

Taxogenomics Resolves Conflict in the Genus *Rhodobacter*: A Two and Half Decades Pending Thought to Reclassify the Genus *Rhodobacter*

¹#Suresh G., ¹#^{\$}Tushar D Lodha., ¹Indu B., ²*Sasikala Ch. and ¹*Ramana Ch.V.

¹Department of Plant Sciences, School of Life Sciences, University of Hyderabad, P.O. Central University, Hyderabad-500 046, India.

²Bacterial Discovery Laboratory, Centre for Environment, Institute of Science and Technology, J. N. T. University Hyderabad, Kukatpally, Hyderabad-500085, India.

^{\$}Present address: National Centre for Microbial Resources, National Centre for Cell Sciences, Pune-411011, India.

#both the authors contributed equally

***Authors for correspondence: Ramana, Ch.V., Sasikala, Ch.**

E-mail: cvr449@gmail.com; sasi449@yahoo.ie

Running title: Reclassification of the genus *Rhodobacter*

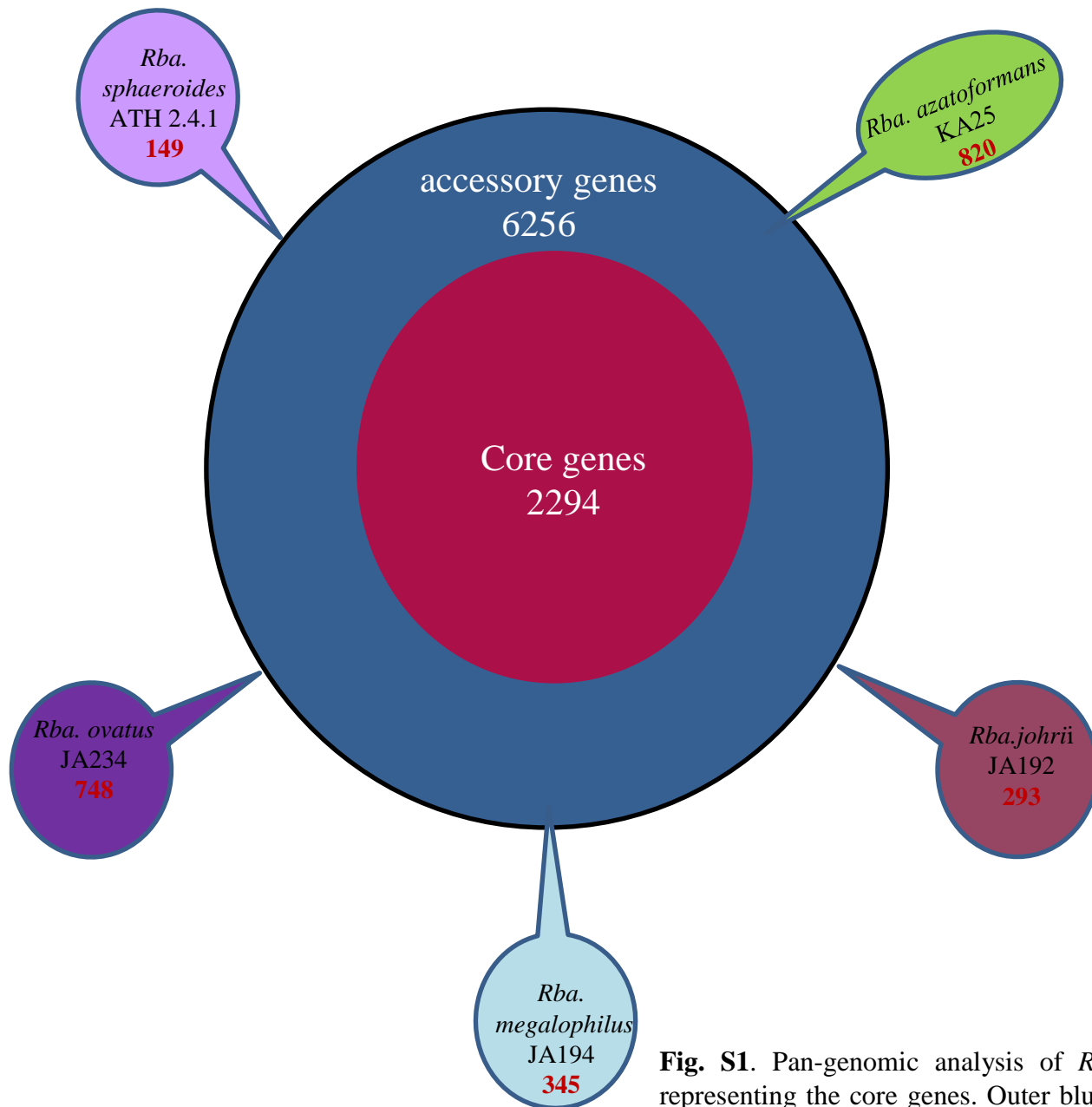


Fig. S1. Pan-genomic analysis of *Rba. sphaeroides* clade , Inner pink circle representing the core genes. Outer blue circle representing the accessory genes of all 5 organisms, and the buds representing the individual organisms unique genes

Pangenomic analysis of Clade II

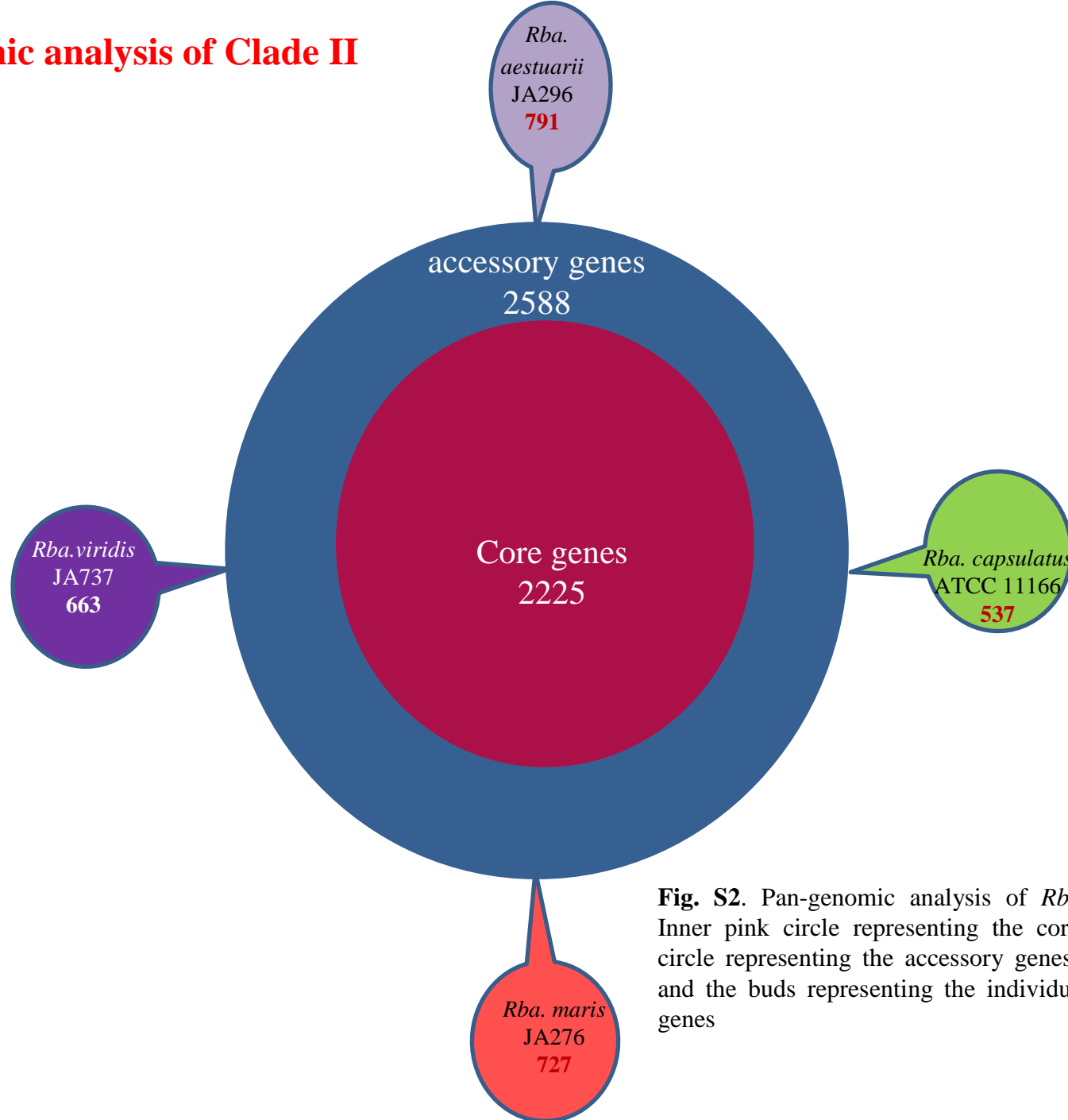


Fig. S2. Pan-genomic analysis of *Rba. capsulatus* clade, Inner pink circle representing the core genes. Outer blue circle representing the accessory genes of all 4 organisms, and the buds representing the individual organisms unique genes

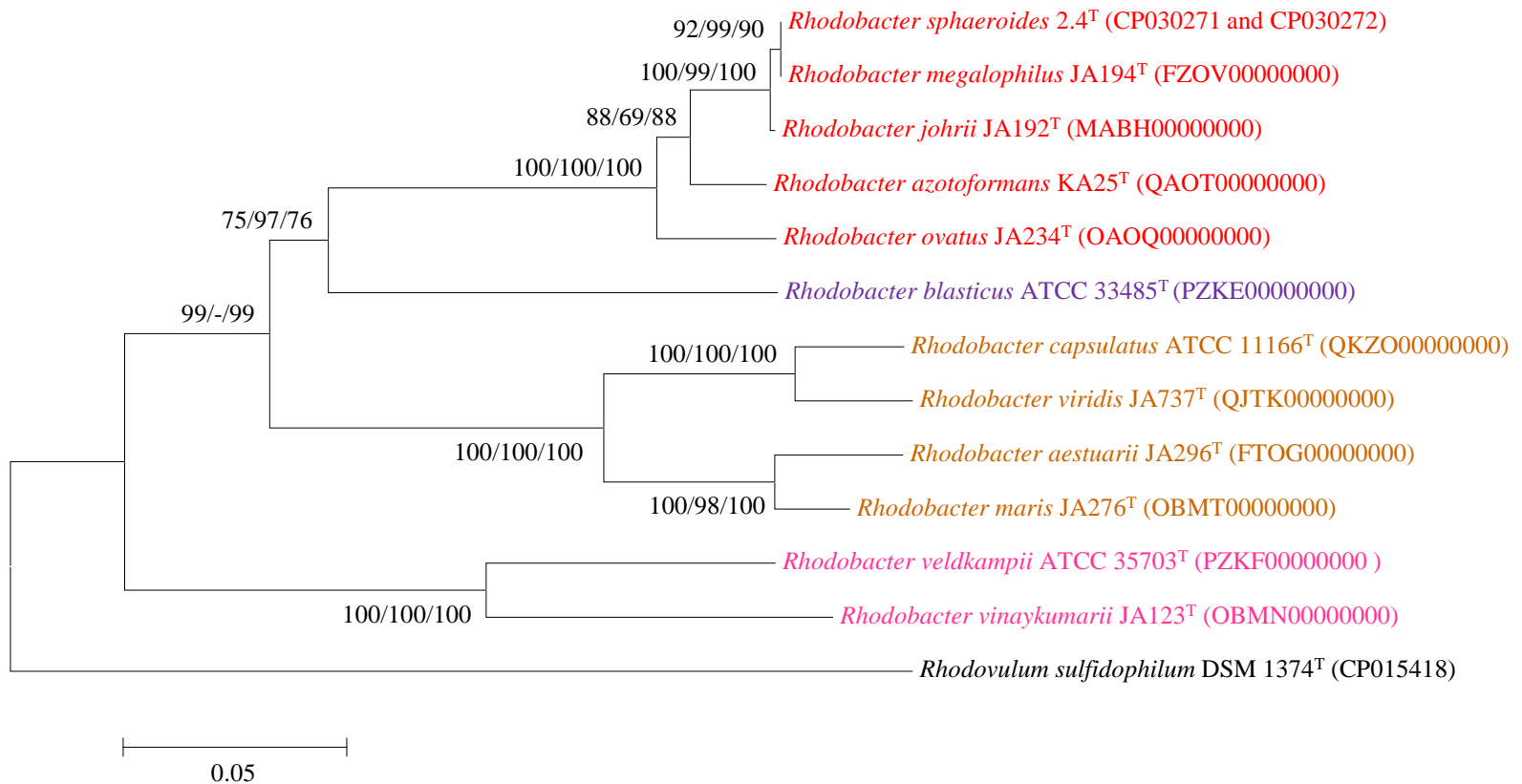


Fig. S3. Phylogenetic analysis Puf L and M concatenated protein sequences, tree was constructed using Mega 7 software. The evolutionary distances were computed using the poisson correction method. The bootstrap values are calculated by 1000 replicates and the values are representing the bootstrap values of NJ/ML/ME tree.

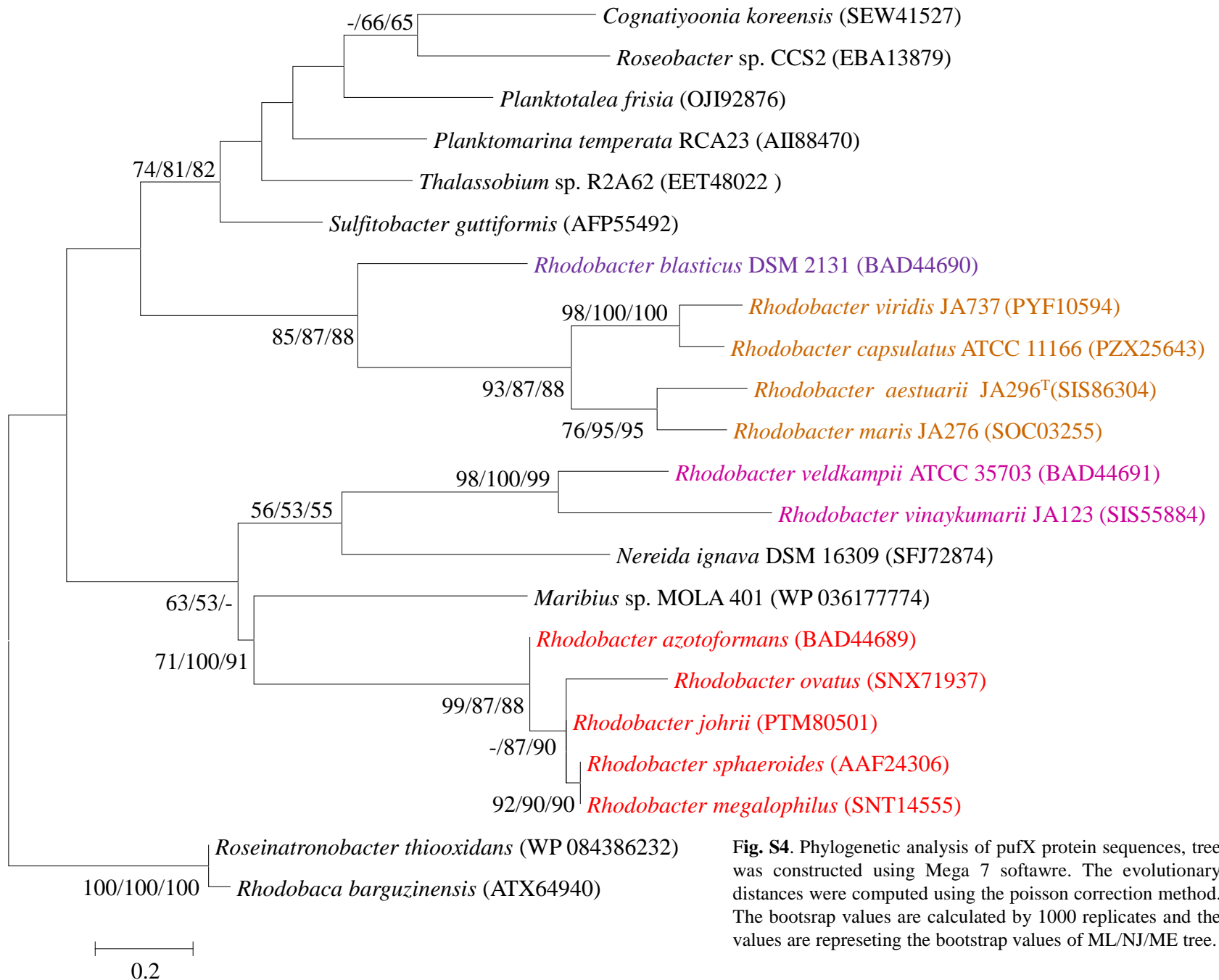


Fig. S4. Phylogenetic analysis of pufX protein sequences, tree was constructed using Mega 7 software. The evolutionary distances were computed using the poisson correction method. The bootstrap values are calculated by 1000 replicates and the values are representing the bootstrap values of ML/NJ/ME tree.

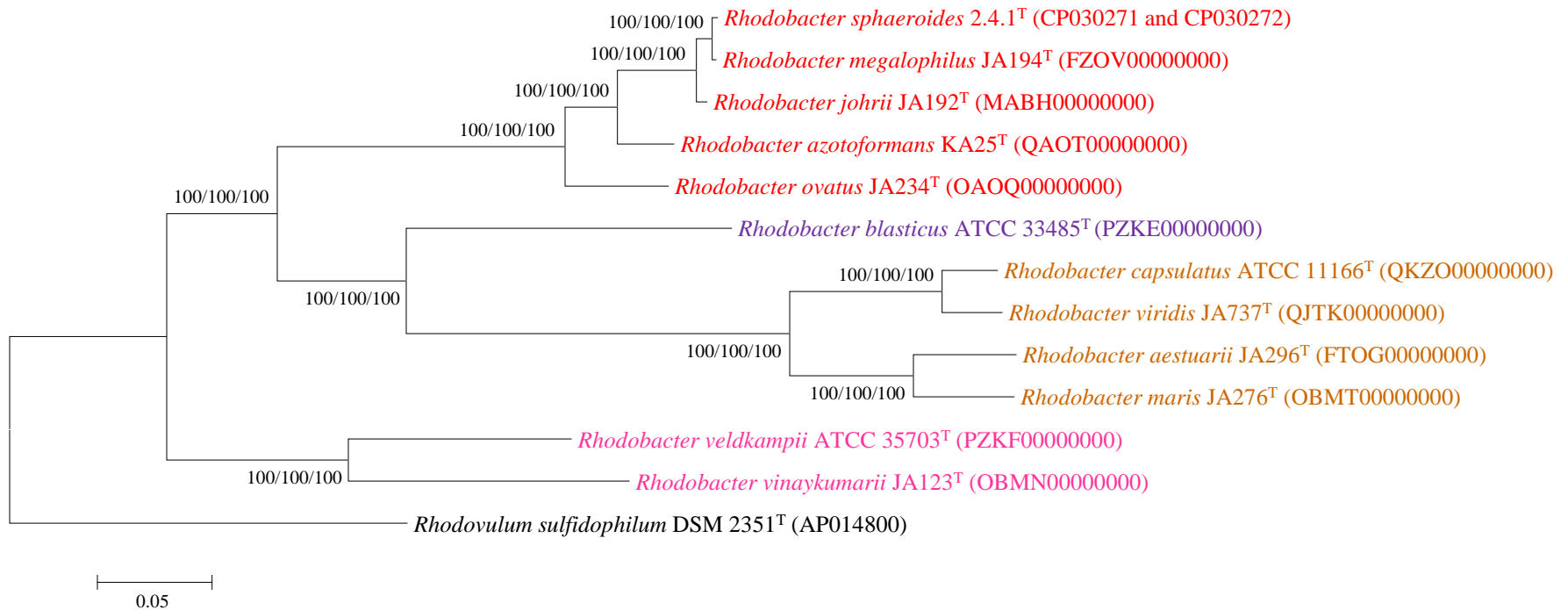


Fig. S5. PGC Phylogenetic analysis of PGC (Photosynthetic gene cluster) concatenated protein sequences, tree was constructed using Mega 7 software. The evolutionary distances were computed using the poisson correction method. The bootstrap values are calculated by 1000 replicates and the values are representing the bootstrap values of NJ/ML/ME tree.

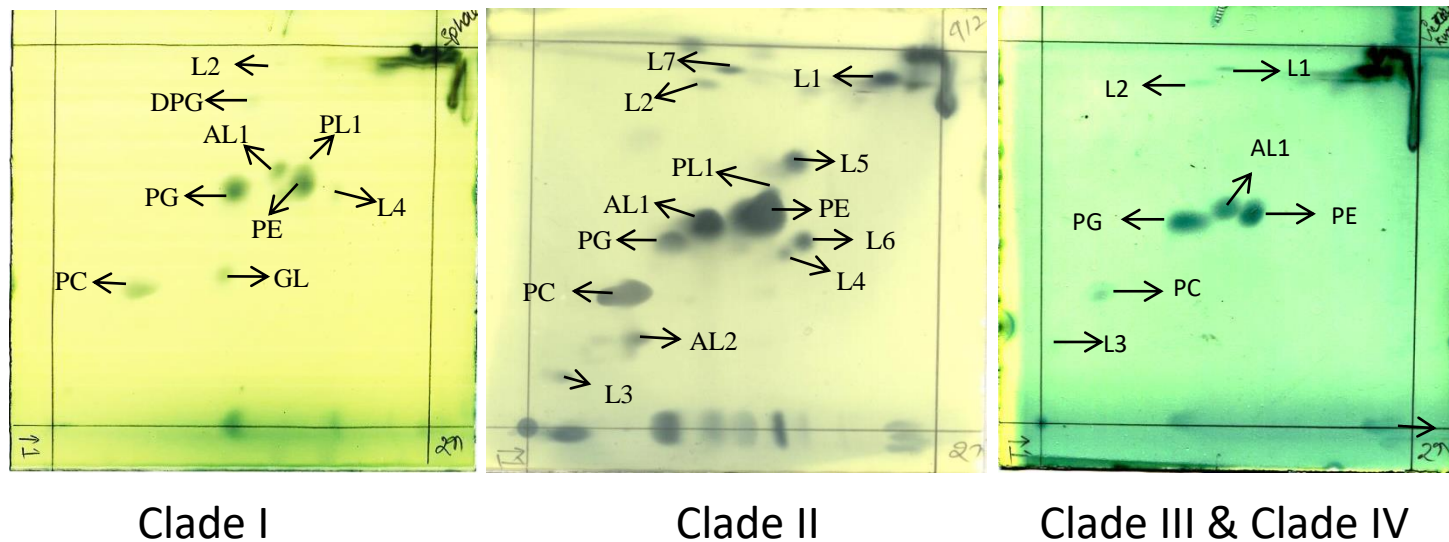


Fig S6. Two-dimensional thin-layer chromatograms of whole cell polar lipids of clade I (*Rba. sphaeroides*, *Rba. johrii*, *Rba. megalophilus*, *Rba. azotoformans*, *Rba. ovatus*, *Rba. alkalitolerans*), clade II (*Rba. capsulatus*, *Rba. viridis*, *Rba. azollae*, *Rba. sediminis*, *Rba. aestuarii*, *Rba. maris*, *Rba. lacus*), Clade III (*Rba. blasticus*); Clade IV (*Rba. veldkampii* clade having *Rba. veldkampii* and *Rba. vinaykumarii*); PE, phosphatidylethanolamine; PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PL1, uncharacterized phospholipid; AL1,2, uncharacterized aminolipids; GL, Glycolipid; L1-7 uncharacterized lipids.

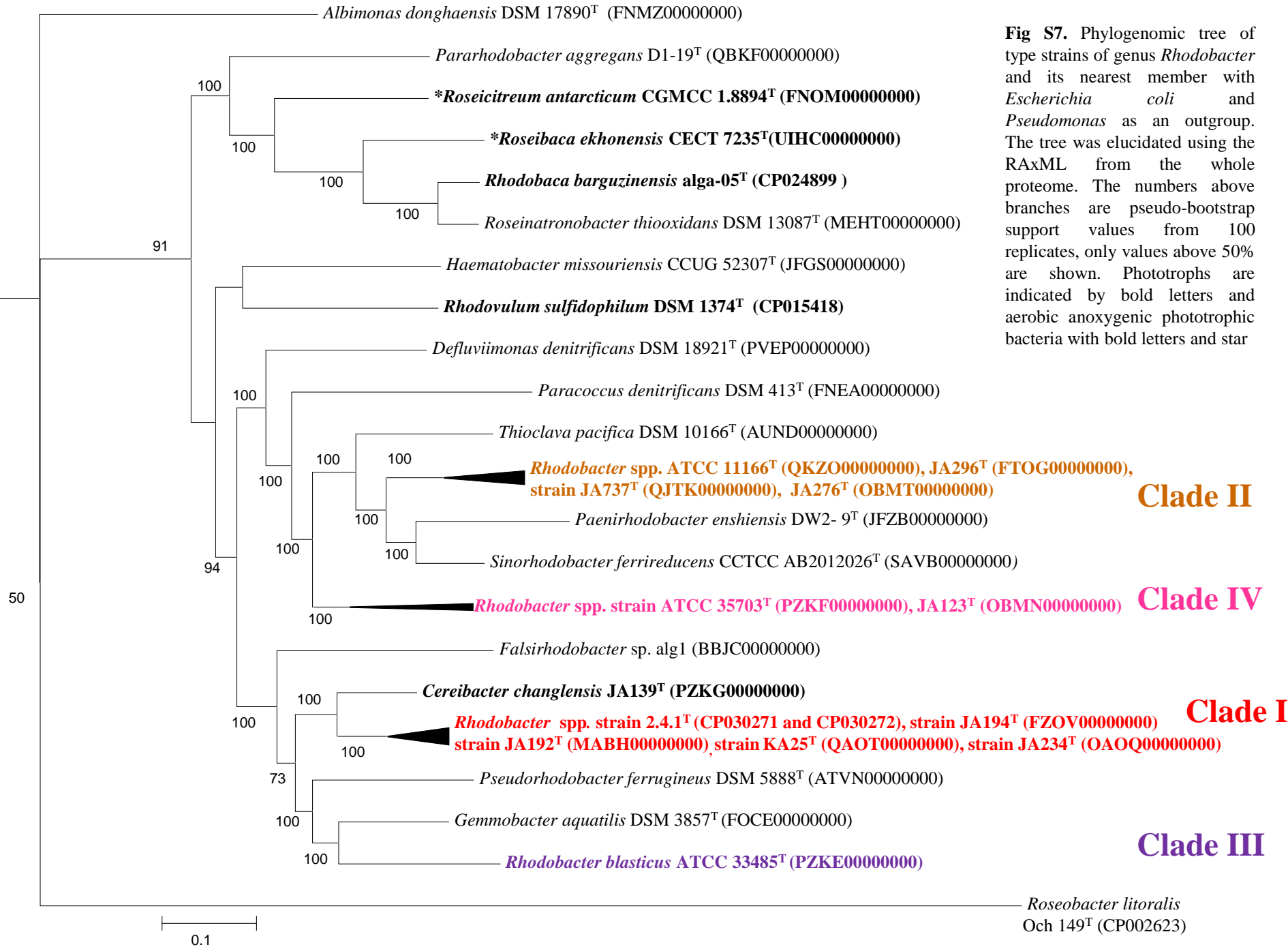


Fig S7. Phylogenomic tree of type strains of genus *Rhodobacter* and its nearest member with *Escherichia coli* and *Pseudomonas* as an outgroup. The tree was elucidated using the RAxML from the whole proteome. The numbers above branches are pseudo-bootstrap support values from 100 replicates, only values above 50% are shown. Phototrophs are indicated by bold letters and aerobic anoxygenic phototrophic bacteria with bold letters and star