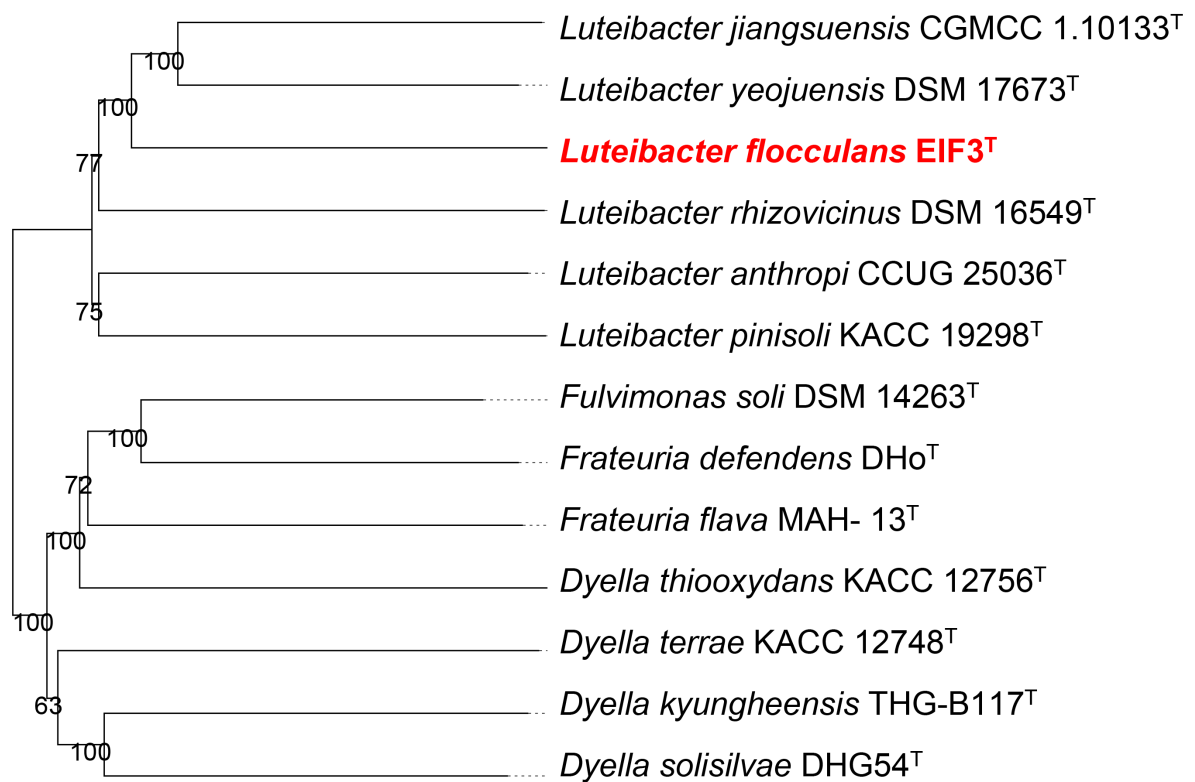




**Figure S1. Flocculation of EIF3<sup>T</sup> in LB medium.**



**Figure S2. Phylogenetic classification of *Luteibacter flocculans* EIF3<sup>T</sup>.** The 12 closest related type strain genomes were used for phylogenetic analysis as described by TYGS (Meier-Kolthoff and Göker, 2019). The tree was inferred with FASTME 2.1.6.1 (Lefort et al., 2015) using Genome Blast Distance Phylogeny (GBDP) distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula  $d_5$ . The numbers above the branches are GBDP pseudo-bootstrap support values of >60% from 100 replications, with an average branch support of 85.1%. The tree was rooted at the midpoint (Farris, 1972).

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