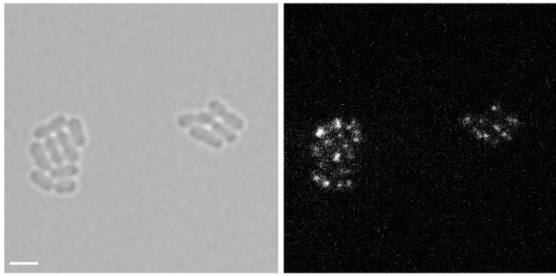
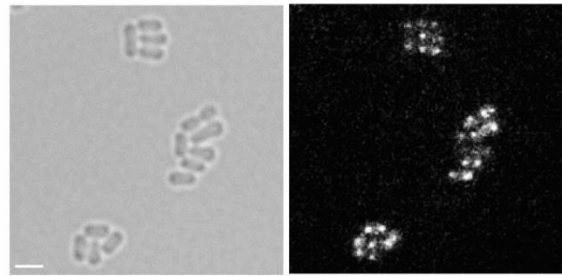


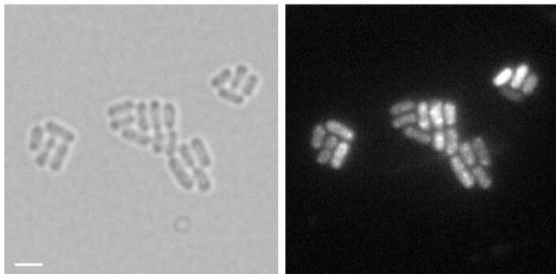
*P. aminophilus* pAMI4 wt



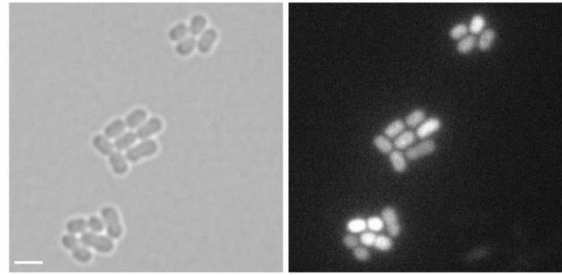
*P. aminophilus* pAMI4Tc



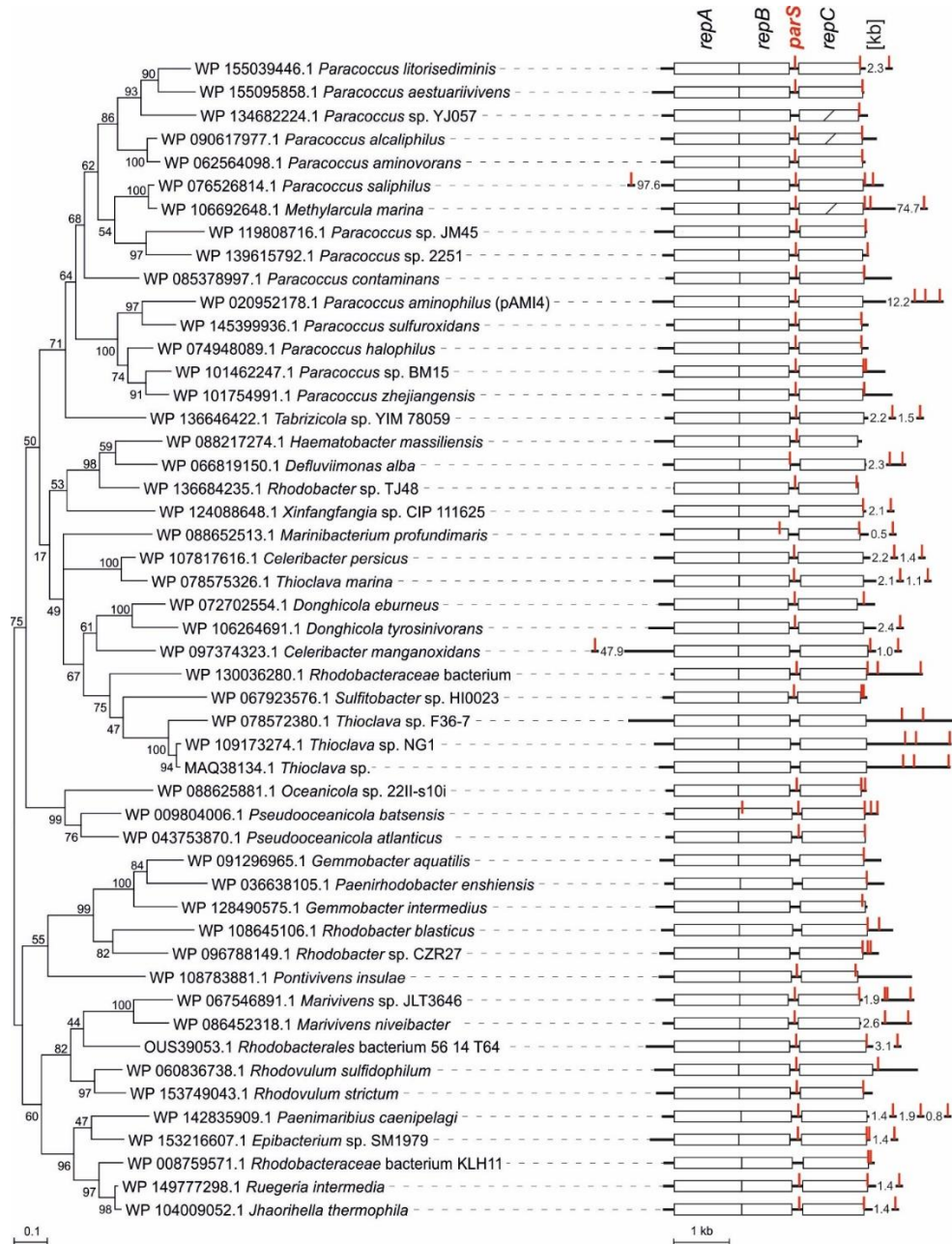
*P. aminophilus* pAMI4Δ3parS



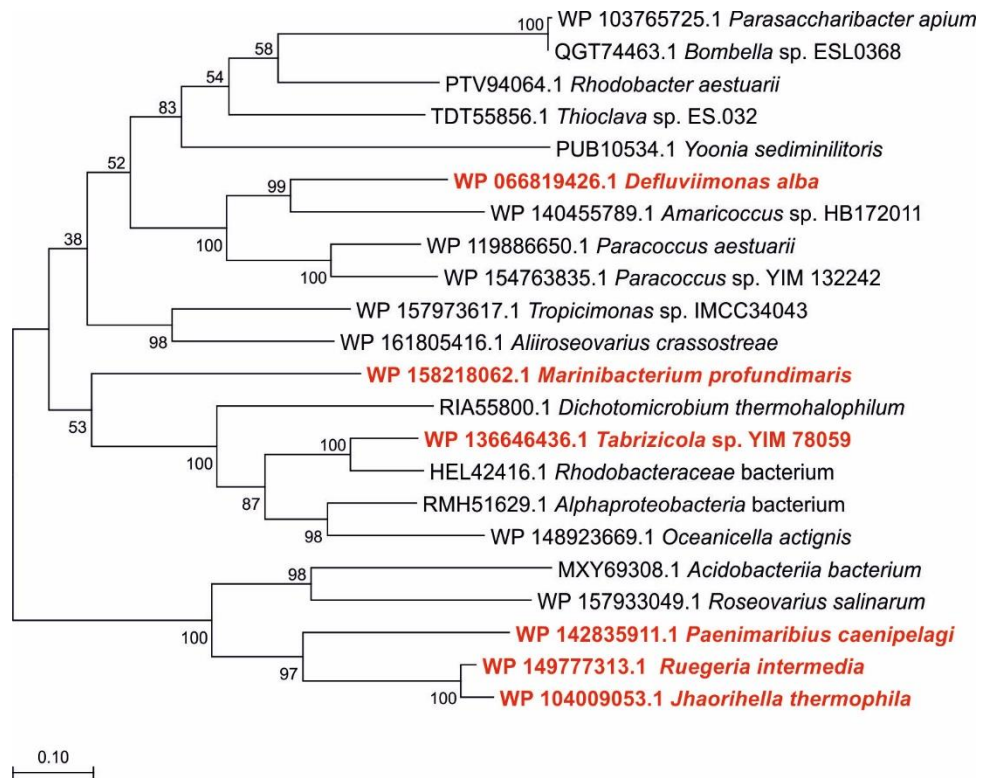
*P. aminophilus* pAMI4-less



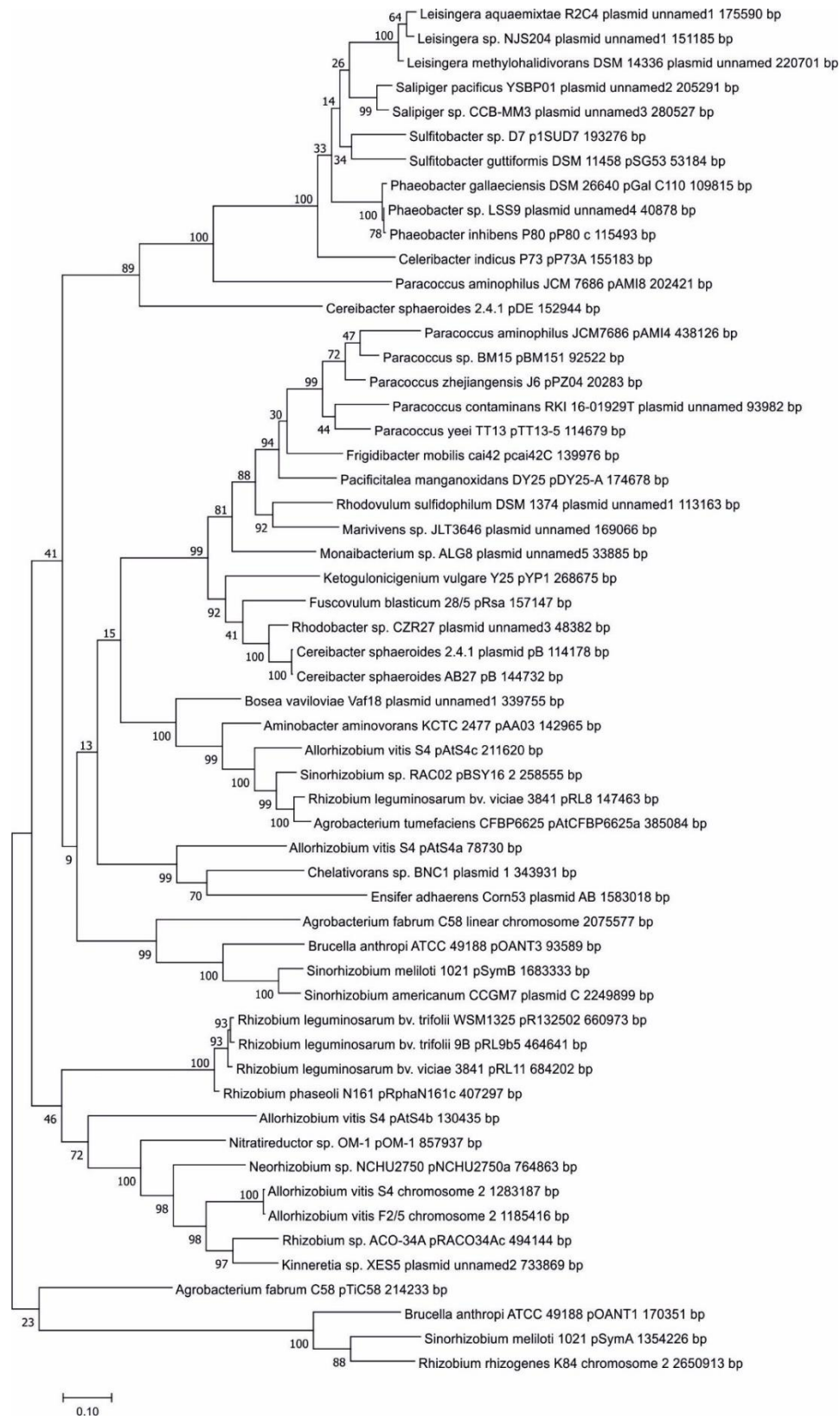
**FIGURE S1.** Expression and localization of GFP-RepBpAMI4 in the various *P. aminophilus* strains. Microscopy images of *P. aminophilus* cells (bright field image) expressing GFP-RepBpAMI4 (fluorescent image). All strains were cultured to mid-exponential phase in LB with gentamycin and taurine. Scale bar in all images is 2 microns.



**FIGURE S2.** Distribution of the putative *parS* sequences within 50 *repABC* replicons of *Rhodobacterales* (replicons selected from database 2, Table S2; complete and partial plasmid sequences). In the left-hand panel, a maximum likelihood tree of RepB protein sequences is presented. In the right-hand panel, the identified *parS* sequences are marked in red on diagrams of *repABC* modules that show the *repA*, *repB* and *repC* genes (rectangles) and intergenic regions upstream of *repA*, between *repA* and *repB*, between *repB* and *repC* and downstream of *repC* (bold lines). The intergenic/intragenic localization of putative *parS* sequences located outside the *repABC* modules (behind the numbers giving the distance from the *repABC* module in kb) is not indicated.



**FIGURE S3.** Maximum likelihood tree of Cas3 proteins. The Cas3 proteins encoded directly downstream *repC* in the dataset 2 (Table S2) of the *repABC* replicon contigs are highlighted in red. Some additional related Cas3 protein sequences were used for the phylogenetic analysis (all non-highlighted), but none of them was encoded in the direct vicinity of *repABC* modules.



**FIGURE S4.** Maximum likelihood tree of RepA-RepB concatenated protein sequences.