Rhizobium leguminosarum **biovar** ***viciae*** **3841, deficient in 27-hydroxyoctacosanoate-modified lipopolysaccharide, is impaired in desiccation tolerance, biofilm formation and motility**

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SUPPLEMENTARY FIGURE LEGEND

Supplementary Fig. S1. (a) Alignment of portions of *Rhizobium leguminosarum* bv *viciae* 3841 FabF1 (Rlegum_1; YP_768399) and FabF2 (Rlegum_2; YP_768400) with *E. coli* W3110 FabF (BAA35903). Stars indicate amino acid identity. Similar sequences are indicated by double and single dots. Catalytic triad residues are shaded. Additional conserved residues within the active site are indicated in bold type (Huang *et al.*, 1998). (b) Alignment of the FabF2 protein sequences from members of the Rhizobiales. *R. leguminosarum* (Rlegum; YP_768400), *R. leguminosarum* bv *trifolii* (Rtrif; ZP_02295003.1), *Rhizobium etli* (Retli; YP_469980.1), *Agrobacterium tumefaciens* (Agrobac; NP_354591.1), *Sinorhizobium meliloti* (Sinorhiz; NP_386046.1), *Bartonella quintana* (Bart; YP_032192.1), *Brucella suis* (B_suis; NP_697867.1), *Mesorhizobium loti* (M_loti; NP_102825.1) and *Bradyrhizobium japonicum* (Brady; NP_770449.1). Similar sequences are indicated by double and single dots.

REFERENCE

Huang, W. J., Jia, J., Edwards, P., Dehesh, K., Schneider, G. & Lindqvist, Y. (1998). Crystal structure of β-ketoacyl-acyl carrier protein synthase II from *E. coli* reveals the molecular architecture of condensing enzymes. *EMBO J* **17**, 1183–1191.