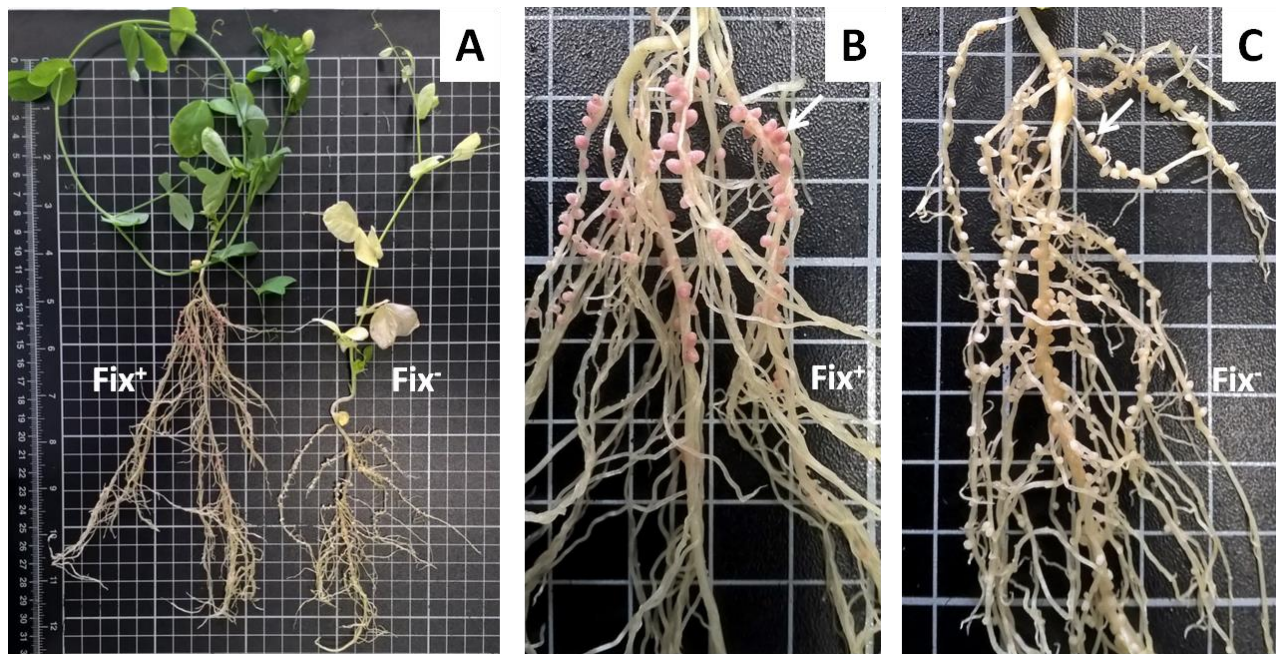


## Supplementary Material

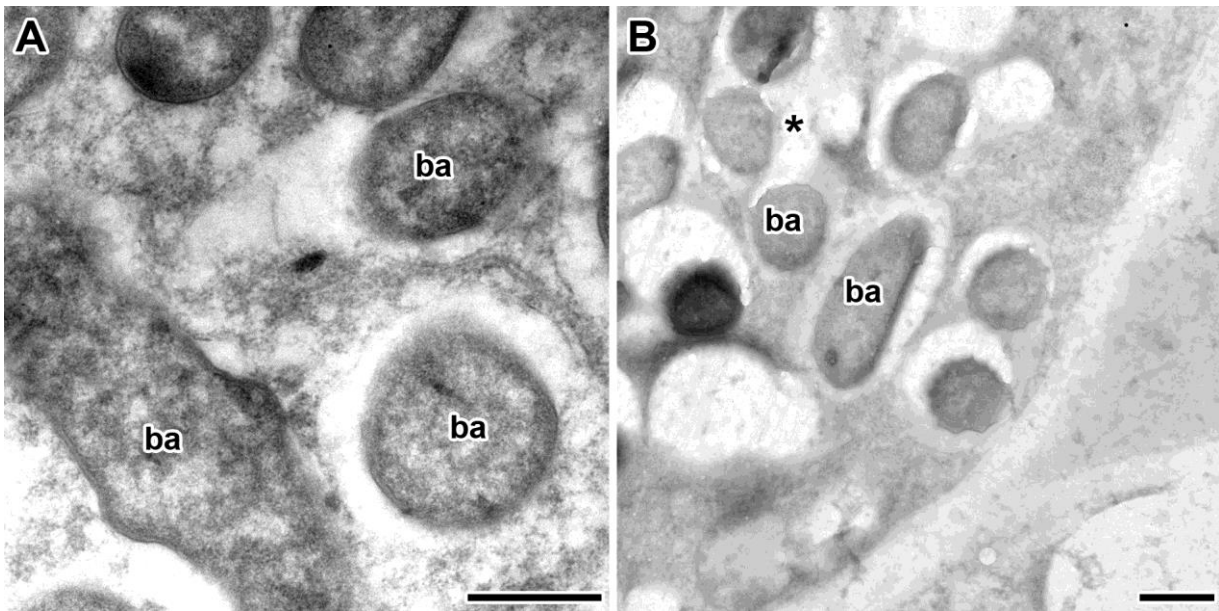


**Supplementary Figure 1.** Development of plants of *Pisum sativum* L. lines Sprint-2 ( $\text{Fix}^+$  phenotype) and Sprint-2 $\text{Fix}^-$  (*sym31*;  $\text{Fix}^-$  phenotype) inoculated with *Rhizobium leguminosarum* bv. *viciae* strain RCAM 1026 (25 days after inoculation). **(A)** Appearance of the whole plants. **(B, C)** Sprint-2 **(B)** and Sprint-2 $\text{Fix}^-$  **(C)** root systems with nodules (arrowed). One grid division is 10 mm.

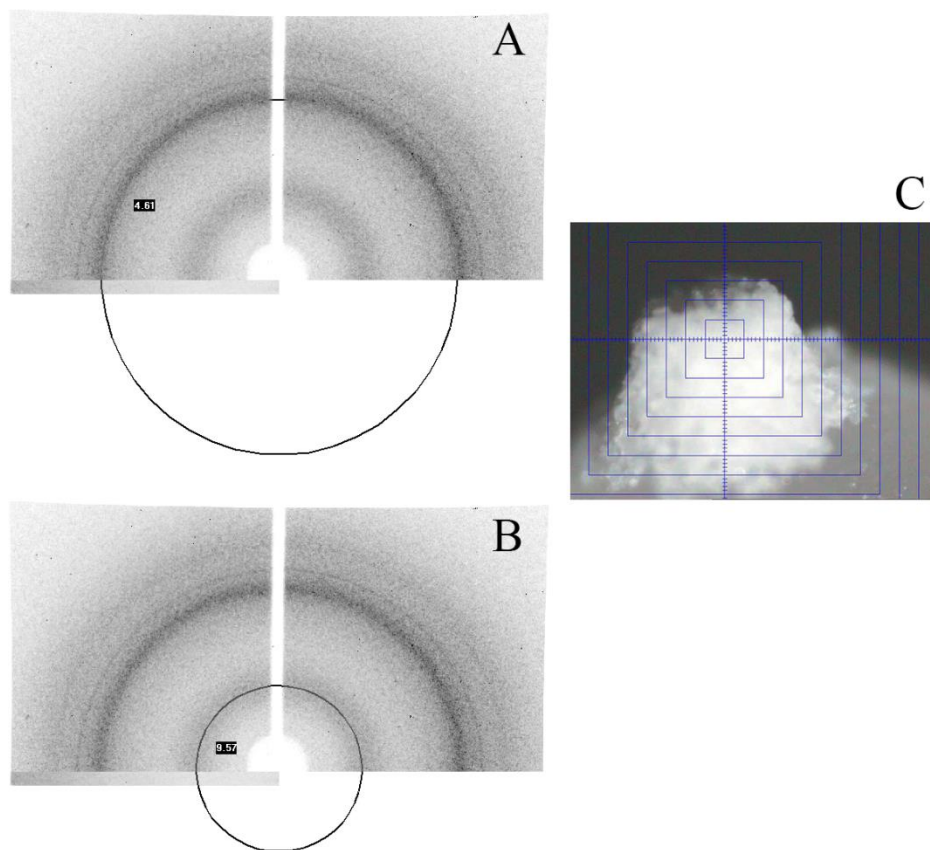
**Supplementary Table 1.** Biometric parameters of the wild-type *Pisum sativum* L. plants Sprint-2 and the mutant Sprint-2 $\text{Fix}^-$  (*sym31*) 25 days after inoculation with *Rhizobium leguminosarum* bv. *viciae* RCAM1026.

Plant genotype	Whole plant fresh weight, g (n = 15)	Shoot fresh weight, g (n = 15)	Nodule number per plant, pcs. (n = 3)	Nodule fresh weight per plant, g (n = 3)	Fresh weight of one nodule, mg
Sprint-2 (Wt)	4.283	1.992	94.7	0.093	1.037
Sprint-2 $\text{Fix}^-$ ( <i>sym31</i> )	1.636*	0.775*	215.3*	0.133	0.623

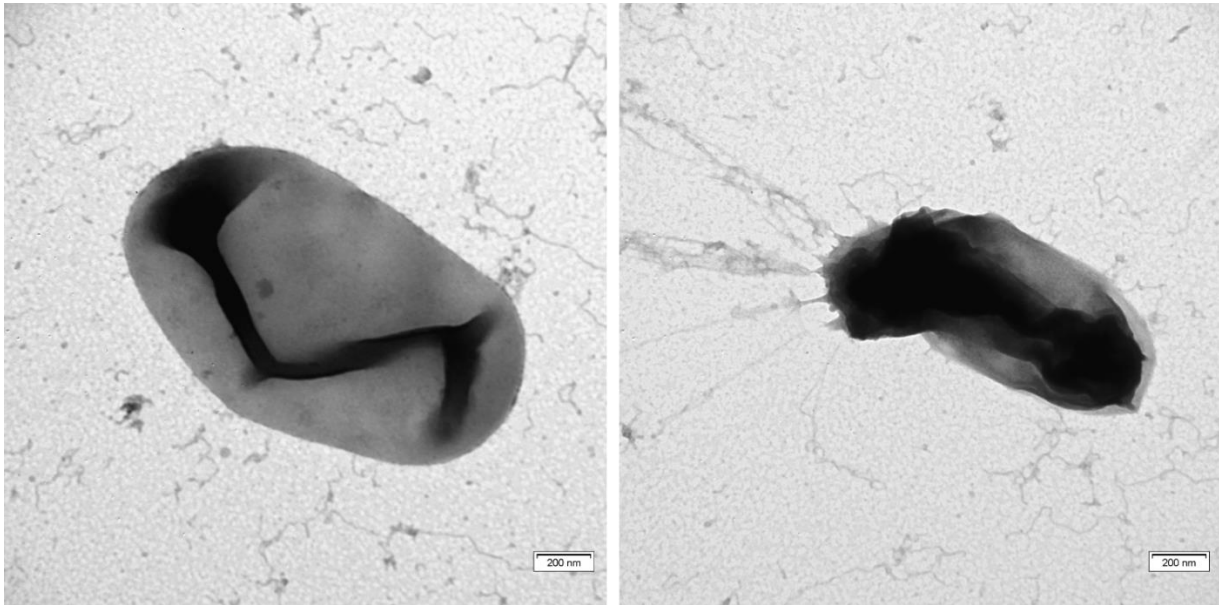
\* – the values of the mutant and the original line differ significantly ( $p \leq 0.05$ ). Pairwise comparison of data was performed using the One-Way ANOVA test in the SigmaPlot 12.0 program (SPSS Inc Chicago, IL, USA).



**Supplementary Figure 2.** Transmission electron micrographs of cells from *Pisum sativum* L. nodule treated as negative control. Gold particles were absent when cells were treated with unspecific secondary antibody (**A**), after the omission of the primary antibody (**B**). ba – bacteroid, \* – multibacteroid symbiosome. (**A**) Wild-type line Sprint-2 of *Pisum sativum* L. labelled with RopB antibody and treated with anti-mouse secondary antibody conjugated to 10 nm diameter colloidal gold. (**B**) Mutant line Sprint-2Fix<sup>-</sup> (*sym31*) of *Pisum sativum* L. after omission of the primary antibody. Bar: (**A**) = 200 nm, (**B**) = 500 nm.



**Supplementary Figure 3.** (A) and (B) x-ray diffraction analysis revealed ring-shaped x-ray reflections of RopB fibrils. Calibration rings corresponding to distances of 9.57 Å and 4.61 Å are shown on top of the reflections. (C) A crystal of aggregated RopB on the surface of a paraffin head prepared according to the technique described in Materials and Methods (x-ray diffraction analysis) of the manuscript. The x-ray beam pointing area is shown.



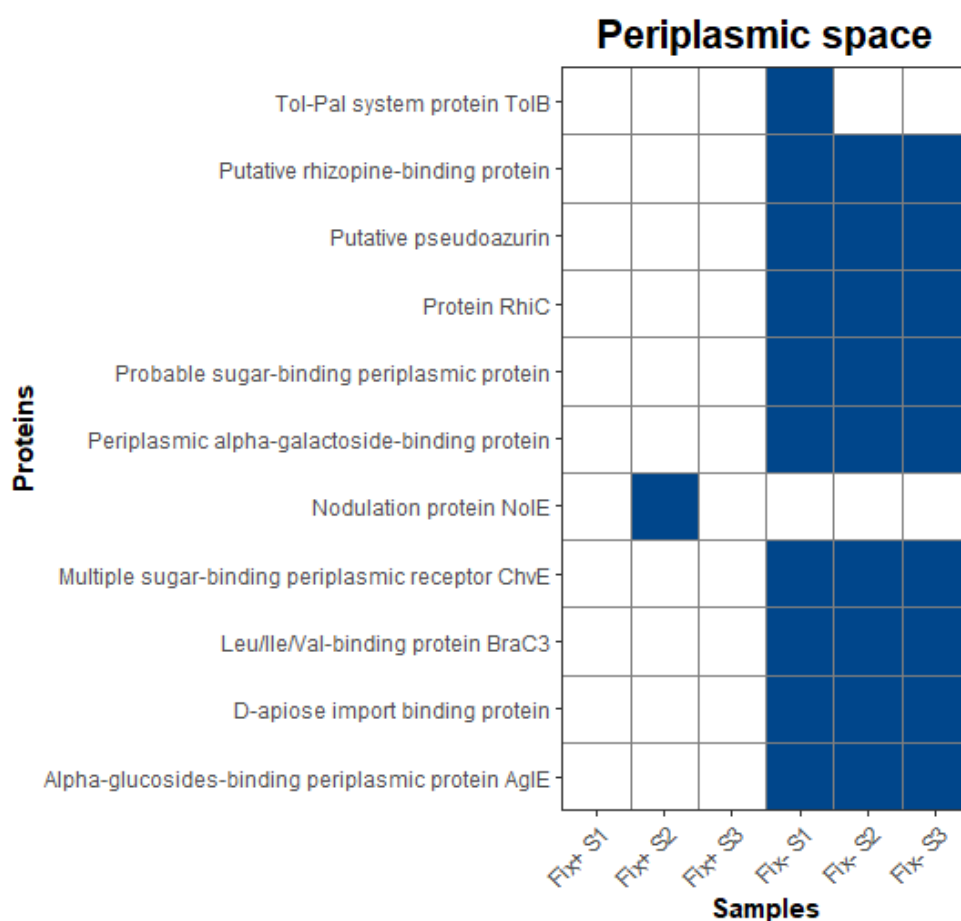
**Supplementary Figure 4.** Transmission electron micrographs of bacteroids treated as negative control. Bacteroids from mutant line Sprint-2Fix<sup>-</sup> (*sym31*) of *Pisum sativum* L. treated only with anti-rabbit secondary antibody conjugated to 10 nm diameter colloidal gold. Bar = 200 nm.

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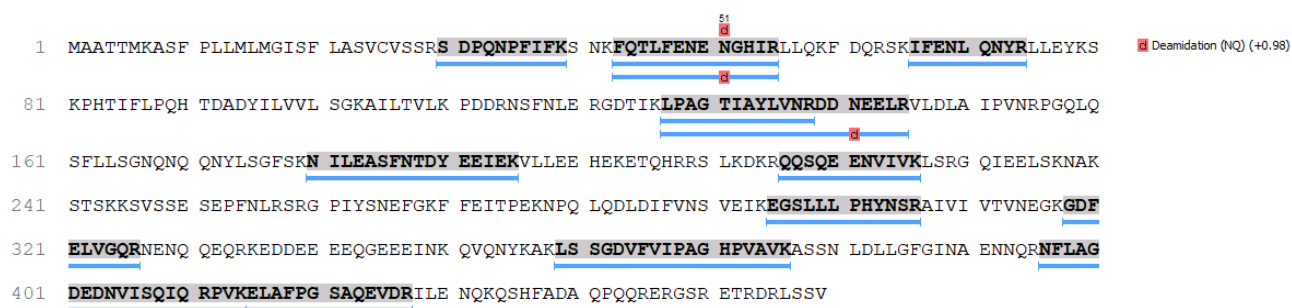
1  MRVLIAGLMA SVFAIAGVSA AQAADRVDQV PEAPVAQEAP VKPAGSWEGF YLGAGTYNM GDFGSDRHTY GFGGQVFTGY
81  NWQQGQIVYG VESDLGYSGD DVSSGGVENK YGWNGSVRGR VGYDMNPFL YGTAGLAIGD VKVSDTSDE SKTNFGYTVG
161 AGVEAFVTNN ITTRLEYRYT DYQSKDYDLD SGSFSGGYDE NSVKLGIGVK F

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**Supplementary Figure 5.** Coverage of RopB protein with peptides identified with mass-spectrometry. Amino acid sequence of RopB is shown. Peptides identified by mass spectrometry are highlighted and underlined.



**Supplementary Figure 6.** Potentially amyloidogenic proteins of *Rhizobium leguminosarum* with “periplasmic space” cellular component GO term identified in protein samples obtained from Fix<sup>+</sup> and Fix<sup>-</sup> nodules. Proteins identified in particular samples (S1-S3) and Fix status of nodules are shown.



**Supplementary Figure 7.** Coverage of vicilin protein with peptide identified with mass-spectrometry. Amino acid sequence of vicilin is shown. Peptides identified by mass spectrometry are highlighted and underlined. Amino acid modifications are marked.