

Table S1. Primers used in this study.

Software/database	Version	Application	Link
Flash	1.2.11	pair-end sequence splicing	<a href="https://ccb.jhu.edu/software/FLASH/index.shtml">https://ccb.jhu.edu/software/FLASH/index.shtml</a>
Qiime	1.9.1	Generate abundance table for each taxonomy level, calculate beta diversity distance	<a href="http://qiime.org/install/index.html">http://qiime.org/install/index.html</a>
Uparse	7.0.1090	OTU cluster	<a href="http://www.drive5.com/uparse/">http://www.drive5.com/uparse/</a>
RDP Classifier	2.1	Sequence classification annotation	<a href="https://sourceforge.net/projects/rdp-classifier/">https://sourceforge.net/projects/rdp-classifier/</a>
Usearch	7.0	OTU statistics	<a href="http://www.drive5.com/usearch/">http://www.drive5.com/usearch/</a>
Mothur	1.30.2	alpha diversity analysis	<a href="https://www.mothur.org/wiki/Download_mothur">https://www.mothur.org/wiki/Download_mothur</a>
PICRUSt	1.1.0	function prediction of KEGG、COG、Pfam	<a href="http://picrust.github.io/picrust/">http://picrust.github.io/picrust/</a>
Mega	7.0	phylogenetic analysis	<a href="https://www.megasoftware.net/">https://www.megasoftware.net/</a>
SILVA	132	rRNA database	<a href="https://www.arb-silva.de/">https://www.arb-silva.de/</a>
RDP	11.5	rRNA database	<a href="http://rdp.cme.msu.edu/">http://rdp.cme.msu.edu/</a>
GreenGenes	135	rRNA database	<a href="http://greengenes.secondgenome.com/">http://greengenes.secondgenome.com/</a>
FunGene	9.6	Functional gene database	<a href="http://www.fungene-db.fr/">http://www.fungene-db.fr/</a>
Tax4fun	0.3.1	Tax4Fun function prediction	<a href="http://tax4fun.gobics.de/">http://tax4fun.gobics.de/</a>
MAFFT	7.2	Multiple sequence alignment	<a href="https://mafft.cbrc.jp/alignment/software/">https://mafft.cbrc.jp/alignment/software/</a>
IQ-TREE	1.6.8	Constructing evolutionary trees	<a href="http://www.iqtree.org/">http://www.iqtree.org/</a>
Fastp	0.19.6	Quality control	<a href="https://github.com/OpenGene/fastp">https://github.com/OpenGene/fastp</a>

