

Supplementary Figures

TITLE: Pyrosequencing of *mcrA* and archaeal 16S rRNA genes reveals diversity and substrate preference of anaerobic digester methanogen communities

RUNNING TITLE: Methanogens in anaerobic digesters

KEY WORDS: Methanogens, anaerobic digestion, biogas, *mcrA* gene, archaea 16S rRNA gene, 454 pyrosequencing

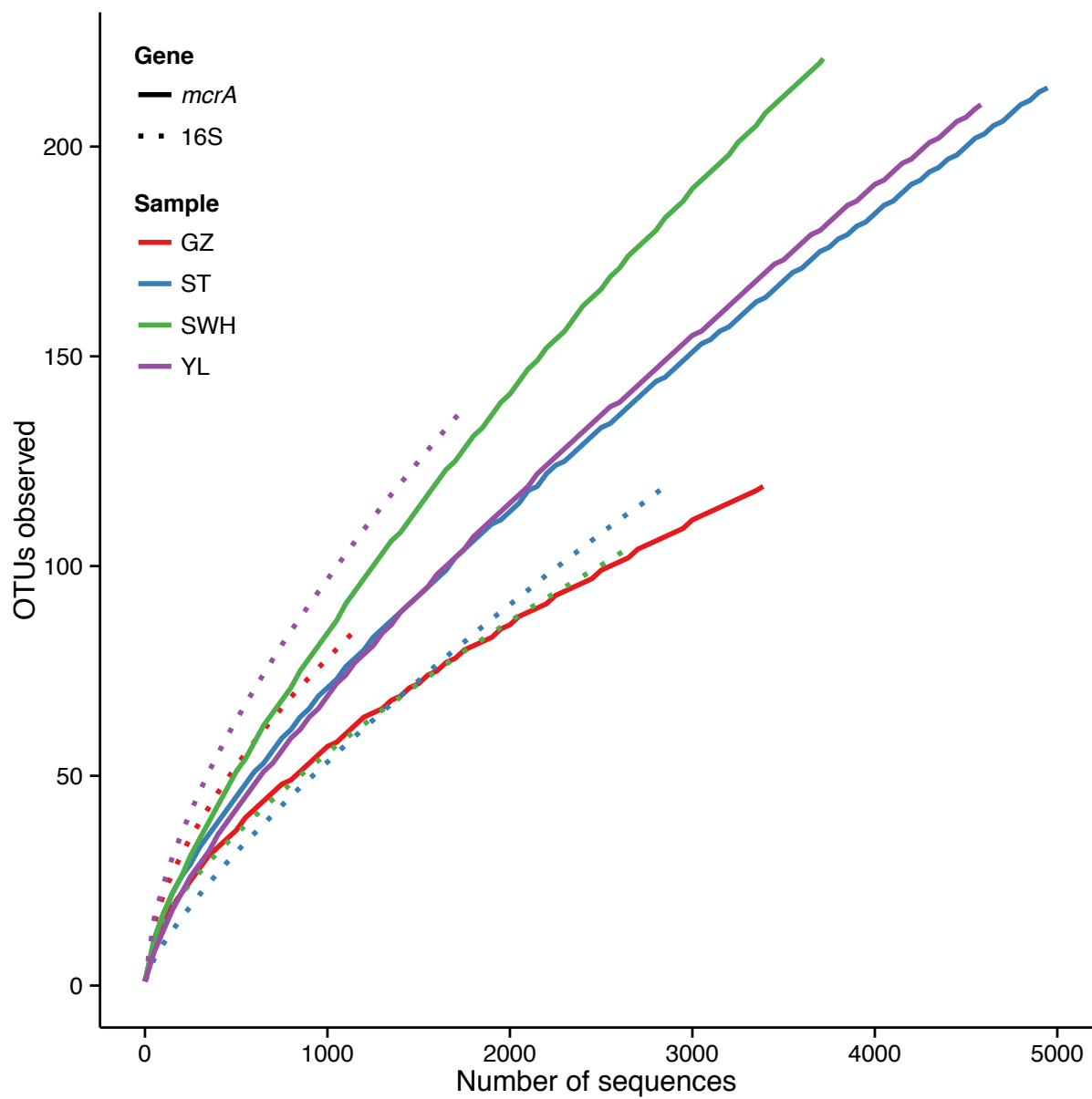
AUTHORS: David Wilkins, Xiao-Ying Lu[†], Zhiyong Shen, Jiapeng Chen, and Patrick K. H. Lee[‡]

AFFILIATION: School of Energy and Environment, City University of Hong Kong, Hong Kong

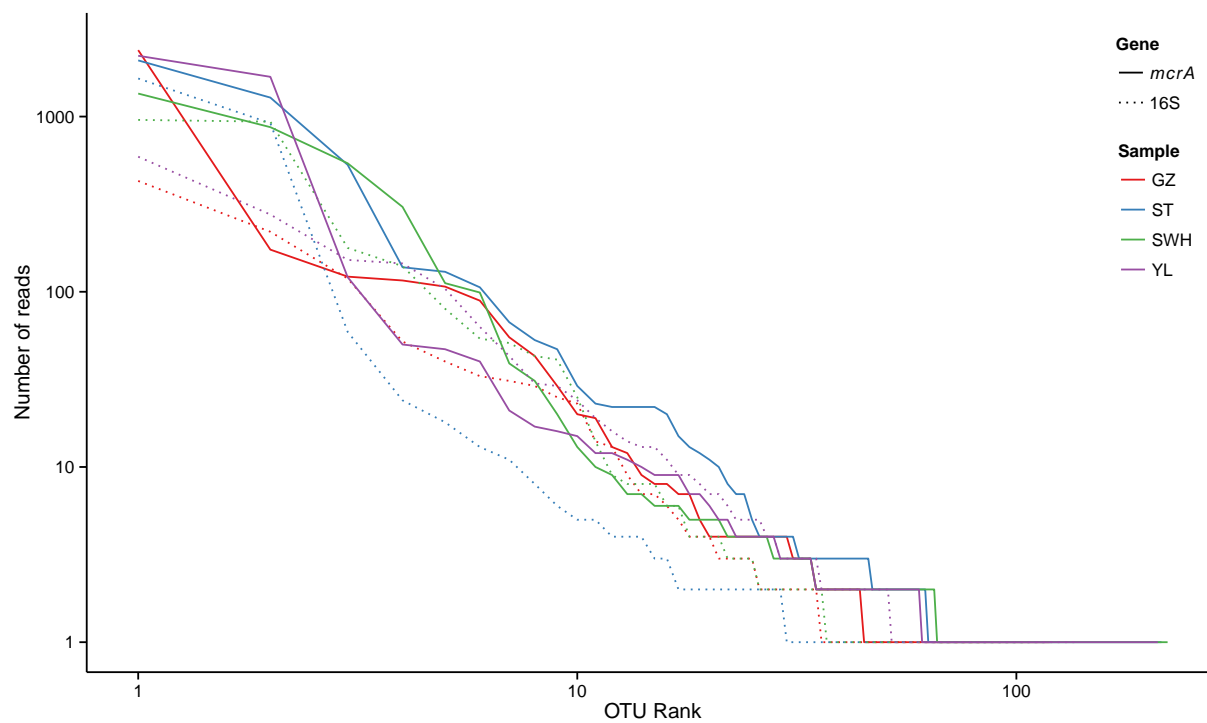
[†]Current address: Faculty of Science and Technology, Technological and Higher Education Institute of Hong Kong, Hong Kong

CORRESPONDENT: [‡]B5424-AC1, School of Energy and Environment, City University of Hong Kong, Tat Chee Avenue, Kowloon, Hong Kong; E-mail: patrick.kh.lee@cityu.edu.hk; Tel: (852) 3442-4625; Fax: (852) 3442-0688.

Supplementary Figure 1: Rarefaction curves for OTUs of each gene and from each digester.

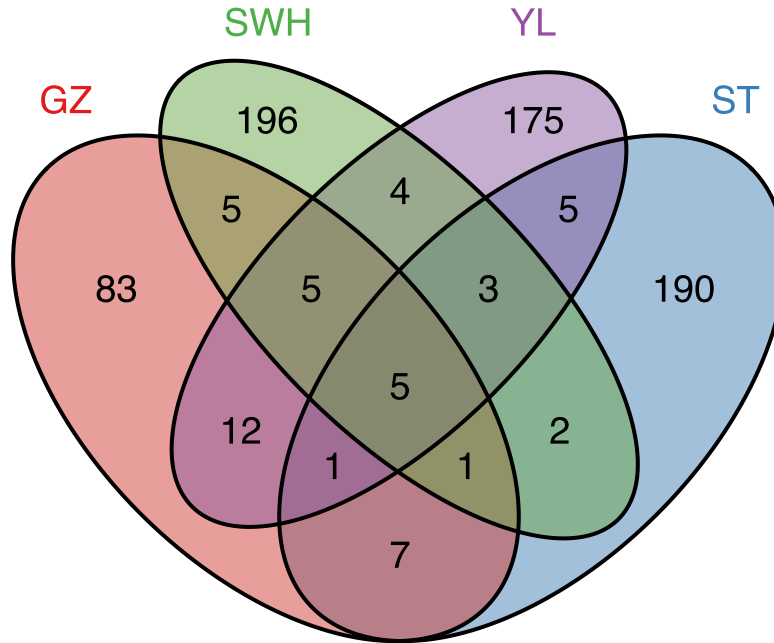


Supplementary Figure 2: Rank-abundance curves for OTUs of each gene and from each digester.



Supplementary Figure 3: Venn diagrams indicating number of overlapping OTUs between the digester methanogen (*mcrA*) and archaea (16S rRNA) communities. Five OTUs_{*mcrA*} (OTU002, OTU029, OTU037 & OTU039, *Methanobacteriaceae*; OTU005, *Methanosaetaceae*) and three OTUs_{16S} (OTU002, WSA2; OTU003, *Methanosaetaceae*; OTU007, *Methanoregulaceae*) were shared between all digesters.

mcrA



16S rRNA

