



Figure S5: Tricarboxylic acid cycle. A modified version of the KEGG pathway map ko00020 [1] displaying the tricarboxylic acid (TCA) cycle is shown. Reactions encoded by the *Ensifer* sp. M14 genome are colored green; those in white are missing. The figure was prepared using the KAAS webserver [2] using BLAST search with the bi-directional best hit assignment method, and with the default organism list for ‘prokaryotes’ plus *Sinorhizobium meliloti* Rm1021.

1. Kanehisa, M.; Sato, Y.; Kawashima, M.; Furumichi, M.; Tanabe, M. KEGG as a reference resource for gene and protein annotation. *Nucleic Acids Res.* **2016**, *44*, D457–D462.
2. Moriya, Y.; Itoh, M.; Okuda, S.; Yoshizawa, A. C.; Kanehisa, M. KAAS: an automatic genome annotation and pathway reconstruction server. *Nucleic Acids Res.* **2007**, *35*, W182–5.