The supporting information provides:

- Schematic diagram of experimental setup (Figure S1);
- Variation of the fluorescence components and Fmax at different C/N identified by PARAFAC analysis (Figure S2);
- Bacterial composition on phylum level (Figure S3).

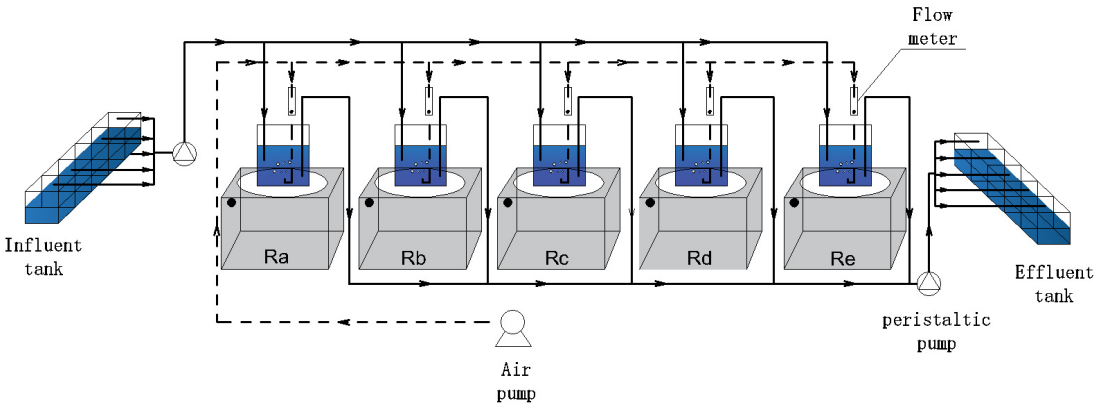


Figure S1. Schematic diagram of experimental setup.

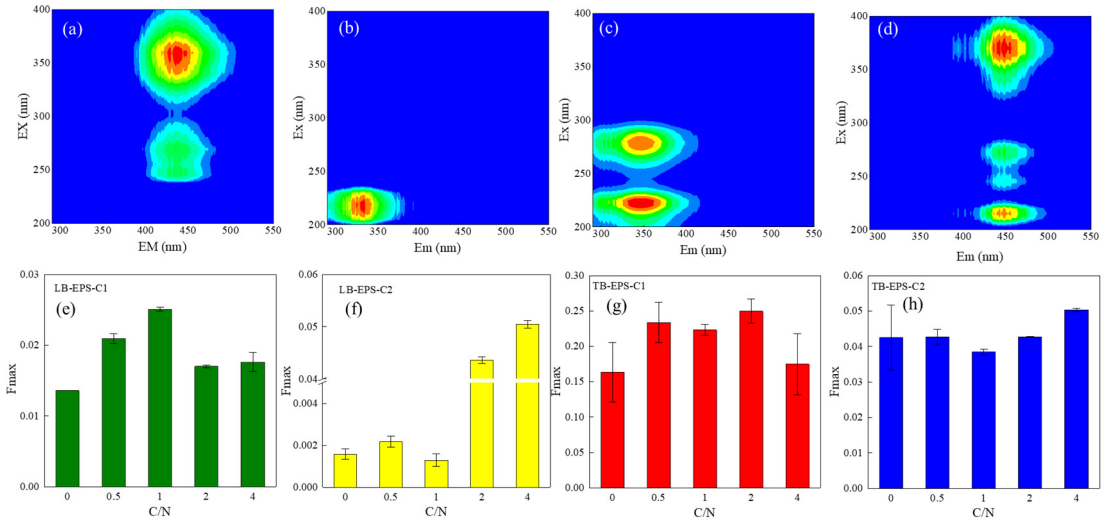


Figure S2. Variation of the fluorescence components and Fmax at different C/N identified by PARAFAC analysis.

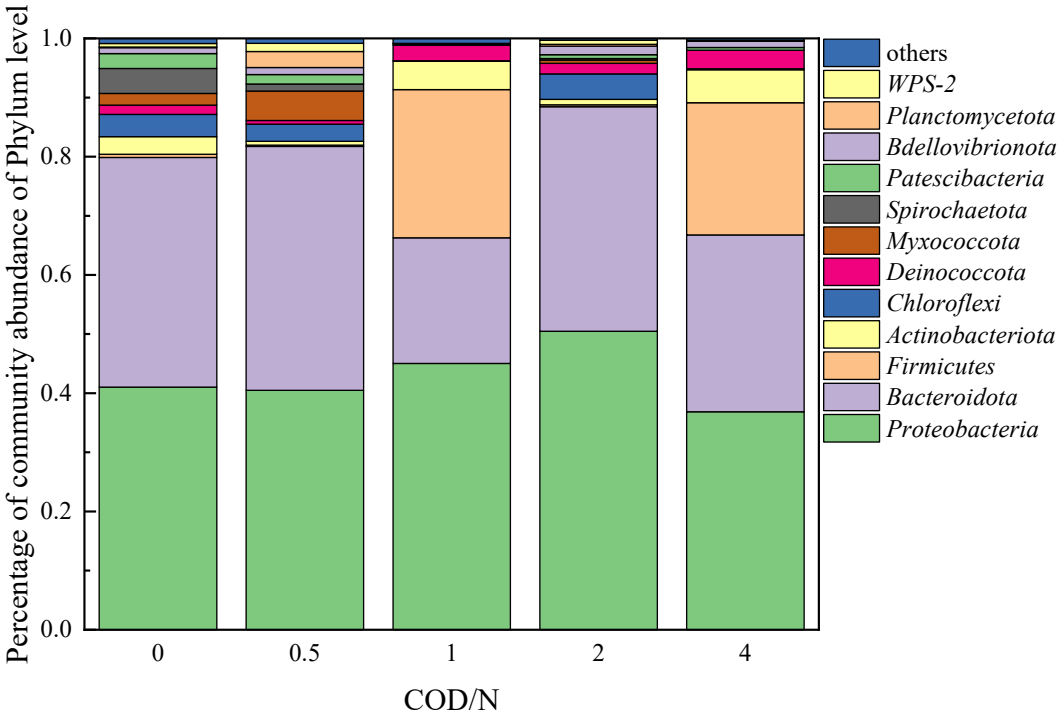


Figure S3. Bacterial composition on phylum level

Figure S3 gives the microbial composition at phylum level under various C/N ratios, and the dominant phylum were *Proteobacteria*, *Bacteroidetes* and *Firmicutes*. *Proteobacteria* were found to have relative abundances of 41.0, 40.5, 50.5, 36.8 and 45.0%, respectively, and relative abundances of *Bacteroidetes* of 38.8, 41.2, 38.0, 30.0 and 21.3%, respectively at C/N ratios of 0, 0.5, 1, 2 and 4. As the vast majority of bacterial phylum, most of the AOB, NOB and denitrifiers belong to *Proteobacteria* [1, 2]. *Bacteroidetes* is also widespread in the nitrification process and the microorganisms in this phylum have the ability to degrade organic matters and potentially release proteinaceous EPS [3]. The relative abundances of *Firmicutes* were as low as 0.5%, 0.2% and 0.3%, respectively, for C/N ratios of 0, 0.5 and 1, while it was quite high at C/N ratios of 2 (22.3%) and 4 (25.1%).

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