF650504, BE941833, CX518468
MtCLE7		AC157502.1
MtCLE8	CLE73	AC151458.10, CX530629, CX530352
MtCLE9		AC155894.1
MtCLE10		AC157779.7
MtCLE11	CLE66	BQ122845
MtCLE12	CLE65	AC144893.15, AL381238, AL381237
MtCLE13	CLE39	AC144893.15, AL380420, AL380419
MtCLE14		AC155894.1
MtCLE15		AC151522.2
MtCLE16	CLE35	AC146785.12
MtCLE17	CLE72	AC123570.7, AC147960.8, AC147961.3, AY379776.1
MtCLE18	CLE36	AC146570.4
MtCLE19		AC150244.2
MtCLE20	CLE37	AC158501.3
MtCLE21	CLE38	CT009655_15.4
MtCLE22	CLE68	AC151522_11.4
MtCLE23		CU024869_31.4
MtCLE24		CR955009_22.5
MtCLE25		CU013514_50.4

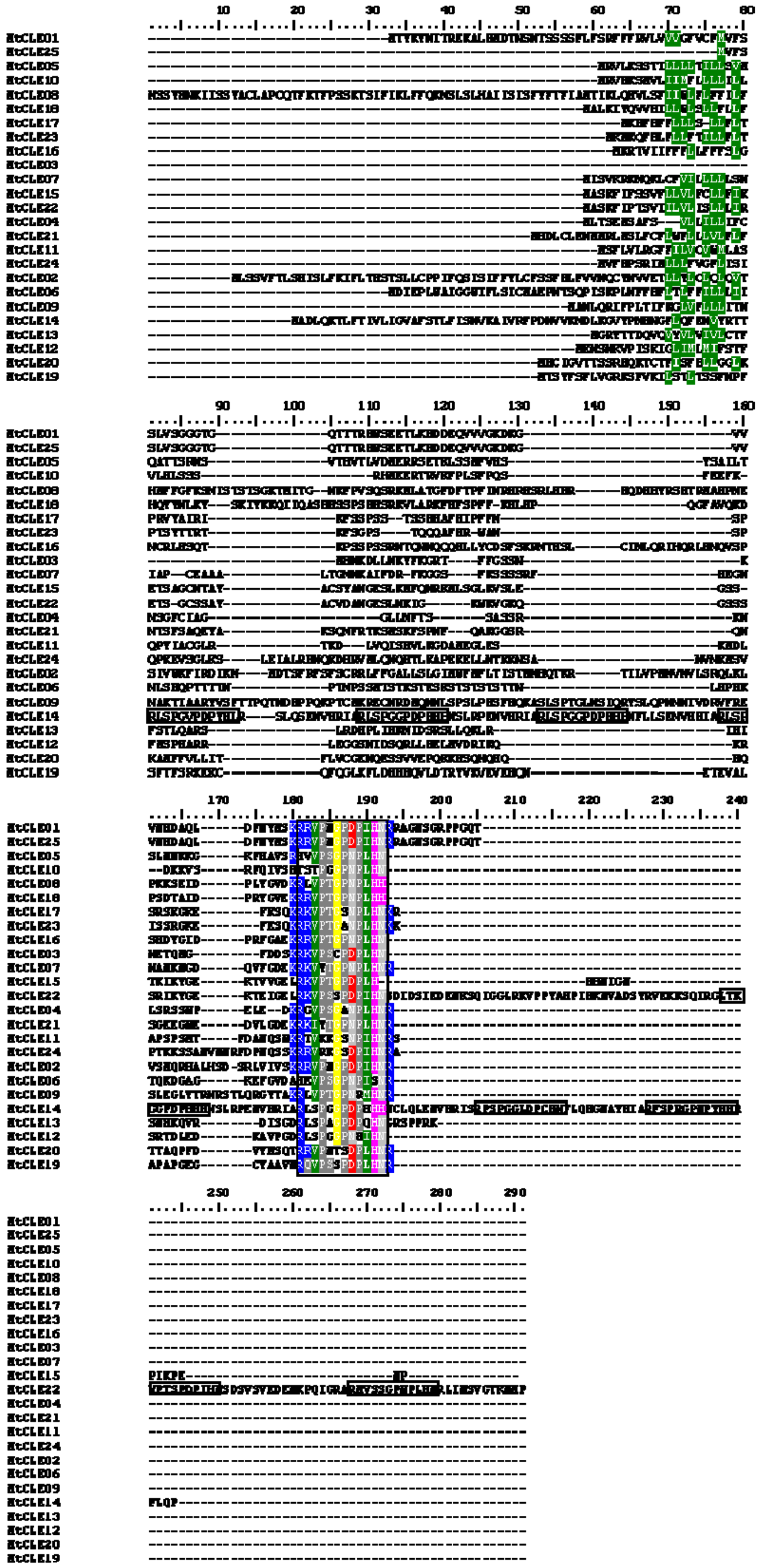
Supplemental Table S2. Comparison of the CLE peptide sequence of *MtCLE4*, *MtCLE12*, and *MtCLE13* with the CLE peptide sequences from Arabidopsis *CLE* genes and of *LjCLE1*, *LjCLE2*, and *LjCLE3*.

CLE peptide sequences homologous to *MtCLE12* and *MtCLE13* are framed in blue and those to *MtCLE4* in red.

MtCLE12	**R**	**L**	**S**	**P**	**G**	**G**	**P**	**N**	**H**	**I**	**H**	**N**
MtCLE13	**R**	**L**	**S**	**P**	**A**	**G**	**P**	**D**	**P**	**Q**	**H**	**N**
LjCLE1	R	L	S	P	G	G	P	D	P	Q	H	N
LjCLE2	R	L	S	P	G	G	P	D	P	Q	H	N
AtCLE7	R	F	S	P	G	G	P	D	P	Q	H	H
AtCLE5/6	R	V	S	P	G	G	P	D	P	Q	H	H
AtCLE2	R	L	S	P	G	G	P	D	P	Q	H	H
AtCLE1/3/4	R	L	S	P	G	G	P	D	P	R	H	H
AtCLE46	H	K	H	P	S	G	P	N	P	T	G	N
AtCLE41/44	H	E	V	P	S	G	P	N	P	I	S	N
AtCLE42	H	G	V	P	S	G	P	N	P	I	S	N
LjCLE3	R	V	V	P	T	G	P	N	P	L	H	N
MtCLE4	**R**	**G**	**V**	**P**	**S**	**G**	**A**	**N**	**P**	**L**	**H**	**N**
AtCLE9/10	R	L	V	P	S	G	P	N	P	L	H	N
AtCLE11	R	V	V	P	S	G	P	N	P	L	H	H
AtCLE12	R	R	V	P	S	G	P	N	P	L	H	H
AtCLE13	R	L	V	P	S	G	P	N	P	L	H	H
AtCLE14	R	L	V	P	K	G	P	N	P	L	H	N
AtCLE16	R	L	V	H	T	G	P	N	P	L	H	N
AtCLE17	R	V	V	H	T	G	P	N	P	L	H	N
AtCLE18	R	Q	I	P	T	G	P	D	P	L	H	N
AtCLE19	R	V	I	P	T	G	P	N	P	L	H	N
AtCLE20	R	K	V	K	T	G	S	N	P	L	H	N
AtCLE21	R	S	I	P	T	G	P	N	P	L	H	N
AtCLE22	R	R	V	F	T	G	P	N	P	L	H	N
AtCLE25	R	K	V	P	N	G	P	D	P	I	H	N
AtCLE26	R	K	V	P	R	G	P	D	P	I	H	N
AtCLE27	R	I	V	P	S	C	P	D	P	L	H	N
AtCLE40	R	Q	V	P	T	G	S	D	P	L	H	H
AtCLE45	R	R	V	R	R	G	S	D	P	I	H	N
AtCLV3	R	T	V	P	S	G	P	D	P	L	H	H

Supplemental Table S3. Primers used in the analysis.

Gene	Sense Primer	Anti-sense Primer
Gateway cloning		
ORF-MtCLE4	ATGCTAACAAGTGAAATGAGCG	CTACCGATTATGCAGAGGATTAGC
ORF-MtCLE12	ATGGAGAATTCAAATAAAGTGCCAAT	TTAGTTATGTATATGGTTTGGTCCAC
ORF-MtCLE13	ATGGGCCGGTATACAACC	CTACTTTCTTGGTGGTGATCT
promoter-MtCLE12	TGTAATGTGATGGTGGACTT	CATGCAAAGAACAAGAAGTTGG
promoter-MtCLE13	TCATTCCTAGTAGAACGGCG	GCCCATGTGTGATTTTAATC
qRT-PCR amplification		
MtCLE1	TGGTGGGGTTTGTTTGTTTTATGG	GTCTTGTAGTTGTTTGTCCTGTTCC
MtCLE2	ATGAATGTGAATGTTCTCTCTAGGC	GGTTGTCTATATTTCCTTGCTCTCC
MtCLE3	GGTTCAAGCAACAAGAATGAAACAC	AGGATCTGGGCAGCTTGGTAC
MtCLE4	AATTTCACAAGTTCTGCTTCATCGC	TGGCACACCTCTCTTGTCTTCC
MtCLE5	AATGCAAGCTACCACGTCTCG	GCAGAGGATTTGGTCCAGAAGG
MtCLE6	TCTATCTCACCAACCAACAACAACC	TCCAAATTCTTTTCCAGCTCCATCC
MtCLE7	AACTGTGTTTTGTTATTCTTCTTC	AGATGATGATGATTTGAATGAACC
MtCLE8	TTCTCAAAGTAGGAAAATGTTAGC	CGATGATGAAGACGACTATGG
MtCLE9	GCTCGCTATGTTTCCTTCAC	AGAGATGGACTTAGATTATTCTGC
MtCLE10	GCACATGGAAGAAAGAACAAGAGTC	CCCCTGGAGTAGATGTATGTGAAAC
MtCLE11	TGTTAGCTTCTCAACCATACATTGC	TGAAGGTGAAGGTGCCAAATCC
MtCLE12	CAACGTCTCTTGCATGAGTTAATGG	ACCTGGTGAAAGCCTATCTCCTG
MtCLE13	CCGAAGCCTTCTACAGAAACTACG	TCTTGGTGGTGATCTTCCATTATGC
MtCLE14	ACACCACCACAATTCCTTAC	ATATGATGAACATTCTCAGATAGC
MtCLE15	CAGTGGTTGGAGAGTTGAGAAAGG	TCAAGGGTTTTCAGGCTTAATAGGG
MtCLE16	AACACTCAAAACAACCAACAACAACATC	ACTCTTCTCTTCTCAGCACCAAATC
MtCLE17	TCTCAAGCCCTTCTTCTACTTC	TCCTGTAGGCACTTTGCGTTTC
MtCLE18	TTCACATTCTACTATGGCTATCTC	ATGATGACTTGCTTGTATGATTTG
MtCLE19	TTGATACTTTTCTTTTCTTGTTGG	TTGAAACTGACATCACTTCT
MtCLE20	TGTTACCACTTCATCACGGCATC	TGTGGCTCAACAACTGAAGACTC
MtCLE21	GCTAAAGGAGGTTCAAGACAG	GTAAAGGATTAGGACCAGTGTAG
MtCLE22	TCATCCCTACCTCTGTCATTATAC	ATCCTTGCTTACCAACCTTCC
MtCLE23	CTTCCTTACACCTACATCTTACAC	TTACCTCTGCTGCTGATTGG
MtCLE24	AAGAAGAGTTCGGCTAATGTC	CTGTTGTGAATAGGATCTGACC
MtCLE25	CACTCAAACATGATGATGAACAAG	TGAATAGGATCTGGTCCATTAGG
40S Ribos	GCCATTGTCCAAGTTTGATGCTG	TTTTCCTACCAACTTCAAAACACCG
GFP	ACGGCATCAAGGTGAACTTC	GTGCTCAGGTAGTGGTTGTC
GUS	CTACACCACGCCGAACAC	CACCACCTGCCAGTCAAC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HtCLE19

Figure S1. Sequence alignment of the *MtCLE* genes. In the *M. truncatula* genome, 25 *MtCLE* peptide genes were found. Alignment was created by ClustalW analysis. Conserved amino acid residues are indicated in color and the conserved 12 amino-acid-long CLE peptides are framed.

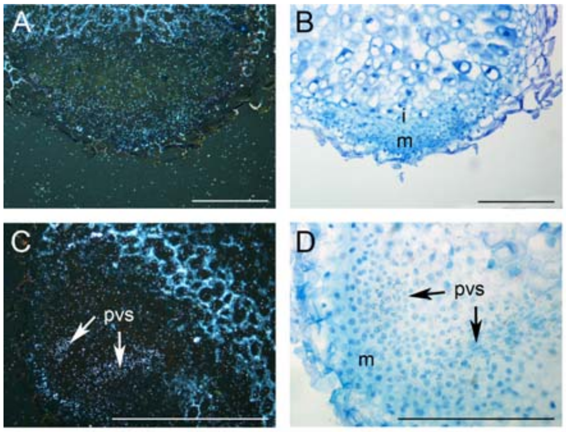

Figure S2. *MtCLE13* transcript accumulation in mature nodules by *in situ* hybridization. *MtCLE13* mRNA was localized by in situ hybridization with a *MtCLE13* antisense probe covering the complete open reading frame. Dark-field (A and C) and bright-field (B and D) microscopic images. Signal is seen as white and black dots in dark-field and bright-field micrographs, respectively. A and B, Detail of the meristematic zone of a mature nodule showing low signal in the meristem (m) and infection zone (i). C and D, Detail of a mature nodule in which the signal is localized in the provascular strands (pvs). Scale bars = 500µm.

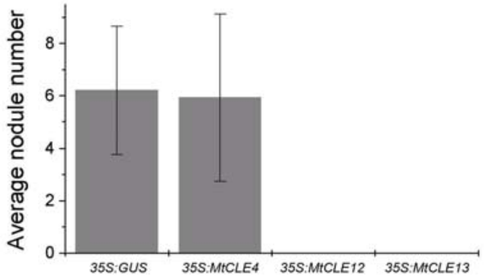

Figure S3. Average nodule number on roots ectopically expressing *GUS*, *MtCLE4*, *MtCLE12*, or *MtCLE13* at 11 dpi with a NF-overproducing *Sinorhizobium meliloti* strain. Average nodule number on plants with transgenic roots carrying the *35S:GUS*, *35S:MtCLE4*, *35S:MtCLE12* or *35S:MtCLE13* constructs at 11 dpi (n=6-17). Inoculation was done with a NF-overproducing *Sinorhizobium meliloti* strain (GMI6390:2011(pMH682)). Data and error bars represent mean ± SD.

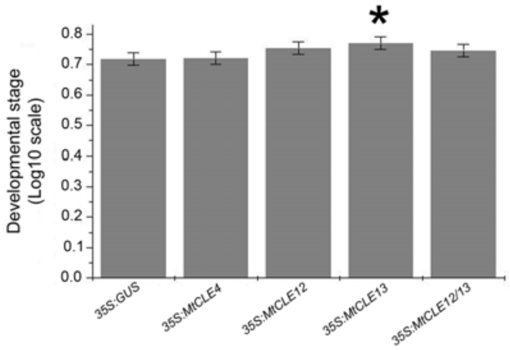

Figure S4. Log10 of the developmental stage of composite plants carrying roots ectopically expressing *GUS*, *MtCLE4*, *MtCLE12*, *MtCLE13*, or *MtCLE12* and *MtCLE13*.

Developmental stage was measured according to Bucciarelli et al., 2006. Data and error bars represent mean ± SE. Asterisk marks a group statistically different from the control (*35S:GUS*).

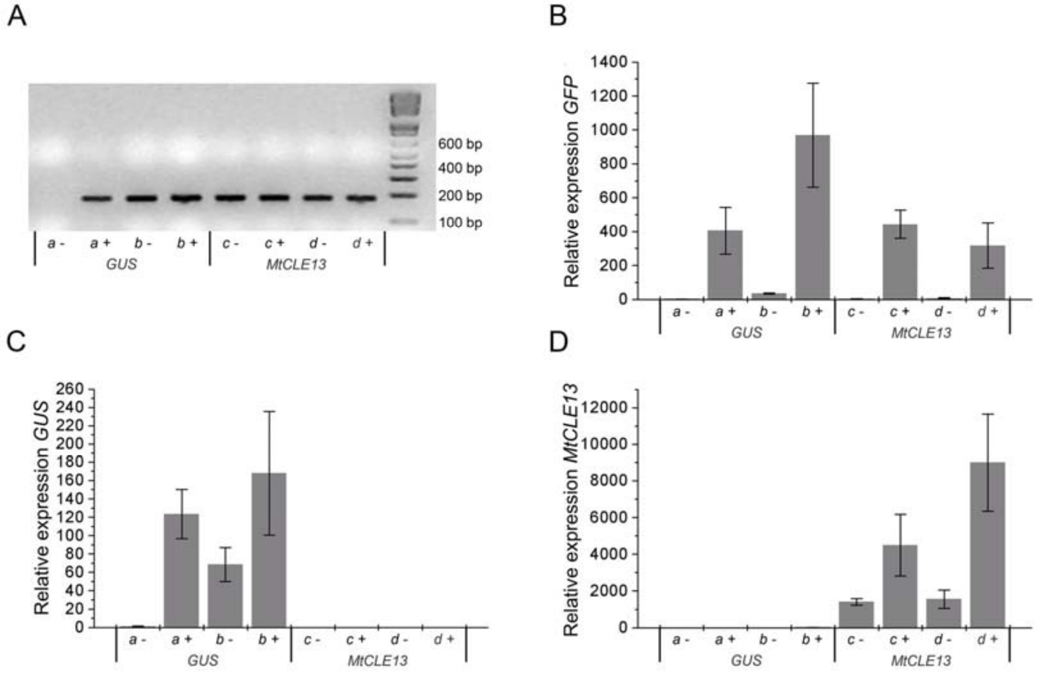

Figure S5. Detailed genotypic analysis of transgenic roots obtained by *A. rhizogenes* transformation.

Jemalong J5 plants were transformed with either *35S:GUS* (plants *a* and *b*) or *35S:MtCLE13* (plants *c* and *d*). Roots with (+) and without (-) GFP fluorescence were kept on the plants and harvested separately at 7 dpi. gDNA as well as cDNA were prepared from these samples. A, Gel electrophoresis of PCR products obtained with GFP-specific primers on the gDNA samples of these roots. B-D, Expression analysis of *GFP*, *GUS*, and *MtCLE13* by qRT-PCR on the cDNA samples of the roots.