**Pan-genome-based analysis as a framework for demarcating two closely related methanotroph genera *Methylocystis* and *Methylosinus***

Igor Y. Oshkin1\*, Kirill K. Miroshnikov1, Denis S. Gruzdev2, Svetlana N. Dedysh1

1*Winogradsky Institute of Microbiology, Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, 119071, Russia*

2*Institute of Bioengineering, Research Center of Biotechnology of the Russian Academy of Sciences, Moscow, 119071, Russia*

\*Author for Correspondence: Igor Y. Oshkin, Winogradsky Institute of Microbiology, Research Center of Biotechnology of the Russian Academy of Sciences, +7-(499)-135-0591, +7-(499)-135-6530, ig.owkin@gmail.com

**Running title:** Pan-genome analysis of the *Methylocystis*/*Methylosinus* group

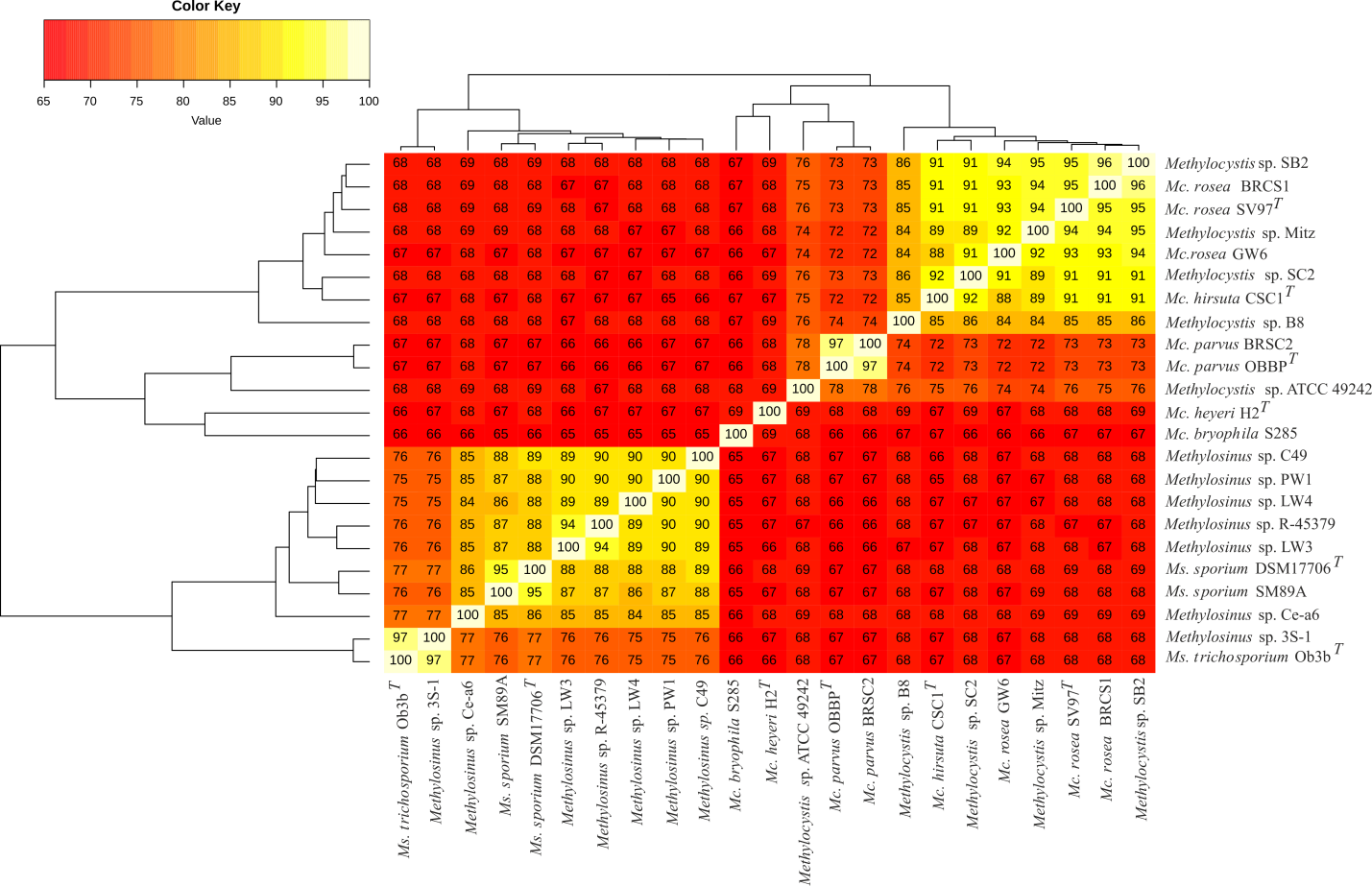


Figure S1. Heatmap derived from an Average Nucleotide Identity (ANI) matrix calculated for each pair of the genomes of *Methylocystis/Methylosinus* group.

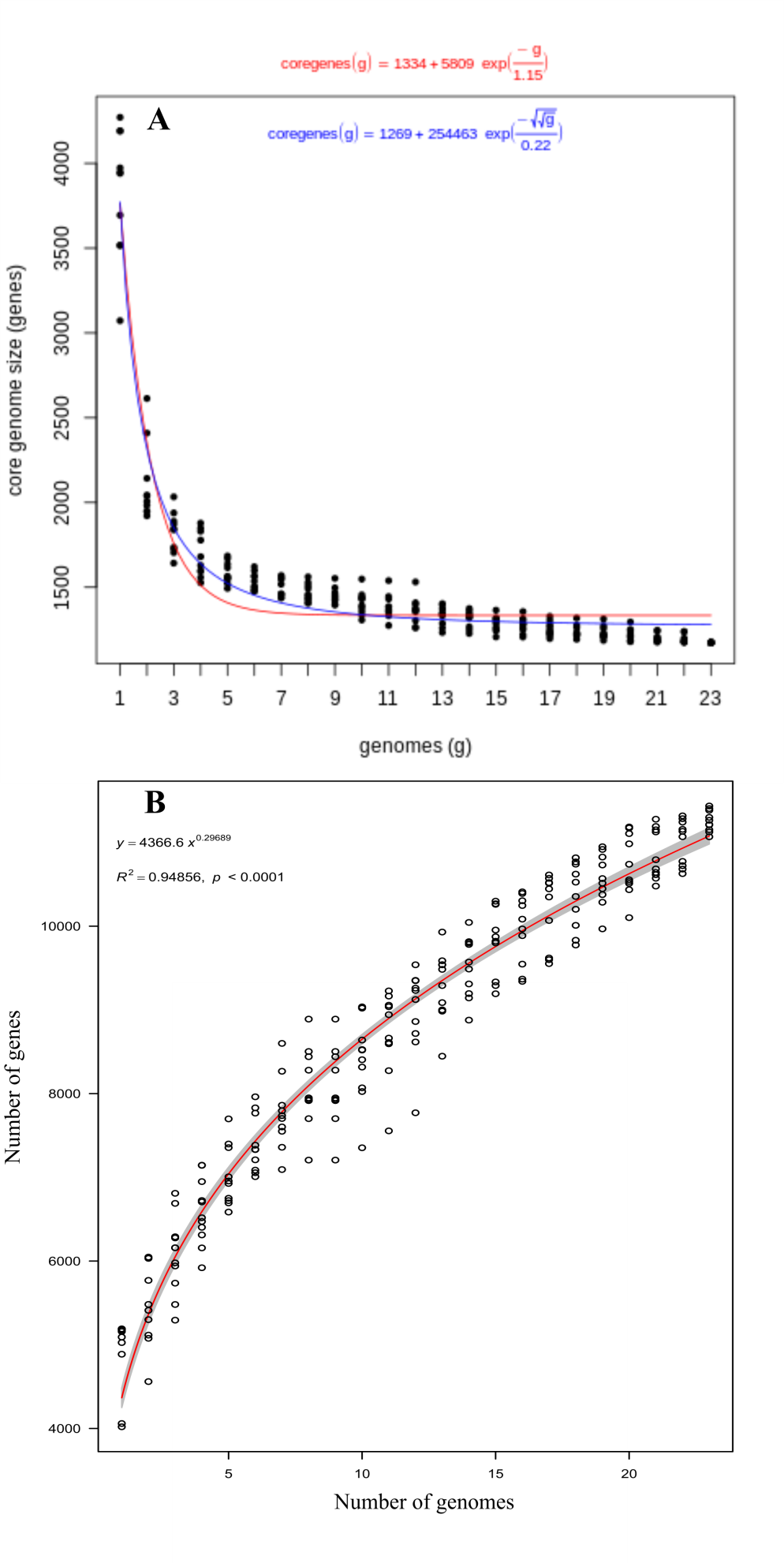


Figure S2. The *Methylocystis/Methylosinus* core genome (A) and pan-genome (B) as a function of the number of genomes included.

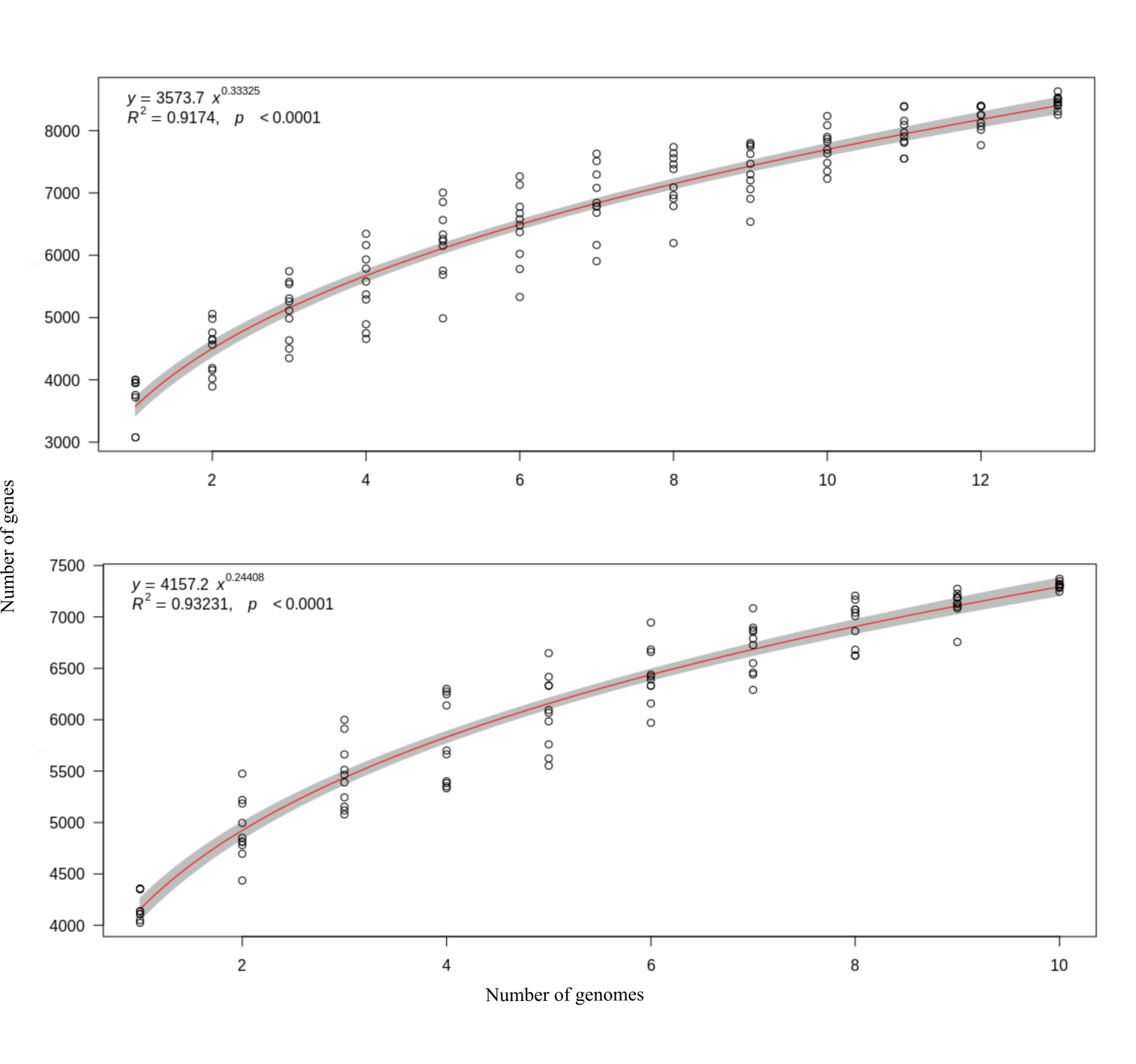


Figure S3. The *Methylocystis* pan-genome (A) and *Methylosinus* pan-genome (B) as a function of the number of genomes included (V1–V24).

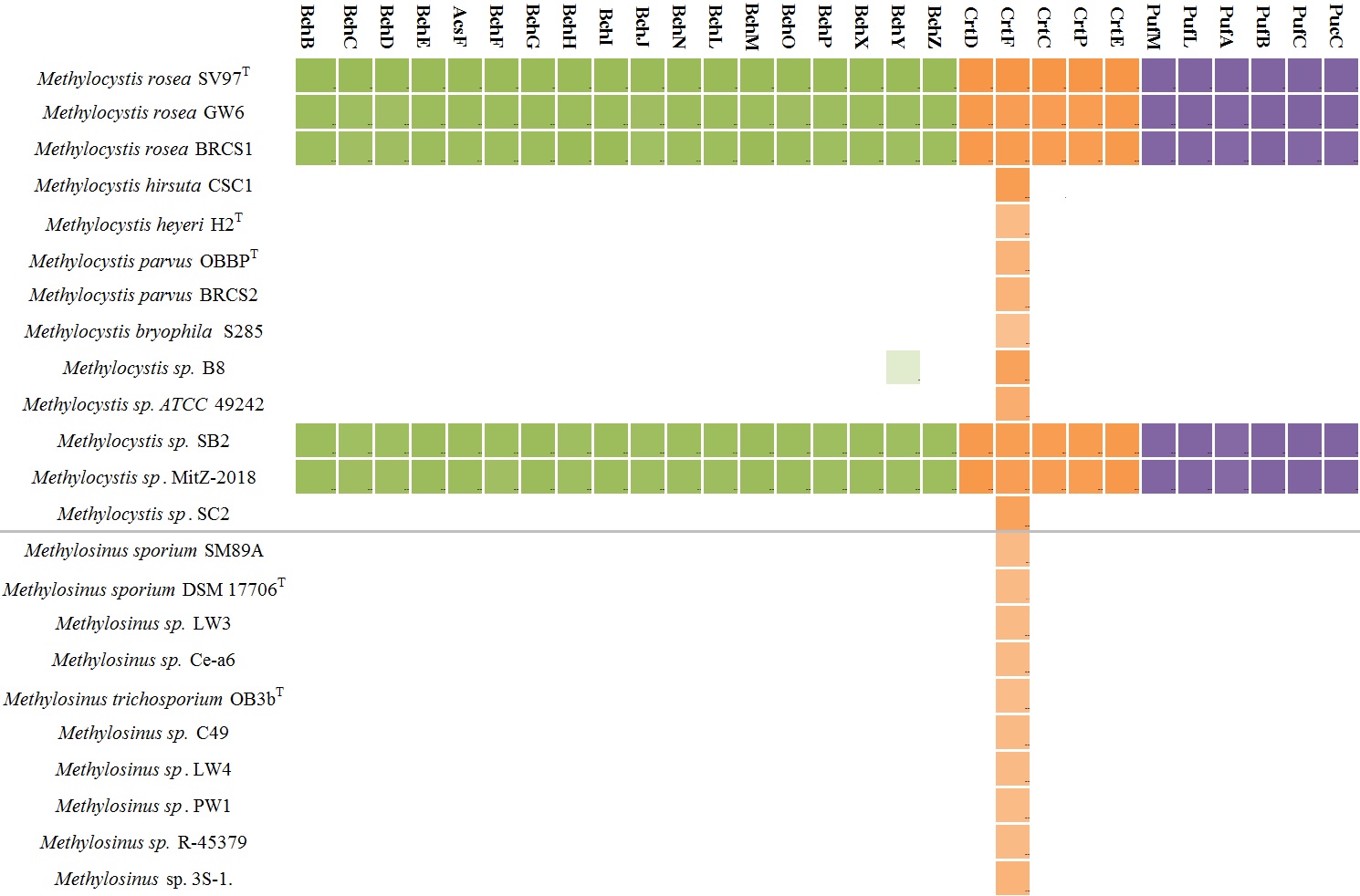


Figure S4. Heatmap displaying distribution of phototrophy-related genes (green) and carotenoids biosynthesis genes (orange).