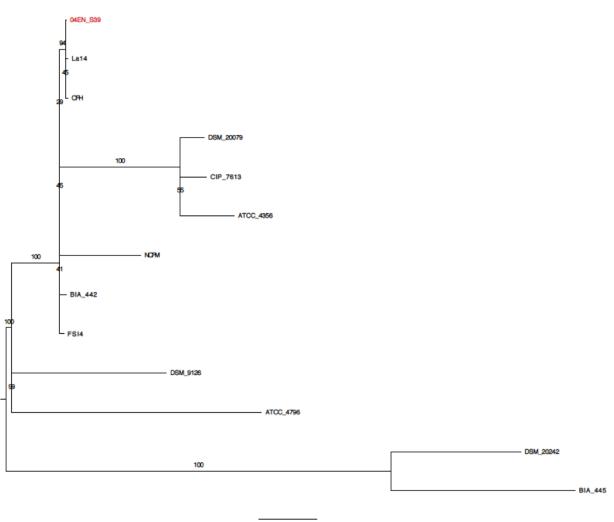
Supplemental Digital Content 1. The phylogenetic structure of Lactobacillus acidophilus

Mid-point rooted maximum likelihood phylogeny of 13 *L. acidophilus* strains, including strain used in this study (highlighted in red) and 12 complete whole genome sequences retrieved from the public database. Numbers above branches indicate bootstrap support values, and horizontal scale bar represents the number of nucleotide substitutions per site.



0.06