

Supporting Information

Physiological and transcriptomic responses of *Chlorella vulgaris* to novel antibacterial nanoparticles of ethyl cyanoacrylate polymer

Di Zhang^{1,5}, Keqing Liu^{1,5}, Chengcheng Feng^{1,5}, Xianmin Wang¹, Ayat J. S. Al-Azab², Han Lu¹, Haiyan Ma³, Ying Tang¹, Li Xu¹, Takeshi Ohama⁴, Fantao Kong^{1,*}

¹ MOE Key Laboratory of Bio-Intelligent Manufacturing, School of Bioengineering, Dalian University of Technology, Dalian, 116024, Liaoning, China

² Department of Biotechnology and Genetic Engineering, Faculty of Science, Philadelphia University, Amman, Jordan

³ Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, Hubei 430072, China

⁴ School of Environmental Science and Engineering, Kochi University of Technology, 185 Miyanokuchi, Tosayamada, Kami-city 782-8502, Japan

* Corresponding author: Fantao Kong (email: kongfantao@dlut.edu.cn; Tel: +86-15642336188)

⁵ These authors contributed equally to this work.

Figure S1. The morphological changes of the cells exposed to ECA-NPs observed by transmission electron microscope (TEM). The cells were exposed to ECA-NPs (100 $\mu\text{g}/\text{mL}$) for 3 days. CW, cell wall; Ch, chloroplast; S, starch; V, vacuole. The red arrows indicate the ECA-NPs. The red arrows indicate the ECA-NPs.

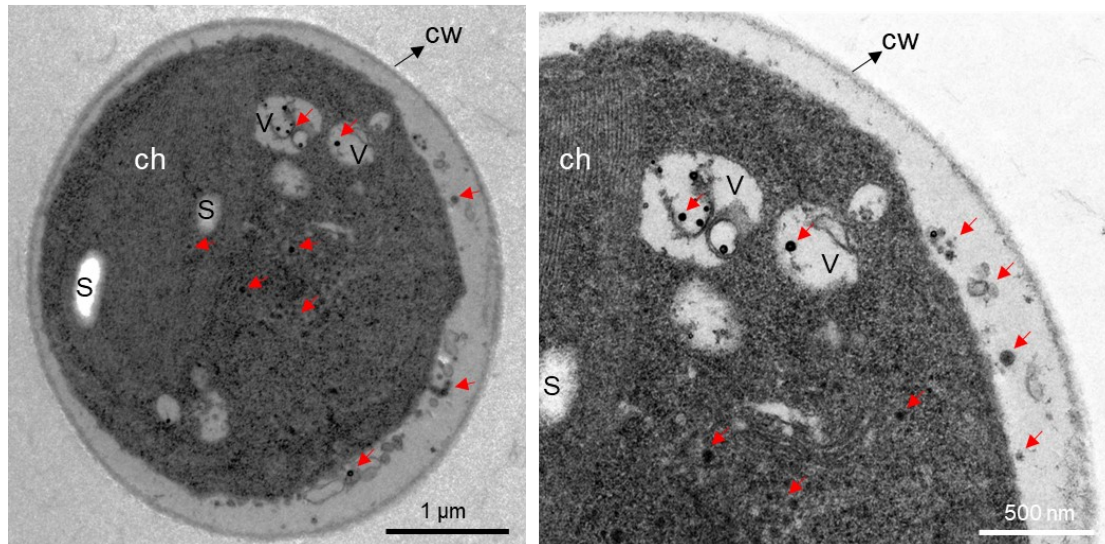
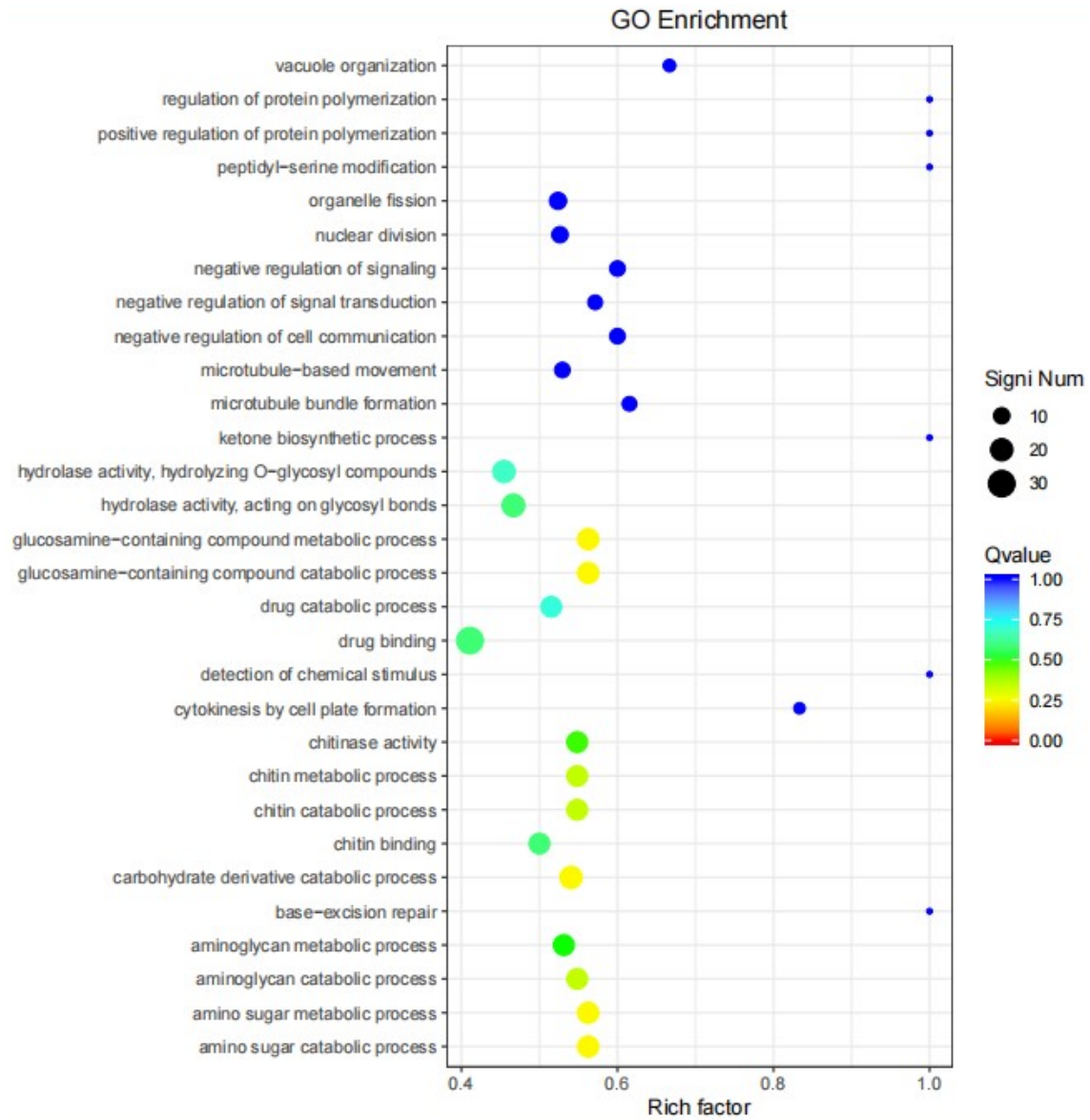


Figure S2. The gene ontology (GO) enrichment analysis showed that differentially expressed genes (DEGs) between ECA-NPs treated cells and control. The downregulated and upregulated DEGs were shown in (A) and (B), respectively.

(A)



(B)

