

Supplementary Figures

CRISPR/Cas9-Mediated Generation of Mutant Lines in *Medicago truncatula* Indicates a Symbiotic Role of *MtLYK10* during Nodule Formation

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Figure S1. Illustration of the cloning procedure to generate CRISPR/Cas9 binary vectors with two sgRNA expression cassettes.

Figure S2. Identification of *M. truncatula* plants with mutations in *MtLYK10*, *MtMFS1* and *MtMFS2*.

Figure S3. PCR analysis of the P3 plant containing a deletion in *MtLYK10*.

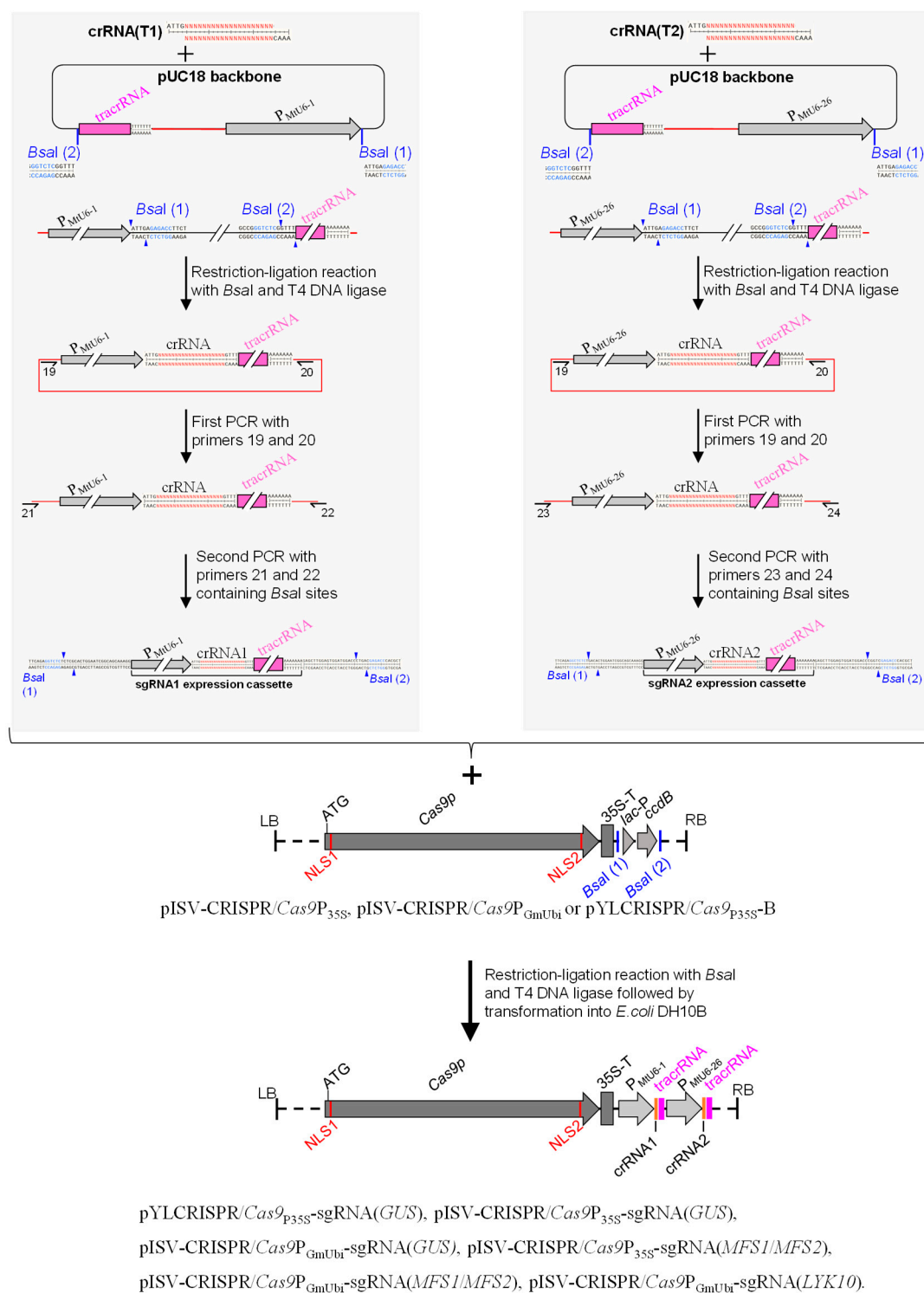


Figure S1. Illustration of the cloning procedure to generate CRISPR/Cas9 binary vectors with two sgRNA expression cassettes. For abbreviations, see legend to Figure 1.

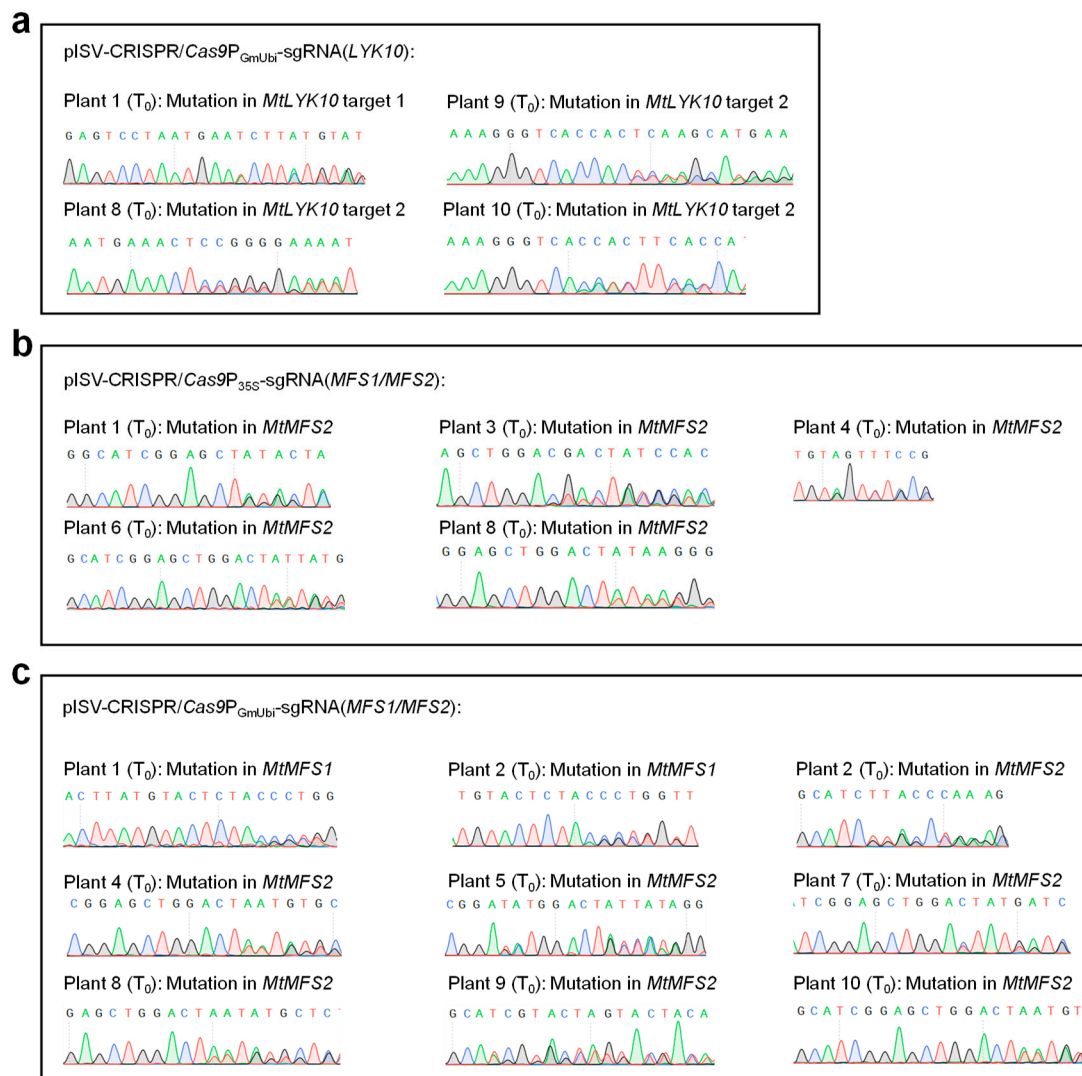


Figure S2. Identification of *M. truncatula* plants with mutations in *MtLYK10*, *MtMFS1* and *MtMFS2*. *M. truncatula* leaf explants were transformed with the indicated binary vectors. Leaf DNA of regenerated plants (T₀ generation) and gene specific primers were used for PCRs and the amplicons were directly sequenced. Sanger sequencing results are shown for plants with mutations at target sites (chromatograms with double peaks). (a) Plants transformed with pISV-CRISPR/Cas9P_{GmUbi}-sgRNA(*LYK10*). (b) Plants transformed with pISV-CRISPR/Cas9P_{35S}-sgRNA(*MFS1/MFS2*). (c) Plants transformed with pISV-CRISPR/Cas9P_{GmUbi}-sgRNA(*MFS1/MFS2*).

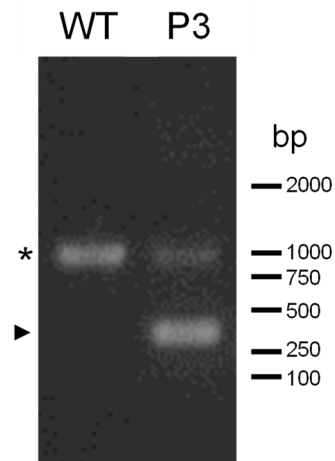


Figure S3. PCR analysis of the P3 plant containing a deletion in *MtLYK10*. *M. truncatula* leaf explants were transformed with pISV-CRISPR/*Cas9*_{GmUbi}-sgRNA (*LYK10*) and a deletion in *MtLYK10* was identified in the P3 plant (T₀ generation) by sequencing. The picture shows an agarose gel with DNA amplified from genomic wild-type and P3 DNA using *MtLYK10* specific primers. Abbreviations: WT, *MtLYK10* DNA amplified from wild-type plants. P3, *MtLYK10* DNA amplified from the heterozygous P3 plant containing a *MtLYK10* wild-type allele (upper band marked by an asterisk) and a mutated *MtLYK10* allele with a 654-bp deletion (lower band marked by an arrowhead).

Supplementary Tables

CRISPR/Cas9-mediated generation of mutant lines in *Medicago truncatula* indicate a symbiotic role of *MtLYK10* during nodule formation

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Table S1. Plasmids used in this study.

Plasmids	Relevant characteristics	Reference/Source
pYLsgRNA-AtU6-1	Vector with a pUC18 backbone, tracrRNA and the AtU6-1 promoter of <i>A. thaliana</i> , Amp ^r	[43]
pYLCRISPR/ <i>Cas9</i> P _{35S} -B	Binary vector with a pCambia1300 backbone and <i>Cas9p/Bar</i> expression cassettes, Kan ^r	[43]
pRT104- <i>DsRed1</i>	A 678-bp <i>DsRed1</i> fragment PCR-amplified from pX-DR and cloned into pRT104 digested with <i>Xba</i> I and <i>Xho</i> I, Amp ^r	[47]
pISV2678	Derivative of pGPTV-BAR with an enhanced double CaMV 35S promoter. Kan ^r	Schultze and Kondorosi; CNRS, Gif-sur-Yvette, France
pUC-tracrRNA-P _{MtU6-1}	Vector with a pUC18 backbone, tracrRNA and the MtU6-1 promoter of <i>M. truncatula</i> R108, Amp ^r	This study
pUC-tracrRNA-P _{MtU6-26}	Vector with a pUC18 backbone, tracrRNA and the MtU6-1 promoter of <i>M. truncatula</i> R108, Amp ^r	This study

pMD19-P _{Gmubi}	P _{Gmubi} (ubiquitin gene promoter of <i>G. max</i> cv. William 82) cloned into pMD-19, Amp ^r	This study
pMD19- <i>DsRed1</i>	<i>DsRed1</i> cassette from pRT104- <i>DsRed1</i> cloned into pMD-19, Amp ^r	This study
pMD19- <i>DsRed1</i> (ΔB)	Point mutated vector of pMD19- <i>DsRed1</i> without <i>BsaI</i> (ΔB) restriction site, Amp ^r	This study
pISV- <i>DsRed1</i> (ΔB)	<i>DsRed1</i> (ΔB) expression cassette cloned into the <i>HindIII</i> site of pISV2678, Kan ^r	This study
pBS- <i>Cas9-ccdB</i>	pBluescript II SK (+) derivative carrying <i>cas9p</i> and <i>ccdB</i> sequences from pYLCRISPR/ <i>Cas9P</i> _{35S} -B, Amp ^r	This study
pISV-CRISPR/ <i>Cas9P</i> _{35S}	pISV- <i>DsRed1</i> (ΔB) derivative carrying <i>Cas9p</i> and <i>ccdB</i> sequences from pBS- <i>Cas9-ccdB</i> , Kan ^r	This study
pISV-CRISPR/ <i>Cas9P</i> _{GmUbi}	pISV- <i>DsRed1</i> (ΔB) derivative carrying P _{Gmubi} , the <i>cas9p</i> coding sequence and a <i>ccdB</i> expression cassette, Kan ^r	This study
pYLCRISPR/ <i>Cas9P</i> _{35S} -sgRNA(<i>GUS</i>)	pYLCRISPR/ <i>Cas9P</i> _{35S} -B derivative carrying two sgRNA expression cassettes for <i>GUSPlus</i> editing, Kan ^r	This study
pISV-CRISPR/ <i>Cas9P</i> _{35S} -sgRNA(<i>GUS</i>)	pISV-CRISPR/ <i>Cas9P</i> _{35S} derivative carrying two sgRNA expression cassettes for <i>GUSPlus</i> editing, Kan ^r	This study
pISV-CRISPR/ <i>Cas9P</i> _{GmUbi} -sgRNA(<i>GUS</i>)	pISV-CRISPR/ <i>Cas9P</i> _{GmUbi} derivative carrying two sgRNA expression cassettes for <i>GUSPlus</i> editing, Kan ^r	This study
pISV-CRISPR/ <i>Cas9P</i> _{35S} -sgRNA(<i>MFS1/MFS2</i>)	pISV-CRISPR/ <i>Cas9P</i> _{35S} derivative carrying a sgRNA expression cassette for <i>MtMFS1</i> editing and a sgRNA expression cassette for <i>MtMFS2</i> editing, Kan ^r	This study

pISV-CRISPR/ <i>Cas9P</i> _{GmUbi} - sgRNA(<i>MFS1/MFS2</i>)	pISV-CRISPR/ <i>Cas9P</i> _{GmUbi} derivative carrying a sgRNA expression cassette for <i>MtMFS1</i> editing and a sgRNA expression cassette for <i>MtMFS2</i> editing, Kan ^r	This study
pISV-CRISPR/ <i>Cas9P</i> _{GmUbi} -sgRNA(<i>LYK10</i>)	pISV-CRISPR/ <i>Cas9P</i> _{GmUbi} derivative carrying two sgRNA expression cassettes for <i>MtLYK10</i> editing, Kan ^r	This study

Table S2. Primers used in this study.

Prim ers	Sequences (5'→3')	Restrictio n sites	Description	Amplico n (bp)
1	GATATCGAATTCCTGCAGCCCGGGTCTCCACTGA	<i>SmaI</i>	Amplification of <i>Cas9p</i> with nuclear localization signals and a terminator sequence from pYLCRISPR/ <i>Cas9P35S-B</i>	4668
2	CCGGTCAACATGTGGAGCACGACCGCGTCACTGG ATTTTGGTT			
3	AACCAAAATCCAGTGACGCGGTCGTGCTCCACAT GTTGACCGG	<i>NotI</i>	Amplification of a <i>ccdB</i> expression cassette from pYLCRISPR/ <i>Cas9P35S-B</i>	765
4	CCGCGGTGGCGGCGCTCTAGATAGCTCGAGAG GCGCGCCA			
5	TCGATTCTAGAGAATTCCCTTAATTAAGGGCCCA ATATAACAACGACGTCG	<i>EcoRI</i> , <i>PacI</i>	Amplification of <i>P</i> _{Gmubi} from genomic DNA of <i>G. max</i> cv. Willams 82	917
6	TCCCTTACGTCAGTGGAGATTAATTAAGGCTGTC GAGTCAACAATCACAGATAA	<i>PacI</i>		
7	GCTTGCGGCAGCGTGAAGCTTAACATGGTGGAGC ACGACACTC		Amplification of a <i>DsRed1</i> cassette from pRT104- <i>DsRed1</i>	1316
8	GGACCTGCAGGCATGCAAGCTTGATTTTGGTTTAA GGAATTAG			

9	GACGGCGTGCTGAAGGGCGAAACACACAAGGCC CTGAAGC		Amplification of pMD19- <i>DsRed1</i> (Δ B)	4008
10	GCTTCAGGGCCTTGTGTGTTTCGCCCTTCAGCACG CCGTC			
11	AACATCGATTCTAGAGAATTCCCTTAATTAATCT CCACTGACGTAAGGGATG	<i>EcoRI</i> , <i>PacI</i>	Amplification of a large DNA fragment containing <i>Cas9p</i> and <i>ccdB</i>	5466
12	GAGCCCGGGGTCGACGAATTCTAGCTCGAGAGG CGCGCCAATG	<i>EcoRI</i>		
13	TCCTTTGCTGCCGATTCCACAGG		Amplification of DNA containing pUC18 and	2846
14	ATTGAGAGACCTCTGAAGATAAC		tracrRNA from pYLsgRNA-AtU6-1	
15	GTGGAATCGGCAGCAAAGGAATCCAACATTTAC TTGAGTTAAC		Amplification of P _{MtU6-1} from genomic DNA of	541
16	TATCTTCAGAGGTCTCTCAATAAACCTGCTGTTC GTCTAGGC		<i>M. truncatula</i> R108	
17	GTGGAATCGGCAGCAAAGGATAGGAAATTTGCT GGGAAAC		Amplification of P _{MtU6-26} from genomic DNA of	536
18	TATCTTCAGAGGTCTCTCAATAAGCCATTGTGCTC TGTGACG		<i>M. truncatula</i> R108	
19	CTCCGTTTTACCTGTGGAATCG		Amplification of sgRNA expression cassettes	634
20	CGGAGGAAAATTCCATCCAC			
21	TTCAGAGGTCTCTCTCGCACTGGAATCGGCAGCA AAGG	<i>BsaI</i>	Amplification of sgRNA expression cassettes with <i>BsaI</i> sites	673
22	AGCGTGGGTCTCGTCAGGGTCCATCCACTCCAAG CTC	<i>BsaI</i>		
23	TTCAGAGGTCTCTCTGACACTGGAATCGGCAGCA AAGG	<i>BsaI</i>	Amplification of sgRNA expression cassettes with <i>BsaI</i> sites	677

24	AGCGTGGGTCTCGACCGGGTCCATCCACTCCAAG CTC	<i>BsaI</i>	
25	TCGGGTACAGACTAGTTCGT	Confirmation of CRISPR/Cas9 binary vectors containing sgRNA for <i>GUSPlus</i>	670
26	CTTCGAATGGCAGGAATCCG		
27	TCAACTTATGTACTCTACGC	Confirmation CRISPR/Cas9 binary vectors containing sgRNA of <i>MFS1/MFS2</i>	670
28	TAATAGTCCAGCTCCGATGC		
29	GAGTCCTAATGAAACTTCTG	Confirmation of pISV-CRISPR/ <i>Cas9</i> _{P_{GmUbi}} -sgRNA(<i>LYK10</i>)	670
30	TGGTAAAGTGGTGACCCTTT		
31	CATGGTAGATCTGAGGGTAAATTTC	Detection of mutations in <i>GUSPlus</i>	940
32	TTCGGAATCTCCACGTTACC		
33	ATGGGTTCAGCTGAAAATGTAGAATC	Detection of mutations in <i>MFS1</i>	1169
34	TACCTGCTAAGAACTTCAGAGTC		
35	ATGGGTGGTGTCTCGTTGAATATGAAG	Detection of mutations in <i>MFS2</i>	1166
36	CTGCTAAGAACTTCAGAGTCATTAGC		
37	ATGGCTTCTCTAATTCAACTTGTTTC	Detection of mutations in <i>LYK10</i>	1000
38	GTGACATTGCTTTCAGTAATTACC		
39	ATGAGCCCAGAACGACGCCCCG	Detection of the <i>Bar</i> gene in transformed plants	552
40	TCAGATCTCGGTGACGGGCAGG		
41	GGAGGCCATAGTGGAATTTTAGGG	Analysis of possible off-target mutations	376
42	CATGGTTGTCACTACAATAGAGCCC		
43	GGATCCTTTTTCTGTTGGCTAGTGG	Analysis of possible off-target mutations	467
44	GCCAGACAGCAACTTTTAGAGTTAGC		
45	CTCTACACCAAGAGACTGGACTGG	Analysis of possible off-target mutations	391
46	AGACATGCTAGTTCCAGATACCATCG		
47	GCAGGAAGCTCCAAGCTTACACAC	Analysis of possible off-target mutations	420

48	GCTATATTGACTACACGTGTTAGCCG		
49	CCAAATGAGTTACAACAGAGTTAGCAGC	Analysis of possible off-target mutations	359
50	CCAAACAATCTGCAATAGCTTCAGC		
51	ATGGGAACCCTCGGAAGAGC	Analysis of possible off-target mutations	368
52	CATACCCATAAAGCATTACTACGACTACC		
53	GCTTCGAGAATGGCAGGTAAGTC	Analysis of possible off-target mutations	471
54	CCTTAAAGGGTCATAATCACTATCGC		
55	GGTTGAACTAATGCTGGGACATCG	Analysis of possible off-target mutations	395
56	GCAGCACAGTGCACTAAAGCTC		
57	TGGCATACATGTCGATCAATGACG	Analysis of possible off-target mutations	426
58	CGACGATGATTCAGCGTATGTG		

Table S3. Target-specific oligonucleotides used in this study.

Name	Sequences (5'→3')	Description	Length (bp)
T-F(<i>GUS</i>)-1 T-R(<i>GUS</i>)-1	attgTCGGGTACAGACTAGTTCGT aaacACGAACTAGTCTGTACCCGA	<i>GUSPlus</i> target 1	20
T-F(<i>GUS</i>)-2 T-R(<i>GUS</i>)-2	attgCGGATTCCTGCCATTCGAAG aaacCTTCGAATGGCAGGAATCCG	<i>GUSPlus</i> target 2	20
T-F(<i>MtMFS1</i>)-1 T-R(<i>MtMFS1</i>)-1	attgTCAACTTATGTACTCTACGC aaacGCGTAGAGTACATAAGTTGA	<i>MtMFS1</i> target 1	20
T-F(<i>MtMFS2</i>)-2 T-R(<i>MtMFS2</i>)-2	attgGCATCGGAGCTGGACTATTA aaacTAATAGTCCAGCTCCGATGC	<i>MtMFS2</i> target 2	20
T-F(<i>MtLYK10</i>)-1 T-R(<i>MtLYK10</i>)-1	attgGAGTCCTAATGAACTTCTG aaacCAGAAGTTTCATTAGGACTC	<i>MtLYK10</i> target 1	20

T-F(<i>MtLYK10</i>)-2	attgAAAGGGTCACCACTTTACCA	<i>MtLYK10</i> target 2	20
T-R(<i>MtLYK10</i>)-2	aaacTGGTAAAGTGGTGACCCTTT		

Table S4. Sequence analysis of possible off-target sites in *lyk10* mutants.

Analyzed mutant	Predicted off-target gene	Predicted off-target site	Used primers	Amplicon length (bp)	Mutations in obtained sequences
<i>lyk10-1</i>	MTR_2g063570	AAGTCCTAATGGAAATTCTG AGG *	41, 42	376	No
<i>lyk10-2</i>	MTR_2g063570				No
<i>lyk10-3</i>	MTR_2g063570				No
<i>lyk10-1</i>	MTR_7g029350	ACGTGCTAATGAACTTCAG TGG *	43, 44	467	No
<i>lyk10-2</i>	MTR_7g029350				No
<i>lyk10-3</i>	MTR_7g029350				No
<i>lyk10-1</i>	MTR_4g127480	GAGTCCAAATGGAACTGATG AGG *	45, 46	391	No
<i>lyk10-2</i>	MTR_4g127480				No
<i>lyk10-3</i>	MTR_4g127480				No
<i>lyk10-1</i>	MTR_2g069950	CAGTCCTAATGAAAATGATT TGG *	47, 48	420	No
<i>lyk10-2</i>	MTR_2g069950				No
<i>lyk10-3</i>	MTR_2g069950				No
<i>lyk10-1</i>	MTR_5g024910	AGAGGATCATCATTTTACCA TGG **	49, 50	359	No
<i>lyk10-2</i>	MTR_5g024910				No
<i>lyk10-3</i>	MTR_5g024910				No
<i>lyk10-1</i>	MTR_3g112020	AAAGGGTCATCAATTTGGTA TGG **	51, 52	368	No
<i>lyk10-2</i>	MTR_3g112020				No
<i>lyk10-3</i>	MTR_3g112020				No
<i>lyk10-1</i>	MTR_1g054795	AAAGTGTCACCTCTTTGCGA TAG **	53, 54	471	No

<i>lyk10-2</i>	MTR_1g054795				No
<i>lyk10-3</i>	MTR_1g054795				No
<i>lyk10-1</i>	MTR_4g116370	AAAAGGTCACCATTTTACCT TCC **	55, 56	395	No
<i>lyk10-2</i>	MTR_4g116370				No
<i>lyk10-3</i>	MTR_4g116370				No
<i>lyk10-1</i>	MTR_7g056073	AAAGCTTCACCACTTCACCA TAT **	57, 58	426	No
<i>lyk10-2</i>	MTR_7g056073				No
<i>lyk10-3</i>	MTR_7g056073				No

* Results from <http://skl.scau.edu.cn/offtarget/> using GAGTCCTAATGAACTTCTGTGG (target 1) in *MtLYK10* as query sequence.

** Results from <http://skl.scau.edu.cn/offtarget/> using AAAGGGTCACCACTTTACCATGG (target 2) in *MtLYK10* as query sequence.