



Figure S1. 16S rDNA maximum likelihood phylogenetic tree. The tree was constructed with MEGA6 using 16S rDNA on *Carnobacterium* genomes and close organisms *Pisciglobus halotolerans* DSM27630T, *Aerococcus urinaequi* CCUG28094T and *Granulicatella adiacens* ATCC49175. *Lactococcus garvieae* ATCC49156 was used as an outgroup. Genomes sequenced in this study are highlighted in red.