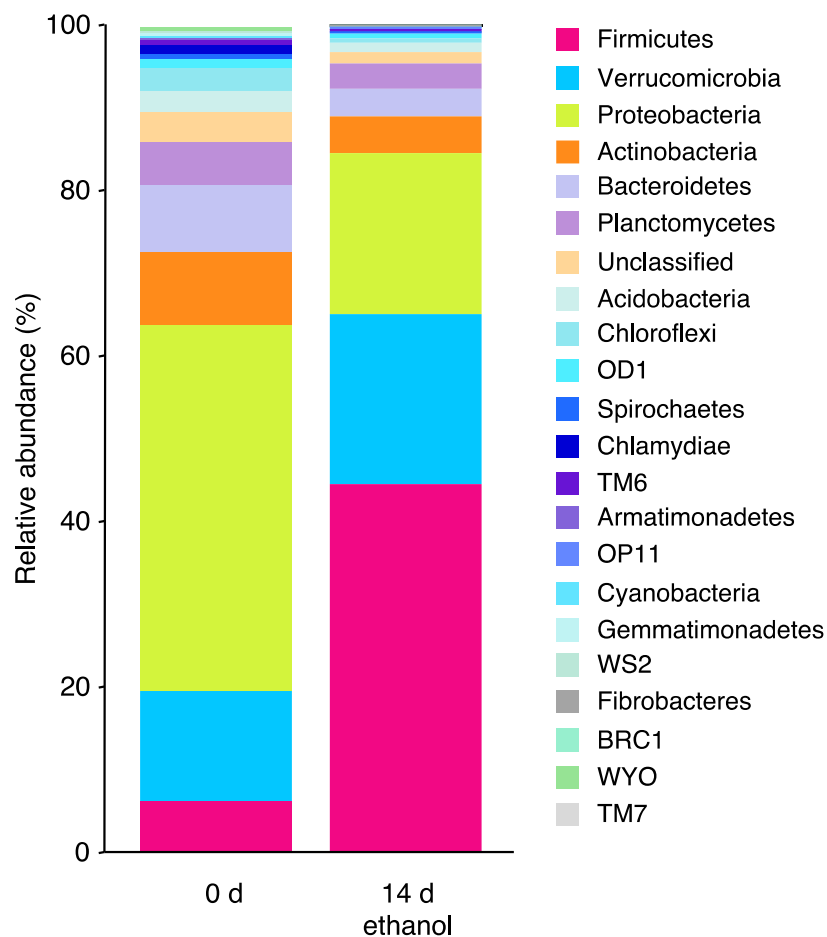
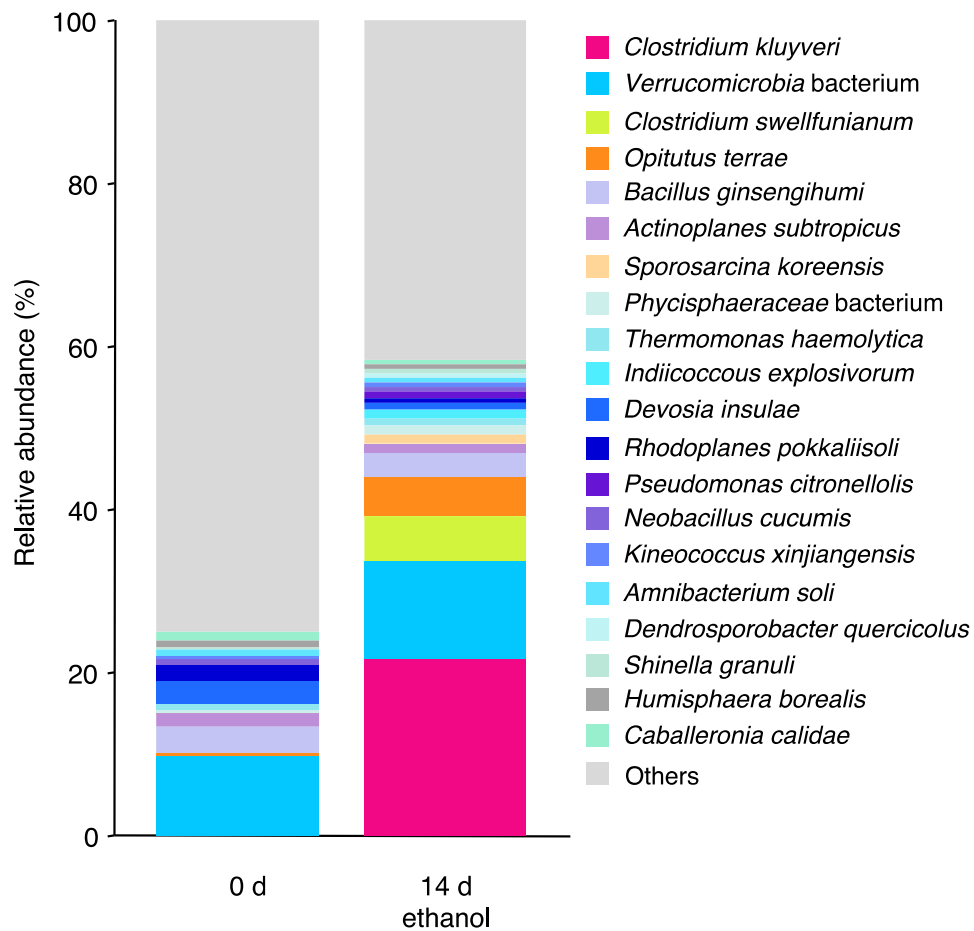


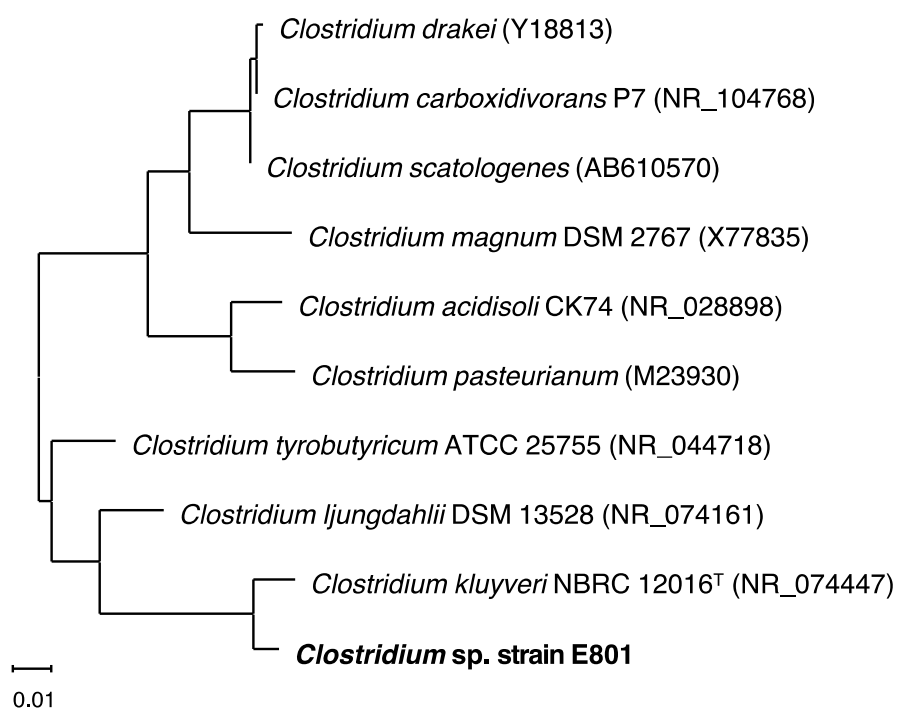
**Figure S1.** Phylum-level bacterial community structures before (0 d) and after (17 d) the laboratory-scale anaerobic soil disinfestation as determined by high-throughput sequencing of 16S rRNA genes.



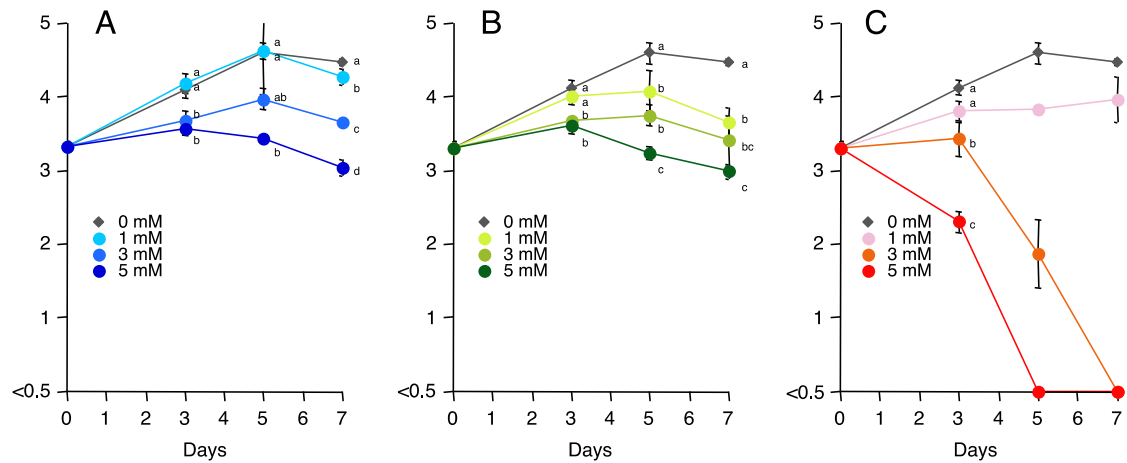
**Figure S2.** Phylum-level bacterial community structures before (0 d) and after (14 d) another laboratory-scale anaerobic soil disinfestation. The V4 region of 16S rRNA gene was amplified by using universal primers 515F and 806R, and the sequences were characterized phylogenetically by use of the QIIME software package as described previously [55].



**Figure S3.** Species-level bacterial community structures before (0 d) and after (14 d) another laboratory-scale anaerobic soil disinfestation. The V4 region of 16S rRNA gene was amplified by using universal primers 515F and 806R, and the sequences were characterized phylogenetically by use of the QIIME software package as described previously [55].



**Figure S4.** Phylogenetic tree showing the relationship between strain E801 and related bacteria within *Clostridium sensu stricto* (*Clostridium* cluster I). The tree was constructed using the neighbor joining method. Scale bar indicates 1 % estimated sequence divergence.



**Figure S5.** Viable number of *Ralstonia solanacearum* cells incubated in MES buffer adjusted at pH 5.5. The buffer contained 0 to 5 mM of acetate (**A**), butyrate (**B**) or caproate (**C**). Values are expressed as means of Log colony forming unit (CFU) of *R. solanacearum* cells mL<sup>-1</sup>  $\pm 1.96 \times$  standard error, when a normal distribution is assumed. Symbols with different alphabets indicate statistically significant differences based on Tukey's HSD ( $\alpha = 0.05$ ).