

## Supplementary Information for Publication

### **Insight into the characteristics of microbial community in single-stage anammox reactor under different oxygen conditions**

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**Figure and Table captions**

Table S1. upstream analysis results of 16S rRNA gene sequencing

A. raw data profile		
total reads count (single-end)	2039675	
average Q30	96.20%	
average Q20	99%	
total reads count after merger	1446925	
B. sample size status		
OTUs counts	582	
	minimum	129139
	25th percentile	148353
	median	163404
raw sample size (reads count)	75th percentile	170176
	maximum	191530
	average	160769
	normalization size	120000

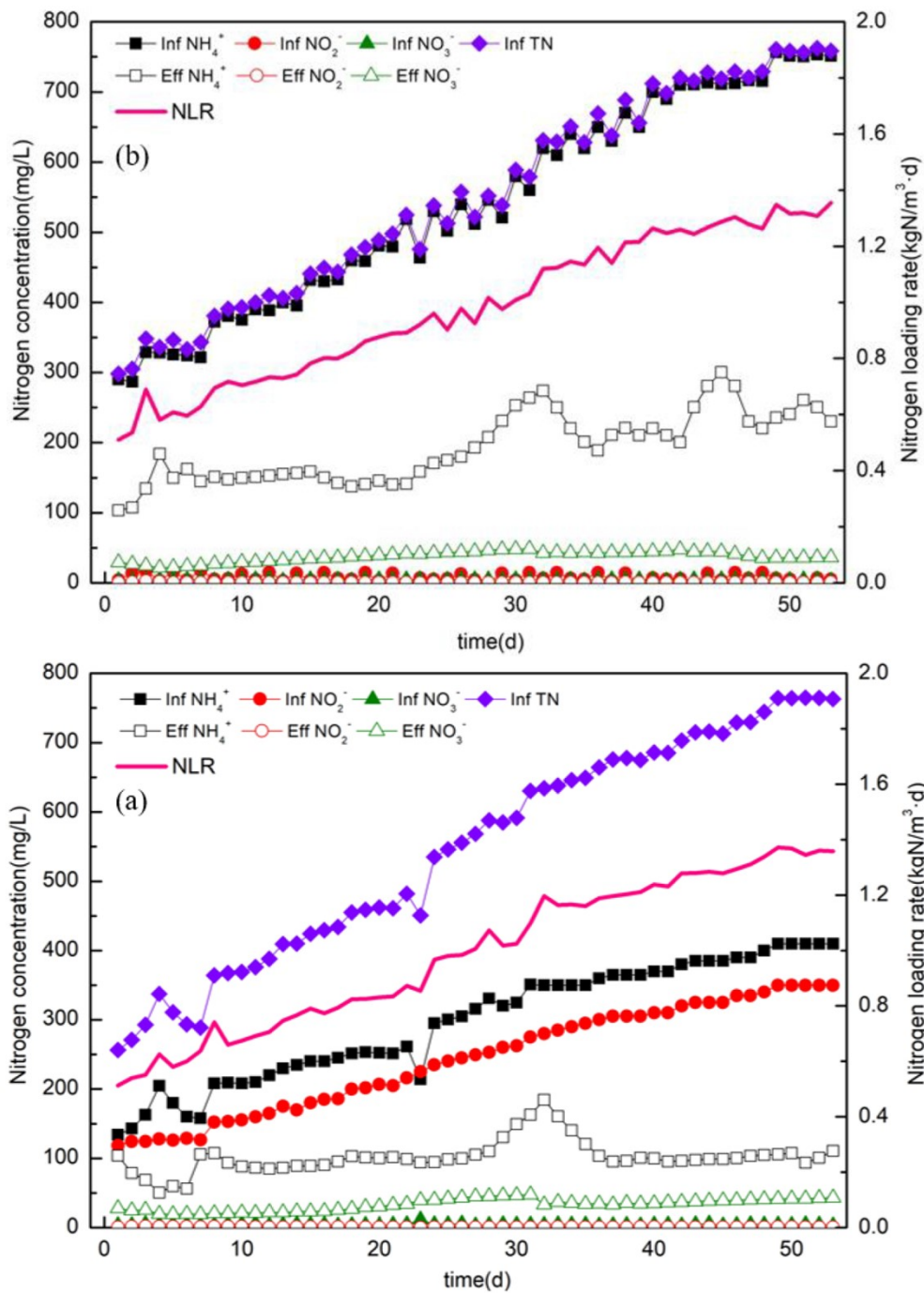


Figure S1. The variation of nitrogen concentration and nitrogen loading rate of the two MBRs in 1-56 d; (a) MBR-O under micro-aerobic condition; (b) MBR-A under anoxic condition (further data under stable operation period were not shown)

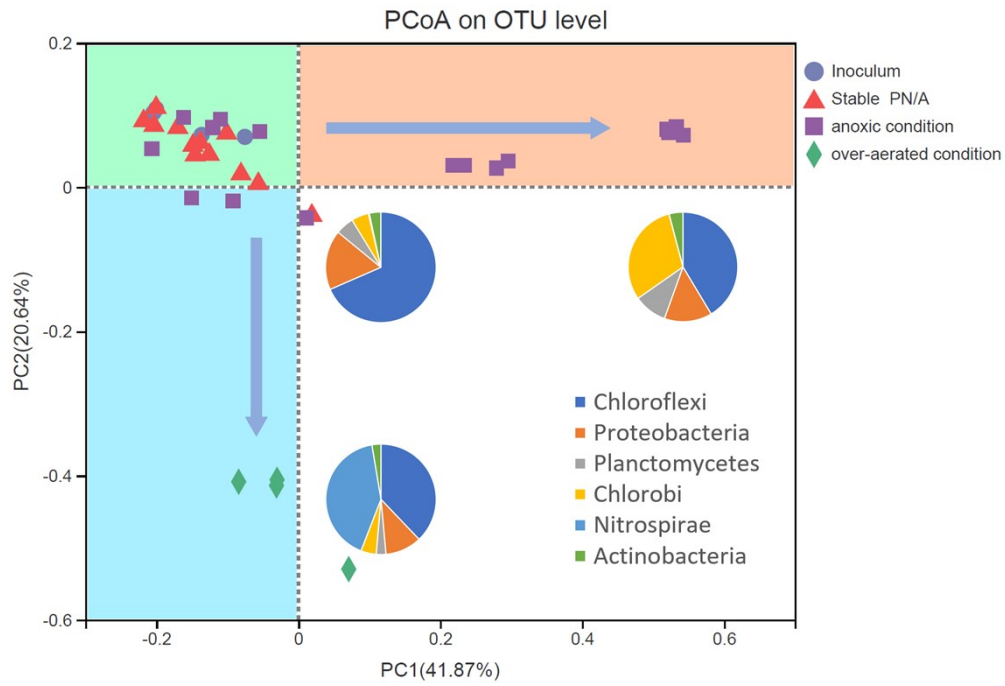


Figure S2. Community dynamics under different conditions characterized by principal coordinate analysis with pie graph of top five phyla

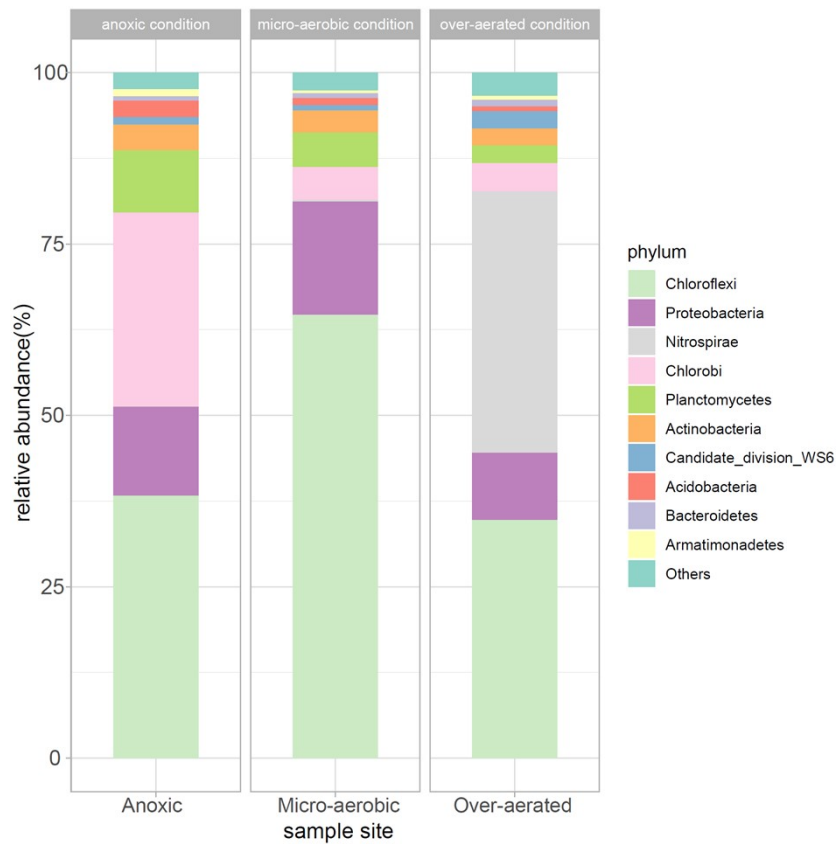


Figure S3. The top 10 phyla of the entire microbial community composition under different conditions