

Supplementary Material

S1. Hydrodynamic properties of QS and GG

Table S1 Hydrodynamic properties of QS and GG

	Particle sizes of fillers (mm)	Total volume of fillers (mL)	Filled volume (mL)	Filling rate (%)	Packing density (g/cm ³)
QS	3-5	600	810	51	1.85
GG			790	49	1.71

S2. COD balance calculation method

COD balance analysis were conducted for QS and GG with the operational data under the HRT of 6 h, the proportion of organic matters in influent (calculated as COD) converted to gaseous and dissolved methane, residual soluble organics in effluent, suspended organic matters in effluent (including detached biomass and intercellular polymers) and other unknown lost, were calculated as follows:

- 1) The proportion of gaseous methane:

$$P_{gaseous_methane} = 64 \times \frac{P \times V_{CH_4}}{R \times T \times COD_{in} \times V_R} \times 100\%$$

Where P was atmospheric pressure (Pa); R was gas constant, (8.314 J/mol/K); T was temperature (K); COD_{in} was the COD concentration of influent (g/m³); V_{CH_4} was the volume of methane produced within one HRT (m³); V_R was the volume of reactor (m³).

- 2) The proportion of dissolved methane:

$$P_{dissolved_methane} = 64 \times \frac{H \times p_{CH_4}}{COD_{in}} \times 100\%$$

Where H was henry constant of methane (mol/m³/Pa); p_{CH_4} was the partial pressure of methane (Pa).

- 3) The proportion of soluble organics in effluent:

$$P_{soluble\ effluent} = \frac{SCOD_{eff}}{COD_{in}} \times 100\%$$

Where $SCOD_{eff}$ was the soluble COD concentration of effluent (g/m³), which was measured with filtered effluent.

- 4) The proportion of suspended organic matters:

$$P_{suspended\ effluent} = \frac{(TCOD_{eff} - SCOD_{eff})}{COD_{in}} \times 100\%$$

Where $TCOD_{eff}$ was the total COD concentration of effluent (g/m³).

- 5) The other unknown lost:

$$P_{others} = 100\% - P_{gaseous_methane} - P_{dissolved_methane} - P_{soluble\ effluent} - P_{suspended\ effluent}$$

S3. Total genomic DNA extraction and Illumina sequencing method

Total genomic DNA of biomass sample was extracted with E.Z.N.A. Soil DNA Isolation Kit (OMEGA), according to the manufacturer's instructions. The quantity and quality of the

extracted DNA were checked by agarose gel test (Gel imaging system from UVP Co. Ltd., USA). Bacterial V3-V4 region of 16S rDNA gene was amplified using general primers Nobar_341F (CCTACGGGNGGCWGCAG) and Nobar_805R (GACTACHVGGGTATCTAATC C). Archaeal V3-V4 region of 16S rDNA was amplified using general primers 340F (CCCTAYGGGGYGCASCAG) and 1000R (GGCCATGCACYWCYTCTC) for first round amplification, 349F (GYGCASCAG KCGMGAAW) and 806R (GGACTACVSGGGTATCTAAT) for the second round amplification. PCR products of both bacterial and archaeal amplification were purified using Agencourt AMPure XP kit (Beckman Coulter Commercial Enterprise (China) Co., Ltd.) and went for Illumina Miseq sequencing.