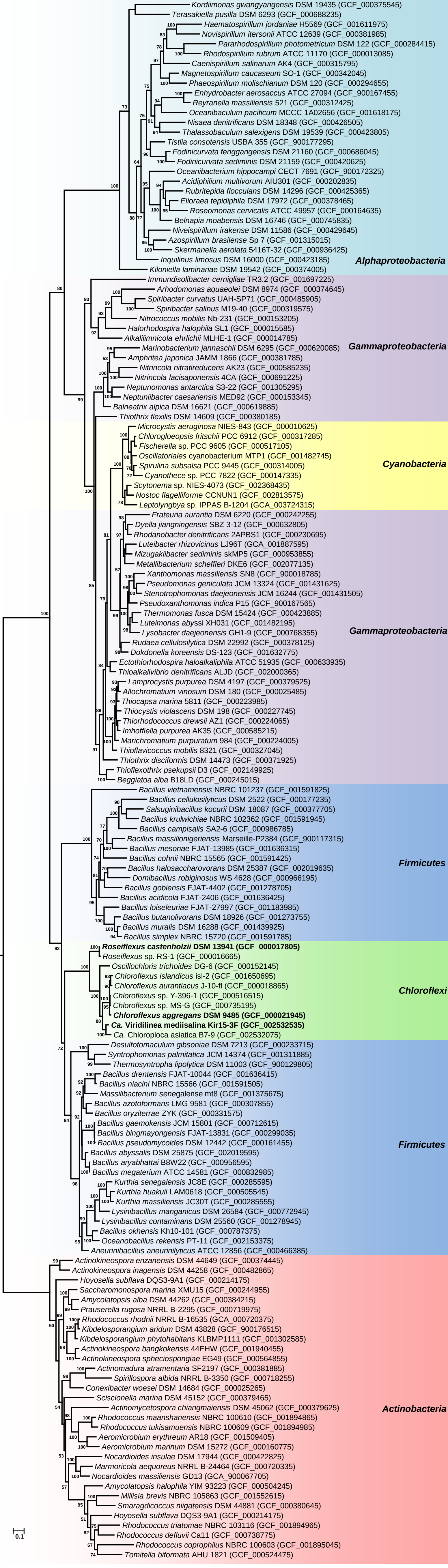

Supplementary Figure S4. Maximum likelihood phylogenetic tree of polyhydroxyalkanoate synthase (PhaC) amino acid sequences, based on a LG+F+I+G4 protein substitution model. Black numbers represent ultrafast bootstrap values (>50%) expressed in percent. The scale bar represents amino acid substitutions per site.