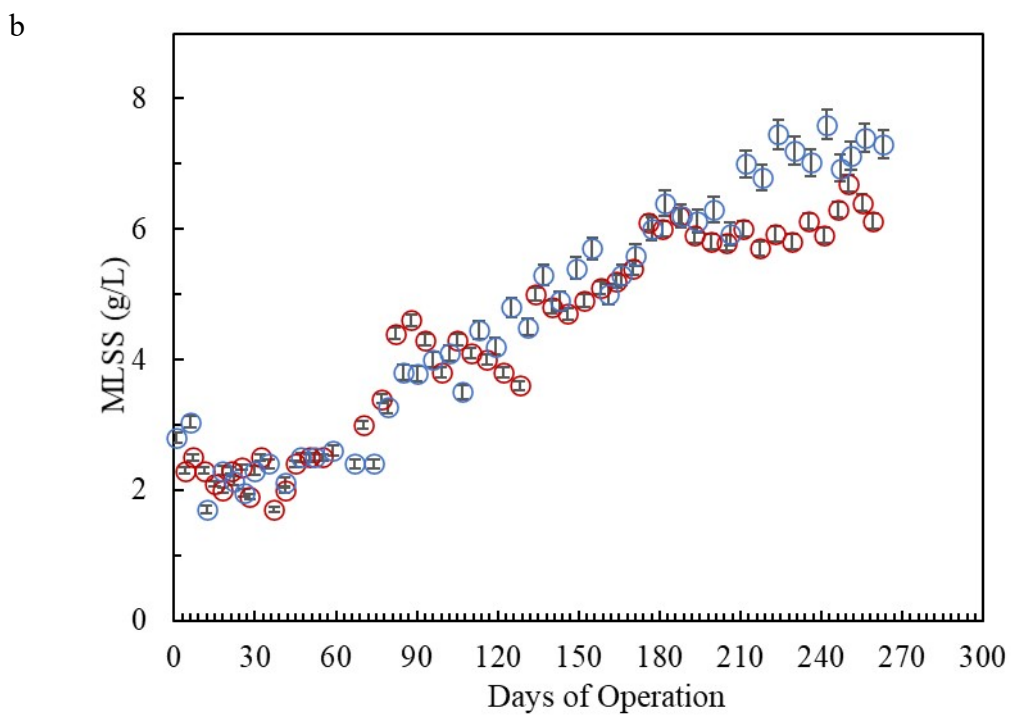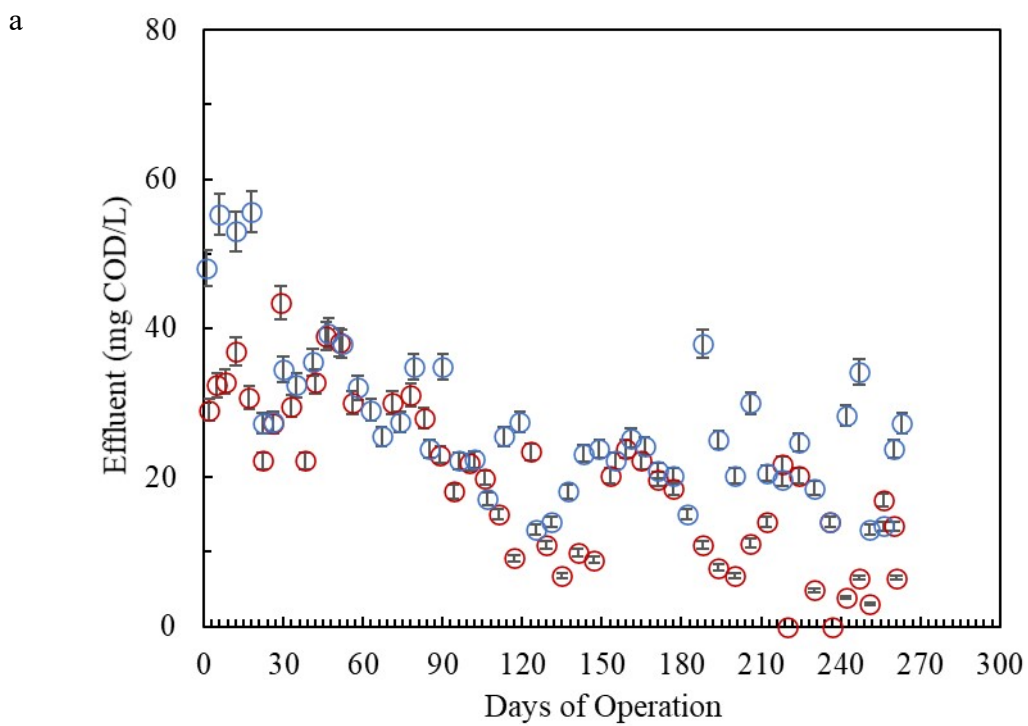*Supplemental Materials*

a

b

Figure S1 Effluent COD (a) and MLSS (b) concentrations from the two AnMBRs (red circles for AnMBR-A; blue circles for AnMBR-G) at decreasing HRTs (24 h from day 1 to day 60, 12 h from day 61 to day 170, and 6 h from day 170 to day 270).
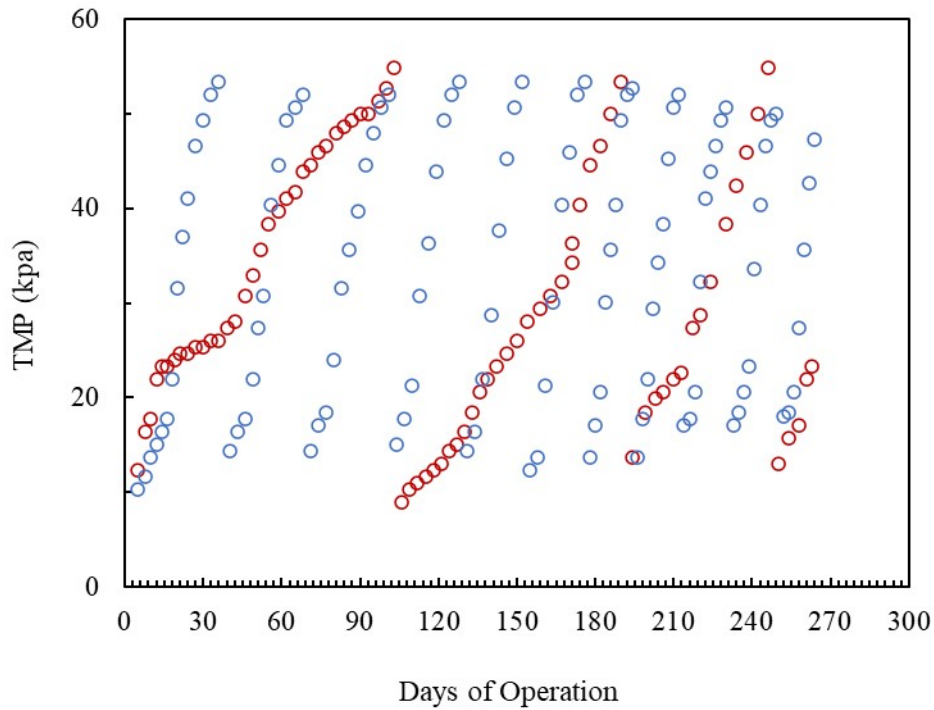

Figure S2 Changes in TMP with time from the two AnMBRs (red circles for AnMBR-A; blue circles for AnMBR-G) over a period of approximately 270 days.
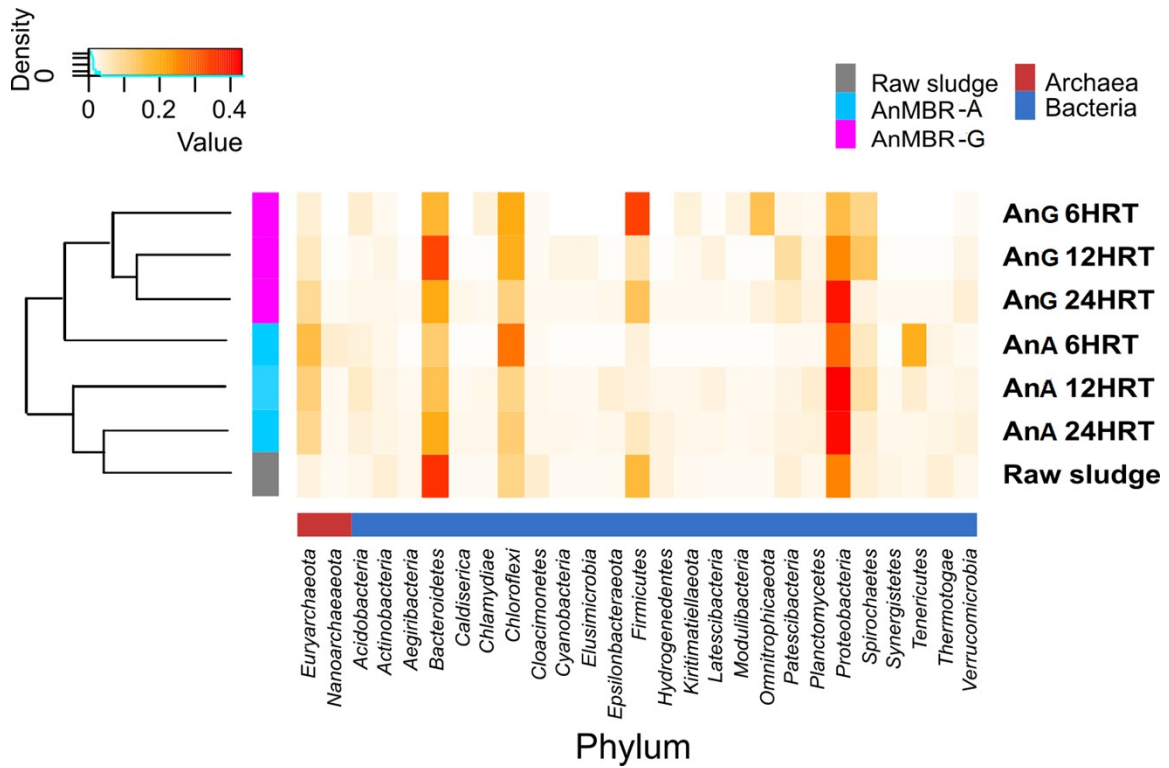
Figure S3 Heatmap of the distribution of dominant phyla and Joining clustering by using Bray-Curtis similarity index of anaerobic sludge obtaining from the AnMBRs (AnA stands for AnMBR-A and AnG stands for AnMBR-G) at decreasing HRTs.

Table S1 Operating conditions of AnMBR systems.

Treatment	AnMBR-A			AnMBR-G		
	Run 1	Run 2	Run 3	Run 1	Run 2	Run 3
Carbon Source		Sodium acetate			Glucose	
HRT (h)	24	12	6	24	12	6
SRT (d)				40		

Table S2 Significance tests of the structures of the whole communities between samples obtaining from the AnMBRs at decreasing HRTs (from 24, to 12, and to 6 h).

Sludge samples		Raw sludge	24 h	12 h	6 h
	24 h	$p < 0.01$		$p < 0.01$	$p < 0.01$
AnMBR-A	12 h	$p < 0.01$	$p < 0.01$		$p < 0.01$
	6 h	$p < 0.01$	$p < 0.01$	$p < 0.01$	
	24 h	$p < 0.01$		$p < 0.01$	$p < 0.01$
AnMBR-G	12 h	$p < 0.01$	$p < 0.01$		$p < 0.05$
	6 h	$p < 0.01$	$p < 0.01$	$p < 0.05$	

Table S3 Significance tests of the structures of the whole communities between samples obtaining from each reactor in the middle and end of each operational stage.

Treatment		AnMBR-A	
		Middle*	End*
24 h	Middle		$p > 0.05$
	End	$p > 0.05$	
12 h	Middle		$p > 0.05$
	End	$p > 0.05$	
6 h	Middle		$p > 0.05$
	End	$p > 0.05$	
		AnMBR-G	
24 h	Middle		$p > 0.05$
	End	$p > 0.05$	
12 h	Middle		$p > 0.05$
	End	$p > 0.05$	
6 h	Middle		$p > 0.05$
	End	$p > 0.05$	

Middle*: Sludge obtaining in the middle of the run
End*: Sludge obtaining at the end of the run

Table S4 Conversion of the average copies/L to cells/L, cells/g, and percent of dominant species in anaerobic sludge obtained from AnMBRs at decreasing HRTs.

		AnMBR-A				AnMBR-G			
		copies/L	cells/L[a]	cells/g[b]	% Biomass[c]	copies/L	cells/L[a]	cells/g[b]	% Biomass[c]
Raw sludge	Bacteria	2.07E+11	5.19E+10	3.99E+10	78.52	2.07E+11	5.19E+10	3.99E+10	78.52
	Archaea	2.33E+10	1.42E+10	1.09E+10	21.48	2.33E+10	1.42E+10	1.09E+10	21.48
	Methanosaeta	1.33E+10	8.85E+09	6.81E+09	13.39	1.33E+10	8.85E+09	6.81E+09	13.39
	Methanosarcina	6.78E+08	2.26E+08	1.74E+08	0.34	6.78E+08	2.26E+08	1.74E+08	0.34
	Methanomicrobiales	4.90E+09	2.72E+09	2.09E+09	4.12	4.90E+09	2.72E+09	2.09E+09	4.12
	Methanobacteriales	1.02E+08	4.61E+07	3.55E+07	0.07	1.02E+08	4.61E+07	3.55E+07	0.07
		copies/L	cells/L	cells/g	% Biomass	copies/L	cells/L	cells/g	% Biomass
Sludge at HRT of 24 h	Bacteria	2.46E+11	6.17E+10	2.80E+10	59.32	3.61E+11	9.08E+10	3.95E+10	51.18
	Archaea	6.94E+10	4.23E+10	1.92E+10	40.68	1.42E+11	8.66E+10	3.76E+10	48.82
	Methanosaeta	5.78E+10	3.85E+10	1.59E+10	33.67	4.40E+10	2.94E+10	1.28E+10	16.55
	Methanosarcina	1.47E+09	4.88E+08	2.22E+08	0.47	1.88E+09	6.27E+08	2.72E+08	0.35
	Methanomicrobiales	1.96E+10	1.09E+10	4.51E+09	9.54	3.28E+10	1.82E+10	7.92E+09	10.28
	Methanobacteriales	6.83E+07	3.10E+07	1.41E+07	0.03	2.49E+10	1.13E+10	4.92E+09	6.38
		copies/L	cells/L	cells/g	% Biomass	copies/L	cells/L	cells/g	% Biomass
Sludge at HRT of 12 h	Bacteria	2.54E+11	6.39E+10	1.49E+10	40.51	5.90E+11	1.48E+11	3.37E+10	78.67
	Archaea	1.54E+11	9.38E+10	2.18E+10	59.49	6.60E+10	4.02E+10	9.14E+09	21.33
	Methanosaeta	1.32E+11	8.82E+10	2.05E+10	55.59	4.14E+10	2.76E+10	6.27E+09	14.63
	Methanosarcina	6.74E+09	2.25E+09	5.22E+08	1.43	3.17E+09	1.06E+09	2.40E+08	0.56
	Methanomicrobiales	5.65E+09	3.14E+09	7.30E+09	1.99	1.05E+10	5.84E+09	1.33E+09	3.10
	Methanobacteriales	1.38E+08	6.27E+07	1.46E+07	0.04	2.01E+10	9.15E+09	2.08E+09	4.85
		copies/L	cells/L	cells/g	% Biomass	copies/L	cells/L	cells/g	% Biomass
Sludge at HRT of 6 h	Bacteria	2.58E+11	6.48E+10	1.62E+10	37.57	5.20E+10	1.31E+10	1.00E+10	82.81
	Archaea	1.77E+1	1.08E+	2.69E+	62.43	4.45E+0	2.71E+	2.08E+	17.19

	1	11	10		9	09	09	
Methanosaeta	1.58E+11	1.05E+11	2.63E+10	61.08	2.98E+09	1.99E+09	1.53E+09	12.60
Methanosarcina	9.14E+09	3.05E+09	7.62E+08	1.77	1.17E+08	3.90E+07	3.00E+07	0.25
Methanomicrobiales	2.55E+09	1.42E+09	3.54E+08	0.82	1.08E+09	6.00E+08	4.62E+08	3.81
Methanobacteriales	2.19E+08	9.95E+07	2.49E+07	0.06	1.75E+09	7.95E+08	6.12E+08	5.05

Values are averaged for samples.

[a] Cells/L = copies/L ÷ gene copy number/cell. (The average 16S rDNA copies per genome in bacteria, archaea, *Methanosaeta*, *Methanosarcina, Methanomicrobiales*, and *Methanobacteriales* was 3.98, 1.64, 1.5, 3, 1.8, and 2.2, repetitively, according to previous studies (Hou et al., 2020; Klappenbach et al., 2001))

[b] Cells/g = cells/L ÷ g/L (mean mixed liquor suspended solids (MLSS)).

[c] The total of Bacterial and Archaeal 16S rRNA gene provides normalization for comparison to the subpopulations and is set at 100%.

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