Supplementary information

Text S1

The contents of the mineral medium were (g/L except for trace element solution): $MgSO_4$ 0.1, $CaCl_2 \cdot 2H_2O$ 0.3, KH_2PO_4 0.1, $NaHCO_3$ 1 and 1 mL trace elements solution per liter synthetic wastewater. The trace elements solution contained (g/L): 10 EDTA, 0.15 H_3BO_3, 1.54 $FeSO_4 \cdot 7H_2O$, 0.02 $CuCl_2 \cdot 2H_2O$, 0.12 $ZnSO_4 \cdot 7H_2O$, 0.15 $CoCl_2 \cdot 6H_2O$, 0.12 $NaMoO_4 \cdot 2H_2O$ and 0.18 KI.

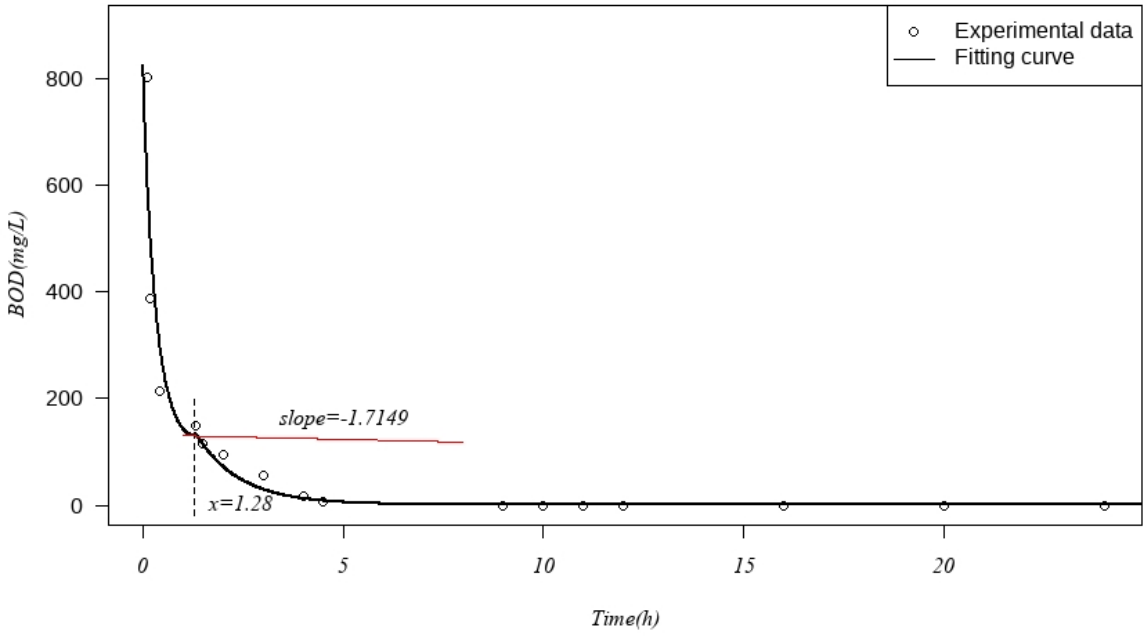

Fig. S1 Fitting curve for determining feast and famine conditions in SBR. The fitting curve is drawn by Rstudio software using least square algorithm.

Text S2

1) Analysis method for gaseous N_2O

The 0.5% N_2O standard gases of 0.2 mL, 0.4 mL, 0.6 mL, 0.8 mL and 1 mL were extracted by gas injection needle, and then the air was extracted to a total volume of 1 mL for gas chromatography analysis, respectively. After the gaseous N_2O standard curve was completed the gas samples were injected into the

gas chromatograph for quantitative determination. Gas chromatographic conditions: Porapak Q column (80–100 mesh, 3 m×3 mm×2 mm), inlet temperature 200℃; detector temperature 340℃, column temperature 50℃. The carrier gas was N_2 and the carrier gas flow was 15 cm^3/min.

2) Analysis method of dissolved N_2O

N_2O was injected into reactors effluent to prepare saturated N_2O solution. The concentration of N_2O of the saturated solution was determined to be approximately 0.027 mol/L (756 mg/L) based on the solubility of N_2O of ambient temperature 25℃. Five different N_2O concentration points were set, the corresponding microelectrode signal values were read, and a standard curve was made. After the dissolved N_2O standard curve was completed the N_2O microelectrode was inserted into microelectrode fittings to read the corresponding microelectrode signal value under different N_2O concentrations for quantitative determination.

Table S1 The experimental measurements of both reactors.

Reactor	Parameter						
	Influent NH_4^+-N (mg/L)	Effluent NH_4^+-N (mg/L)	Influent NO_3^--N (mg/L)	Effluent NO_3^--N (mg/L)	VSS (mg/L)	DO (mg/L)	pH
SBR	0.45	<0.01	0.76	<0.01	3.70	<0.1	8.73
CSTR	0.45	<0.01	0.76	<0.01	3.70	<0.1	8.71

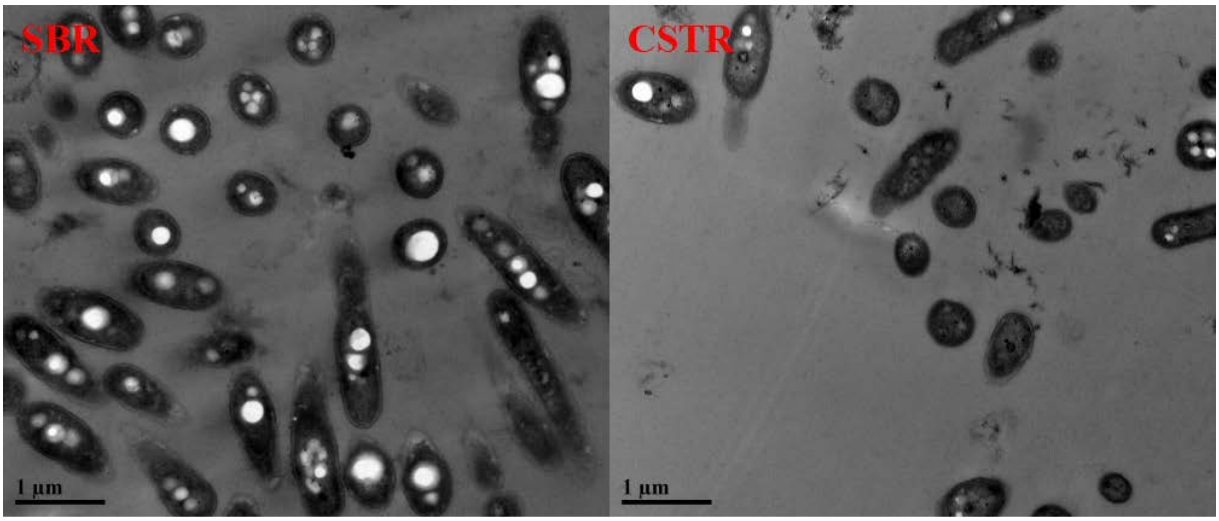

Fig. S2 TEM observation of sludge. SBR represent the sludge sampled from feast period in SBR, CSTR represent the raw sludge sampled from CSTR.

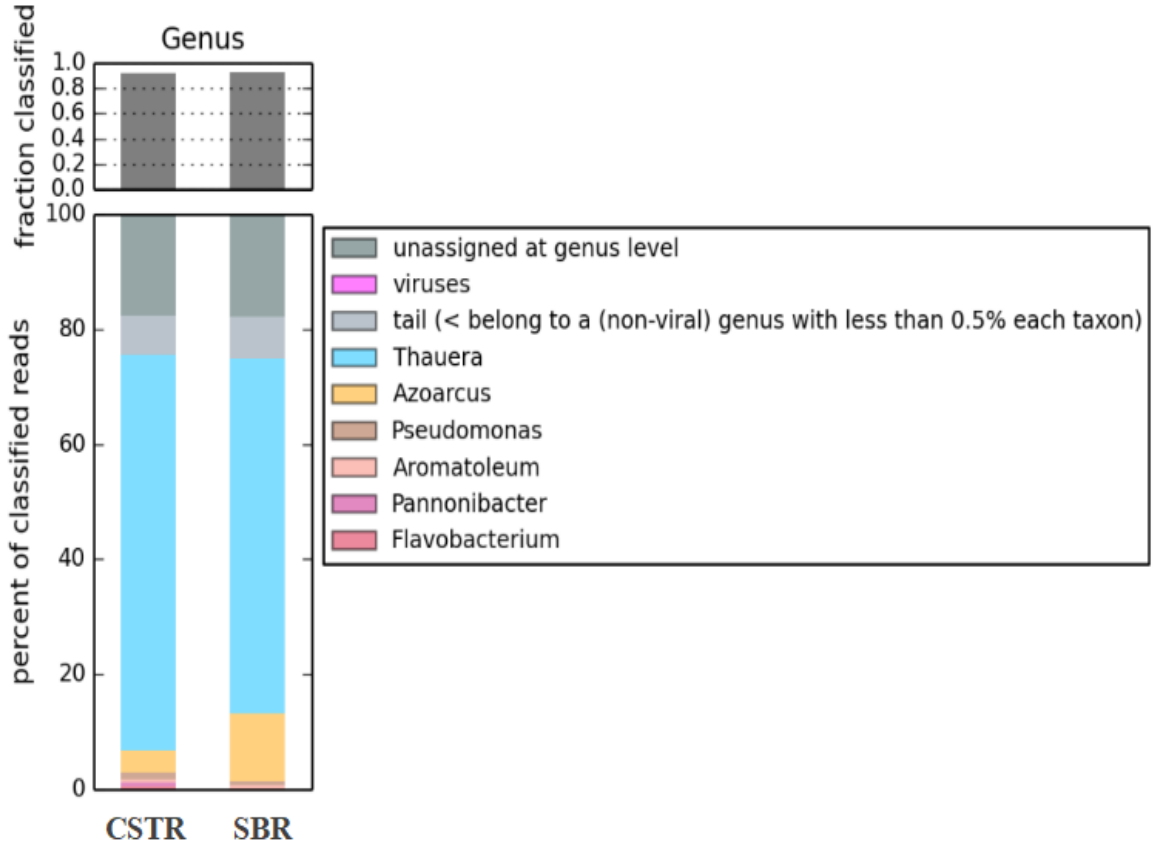

Fig. S3 Taxonomic classification of bacterial communities at genus level. CSTR represent the raw sludge sampled from CSTR, SBR represent the sludge sampled from feast period in SBR.

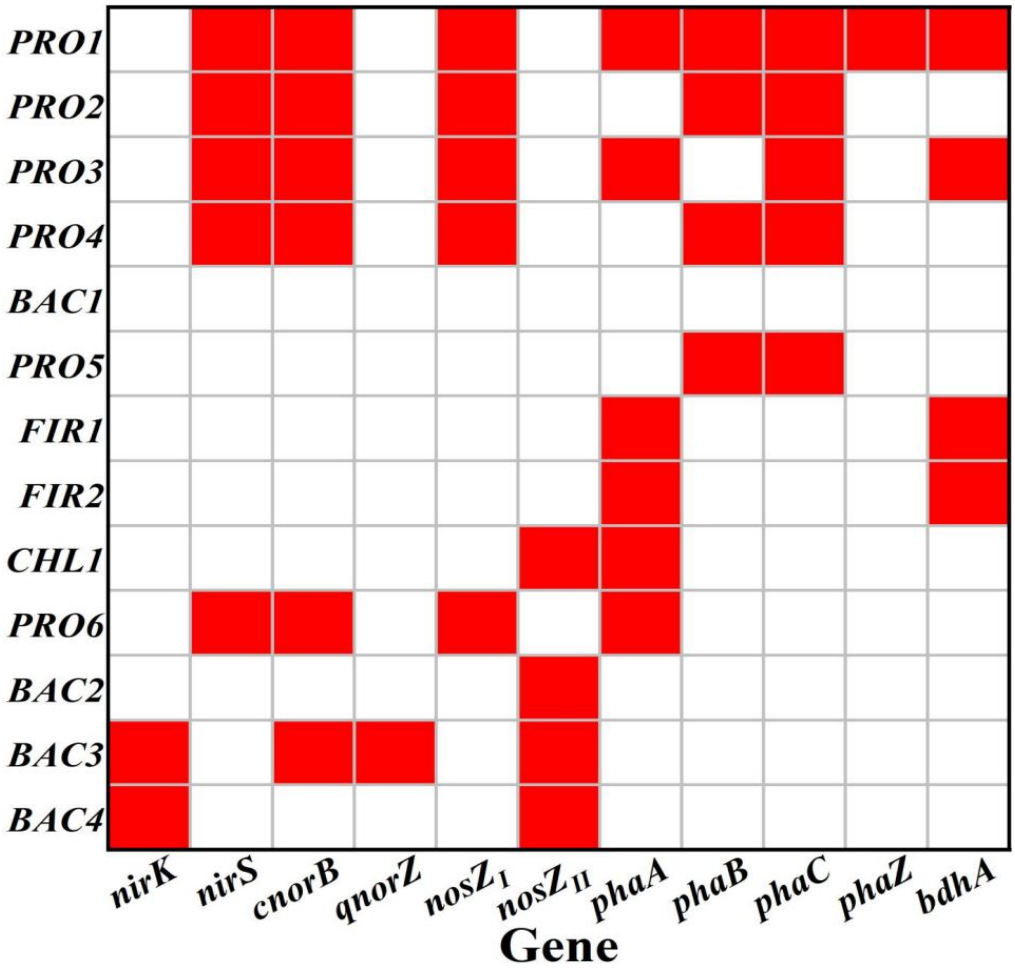

Fig. S4 Gene occurrence/absence of relevant genes from the annotations of 13 dominant organisms. The presence/absence analysis of key denitrification genes (*nirK*, *nirS*, *cnorB*, *qnorZ*, *nosZ*$_{I}$, *nosZ*$_{II}$), PHB synthesis genes (*phaA*, *phaB*, *phaC*) and PHB degradation genes (*phaZ*, *bdhA*) from the draft genomes. Red indicates gene presence and white indicates gene absence.

Table S2 Gene expression profiles of relevant genes in PRO1.

Gene_ID	KO_ID	Name	SBR-feast period FPKM	SBR-early famine period FPKM5	SBR-final famine period FPKM9	CSTR FPKM13
PRO1	K15864	nirS; cytochrome cd1 nitrite reductase[EC:1.7.2.1 1.7.99.1]	232096.8	1454.5	688.7	121026.5
PRO1	K02569	napC; cytochrome c-type protein NapC	64125.4	471.7	744.1	30497.3
PRO1	K00376	nosZ; nitrous oxide reductase [EC:1.7.2.4]	17533.7	77.0	55.7	5809.2
PRO1	K04561	norB; nitric oxide reductase subunit B [EC:1.7.2.5]	10073.2	124.6	130.2	5556.6
PRO1	K02305	norC; nitric oxide reductase subunit C	9214.5	143.0	247.0	13948.8
PRO1	K02569	napC; cytochrome c-type protein NapC	64125.4	471.7	744.1	30497.3
PRO1	K01647	CS, gltA; citrate synthase [EC:2.3.3.1]	5389.7	5312.4	2232.4	4939.7
PRO1	K01637	aceA; isocitrate lyase [EC:4.1.3.1]	1544.7	761.2	979.6	3720.2
PRO1	K01907	AACS, acsA; acetoacetyl-CoA synthetase [EC:6.2.1.16]	12.2	72.3	63.3	147.6
PRO1	K00626	ACAT, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	0.0	0.0	0.0	0.0
PRO1	K00626	ACAT, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	90.9	240.9	235.9	55.9
PRO1	K00626	ACAT, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	0.0	28.0	0.0	11.4
PRO1	K00626	ACAT, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	1127.8	1123.1	643.1	1047.5
PRO1	K00626	ACAT, atoB; acetyl-CoA C-acetyltransferase [EC:2.3.1.9]	0.0	19.0	0.0	17.8
PRO1	K05559	phaA; multicomponent K^+:H^+ antiporter subunit A	4.4	7.4	0.0	11.2
PRO1	K00023	phbB; acetoacetyl-CoA reductase [EC:1.1.1.36]	9404.0	24123.7	7650.2	5562.6
PRO1	K00023	phbB; acetoacetyl-CoA reductase [EC:1.1.1.36]	645.2	78.3	0.0	446.3
PRO1	K03821	phaC, phbC; poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]	21.8	24.5	0.0	0.0
PRO1	K03821	phaC, phbC; poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]	201.2	212.4	144.1	186.4
PRO1	K03821	phaC, phbC; poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]	905.4	1547.0	935.0	867.6
PRO1	K03821	phaC, phbC; poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]	79.4	189.9	297.6	182.5
PRO1	K00114	exaA; alcohol dehydrogenase (cytochrome c) [EC:1.1.2.8]	19.2	107.3	2237.8	93.8
PRO1	K20937	boh; 1-butanol dehydrogenase (quinone) [EC:1.1.5.11]	0.0	32.6	12172.9	5.0