TABLE S1. Bacterial strains and plasmids used in this work.

Strain or plasmid	Relevant genotype or phenotype	Source of reference
Strains		
E. coli strains		
DH5α	*supE44* Δ*lacU*169-(Ψ80*lacZ*Δ*M15*)*hsdR1* *recA1* *gyrA96 thi-1 relA1*	Bethesda Research Laboratories, Inc., Gaithersburg, U.S.A.
S17-1	Sm^r Sp^r; *hdsR* (RP4-2 *kan*::Tn7 *tet*::Mu, integrated in the chromosome)	(1)
B. japonicum strains		
110*spc*4	Sp^r; wild type	(2)
6243	Sp^r Km^r; Δbll3156-3157*::aph*II (same orientation)	This work
Plasmids		
pGEM-T Easy	Ap^r; cloning vector	Promega Corporation, Madison, U.S.A.
pBSL15	Ap^r Km^r; cloning vector	(3)
pSUP202pol4	Tc^r; (pSUP202) part of the polylinker from pBlueskript II KS+ between *EcoR*I and *Pst*I	(4)
pRJ6240	Ap^r; (pGEM-T Easy) 623 bp amplicon of the bll3156 downstream region comprising the *B. japonicum* genome sequence from coordinate 3489814 to 3490437	This work
pRJ6241	Ap^r; (pGEM-T Easy) 636 bp amplicon of the bll3157 upstream region comprising the *B. japonicum* genome sequence from coordinate 3493519 to 3494155	This work
pRJ6242	Tc^r; (pSUP202pol4) 1259 bp *Eco*RI/*Not*I up- and downstream region of bll3156-bll3157	This work
pRJ6243	Tc^r Km^r; (pSUP202pol4) the *aph*II cassette flanked by the up-and downstream region of bll3156-bll3157	This work

1. **Simon R, Priefer U, Pühler A.** 1983. Vector plasmids for *in vivo* and *in vitro* manipulation of gram-negative bacteria. Springer Verlag, Heidelberg, Germany.
2. **Regensburger B, Hennecke H.** 1983. RNA polymerase from *Rhizobium japonicum*. Arch Microbiol **135:**103-109.
3. **Alexeyev MF.** 1995. Three kanamycin resistance gene cassettes with different polylinkers. Biotechniques **18:**52-56.
4. **Fischer HM, Babst M, Kaspar T, Acuna G, Arigoni F, Hennecke H.** 1993. One member of a *groESL*-like chaperonin multigene family in *Bradyrhizobium japonicum* is co-regulated with symbiotic nitrogen fixation genes. EMBO J **12:**2901-2912.

TABLE S2. Specific nitrogenase activity (% C_2H_4 min^{-1} g^{-1}) of *B. japonicum* wild type and 6243 mutant on soybean, mungbean, cowpea and siratro plants.

	Relevant genotype	Soybean	Mungbean	Cowpea	Siratro
110*spc*4	Wild type	1.9 ± 0.7	1.9 ± 0.9	2.5 ± 0.7	1.7 ± 0.8
6243	Δ*frc-oxc*	1.7 ± 1.2	2.2 ± 0.8	2.9 ± 1.7	1.2 ± 0.7