Supplementary information

Identification, characterization and molecular analysis of the viable but nonculturable *Rhodococcus biphenylivorans*

Xiaomei Su[1,2], Faqian Sun[1,2], Yalin Wang[1,2], Muhammad Zaffar Hashmi[3], Li Guo[1,2], Linxian Ding[4], Chaofeng Shen[1,2]*

[1]Department of Environmental Engineering, College of Environmental and Resource Sciences, Zhejiang University, Hangzhou 310058, China

[2]Key Laboratory for Water Pollution Control and Environmental Safety, Zhejiang Province, China

[3]Department of Meteorology, COMSATS Institute of Information Technology, Islamabad 44000, Pakistan

[4]College of Geography and Environmental Science, Zhejiang Normal University, Jinhua 321004, China

*Corresponding author: Chaofeng Shen

Address: Yuhangtang Road 866#, Hangzhou, 310058, China

E-mail: ysxzt@zju.edu.cn; purple@zju.edu.cn

Tel: +86-571-88982016

Fax: +86-571-88982010

Table S1. qPCR primers used in this study.

Table S2. Gene expression value of annotated genes.

Table S3. Differentially expressed genes.

Table S4. Genes >20 fold up- or down-regulated in t_TG9 versus c_TG9 cultures.

Table S5. Gene Ontology function of differentially expressed genes.

Table S6. GO enrichment analysis of up-regulated genes.

Table S7. GO enrichment analysis of down-regulated genes.

Table S8. KEGG pathway enrichment of differentially expressed genes in t_TG9 and c_TG9 libraries.

Table S9. KEGG enrichment analysis of up-regulated genes.

Table S10. KEGG enrichment analysis of down-regulated genes.

Table S11. qRT-PCR validation of transcriptomic profiles.

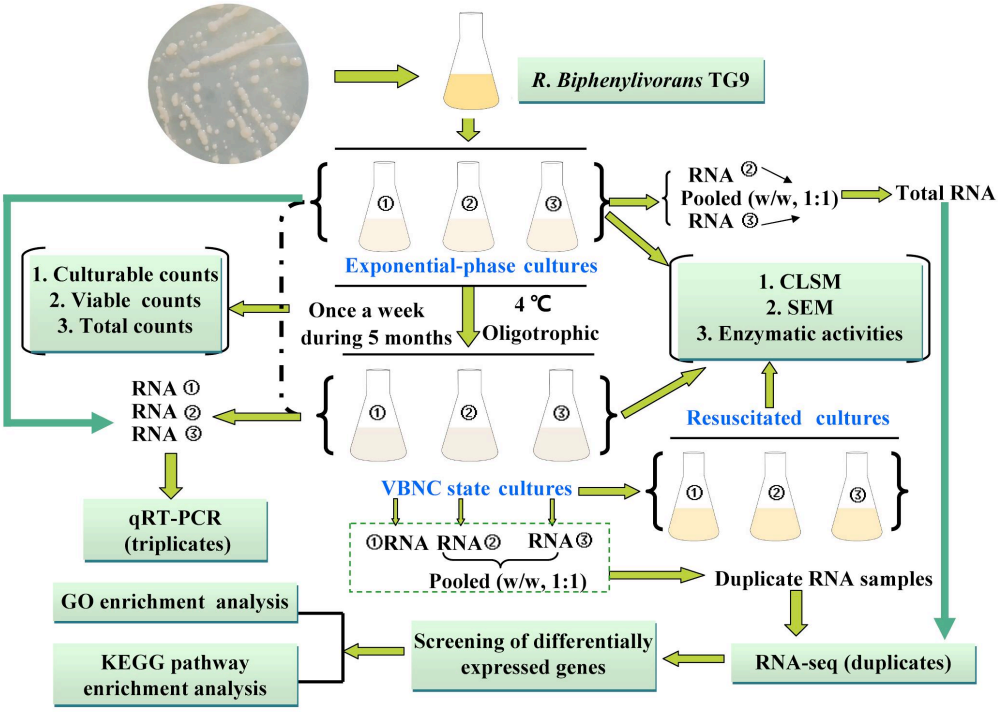

Fig. S1. Schematic flow diagram of the experimental design.

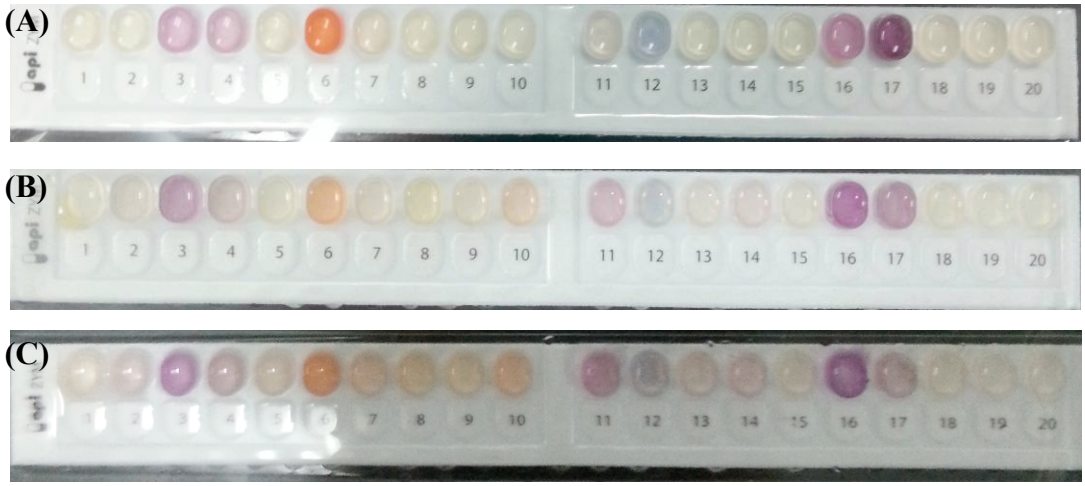

Fig. S2. Enzymatic activities of *Rhodococcus biphenylivorans* TG9^{T} measured by the API ZYM system. (A) exponential-phase cells; (B) VBNC cells; (C) resuscitated cells.