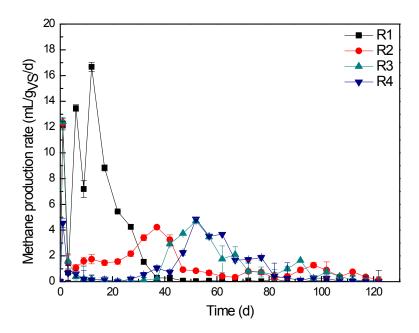
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Fig.S1. Methane production rate of the reactors at different TS contents.



**Table S1**Concentrations of soluble organic matters at different periods of the anaerobic digestion. Acetate, propionate, butyrate and valerate were summed as VFAs. Mean values were in triplicate.

Sample		VFAs	Protein	Polysaccharide	Unknown
		$(mg_{COD}/g_{VS})$	$(mg_{COD}/g_{VS})$	$(mg_{COD}/g_{VS})$	$(mg_{COD}/g_{VS})$
6 d	R1	270.7	9.6	15.0	29.7
	R2	287.7	6.9	13.7	87.5
	R3	331.0	13.1	16.6	85.1
	R4	346.2	7.8	18.8	230.3
37 d	R1	28.4	10.7	25.6	194.3
	R2	403.8	5.3	21.9	295.9
	R3	402.4	7.6	21.3	310.5
	R4	386.7	6.8	20.5	395.1
87 d	R1	41.5	23.4	30.7	175.9
	R2	315.0	13.7	24.3	185.0
	R3	275.9	11.1	24.7	271.9
	R4	285.8	9.3	25.1	369.0
122 d	R1	51.7	19.7	31.3	195.3
	R2	187.2	15.0	30.1	198.8
	R3	246.0	14.3	32.3	284.0
	R4	294.1	11.8	32.9	298.7

**Table S2**Relative abundance of major bacterial communities at genus level at different TS contents. Each represented by more than 0.5% total sequences in at least one sample and the rest was defined as "Unclassified".

Taxonomy assignment	R1	R2	R3	R4
Coprothermobacter	25.0	20.8	5.5	2.1
Allochromatium	9.8	7.3	4.9	4.1
Anaerobaculum	2.4	2.7	2.6	0.5
VadinCA02	1.4	0.2	0.4	1.1
Rhodobacter	1.2	1.1	2.4	3.5
Caldicoprobacter	0.9	0.7	1.5	2.0
Bacillus	0.7	0.8	0.2	0.5
Dechloromonas	0.7	0.2	0.2	0.5
KD1-23	0.5	0.2	0.6	0.3
Clostridium	0.4	1.2	1.1	0.2
Nevskia	0.3	1.0	3.5	5.4
Tepidimicrobium	0.2	1.7	1.9	2.6
Syntrophomonas	0.1	1.2	1.0	0.1
Thermacetogenium	-	0.4	2.1	1.9
Unclassified	56.4	60.5	72.1	75.2

<sup>&#</sup>x27;-' indicates the presence of OTU is less than 0.1 % in the sample.

**Table S3**Relative abundance of major archaea communities at genus level at different TS contents. Each represented by more than 0.5% total sequences in at least one sample and the rest was defined as "Unclassified".

Taxonomy assignment	R1	R2	R3	R4
Methanosarcina	34.5	15.5	6.3	3.6
Methanosaeta	19.0	22.9	22.5	21.4
Methanothermobacter	36.7	42.0	21.8	2.1
Methanobacterium	2.2	1.2	1.4	3.0
Methanospirillum	2.2	0.4	1.1	2.0
Methanomassiliicoccus	0.7	0.6	0.1	0.3
Methanoculleus	0.2	11.6	39.9	43.2
Methanobrevibacter	0.1	0.1	0.5	1.5
Unclassified	4.4	5.7	6.4	22.9