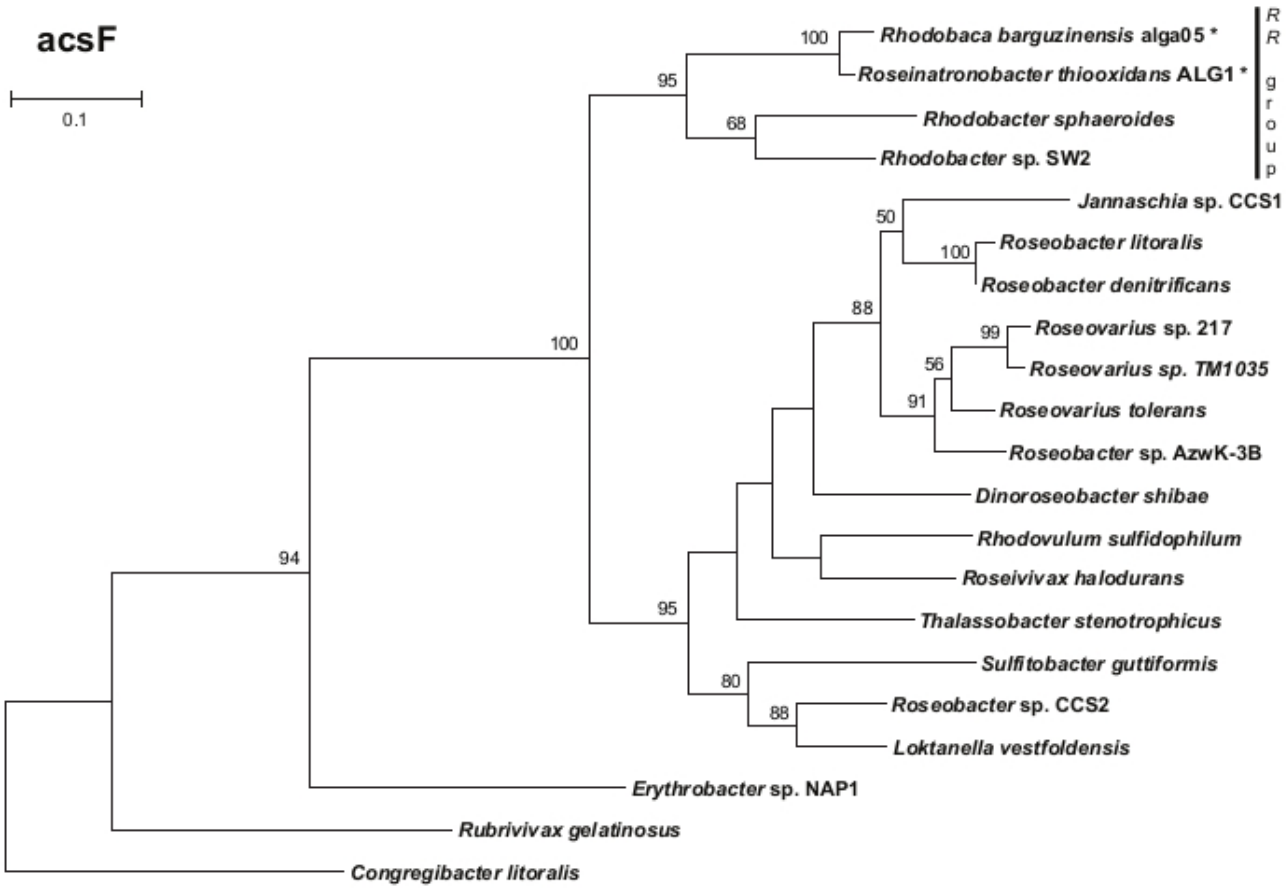

Suppl. Fig. 2. Maximum likelihood phylogenetic tree based on protein sequences of the oxygen-dependent (*acsF* gene product, 334 common amino acid positions), bootstrap 500x. *Congregibacter litoralis* was used as an outgroup organism. Scale bar represents changes per position. Bootstrap values >50% are shown. Studied strains are marked by the asterisk.