

Supplemental Fig. S1. Neighbor-joining phylogenetic tree based on the 16S rRNA gene sequences of the carotenoid-producing LAB isolated in this study and other related taxa. Nucleotide sequences were aligned using a CLUSTALW program and phylogenetic analysis was performed with the MEGA6 program. *Enterococcus faecalis* ATCC 19433T was used as an out-group. The scale bar represents 0.01 substitutions per nucleotide position.

