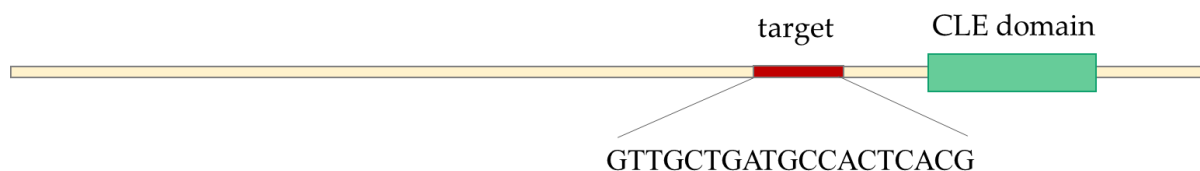
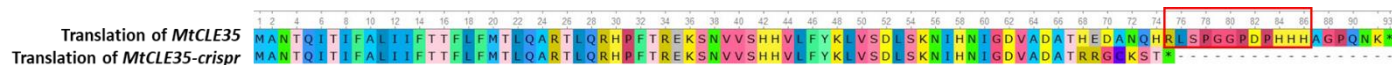


A

MtCLE35 CDS (279 bp)

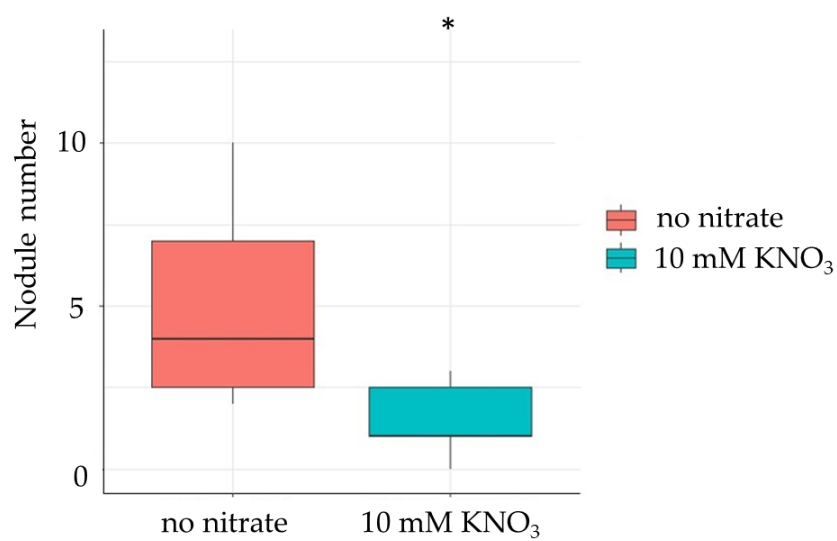


B



T0 plant ID (№/sample ID)		In/del
1	#1	+1(G)/ +1(C)
2	#2	-15/+1
3	#4	deletions of various length
4	#6	+1/-3
5	#8	deletions of various length
6	#9	-4/-3
7	#10	-15
8	#11	-20/-1
9	#12	-4/-5
10	#13	+1/-2
11	#14	deletions of various length
12	#15	-1/-5
13	#16	0 (wild type)
14	#17	+1(G)/ +1(C)
15	#18	-20/-1
16	#19	0 (wild type)
17	#20	-1/-5
18	#21	+1/-2
19	#25	-5/-1
20	#27	-20/-1

Supplementary Table S1. Genotypes of T0 plants obtained after transformation with the construct for CRISPR/Cas9-mediated editing of the *MtCLE35* gene. The data are obtained based on the analysis of sequencing chromatogram for the *MtCLE35* gene using Synthego ICE tool. For two plants, #16 and #19, no editing events were found (wild type genotype). In/del – insertions and deletions within the *MtCLE35* CDS, negative numbers correspond to the length of deletions in bp, +1 corresponds to 1 bp insertion. Three plants (#4, #8, #14) had deletions of various length according to Synthego ICE analysis indicating multiallelic changes in the *MtCLE35* gene in these plants.



Supplementary Figure S2. Number of nodules at 28 dpi in wild-type plants (R108) grown without nitrate and in presence of 10 mM KNO₃. * $p < 0.05$ (wilcoxon test, $n = 15$).