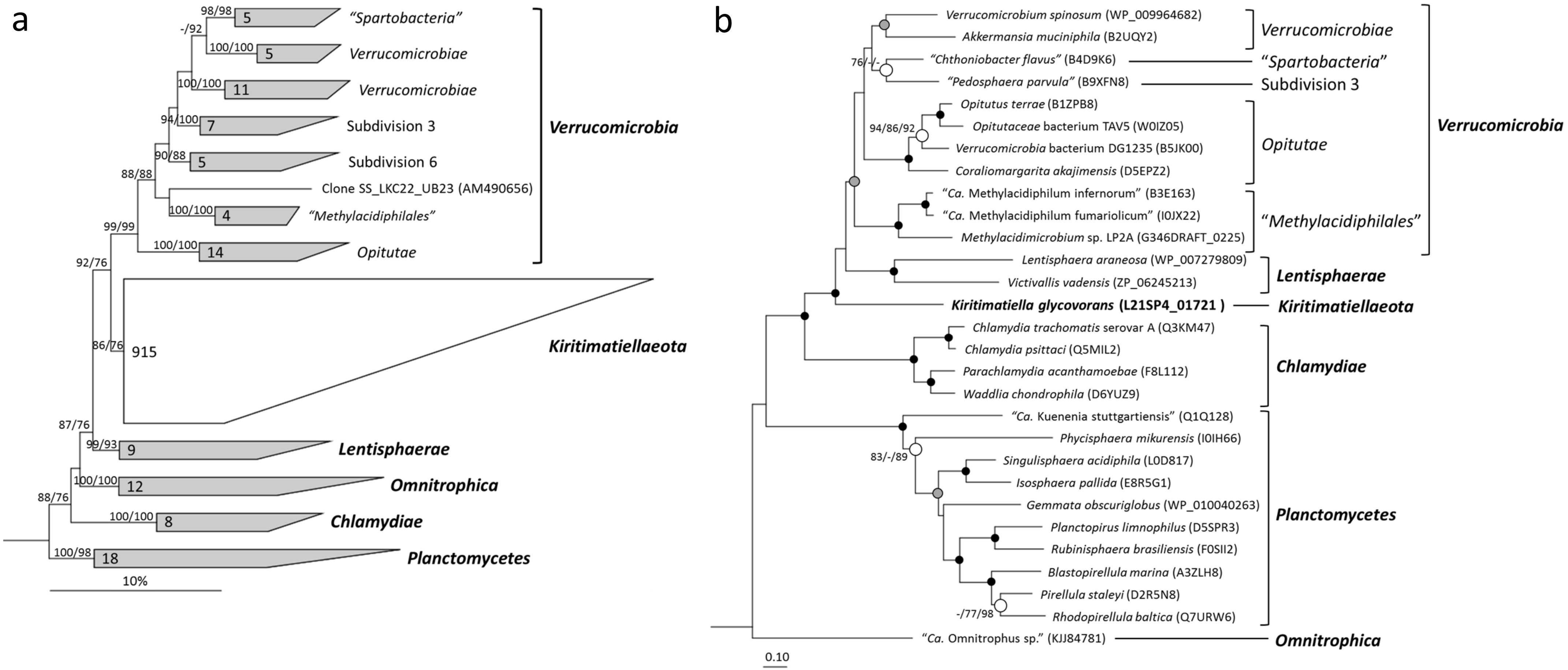

Supplementary Figure S1. Phylogenetic position of *K. glycovorans* L21-Fru-AB^T and related bacteria within the PVC superphylum determined by using various sequence data sets for tree reconstruction.

(a) Phylogenetic tree based on a data set of 1015 almost complete 16S rRNA gene sequences. The tree topology was reconstructed with the neighbor-joining algorithm and rooted with the sequence of Escherichia coli K12 (AKVX01000001, not shown). Phylogenetic distances were calculated with the correction of Jukes Cantor as implemented in the ARB neighbor-joining program. Based on the used alignment a filter was calculated that excluded all positions which show less than 50% conservation. Bootstrap values based on 1000 replicates are given at each node with the first number indicating tree reconstruction using the 50% conservation filter and the second number tree reconstruction without filter. Numbers within polygons indicate the number of used sequences. Scale bar, 10% estimated sequence divergence. **(b)** Phylogenetic tree based on amino acid sequences of complete RpoB proteins. The tree topology was reconstructed under the maximum-likelihood criterion and rooted using the RpoB protein sequence of *Escherichia coli* K12 (P0A8V2, not shown). Support of a distinct branching by bootstrap analyses is indicated by symbols as explained in the legend of Fig. 1. Scale bar, 0.10 changes per nucleotide position.