

Supplementary Material

Table S1 Characteristics of the PCR primers.

Target organism	Primer pair	Sequences(5'-3')	Size(bp)
Total bacteria	27F	AGAGTTTGATCCTGGCTCAG	311
	338R	TGCTGCCTCCCGTAGGAGT	

Table S2 Relative abundances (%) of the genus in the three activated sludge samples at 0,100 and 400 mg/L NB

phylums	0 ppm	100 ppm	400 ppm
	NB	NB	NB
<i>Zoogloea</i>	0.01%	0.58%	19.88%
<i>Hydrogenophaga</i>	0.00%	0.15%	11.64%
<i>Lactobacillus</i>	12.12%	42.69%	5.47%
<i>Micropruina</i>	0.00%	0.06%	4.09%
<i>Microbacterium</i>	0.00%	0.10%	2.55%
<i>Sphaerotilus</i>	12.42%	0.20%	2.12%
<i>Nakamurella</i>	0.00%	0.04%	1.83%
<i>Gp4</i>	0.00%	0.03%	1.48%
<i>Luteimonas</i>	0.00%	0.08%	1.38%
<i>Nitrospira</i>	0.00%	0.19%	1.36%
<i>Bacteroides</i>	2.75%	1.40%	1.33%
<i>Ferruginibacter</i>	0.00%	0.01%	1.25%
<i>Enterobacter</i>	0.61%	0.36%	1.23%
<i>Clostridium sensu stricto</i>	0.96%	12.03%	0.98%
<i>Dechloromonas</i>	0.00%	0.02%	0.80%
<i>Ideonella</i>	0.00%	0.03%	0.80%

<i>Terrimonas</i>	0.00%	0.02%	0.75%
<i>Pseudomonas</i>	1.16%	5.19%	0.72%
<i>Serratia</i>	0.00%	3.16%	0.01%
<i>Acetobacter</i>	0.00%	3.02%	0.28%
<i>Lactococcus</i>	12.16%	1.55%	0.54%
<i>Pectinatus</i>	9.24%	1.54%	0.01%
<i>Desulfovibrio</i>	11.76%	0.05%	0.14%
<i>Clostridium XVIII</i>	3.88%	0.10%	0.06%
<i>Aeromonas</i>	2.38%	0.13%	0.01%
<i>Clostridium XIVb</i>	1.50%	0.02%	0.01%
<i>Klebsiella</i>	1.26%	0.00%	0.00%
<i>unclassified</i>	27.76%	27.21%	37.81%

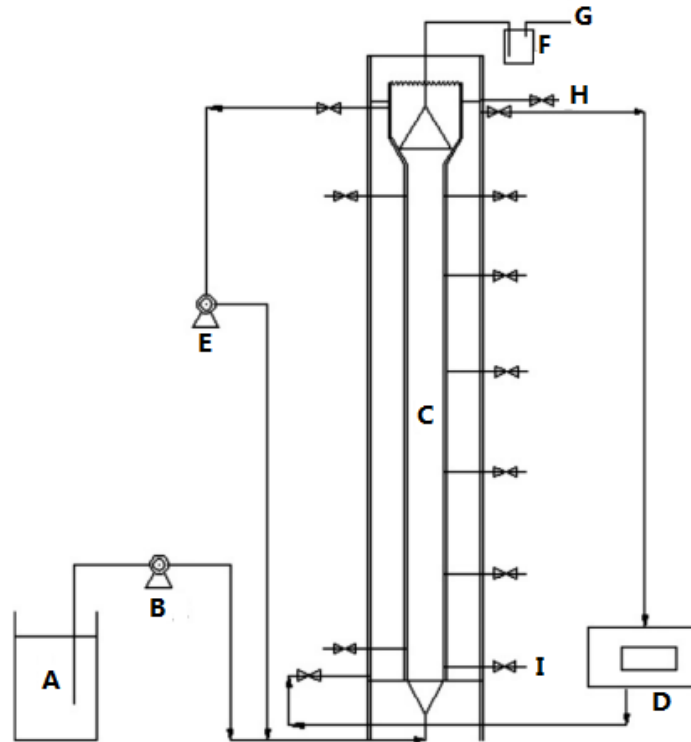


Fig. S1 The EGSB reactor structure. (A) influent tank; (B) influent pump; (C) main body of EGSB reactor; (D)

water bath temperature control system; (E) recycling

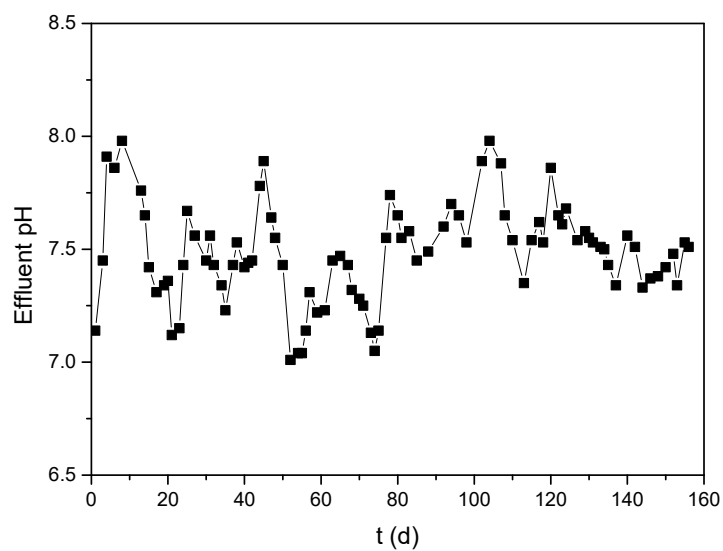


Fig. S2 Variation of effluent pH value during the whole operation