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ORIGINAL ARTICLE

Composition and function of the microbiotas in the different parts of the midgut of *Pyrrhocoris sibiricus* (Hemiptera: Pyrrhocoridae) revealed using high-throughput sequencing of 16S rRNA

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Key words. Pyrrhocoridae, *Pyrrhocoris sibiricus*, digestion, gut microbiota, community structure, functional profiling, next-generation sequencing, 16S rRNA gene

Abstract. In pyrrhocorids, digestion of food occurs mainly in the midgut, which is divided into four parts (M1–M4), and takes between three and four days. Food is retained in M1 for about 5 h and passes quickly through M4. However, food is retained in M2 and M3 much longer, about 70 to 90 h. The different stages in digestion may be influenced by different microbial populations in the different parts of the midgut. In the present study, the microbiota in the four parts of the midgut of *Pyrrhocoris sibiricus* were analysed in detail using high-throughput sequencing of the 16S rRNA V3–V4 region. The most abundant bacteria in M3 were Actinobacteria (Coriobacteriaceae) whereas it was Proteobacteria (gammaproteobacteria) in M1, M2 and M4. Actinobacteria was the second most abundant bacterial group in M2. According to the PCA analysis, M2 and M3 have the most similar bacterial communities. *Burkholderia*, which is closely related to the plant-associated beneficial and environmental (PBE) group, was also found in M1, M2 and M4. Predictive functional profiles of the metagenomes revealed that metabolism mostly occurred in M2 and M3. The PICRUSt results were consistent with the 16S rRNA metagenomic analysis and indicate that the bacteria in M2 and M3 play an important role in degrading complex dietary components.

INTRODUCTION

Symbiotic interactions between animals and beneficial microorganisms are very common in nature, including insects (Buchner, 1965; Smith, 1989; Moran et al., 2008). In many cases, these symbionts are housed in the gut of their hosts and play an essential nutritional role in maintaining the fitness of the host insect. Their role can involve detoxifying plant allelochemicals, promoting digestion and providing digestive enzymes or nutrients, especially when the insect is either a blood, sap or cellulose feeder (Buchner, 1965; Douglas, 1992; Akman et al., 2002; Genta et al., 2006; Sudakaran et al., 2012; Taylor et al., 2014; Onchuru et al., 2018).

The Pyrrhocoridae are terrestrial bugs of which there are ~340 species belonging to 33 genera worldwide (Schaefer & Ahmad, 2000; Henry, 2009). Most of them prefer to feed on the seeds of Malvales plants, which are vitamin limited and avoided by other insects due to their phytochemical defences (Allen et al., 1967; Abou-Donia, 1976; Ahmad & Schaefer, 1987; Kristenová et al., 2011). The midgut of Pyrrhocoridae is differentiated into four distinct parts, namely M1–M4. The digestion of food in pyrrhocorids takes three or four days, with most of the time spent in M2 and M3 (Silva & Terra, 1994). It is suggested that the final stages of digestion occur in the midgut as the salivary digestive enzymes in seed feeders only have a minor role (Saxena, 1963; Silva & Terra, 1994). Previous studies on the gut microbiota of cotton stainers (*Dysdercus fasciatus* Signoret) and red firebugs (*Pyrrhocoris apterus* Linnaeus) indicate that a special microbiota, Actinobacteria, dominate in M3 and provide the host with B vitamins and protects it from parasites (Sudakaran et al., 2012; Salem et al., 2014; Onchuru et al., 2018). However, the role of microbiota in the digestion of food is still unclear.

Pyrrhocoris sibiricus Kuschakevich, a ground-dwelling seed-feeder, is widely distributed in Russian Far East, Central and East Mongolia, China, North Korea and Japan (Zhang, 1985; Matolin & Štys, 1987). Both nymphs and adults of *P. sibiricus* feed on the seeds of leguminous and gramineous plants, which subsequently affects the health

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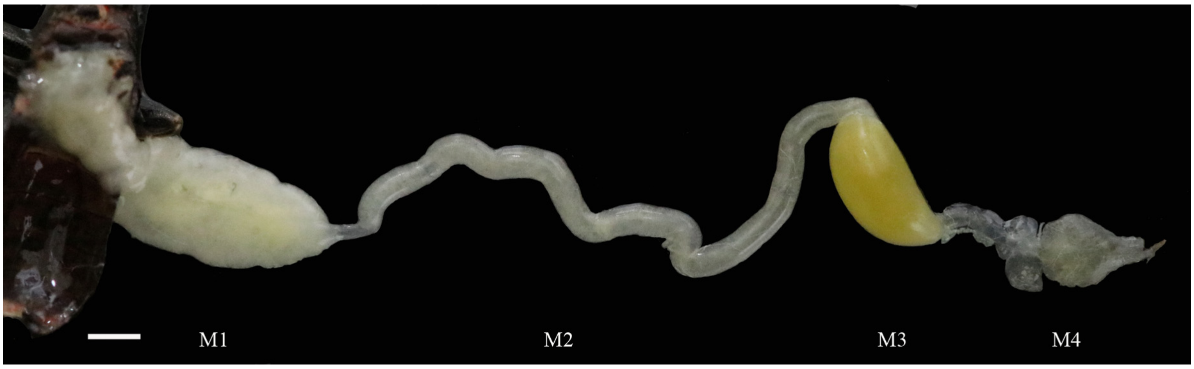

Fig. 1. Photograph of a dissected midgut of *Pyrrhocoris sibiricus* (M1–M4). Scale bar = 1 mm.

of these plants (Zhang, 1985; Matolin & Štys, 1987). In the present study, 16S rRNA metagenomic analysis was used to characterize the microbes that inhabit the different parts of the midgut of *P. sibiricus*. Furthermore, a PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) analysis was used to determine the functional potentials of the bacteria in the M1, M2, M3 and M4 using the 16S rRNA marker gene.

MATERIALS AND METHODS

Sample collection

Adult specimens of *P. sibiricus* feeding on the seeds of *Abutilon theophrasti* Medicus were collected between September and December 2018 in Jinzhong, Shanxi Province (37.68°N, 112.75°E). Prior to dissection, they were soaked in 70% ethyl alcohol for 3 min and then washed 3 times with sterile deionized water in order to remove exogenous contaminants. The guts were then dissected under sterile deionized water using sterilized tweezers and eye scissors under aseptic conditions. Each midgut was separated into four parts, M1, M2, M3 and M4 (Fig. 1), which were treated separately. Since there were three replicates for each part and each replicate consisted of a mixture of samples from 20 adults regardless of sex, a total of 60 adults were dissected. Five hundred milligrams of each part were collected and immediately frozen in liquid nitrogen for subsequent DNA extraction. The remains of the material of each of the parts were also frozen in liquid nitrogen and preserved at –80°C.

DNA extraction and sequencing

DNA was extracted using a Mag-Bind Soil DNA extraction kit (Omega, Norcross, GA, USA) according to the manufacturer's instructions with slight modifications to improve the efficiency of the DNA extraction from the gut samples. DNA concentration was measured using a NanoDrop ND-1000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA) and its quality confirmed using agarose gel electrophoresis. The V3–V4 hypervariable region of the 16S rRNA gene was then amplified using PCR and the universal primers 338F (5'-ACTCCTACGGGAGGCAGCA-3') and 806R (5'-GGACTACHVGGGTWTCTAAT-3') (Mizrahi-Man et al., 2013). The reaction solution consisted of: 5 µl of Q5 reaction buffer (5×), 5 µl of Q5 High-Fidelity GC buffer (5×), 2 µl of dNTPs (2.5 mM), 1 µl each of forward and reverse primer (10 uM), 2 µl of DNA template, 0.25 µl of Q5 High-Fidelity DNA Polymerase (5 U/µl) and 8.75 µl of ddH_2O. PCR conditions consisted of initial denaturation at 98°C for 5 min, followed by 25 cycles of denaturation at 98°C for 30 s, annealing at 52°C for 30 s and extension at 72°C for 1 min, with a final extension at 72°C for 5 min. PCR products were verified by 2% agarose gel electrophoresis and target fragments were purified using an AxyPrep gel extraction kit (Axygen, Union City, CA, USA). The purified PCR products were then sequenced on an Illumina Miseq platform using 2 × 300 base pairs (bp) paired-end reads (Personalbio, Shanghai, China).

Sequence analysis

Sequencing data was processed using the Quantitative Insights Into Microbial Ecology (QIIME, v.1.8.0) pipeline as previously described (Caporaso et al., 2010). Resulting sequence with average Phred scores lower than 20, ambiguous bases, mononucleotide repeats longer than 8 bp, or those which had a length shorter than 100 bp were removed. Sequences that passed the filter without any mismatches were trimmed and merged using FLASH v.1.2.11 (Magoc & Salzberg, 2011), according to the principle of 98% overlap of 19 bases. The resulting sequences of each sample were clustered into operational taxonomic units (OTUs) based on 97% identity using the UCLUST function in QIIME (Caporaso et al., 2010; Edgar et al., 2010). OTU taxonomic classification was conducted using a BLAST search of the representative sequences set against the Greengenes database (Release 13.8, http://greengenes.secondgenome.com/) (DeSantis et al., 2006) and using the best hit (Altschul et al., 1997). An OTU table was generated to record the abundance and taxonomy of each OTU in each sample. OTUs with a sequence frequency below 0.001% were not included in the analysis (Bokulich et al., 2013). To minimize the difference of sequencing depth across samples, an averaged, rounded rarefied OTU table was generated by averaging 100 evenly resampled OTU subsets under the 90% of the minimum sequencing depth for further analysis.

Bioinformatics analysis

Rarefaction curves were calculated at a 97% similarity level in QIIME. Richness (Chao1 and ACE) and diversity (Simpson and Shannon) indices were calculated for the microbiota using an out table in QIIME. Structural variation in the microbiota in the four parts of the midgut was investigated using Weighted UniFrac principal coordinate analysis (PCoA) in QIIME (Lozupone & Knight, 2005; Lozupone et al., 2007). A maximum likelihood (ML) tree was constructed based on the Kimura 2-parameter model using MEGA X with 1000 bootstrap replicates (Kumar et al., 2018). The function of the gut microbiota was predicted using PICRUSt v1.1.3 Release and Greengenes as the sequenced reference, according to the online protocol (http://picrust.github.io/picrust/index.html) (DeSantis et al., 2006; McDonald et al., 2012; Langille et al., 2013). Firstly, OTUs which mapped to the GG13.5 database with a 97% similarity were selected by QIIME. The OTUs counts were normalized by dividing by the 16S rRNA gene copy numbers from known bacterial genomes in Integrated Microbial Genomes (IMG); normalized OTU tables were

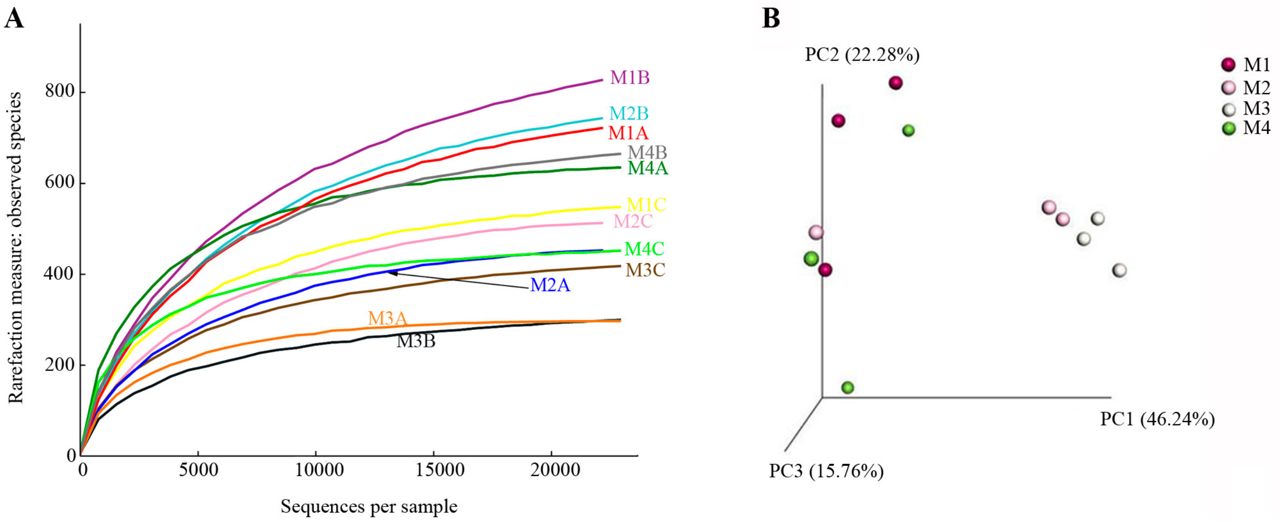

Fig. 2. Rarefaction curve of the samples (A) and PCA analysis of their microbiota (B) for each treatment.

then aligned to the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. The nearest sequenced taxon index (NSTI) was calculated to quantify the quality of the predictions. Heatmap was generated using hemI (Deng et al., 2014). PCA analysis was conducted in STAMP v.2.1.3 (Parks et al., 2014) and contributions of core genera were generated from PICRUSt results using Excel. The functional differences between two-groups were compared using two-sided Welch's *t*-test in the Majorbio Cloud (cloud.majorbio.com).

RESULTS

The microbiota in the M1, M2, M3 and M4 of *P. sibiricus* were characterized using 16S rRNA high-throughput sequencing. A total of 463,717 reads were generated from all of the independent biological treatments and replicates. The average amplicon length of the 16S rRNA variable V3–V4 region was 420 bp. After quality filtering and read merging, 405,095 (87.36%) sequences were obtained (105,842, 96,241, 98,594 and 104,418 sequences for M1, M2, M3 and M4, respectively). After assignment using UCLUST and removing OTUs with a relative abundance less than 0.001%, a total of 1,111, 1,060, 496 and 1,217 OTUs were obtained for M1, M2, M3 and M4, respectively. All taxa with relative abundances > 0.001% are cited in Table S3. Rarefaction curves indicate sufficient sequenc-

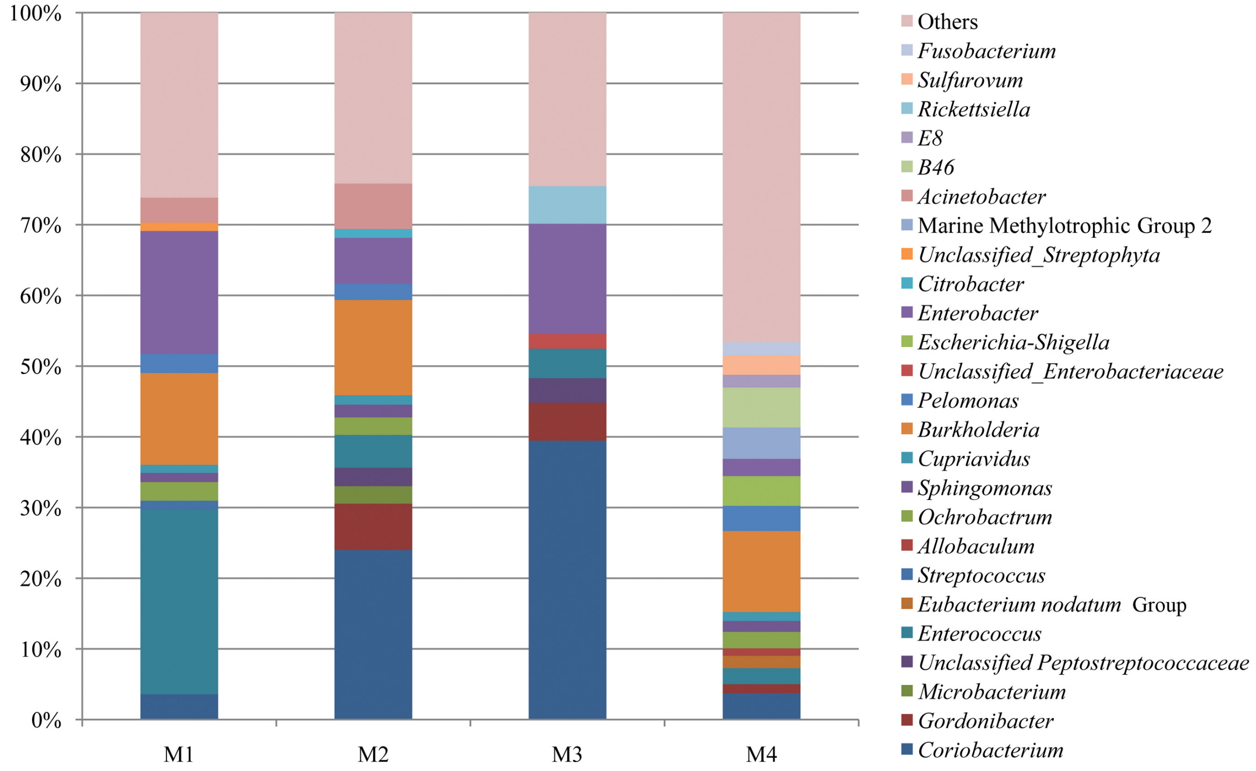

Fig. 3. Bacterial composition in terms of genera in the four parts of the midgut. Genera with an abundance lower than 1% are referred to as "Others".

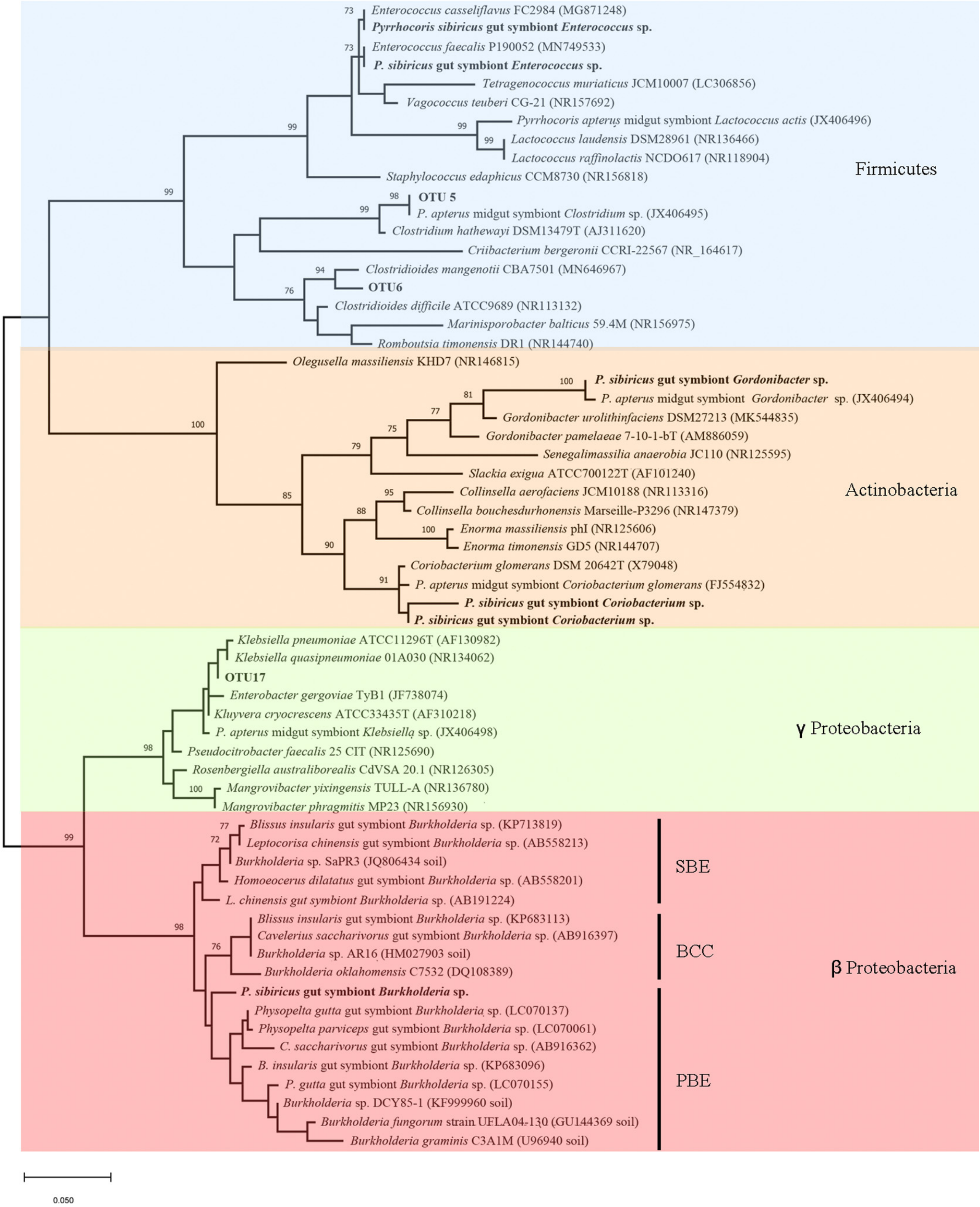

Fig. 4. Phylogenetic analysis based on the sequences of *Coriobacterium* sp., *Gordonibacter* sp., *Enterococcus* sp., *Burkholderia* sp. and unassigned OTUs in the different parts of the midgut of *Pyrrhocoris sibiricus*. Bootstrap values more than 70% are displayed on the bacterial phylogenies. Abbreviations of clades: BCC – *Burkholderia cepacia* complex; PBE – plant-associated beneficial and environmental group; SBE – stinkbug-associated beneficial and environmental group.

ing depth for taxonomic classification (Fig. 2A). For all samples, estimates of ACE richness indicate that M2 had the richest microbiota and the Shannon index suggests that diversity in M4 was significantly higher than in the other parts of the midgut (Table S1).

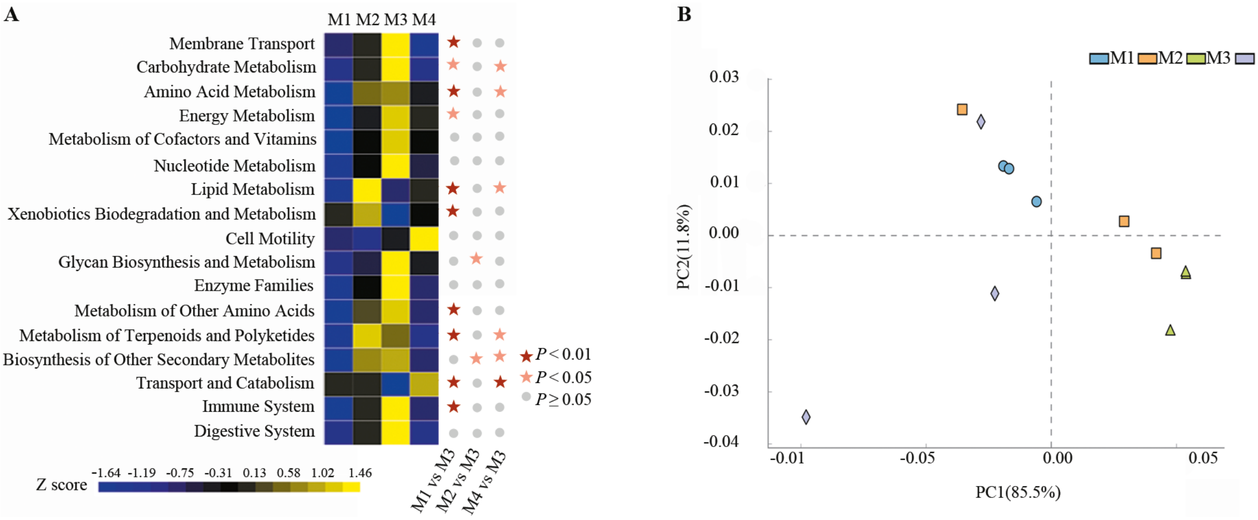

Fig. 5. Predicted KEGG pathways in different parts of the midgut of *Pyrrhocoris sibiricus*. A – heatmap of the KEGG modules differentially enriched in the different midgut microbiomes. KEGG pathways with a *P*-value < 0.01 are marked with a dark red star, < 0.05 with light red star and ≥ 0.05 with a grey circle. B – PCA based on the relative abundance of KEGG orthology groups.

Diversity of bacteria in gut microbiota

At the phylum level Proteobacteria, Actinobacteria, Firmicutes and Bacteroidetes were present in all samples of the midgut of *P. sibiricus*. Proteobacteria was the most abundant in M1 (56.39%), M2 (51.68%) and M4 (68.31%) followed by Firmicutes in M1 and M4 (31.60% and 15.97%, respectively). In M2, Actinobacteria was the second most abundant, accounting for 35.51% of all bacteria. The M3 region was unique in that Actinobacteria dominated followed by Proteobacteria with abundances of 49.58% and 37.11%, respectively (Fig. S1). Principal component analysis revealed that M2 and M3 were most similar in terms of their microbiota (Fig. 2B).

When OTUs with an abundance lower than 1% were removed, 10, 13, 8 and 18 core genera were identified in M1, M2, M3 and M4, respectively (Fig. 3). All OTUs with abundances greater than 1% are cited in Table S2. For the phylum Proteobacteria, the most dominant bacterial group was the gammaproteobacterial genus *Enterobacter*, which was present throughout the midgut. An unassigned OTU is closely related to *Klebsiella pneumoniae* with a 99.17% similarity (AF130982, Fig. 4). The Betaproteobacterial genus *Burkholderia* was detected in M1, M2 and M4. According to the maximum likelihood (ML) tree, which was constructed based on the sequence obtained from next-generation sequencing as well as representative sequences of in- and outgroup taxa, the *Burkholderia* detected in the midgut of *P. sibiricus* closely matched sequences of the PBE clade (Fig. 4).

Within the phylum Actinobacteria, the genus *Coriobacterium* was recorded in all samples, mostly with high levels of relative abundance in M2 and M3. According to the ML phylogenetic tree, the two *Coriobacterium* OTUs were closely related to strains of *Coriobacterium glomerans* (X79048, FJ554832) that occur in the intestinal tract of *P. apterus* with 97.66% 16S rRNA gene sequence similarity. A *Gordonibacter* OTU was identified in *P. sibiricus* that only had a 92.57% 16S rDNA similarity with its closest relative, *Gordonibacter pamelaeae* (AM886059), and 99.26% with *Gordonibacter* sp. (JX406494) strain in the gut of *P. apterus*. This OTU was first clustered with *Gordonibacter* sp. with an overall mean genetic distance of 0.022 and then with cultured strains of the genus *Gordonibacter* (Fig. 4).

Members of the phylum Firmicutes also occurred in gut micribiota. One unassigned Firmicutes OTU was closely related to a strain in the gut of *P. apterus* (JX406495, with 98.03% similarity), one was clustered with a cultured strain of *Clostridioides mangenotii* (MN646967, with 97.28% similarity) and the other two with *Enterococcus faecalis* (MN749533, with 98.47% similarity) and *E. casseliflavus* (MG871248, with 98.08% similarity) (Fig. 4).

Predictive functional profiles

In order to determine differences in the functions of the microbiota in the different parts of the midgut we carried out a functional analysis using PICRUSt. This revealed that 17 level2 KEGG orthology groups (KOs) differentially occurred in the four parts of the midgut, which is depicted in a heatmap (Fig. 5A). The mean NSTI values were 0.06, 0.04, 0.02 and 0.08 for M1, M2, M3 and M4, respectively. Significant differences in predicted microbial functions (two-sided Welch's *t*-test, $P < 0.05$) were detected between M3 and the other parts of the midgut (Fig. 5A, Table S4). PCA analysis showed that M2 and M3 have the most similar predicted microbial functions (Fig. 5B). Contributions of core genera to the predicted functions, which differ significantly among groups, are presented in Fig. 6. *Enterobacter* and *Burkholderia* contribute most to the predicted functions in M1, M2 and M4, while in M3 it is *Enterobacter* and *Coriobacterium* (Fig. 6).

DISCUSSION

In the present study, the microbiota inhabiting the midgut of *P. sibiricus* were characterized using 16S rRNA metagenomic analysis. The results indicate that it differs

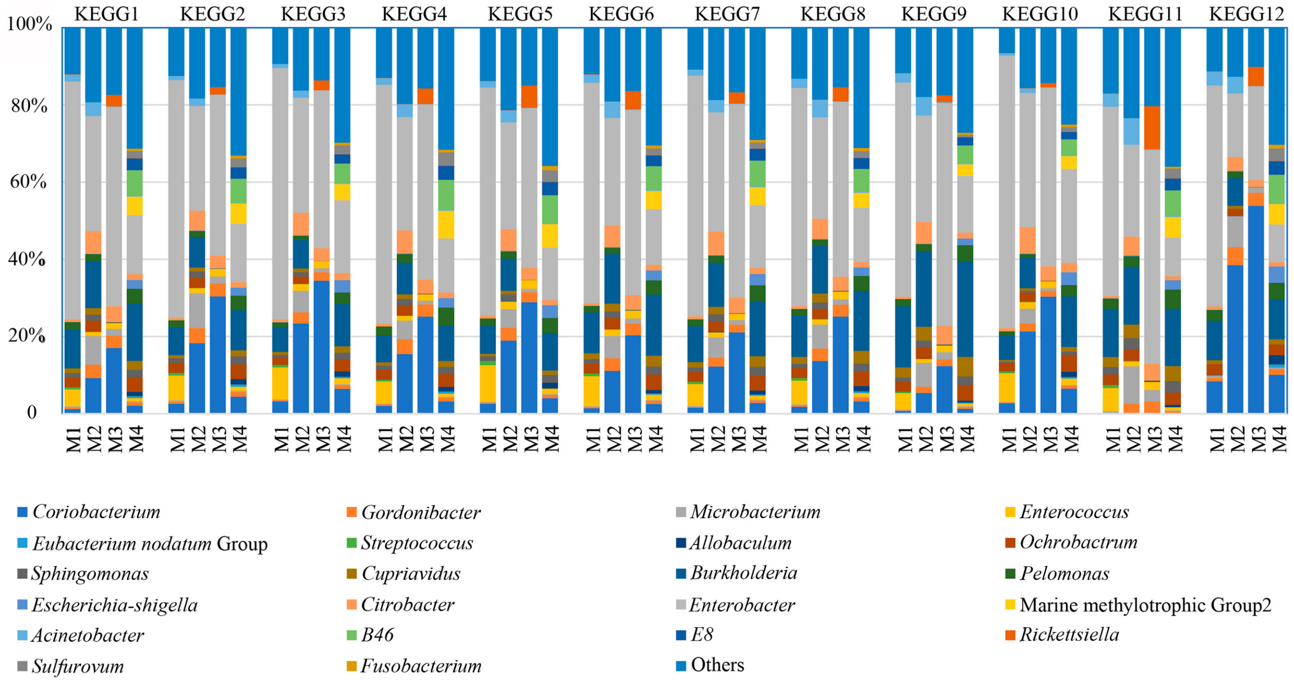

Fig. 6. Contributions of core genera to the predicted KEGG pathways. KEGG1-12: Amino acid metabolism; Biosynthesis of other secondary metabolites; Carbohydrate metabolism; Energy metabolism; Glycan Biosynthesis and Metabolism; Lipid metabolism; Metabolism of other amino acids; Metabolism of terpenoids and polyketides; Xenobiotic biodegradation and metabolism; Membrane transport; Transport and catabolism; Immune system.

in the different parts of the midgut (Fig. S1). Proteobacteria are the dominant bacteria in M1, M2 and M4. In M3, however, there is a distinct microbiota, consisting predominantly of Actinobacteria (Fig. S1). These results are in accord with previous studies on *D. fasciatus* and *P. apterus* (Sudakaran et al., 2012; Salem et al., 2013). The composition of the microbiota in M2 is particularly interesting in having a similar microbial profile of proteobacteria to M1 whilst sharing some core bacterial taxa with M3 (Fig. 2).

C. glomerans and *Gordonibacter* sp. (Actinobacteria), *Clostridium* sp. (Firmicutes) and *Klebsiella* sp. (Proteobacteria) occur in most species of Pyrrhocoridae (Salem et al., 2013; Sudakaran et al., 2015). Similarly, M3 in *P. sibiricus* is dominated by species of *Coriobacterium* and *Gordonibacter*, which are closely related to those recorded in *P. apterus* (*C. glomerans* and *Gordonibacter* sp., respectively; Figs 3, 4). In addition, there were also some OTUs with high sequence similarity with species of *Clostridium* and *Klebsiella*.

There were, however, some differences, the most notable being the distribution of *Gordonibacter* sp. and *C. glomerans*. In previous studies, they were recorded mainly in M3 (Sudakaran et al., 2012). However, they also make up a high proportion of the microbiota in M2. Furthermore, *Lactococcus lactis* and an undescribed Rickettsiales bacterium, which are core bacteria in M3 in *P. apterus* (Sudakaran et al., 2012), were absent in all our samples. We also recorded a relatively high abundance of *Burkholderia* and *Enterobacter*. Previously, *Burkholderia* was thought to be absent in Pyrrhocoridae, including *Pyrrhocoris* (Sudakaran et al., 2015), however, Gordon et al. (2016) report a high concentration of *Burkholderia* in the pyrrhocorid *Euscopus rufipes*. Hence, particular symbionts may be restricted to certain species of Pyrrhocoridae.

Species of *Burkholderia* are symbiotic partners of species of the superfamilies Lygaeoidea and Coreoidea, and particularly the Largidae in Pyrrhocoroidea (Kikuchi et al., 2011a; Itoh et al., 2014; Gordon et al., 2016). Generally, *Burkholderia* are acquired directly from the soil by early instar nymphs and stored in well-developed crypts in the posterior midgut (Kikuchi et al., 2011b; Boucias et al., 2012). However, in *P. sibiricus*, these symbionts are not only to the posterior midgut but also present in M1, M2 and M4. Early microscopic studies indicate that *Burkholderia* in Hemiptera belong to three distinct clades: the *Burkholderia cepacia* complex (BCC), the plant-associated beneficial and environmental (PBE) group, and the stinkbug-associated beneficial and environmental group (SBE) (Itoh et al., 2014). Unlike other *Burkholderia* associations in Alydidae (SBE clade) and Blissidae (all clades), the *Burkholderia* in *P. sibiricus* are closely related to the PBE clade (Itoh et al., 2014; Takeshita et al., 2015; Gordon et al., 2016). The function of *Burkholderia* symbionts in stinkbugs is unknown (Kaltenpoth & Flórez, 2020). It is hypothesized (Takeshita et al., 2015) that they fix nitrogen for their insect hosts, however, this is still be tested experimentally. In this study, *Burkholderia* contributes a high proportion of the genes in the metagenome associated with xenobiotic biodegradation and metabolism than any of the other pathways studied. This may indicate that *Burkholderia* in *P. sibiricus* provides a secondary context-dependent benefit, namely resistance to insecticides, which is reported in the bean bug, *Riptortus pedestris* and oriental chinch bug, *Cavelerius saccharivorus* (Kikuchi et al., 2012).

Many herbivorous insects have symbionts that supply nitrogen, essential amino acids, B vitamins and sterols, which are not present in the plant material they consume (Jones, 1984; Douglas, 1992, 1998). Seeds of Malvales are vitamin-limited and are generally avoided by other phytophagous bugs. Furthermore, phytochemical defences (gossypol and cyclopropenoic fatty acids) of the seeds interfere with digestion and so retarded growth, which can result in sterility (Allen et al., 1967; Abou-Donia, 1976; Kristenová et al., 2011). In previous studies, symbionts of Coriobacteriaceae are reported to activate food polyphenols and dietary phytoestrogens (Clavel et al., 2014; Chew et al., 2018). Some species, such as *C. glomerans*, can supply B vitamins to the host and protect them from parasites (Salem et al., 2014; Onchuru et al., 2018) and species of Clostridia play a role in the fermentation of carbohydrates, including the degradation of cellulose (Makonde et al., 2013; Sabree & Moran, 2014). *Enterobacter* belonging to the Enterobacteriaceae are present in the gut of Mediterranean fruit flies (*Ceratitis capitate*) (Aharon et al., 2013; Kyritsis et al., 2019). They are important in nitrogen and carbon metabolism and used as a dietary supplement (probiotic) in the diets to rear their larvae (Behar et al., 2005, 2008; Ben-Yosef et al., 2008; Augustinos et al., 2015; Kyritsis et al., 2019). Our study revealed that *Enterobacter*, *Coriobacterium* and *Burkholderia* make up a big proportion of the bacteria and contribute to most of the functions. The heatmap of the metabolic processes occurring in the different parts of the midgut reveals that M2 and M3 are involved in carbohydrate, amino acid, energy, lipid and vitamin metabolism, which accords with our 16S rRNA metagenomic results, which also indicate that these parts of the midgut are the main sites for food digestion, but the mechanism needs further study.

With the help of bacterial symbionts, Hemiptera are able to exploit plant tissues, such as xylem and phloem, which are nutrient-limited and contain phytochemicals (Buchner, 1965). In recent decades, our knowledge of Hemiptera and their microbes has increased considerably, particularly the identification of their core microbiota, genome sequencing, phylogenetic relationships, and the role of symbionts in the provision of nutrients, insecticide-resistance and defence against parasites (Kikuchi et al., 2012; Stackebrandt et al., 2013; Kaiwa et al., 2014; Hosokawa et al., 2016; Sudakaran et al., 2017; Onchuru et al., 2018; Onchuru & Kaltenpoth, 2019; Kaltenpoth & Flórez, 2020). However, few studies have focused on the role symbionts in the digestion of food. Although further study is needed to verify the exact mechanism, our results indicate that the microbiota in the M2 and M3 parts of the midgut play an important role in degrading complex dietary components.

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Supplementary material follows (Tables S1–S4, Fig. S1).

Table S1. 16S rRNA gene sequence reads and alpha-diversity indices recorded in the different treatments.

Sample	High quality sequence	No. of modified OTUs	Richness indices		Diversity indices	
			Chao1	ACE	Shannon	Simpson
M1A	36317	32192	792.57	813.99	0.814697	4.32
M1B	41975	36801	972.58	998.37	0.810928	4.52
M1C	37358	31019	568.45	584.64	0.797064	4.42
M2A	36515	30417	457.38	469.54	0.848671	4.27
M2B	39843	32413	839.93	849.29	0.854713	4.77
M2C	32096	29578	515.07	523.25	0.892772	4.68
M3A	33453	25624	297	297	0.802357	4.06
M3B	42176	33720	340.92	338.49	0.829836	4.03
M3C	48319	37869	446.99	454.83	0.845618	4.49
M4A	37697	31176	647.13	652.57	0.966306	6.53
M4B	37213	34148	734.12	712.98	0.896785	5.23
M4C	40755	34544	490.33	471.62	0.950102	5.99

The "No. of modified OTUs" means the clean OTUs with abundance > 0.001%.

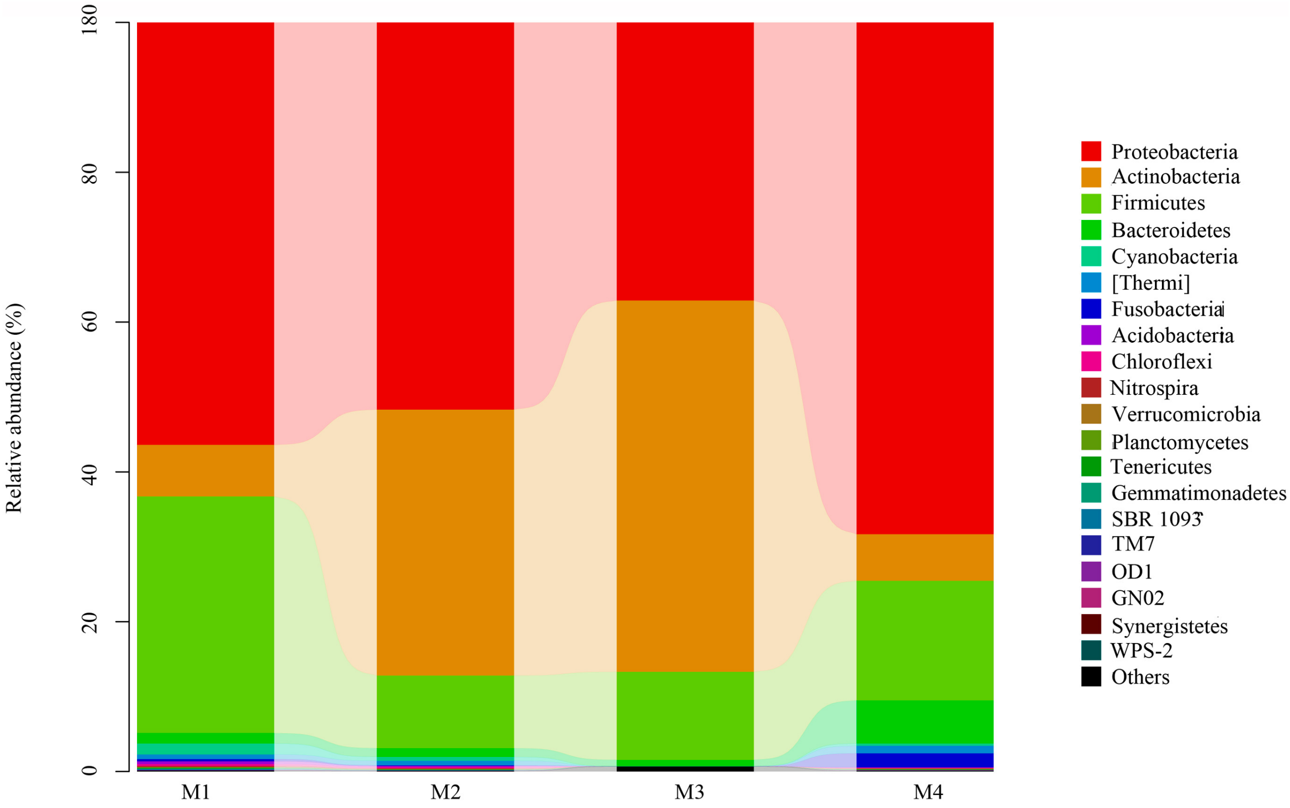

Fig. S1. Bacterial composition in terms of phyla in the four parts of the midgut.

Table S2. Bacterial taxonomy and relative abundance of bacterial OTUs (> 0.1%) in the different parts of the midgut of *Pyrrhocoris sibiricus*.

OTU ID	Relative aboundance of OTUs				Taxonomy						
	M1	M2	M3	M4							
OTU1	0.00%	0.28%	1.01%	0.01%	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Coriobacterium	s_
OTU2	3.60%	23.99%	38.44%	3.75%	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Coriobacterium	s_
OTU3	0.76%	6.55%	5.38%	1.27%	k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Eggerthellaceae	g_Gordonibacter	s_
OTU4	0.12%	2.47%	0.49%	0.05%	k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Microbacterium	s_
OTU5	0.01%	2.60%	1.49%	0.07%	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptostreptococcaceae	g_	s_
OTU6	0.11%	0.28%	1.97%	0.18%	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptostreptococcaceae	g_	s_
OTU7	26.03%	3.30%	0.84%	2.30%	k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Enterococcaceae	g_Enterococcus	s_
OTU8	0.40%	1.36%	4.17%	0.25%	k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Enterococcaceae	g_Enterococcus	s_
OTU9	0.00%	0.00%	0.00%	1.75%	k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_XIII	g_[Eubacterium] nodatum group	s_
OTU10	1.33%	0.19%	0.00%	0.01%	k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Streptococcus	s_
OTU11	0.02%	0.01%	0.00%	1.05%	k_Bacteria	p_Firmicutes	c_Erysipelotrichi	o_Erysipelotrichales	f_Erysipelotrichaceae	g_Allobaculum	s_
OTU12	2.63%	2.49%	0.03%	2.32%	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Brucellaceae	g_Ochrobactrum	s_
OTU13	1.32%	1.81%	0.01%	1.54%	k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Sphingomonas	s_Sphingomonas_azotifigens
OTU14	1.14%	1.33%	0.00%	1.26%	k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Oxalobacteraceae	g_Cupriavidus	s_
OTU15	12.98%	13.45%	0.06%	11.47%	k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Burkholderiaceae	g_Burkholderia	s_
OTU16	2.70%	2.29%	0.06%	3.58%	k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Burkholderiaceae	g_Pelomonas	s_
OTU17	0.00%	0.05%	2.08%	0.00%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_	s_
OTU18	0.06%	0.35%	0.07%	4.20%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Escherichia-Shigella	s_
OTU19	17.39%	6.51%	4.32%	2.46%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_turicensis
OTU20	0.48%	0.86%	4.63%	0.22%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_gergoviae
OTU21	0.72%	0.97%	6.66%	0.61%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_gergoviae
OTU22	0.14%	1.25%	0.80%	0.23%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Citrobacter	s_
OTU23	1.18%	0.09%	0.01%	0.04%	k_Bacteria	p_Cyanobacteria	c_Chloroplast	o_Streptophyta	f_Unclassified_Streptophyta	g_	s_
OTU24	0.00%	0.00%	0.00%	1.66%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Methylococcales	f_Methylomonaceae	g_Marine Methylotrophic Group 2	s_
OTU25	0.00%	0.00%	0.00%	2.78%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Methylococcales	f_Methylomonaceae	g_Marine Methylotrophic Group 2	s_Marine Methylotrophic Group
OTU26	3.52%	6.43%	0.01%	0.01%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Acinetobacter	s_
OTU27	0.00%	0.00%	0.00%	5.68%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_B46	s_
OTU28	0.00%	0.00%	0.00%	1.81%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_E8	s_
OTU29	0.06%	0.03%	5.31%	0.06%	k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Legionellales	f_Coxiellaceae	g_Rickettsiella	s_
OTU30	0.00%	0.00%	0.00%	2.73%	k_Bacteria	p_Epsilonbacteraeota	c_Campylobacteria	o_Campylobacterales	f_Sulfurovaceae	g_Sulfurovum	s_
OTU31	0.01%	0.00%	0.00%	1.87%	k_Bacteria	p_Fusobacteria	c_Fusobacteriia	o_Fusobacteriales	f_Fusobacteriaceae	g_Fusobacterium	s_

Table S3. All taxa with a relative abundance > 0.001% recorded in the different parts of the midgut of *Pyrrhocoris sibiricus*.

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_[Thermi]	c_Deinococci	o_Deinococcales	f_Trueperaceae	g_B-42	s_Unclassified_B-42	0.02%	0.01%	0.00%	0.00%
k_Bacteria	p_[Thermi]	c_Deinococci	o_Deinococcales	f_Trueperaceae	g_Unclassified_Trueperaceae	s_Unclassified_Trueperaceae	0.01%	0.00%	0.00%	0.08%
k_Bacteria	p_[Thermi]	c_Deinococci	o_Thermales	f_Thermaceae	g_Thermus	s_Unclassified_Thermus	0.60%	0.59%	0.00%	0.93%
k_Bacteria	p_Acidobacteria	c_[Chloracidobacteria]	o_RB41	f_Ellin6075	g_Unclassified_Ellin6075	s_Unclassified_Ellin6075	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_[Chloracidobacteria]	o_RB41	f_Unclassified_RB41	g_Unclassified_RB41	s_Unclassified_RB41	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Acidobacteria	c_Acidobacteria-5	o_Unclassified_Acidobacteria-5	f_Unclassified_Acidobacteria-5	g_Unclassified_Acidobacteria-5	s_Unclassified_Acidobacteria-5	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Acidobacteria-6	o_BPC015	f_Unclassified_BPC015	g_Unclassified_BPC015	s_Unclassified_BPC015	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Acidobacteria-6	o_CCU21	f_Unclassified_CCU21	g_Unclassified_CCU21	s_Unclassified_CCU21	0.02%	0.02%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Acidobacteria-6	o_iii1-15	f_mb2424	g_Unclassified_mb2424	s_Unclassified_mb2424	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Acidobacteria-6	o_iii1-15	f_Unclassified_iii1-15	g_Unclassified_iii1-15	s_Unclassified_iii1-15	0.05%	0.02%	0.00%	0.01%
k_Bacteria	p_Acidobacteria	c_Acidobacteriia	o_Acidobacteriales	f_Acidobacteriaceae	g_Acidopila	s_Acidopila_rosea	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Acidobacteriia	o_Acidobacteriales	f_Koribacteraceae	g_Unclassified_Koribacteraceae	s_Unclassified_Koribacteraceae	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_AT-s2-57	o_Unclassified_AT-s2-57	f_Unclassified_AT-s2-57	g_Unclassified_AT-s2-57	s_Unclassified_AT-s2-57	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_BPC102	o_B110	f_Unclassified_B110	g_Unclassified_B110	s_Unclassified_B110	0.05%	0.02%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_BPC102	o_MVS-40	f_Unclassified_MVS-40	g_Unclassified_MVS-40	s_Unclassified_MVS-40	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Acidobacteria	c_OS-K	o_Unclassified_OS-K	f_Unclassified_OS-K	g_Unclassified_OS-K	s_Unclassified_OS-K	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_RB25	o_Unclassified_RB25	f_Unclassified_RB25	g_Unclassified_RB25	s_Unclassified_RB25	0.03%	0.01%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Solibacteres	o_Solibacterales	f_PAUC26f	g_Unclassified_PAUC26f	s_Unclassified_PAUC26f	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Solibacteres	o_Solibacterales	f_Solibacteraceae	g_Candidatus_Solibacter	s_Unclassified_Candidatus_Solibacter	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Solibacteres	o_Solibacterales	f_Solibacteraceae	g_Unclassified_Solibacteraceae	s_Unclassified_Solibacteraceae	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Solibacteres	o_Solibacterales	f_Unclassified_Solibacterales	g_Unclassified_Solibacterales	s_Unclassified_Solibacterales	0.01%	0.01%	0.00%	0.01%
k_Bacteria	p_Acidobacteria	c_Sva0725	o_Sva0725	f_Unclassified_Sva0725	g_Unclassified_Sva0725	s_Unclassified_Sva0725	0.13%	0.03%	0.00%	0.00%
k_Bacteria	p_Acidobacteria	c_Unclassified_Acidobacteria	o_Unclassified_Acidobacteria	f_Unclassified_Acidobacteria	g_Unclassified_Acidobacteria	s_Unclassified_Acidobacteria	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_C111	g_Unclassified_C111	s_Unclassified_C111	0.03%	0.01%	0.00%	0.02%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_JdFBGBact	g_Unclassified_JdFBGBact	s_Unclassified_JdFBGBact	0.00%	0.00%	0.00%	0.29%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_koll13	g_Unclassified_koll13	s_Unclassified_koll13	0.18%	0.09%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_ntu14	g_Unclassified_ntu14	s_Unclassified_ntu14	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_TK06	g_Unclassified_TK06	s_Unclassified_TK06	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_Unclassified_Acidimicrobiales	g_Unclassified_Acidimicrobiales	s_Unclassified_Acidimicrobiales	0.13%	0.09%	0.00%	0.03%
k_Bacteria	p_Actinobacteria	c_Acidimicrobiia	o_Acidimicrobiales	f_wb1_P06	g_Unclassified_wb1_P06	s_Unclassified_wb1_P06	0.05%	0.03%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Actinomycetaceae	g_Actinomyces	s_Unclassified_Actinomyces	0.39%	0.05%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Actinosynnemataceae	g_Lentzea	s_Unclassified_Lentzea	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Brevibacteriaceae	g_Brevibacterium	s_Unclassified_Brevibacterium	0.03%	0.02%	0.00%	0.02%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Cellulomonadaceae	g_Cellulomonas	s_Unclassified_Cellulomonas	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Corynebacteriaceae	g_Corynebacterium	s_Unclassified_Corynebacterium	0.14%	0.24%	0.00%	0.09%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Cryptosporangiaceae	g_Unclassified_Cryptosporangiaceae	s_Unclassified_Cryptosporangiaceae	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Dermabacteraceae	g_Brachybacterium	s_Brachybacterium_conglomeratum	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Dermabacteraceae	g_Brachybacterium	s_Unclassified_Brachybacterium	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Dietziaceae	g_Dietzia	s_Unclassified_Dietzia	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Geodermatophilaceae	g_Unclassified_Geodermatophilaceae	s_Unclassified_Geodermatophilaceae	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Gordoniaceae	g_Gordonia	s_Unclassified_Gordonia	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Intrasporangiaceae	g_Kytococcus	s_Unclassified_Kytococcus	0.00%	0.00%	0.00%	0.04%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Intrasporangiaceae	g_Unclassified_Intrasporangiaceae	s_Unclassified_Intrasporangiaceae	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Agromyces	s_Unclassified_Agromyces	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Cryocola	s_Unclassified_Cryocola	0.01%	0.04%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Curtobacterium	s_Unclassified_Curtobacterium	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Microbacterium	s_Unclassified_Microbacterium	0.12%	2.57%	0.54%	0.06%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Mycetocola	s_Unclassified_Mycetocola	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Microbacteriaceae	g_Unclassified_Microbacteriaceae	s_Unclassified_Microbacteriaceae	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Arthrobacter	s_Unclassified_Arthrobacter	0.01%	0.06%	0.05%	0.02%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Micrococcus	s_Unclassified_Micrococcus	0.01%	0.02%	0.00%	0.03%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Rothia	s_Rothia_aeria	0.23%	0.04%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Rothia	s_Rothia_mucilaginosa	0.75%	0.09%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Rothia	s_Unclassified_Rothia	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micrococcaceae	g_Unclassified_Micrococcaceae	s_Unclassified_Micrococcaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Micromonospora	s_Micromonospora_carbonacea	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Phytohabitans	s_Phytohabitans_suffuscus	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Micromonosporaceae	g_Virgisporangium	s_Virgisporangium_ochraceum	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Mycobacteriaceae	g_Mycobacterium	s_Mycobacterium_llatzerense	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Mycobacteriaceae	g_Mycobacterium	s_Unclassified_Mycobacterium	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Nocardiaceae	g_Rhodococcus	s_Unclassified_Rhodococcus	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Nocardioidaceae	g_Aeromicrobium	s_Unclassified_Aeromicrobium	0.00%	0.00%	0.00%	0.00%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Nocardioidaceae	g_Nocardioides	s_Unclassified_Nocardioides	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Nocardioidaceae	g_Unclassified_Nocardioidaceae	s_Unclassified_Nocardioidaceae	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Propionibacteriaceae	g_Propionibacterium	s_Propionibacterium_acnes	0.05%	0.05%	0.00%	0.07%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Propionibacteriaceae	g_Propionibacterium	s_Propionibacterium_granulosum	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Pseudonocardiaceae	g_Amycolatopsis	s_Unclassified_Amycolatopsis	0.13%	0.11%	0.00%	0.12%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Sanguibacteraceae	g_Sanguibacter	s_Sanguibacter_soli	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Sporichthyaceae	g_Unclassified_Sporichthyaceae	s_Unclassified_Sporichthyaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Streptomyces	s_Streptomyces_lanatus	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Streptomyces	s_Streptomyces_mashuensis	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Streptomycetaceae	g_Unclassified_Streptomycetaceae	s_Unclassified_Streptomycetaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Thermomonosporaceae	g_Actinomadura	s_Actinomadura_vinacea	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Actinomycetales	f_Unclassified_Actinomycetales	g_Unclassified_Actinomycetales	s_Unclassified_Actinomycetales	0.00%	0.01%	0.00%	0.02%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Bifidobacteriales	f_Bifidobacteriaceae	g_Bifidobacterium	s_Bifidobacterium_animalis	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Bifidobacteriales	f_Bifidobacteriaceae	g_Bifidobacterium	s_Bifidobacterium_pseudolongum	0.02%	0.01%	0.00%	0.05%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_Bifidobacteriales	f_Bifidobacteriaceae	g_Gardnerella	s_Unclassified_Gardnerella	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Actinobacteria	o_WCHB1-81	f_At425_EubF1	g_Unclassified_At425_EubF1	s_Unclassified_At425_EubF1	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Adlercreutzia	s_Unclassified_Adlercreutzia	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Atopobium	s_Unclassified_Atopobium	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Collinsella	s_Collinsella_aerofaciens	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Coriobacterium	s_Unclassified_Coriobacterium	3.60%	24.31%	39.61%	3.76%
k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Eggerthellaceae	g_Gordonibacter	s_ Unclassified_Gordonibacter	0.76%	6.55%	5.38%	1.27%
k_Bacteria	p_Actinobacteria	c_Coriobacteriia	o_Coriobacteriales	f_Coriobacteriaceae	g_Unclassified_Coriobacteriaceae	s_Unclassified_Coriobacteriaceae	0.07%	0.97%	3.97%	0.10%
k_Bacteria	p_Actinobacteria	c_MB-A2-108	o_Unclassified_MB-A2-108	f_Unclassified_MB-A2-108	g_Unclassified_MB-A2-108	s_Unclassified_MB-A2-108	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Nitriliruptoria	o_Nitriliruptorales	f_Nitriliruptoraceae	g_Unclassified_Nitriliruptoraceae	s_Unclassified_Nitriliruptoraceae	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_OPB41	o_Unclassified_OPB41	f_Unclassified_OPB41	g_Unclassified_OPB41	s_Unclassified_OPB41	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Rubrobacteria	o_Rubrobacterales	f_Rubrobacteraceae	g_Rubrobacter	s_Unclassified_Rubrobacter	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Gaiellales	f_Gaiellaceae	g_Unclassified_Gaiellaceae	s_Unclassified_Gaiellaceae	0.04%	0.04%	0.00%	0.04%
k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Gaiellales	f_Unclassified_Gaiellales	g_Unclassified_Gaiellales	s_Unclassified_Gaiellales	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Solirubrobacterales	f_Patulibacteraceae	g_Unclassified_Patulibacteraceae	s_Unclassified_Patulibacteraceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Solirubrobacterales	f_Solirubrobacteraceae	g_Solirubrobacter	s_Unclassified_Solirubrobacter	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Actinobacteria	c_Thermoleophilia	o_Solirubrobacterales	f_Solirubrobacteraceae	g_Unclassified_Solirubrobacteraceae	s_Unclassified_Solirubrobacteraceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_AD3	c_ABS-6	o_Unclassified_ABS-6	f_Unclassified_ABS-6	g_Unclassified_ABS-6	s_Unclassified_ABS-6	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Armatimonadetes	c_[Fimbriimonadia]	o_[Fimbriimonadales]	f_[Fimbriimonadaceae]	g_Fimbriimonas	s_Unclassified_Fimbriimonas	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Armatimonadetes	c_Chthonomonadetes	o_Chthonomonadales	f_Chthonomonadaceae	g_Chthonomonas	s_Unclassified_Chthonomonas	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_[Rhodothermi]	o_[Rhodothermales]	f_Rhodothermaceae	g_Unclassified_Rhodothermaceae	s_Unclassified_Rhodothermaceae	0.02%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_[Saprospirae]	o_[Saprospirales]	f_Chitinophagaceae	g_Sediminibacterium	s_Unclassified_Sediminibacterium	0.52%	0.73%	0.00%	0.17%
k_Bacteria	p_Bacteroidetes	c_[Saprospirae]	o_[Saprospirales]	f_Saprospiraceae	g_Unclassified_Saprospiraceae	s_Unclassified_Saprospiraceae	0.07%	0.02%	0.00%	0.15%
k_Bacteria	p_Bacteroidetes	c_[Saprospirae]	o_[Saprospirales]	f_Unclassified_[Saprospirales]	g_Unclassified_[Saprospirales]	s_Unclassified_[Saprospirales]	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_[Barnesiellaceae]	g_Unclassified_[Barnesiellaceae]	s_Unclassified_[Barnesiellaceae]	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_[Paraprevotellaceae]	g_Paraprevotella	s_Unclassified_Paraprevotella	0.00%	0.00%	0.00%	0.09%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Bacteroidaceae	g_Bacteroides	s_Bacteroides_fragilis	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Bacteroidaceae	g_Bacteroides	s_Bacteroides_ovatus	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Bacteroidaceae	g_Bacteroides	s_Bacteroides_plebeius	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Bacteroidaceae	g_Bacteroides	s_Bacteroides_uniformis	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Bacteroidaceae	g_Bacteroides	s_Unclassified_Bacteroides	0.02%	0.03%	0.00%	1.12%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_BS11	g_Unclassified_BS11	s_Unclassified_BS11	0.04%	0.02%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Dysgonomonas	s_Dysgonomonas_gadei	0.00%	0.00%	0.83%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Dysgonomonas	s_Unclassified_Dysgonomonas	0.00%	0.01%	0.01%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Dysgonomonas	s_Unclassified_Dysgonomonas	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Parabacteroides	s_Parabacteroides_distasonis	0.00%	0.00%	0.00%	0.12%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Parabacteroides	s_Unclassified_Parabacteroides	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Porphyromonas	s_Porphyromonas_endodontalis	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Porphyromonas	s_Unclassified_Porphyromonas	0.05%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Porphyromonadaceae	g_Unclassified_Porphyromonadaceae	s_Unclassified_Porphyromonadaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Prevotellaceae	g_Prevotella	s_Prevotella_copri	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Prevotellaceae	g_Prevotella	s_Prevotella_melaninogenica	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_RF16	g_Unclassified_RF16	s_Unclassified_RF16	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_Alistipes	s_Alistipes_indistinctus	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Rikenellaceae	g_Unclassified_Rikenellaceae	s_Unclassified_Rikenellaceae	0.01%	0.00%	0.00%	0.09%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_S24-7	g_Unclassified_S24-7	s_Unclassified_S24-7	0.19%	0.17%	0.00%	2.53%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_SB-1	g_Unclassified_SB-1	s_Unclassified_SB-1	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Bacteroidia	o_Bacteroidales	f_Unclassified_Bacteroidales	g_Unclassified_Bacteroidales	s_Unclassified_Bacteroidales	0.02%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Cytophagia	o_Cytophagales	f_Cytophagaceae	g_Cytophaga	s_Unclassified_Cytophaga	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Cytophagia	o_Cytophagales	f_Cytophagaceae	g_Unclassified_Cytophagaceae	s_Unclassified_Cytophagaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Cytophagia	o_Cytophagales	f_Flammeovirgaceae	g_Reichenbachiella	s_Unclassified_Reichenbachiella	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Cytophagia	o_Cytophagales	f_Flammeovirgaceae	g_Unclassified_Flammeovirgaceae	s_Unclassified_Flammeovirgaceae	0.09%	0.02%	0.00%	0.63%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_[Weeksellaceae]	g_Chryseobacterium	s_Unclassified_Chryseobacterium	0.03%	0.01%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Cryomorphaceae	g_Crocinitomix	s_Unclassified_Crocinitomix	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Cryomorphaceae	g_Fluviicola	s_Unclassified_Fluviicola	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Cryomorphaceae	g_Unclassified_Cryomorphaceae	s_Unclassified_Cryomorphaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Capnocytophaga	s_Capnocytophaga_ochracea	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Capnocytophaga	s_Unclassified_Capnocytophaga	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Croceimarina	s_Croceimarina_litoralis	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Flavobacterium	s_Unclassified_Flavobacterium	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Formosa	s_Formosa_crassostrea	0.04%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Lutimonas	s_Unclassified_Lutimonas	0.02%	0.00%	0.00%	0.01%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Polaribacter	s_Unclassified_Polaribacter	0.00%	0.00%	0.00%	0.03%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Robiginitalea	s_Unclassified_Robiginitalea	0.03%	0.01%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Flavobacteriia	o_Flavobacteriales	f_Flavobacteriaceae	g_Unclassified_Flavobacteriaceae	s_Unclassified_Flavobacteriaceae	0.18%	0.06%	0.00%	0.66%
k_Bacteria	p_Bacteroidetes	c_Sphingobacteriia	o_Sphingobacteriales	f_Sphingobacteriaceae	g_Sphingobacterium	s_Sphingobacterium_multivorum	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Bacteroidetes	c_Sphingobacteriia	o_Sphingobacteriales	f_Unclassified_Sphingobacteriales	g_Unclassified_Sphingobacteriales	s_Unclassified_Sphingobacteriales	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Caldithrix	c_Caldithrixae	o_Caldithrixales	f_Caldithrixaceae	g_LCP-26	s_Unclassified_LCP-26	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Chlamydiae	c_Chlamydiia	o_Chlamydiales	f_Rhabdochlamydiaceae	g_Candidatus_Rhabdochlamydia	s_Unclassified_Candidatus_Rhabdochlamydia	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Chlorobi	c_BSV26	o_PK329	f_Unclassified_PK329	g_Unclassified_PK329	s_Unclassified_PK329	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Chlorobi	c_Ignavibacteria	o_Ignavibacteriales	f_Ignavibacteriaceae	g_Unclassified_Ignavibacteriaceae	s_Unclassified_Ignavibacteriaceae	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Chlorobi	c_Ignavibacteria	o_Ignavibacteriales	f_lheB3-7	g_Unclassified_lheB3-7	s_Unclassified_lheB3-7	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_Caldilineales	f_Caldilineaceae	g_Unclassified_Caldilineaceae	s_Unclassified_Caldilineaceae	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_CFB-26	f_Unclassified_CFB-26	g_Unclassified_CFB-26	s_Unclassified_CFB-26	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_GCA004	f_Unclassified_GCA004	g_Unclassified_GCA004	s_Unclassified_GCA004	0.14%	0.09%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_OPB11	f_Unclassified_OPB11	g_Unclassified_OPB11	s_Unclassified_OPB11	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_S0208	f_Unclassified_S0208	g_Unclassified_S0208	s_Unclassified_S0208	0.02%	0.01%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SB-34	f_Unclassified_SB-34	g_Unclassified_SB-34	s_Unclassified_SB-34	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SBR1031	f_A4b	g_Unclassified_A4b	s_Unclassified_A4b	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SBR1031	f_oc28	g_Unclassified_oc28	s_Unclassified_oc28	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SBR1031	f_SHA-31	g_Unclassified_SHA-31	s_Unclassified_SHA-31	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SBR1031	f_SJA-101	g_Unclassified_SJA-101	s_Unclassified_SJA-101	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Anaerolineae	o_SHA-20	f_Unclassified_SHA-20	g_Unclassified_SHA-20	s_Unclassified_SHA-20	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Chloroflexi	o_Chloroflexales	f_FFCH7168	g_Unclassified_FFCH7168	s_Unclassified_FFCH7168	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Dehalococcoidetes	o_Unclassified_Dehalococcoidetes	f_Unclassified_Dehalococcoidetes	g_Unclassified_Dehalococcoidetes	s_Unclassified_Dehalococcoidetes	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Ellin6529	o_Unclassified_Ellin6529	f_Unclassified_Ellin6529	g_Unclassified_Ellin6529	s_Unclassified_Ellin6529	0.01%	0.01%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Gitt-GS-136	o_Unclassified_Gitt-GS-136	f_Unclassified_Gitt-GS-136	g_Unclassified_Gitt-GS-136	s_Unclassified_Gitt-GS-136	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Ktedonobacteria	o_JG30-KF-AS9	f_Unclassified_JG30-KF-AS9	g_Unclassified_JG30-KF-AS9	s_Unclassified_JG30-KF-AS9	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_S085	o_Unclassified_S085	f_Unclassified_S085	g_Unclassified_S085	s_Unclassified_S085	0.01%	0.02%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_Thermomicrobia	o_AKYG1722	f_Unclassified_AKYG1722	g_Unclassified_AKYG1722	s_Unclassified_AKYG1722	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Thermomicrobia	o_JG30-KF-CM45	f_Unclassified_JG30-KF-CM45	g_Unclassified_JG30-KF-CM45	s_Unclassified_JG30-KF-CM45	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_Thermomicrobia	o_Thermomicrobiales	f_Unclassified_Thermomicrobiales	g_Unclassified_Thermomicrobiales	s_Unclassified_Thermomicrobiales	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_TK10	o_B07_WMSP1	f_Unclassified_B07_WMSP1	g_Unclassified_B07_WMSP1	s_Unclassified_B07_WMSP1	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Chloroflexi	c_TK17	o_mle1-48	f_Unclassified_mle1-48	g_Unclassified_mle1-48	s_Unclassified_mle1-48	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Chloroflexi	c_TK17	o_Unclassified_TK17	f_Unclassified_TK17	g_Unclassified_TK17	s_Unclassified_TK17	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Cyanobacteria	c_4C0d-2	o_MLE1-12	f_Unclassified_MLE1-12	g_Unclassified_MLE1-12	s_Unclassified_MLE1-12	0.12%	0.12%	0.00%	0.08%
k_Bacteria	p_Cyanobacteria	c_4C0d-2	o_YS2	f_Unclassified_YS2	g_Unclassified_YS2	s_Unclassified_YS2	0.00%	0.00%	0.00%	0.06%
k_Bacteria	p_Cyanobacteria	c_Chloroplast	o_Stramenopiles	f_Unclassified_Stramenopiles	g_Unclassified_Stramenopiles	s_Unclassified_Stramenopiles	0.03%	0.17%	0.00%	0.02%
k_Bacteria	p_Cyanobacteria	c_Chloroplast	o_Streptophyta	f_Unclassified_Streptophyta	g_Unclassified_Streptophyta	s_Unclassified_Streptophyta	1.30%	0.22%	0.01%	0.14%
k_Bacteria	p_Cyanobacteria	c_ML635J-21	o_Unclassified_ML635J-21	f_Unclassified_ML635J-21	g_Unclassified_ML635J-21	s_Unclassified_ML635J-21	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Cyanobacteria	c_Synechococcophycideae	o_Synechococcales	f_Synechococcaceae	g_Synechococcus	s_Unclassified_Synechococcus	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Elusimicrobia	c_Elusimicrobia	o_Elusimicrobiales	f_Unclassified_Elusimicrobiales	g_Unclassified_Elusimicrobiales	s_Unclassified_Elusimicrobiales	0.01%	0.01%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_[Exiguobacteraceae]	g_Exiguobacterium	s_Unclassified_Exiguobacterium	0.01%	0.14%	0.02%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_[Exiguobacteraceae]	g_Unclassified_[Exiguobacteraceae]	s_Unclassified_[Exiguobacteraceae]	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Bacillaceae	g_Anoxybacillus	s_Anoxybacillus_kestanbolensis	0.02%	0.01%	0.00%	0.02%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Bacillaceae	g_Bacillus	s_Unclassified_Bacillus	0.00%	0.01%	0.02%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Bacillaceae	g_Geobacillus	s_Unclassified_Geobacillus	0.09%	0.08%	0.00%	0.15%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Listeriaceae	g_Listeria	s_Listeria_seeligeri	0.00%	0.00%	0.18%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Paenibacillaceae	g_Unclassified_Paenibacillaceae	s_Unclassified_Paenibacillaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Planococcaceae	g_Rummeliibacillus	s_Unclassified_Rummeliibacillus	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Planococcaceae	g_Solibacillus	s_Unclassified_Solibacillus	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Planococcaceae	g_Unclassified_Planococcaceae	s_Unclassified_Planococcaceae	0.01%	0.03%	0.30%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Staphylococcaceae	g_Jeotgalicoccus	s_Jeotgalicoccus_psychrophilus	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Staphylococcaceae	g_Staphylococcus	s_Staphylococcus_epidermidis	0.06%	0.10%	0.00%	0.08%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Staphylococcaceae	g_Staphylococcus	s_Staphylococcus_sciuri	0.06%	0.10%	0.00%	0.03%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Staphylococcaceae	g_Staphylococcus	s_Unclassified_Staphylococcus	0.00%	0.00%	0.02%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Bacillales	f_Thermoactinomycetaceae	g_Thermoactinomyces	s_Unclassified_Thermoactinomyces	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Gemellales	f_Gemellaceae	g_Unclassified_Gemellaceae	s_Unclassified_Gemellaceae	0.14%	0.02%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Aerococcaceae	g_Aerococcus	s_Unclassified_Aerococcus	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Aerococcaceae	g_Alloiococcus	s_Unclassified_Alloiococcus	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Aerococcaceae	g_Unclassified_Aerococcaceae	s_Unclassified_Aerococcaceae	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Carnobacteriaceae	g_Granulicatella	s_Unclassified_Granulicatella	0.10%	0.02%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Carnobacteriaceae	g_Isobaculum	s_Isobaculum_melis	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Enterococcaceae	g_Enterococcus	s_Enterococcus_cecorum	0.04%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Enterococcaceae	g_Enterococcus	s_Unclassified_Enterococcus	26.51%	4.75%	5.93%	2.59%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Enterococcaceae	g_Vagococcus	s_Unclassified_Vagococcus	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Lactobacillaceae	g_Lactobacillus	s_Lactobacillus_brevis	0.00%	0.00%	0.02%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Lactobacillaceae	g_Lactobacillus	s_Lactobacillus_iners	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Lactobacillaceae	g_Lactobacillus	s_Lactobacillus_zeae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Lactobacillaceae	g_Lactobacillus	s_Unclassified_Lactobacillus	0.55%	0.11%	0.00%	0.24%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Lactobacillaceae	g_Unclassified_Lactobacillaceae	s_Unclassified_Lactobacillaceae	0.02%	0.02%	0.01%	0.05%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Leuconostocaceae	g_Leuconostoc	s_Unclassified_Leuconostoc	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Leuconostocaceae	g_Unclassified_Leuconostocaceae	s_Unclassified_Leuconostocaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Lactococcus	s_Lactococcus_garvieae	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Lactococcus	s_Unclassified_Lactococcus	0.01%	0.01%	0.10%	0.01%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Streptococcus	s_Unclassified_Streptococcus	2.32%	0.33%	0.00%	0.03%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Streptococcaceae	g_Unclassified_Streptococcaceae	s_Unclassified_Streptococcaceae	0.03%	0.01%	0.04%	0.00%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Lactobacillales	f_Unclassified_Lactobacillales	g_Unclassified_Lactobacillales	s_Unclassified_Lactobacillales	0.28%	0.09%	0.29%	0.05%
k_Bacteria	p_Firmicutes	c_Bacilli	o_Turicibacterales	f_Turicibacteraceae	g_Turicibacter	s_Unclassified_Turicibacter	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_[Mogibacteriaceae]	g_Anaerovorax	s_Unclassified_Anaerovorax	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_XIII	g_[Eubacterium] nodatum group	s_Unclassified_[Eubacterium] nodatum group	0.00%	0.00%	0.00%	1.75%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_[Mogibacteriaceae]	g_Unclassified_[Mogibacteriaceae]	s_Unclassified_[Mogibacteriaceae]	0.04%	0.00%	0.00%	1.87%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_[Tissierellaceae]	g_Anaerococcus	s_Unclassified_Anaerococcus	0.00%	0.00%	0.00%	0.03%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_[Tissierellaceae]	g_Parvimonas	s_Unclassified_Parvimonas	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Caldicoprobacteraceae	g_Caldicoprobacter	s_Unclassified_Caldicoprobacter	0.01%	0.01%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Christensenellaceae	g_Unclassified_Christensenellaceae	s_Unclassified_Christensenellaceae	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium	s_Clostridium_perfringens	0.00%	0.00%	0.00%	0.04%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Clostridium	s_Unclassified_Clostridium	0.02%	0.04%	0.09%	0.06%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Clostridiaceae	g_Unclassified_Clostridiaceae	s_Unclassified_Clostridiaceae	0.09%	0.02%	0.00%	0.50%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Eubacteriaceae	g_Pseudoramibacter_Eubacterium	s_Unclassified_Pseudoramibacter_Eubacterium	0.01%	0.01%	0.03%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_[Ruminococcus]	s_[Ruminococcus]_gnavus	0.00%	0.01%	0.00%	0.06%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_[Ruminococcus]	s_Unclassified_[Ruminococcus]	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Blautia	s_Blautia_producta	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Blautia	s_Unclassified_Blautia	0.01%	0.01%	0.00%	0.02%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Catonella	s_Unclassified_Catonella	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Coprococcus	s_Unclassified_Coprococcus	0.00%	0.01%	0.00%	0.02%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Dorea	s_Unclassified_Dorea	0.01%	0.03%	0.00%	0.27%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Epulopiscium	s_Unclassified_Epulopiscium	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Moryella	s_Unclassified_Moryella	0.04%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Oribacterium	s_Unclassified_Oribacterium	0.23%	0.03%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Roseburia	s_Unclassified_Roseburia	0.02%	0.01%	0.00%	0.03%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Lachnospiraceae	g_Unclassified_Lachnospiraceae	s_Unclassified_Lachnospiraceae	0.11%	0.39%	0.64%	0.17%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptococcaceae	g_Desulfotomaculum_Desulfovirgula	s_Unclassified_Desulfotomaculum_Desulfovirgula	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptococcaceae	g_rc4-4	s_Unclassified_rc4-4	0.00%	0.00%	0.00%	0.06%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptococcaceae	g_Unclassified_Peptococcaceae	s_Unclassified_Peptococcaceae	0.00%	0.00%	0.00%	0.09%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptostreptococcaceae	g_Clostridium	s_Clostridium_venationis	0.00%	0.02%	0.38%	0.01%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptostreptococcaceae	g_Filifactor	s_Unclassified_Filifactor	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptostreptococcaceae	g_Tepidibacter	s_Unclassified_Tepidibacter	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Peptostreptococcaceae	g_Unclassified_Peptostreptococcaceae	s_Unclassified_Peptostreptococcaceae	0.15%	2.89%	3.55%	0.28%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_Faecalibacterium	s_Faecalibacterium_prausnitzii	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_Oscillospira	s_Unclassified_Oscillospira	0.02%	0.02%	0.00%	1.76%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_Ruminococcus	s_Ruminococcus_flavefaciens	0.00%	0.00%	0.00%	0.03%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_Ruminococcus	s_Unclassified_Ruminococcus	0.02%	0.01%	0.00%	0.16%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Ruminococcaceae	g_Unclassified_Ruminococcaceae	s_Unclassified_Ruminococcaceae	0.04%	0.05%	0.00%	3.37%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Dialister	s_Unclassified_Dialister	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Phascolarctobacterium	s_Unclassified_Phascolarctobacterium	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Schwartzia	s_Unclassified_Schwartzia	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Selenomonas	s_Selenomonas_noxia	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Selenomonas	s_Unclassified_Selenomonas	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Unclassified_Veillonellaceae	s_Unclassified_Veillonellaceae	0.00%	0.00%	0.00%	0.04%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Veillonella	s_Unclassified_Veillonella	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Veillonella	s_Veillonella_dispar	0.02%	0.01%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Clostridiales	f_Veillonellaceae	g_Veillonella	s_Veillonella_parvula	0.10%	0.02%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Clostridia	o_Thermoanaerobacterales	f_Unclassified_Thermoanaerobacterales	g_Unclassified_Thermoanaerobacterales	s_Unclassified_Thermoanaerobacterales	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Erysipelotrichi	o_Erysipelotrichales	f_Erysipelotrichaceae	g_[Eubacterium]	s_[Eubacterium]_dolichum	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Erysipelotrichi	o_Erysipelotrichales	f_Erysipelotrichaceae	g_Allobaculum	s_Unclassified_Allobaculum	0.06%	0.06%	0.00%	2.12%
k_Bacteria	p_Firmicutes	c_Erysipelotrichi	o_Erysipelotrichales	f_Erysipelotrichaceae	g_Bulleidia	s_Bulleidia_moorei	0.05%	0.00%	0.00%	0.00%
k_Bacteria	p_Firmicutes	c_Erysipelotrichi	o_Erysipelotrichales	f_Erysipelotrichaceae	g_Unclassified_Erysipelotrichaceae	s_Unclassified_Erysipelotrichaceae	0.00%	0.00%	0.02%	0.01%
k_Bacteria	p_Fusobacteria	c_Fusobacteriia	o_Fusobacteriales	f_Fusobacteriaceae	g_Cetobacterium	s_Cetobacterium_somerae	0.13%	0.04%	0.00%	0.00%
k_Bacteria	p_Fusobacteria	c_Fusobacteriia	o_Fusobacteriales	f_Fusobacteriaceae	g_Fusobacterium	s_Unclassified_Fusobacterium	0.05%	0.01%	0.00%	1.87%
k_Bacteria	p_Fusobacteria	c_Fusobacteriia	o_Fusobacteriales	f_Fusobacteriaceae	g_Propionigenium	s_Unclassified_Propionigenium	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Fusobacteria	c_Fusobacteriia	o_Fusobacteriales	f_Leptotrichiaceae	g_Leptotrichia	s_Unclassified_Leptotrichia	0.12%	0.02%	0.00%	0.00%
k_Bacteria	p_Gemmatimonadetes	c_Gemm-5	o_Unclassified_Gemm-5	f_Unclassified_Gemm-5	g_Unclassified_Gemm-5	s_Unclassified_Gemm-5	0.09%	0.04%	0.00%	0.01%
k_Bacteria	p_Gemmatimonadetes	c_Gemmatimonadetes	o_C114	f_Unclassified_C114	g_Unclassified_C114	s_Unclassified_C114	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Gemmatimonadetes	c_Gemmatimonadetes	o_Ellin5290	f_Unclassified_Ellin5290	g_Unclassified_Ellin5290	s_Unclassified_Ellin5290	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Gemmatimonadetes	c_Gemmatimonadetes	o_KD8-87	f_Unclassified_KD8-87	g_Unclassified_KD8-87	s_Unclassified_KD8-87	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Gemmatimonadetes	c_Gemmatimonadetes	o_Unclassified_Gemmatimonadetes	f_Unclassified_Gemmatimonadetes	g_Unclassified_Gemmatimonadetes	s_Unclassified_Gemmatimonadetes	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_GN02	c_BD1-5	o_Unclassified_BD1-5	f_Unclassified_BD1-5	g_Unclassified_BD1-5	s_Unclassified_BD1-5	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_GN02	c_IIB17	o_Unclassified_IIB17	f_Unclassified_IIB17	g_Unclassified_IIB17	s_Unclassified_IIB17	0.00%	0.00%	0.00%	0.05%
k_Bacteria	p_GN04	c_GN15	o_Unclassified_GN15	f_Unclassified_GN15	g_Unclassified_GN15	s_Unclassified_GN15	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_KSB3	c_Unclassified_KSB3	o_Unclassified_KSB3	f_Unclassified_KSB3	g_Unclassified_KSB3	s_Unclassified_KSB3	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Nitrospirae	c_Nitrospira	o_Nitrospirales	f_[Thermodesulfovibrionaceae]	g_BD2-6	s_Unclassified_BD2-6	0.07%	0.02%	0.00%	0.00%
k_Bacteria	p_Nitrospirae	c_Nitrospira	o_Nitrospirales	f_[Thermodesulfovibrionaceae]	g_GOUTA19	s_Unclassified_GOUTA19	0.03%	0.03%	0.00%	0.00%
k_Bacteria	p_Nitrospirae	c_Nitrospira	o_Nitrospirales	f_[Thermodesulfovibrionaceae]	g_Unclassified_[Thermodesulfovibrionaceae]	s_Unclassified_[Thermodesulfovibrionaceae]	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Nitrospirae	c_Nitrospira	o_Nitrospirales	f_0319-6A21	g_Unclassified_0319-6A21	s_Unclassified_0319-6A21	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Nitrospirae	c_Nitrospira	o_Nitrospirales	f_Nitrospiraceae	g_Unclassified_Nitrospiraceae	s_Unclassified_Nitrospiraceae	0.02%	0.02%	0.00%	0.01%
k_Bacteria	p_OD1	c_ABY1	o_Unclassified_ABY1	f_Unclassified_ABY1	g_Unclassified_ABY1	s_Unclassified_ABY1	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_OD1	c_ZB2	o_Unclassified_ZB2	f_Unclassified_ZB2	g_Unclassified_ZB2	s_Unclassified_ZB2	0.01%	0.03%	0.00%	0.01%
k_Bacteria	p_OP1	c_[Acetothermia]	o_[Acetothermales]	f_Unclassified_[Acetothermales]	g_Unclassified_[Acetothermales]	s_Unclassified_[Acetothermales]	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_OP8	c_OP8_1	o_HMMVPog-54	f_Unclassified_HMMVPog-54	g_Unclassified_HMMVPog-54	s_Unclassified_HMMVPog-54	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Planctomycetes	c_C6	o_d113	f_Unclassified_d113	g_Unclassified_d113	s_Unclassified_d113	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Planctomycetes	c_OM190	o_CL500-15	f_Unclassified_CL500-15	g_Unclassified_CL500-15	s_Unclassified_CL500-15	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Planctomycetes	c_Phycisphaerae	o_Phycisphaerales	f_Phycisphaeraceae	g_Unclassified_Phycisphaeraceae	s_Unclassified_Phycisphaeraceae	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Planctomycetes	c_Phycisphaerae	o_Phycisphaerales	f_Unclassified_Phycisphaerales	g_Unclassified_Phycisphaerales	s_Unclassified_Phycisphaerales	0.05%	0.05%	0.00%	0.03%
k_Bacteria	p_Planctomycetes	c_Pla3	o_Unclassified_Pla3	f_Unclassified_Pla3	g_Unclassified_Pla3	s_Unclassified_Pla3	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Planctomycetes	c_Planctomycetia	o_Gemmatales	f_Isosphaeraceae	g_Unclassified_Isosphaeraceae	s_Unclassified_Isosphaeraceae	0.01%	0.00%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_BD7-3	f_Unclassified_BD7-3	g_Unclassified_BD7-3	s_Unclassified_BD7-3	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Arthrospira	s_Unclassified_Arthrospira	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Asticcacaulis	s_Unclassified_Asticcacaulis	0.05%	0.05%	0.00%	0.05%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Brevundimonas	s_Brevundimonas_diminuta	0.02%	0.02%	0.00%	0.03%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Brevundimonas	s_Brevundimonas_poindexterae	0.10%	0.09%	0.00%	0.12%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Mycoplana	s_Unclassified_Mycoplana	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Caulobacterales	f_Caulobacteraceae	g_Unclassified_Caulobacteraceae	s_Unclassified_Caulobacteraceae	0.77%	0.82%	0.00%	0.79%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Ellin329	f_Unclassified_Ellin329	g_Unclassified_Ellin329	s_Unclassified_Ellin329	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Aurantimonadaceae	g_Aurantimonas	s_Aurantimonas_altamirensis	0.00%	0.03%	0.02%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Beijerinckiaceae	g_Unclassified_Beijerinckiaceae	s_Unclassified_Beijerinckiaceae	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Bradyrhizobiaceae	g_Balneimonas	s_Unclassified_Balneimonas	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Bradyrhizobiaceae	g_Bosea	s_Bosea_genosp.	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Bradyrhizobiaceae	g_Bradyrhizobium	s_Unclassified_Bradyrhizobium	0.07%	0.09%	0.00%	0.09%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Bradyrhizobiaceae	g_Unclassified_Bradyrhizobiaceae	s_Unclassified_Bradyrhizobiaceae	0.12%	0.11%	0.00%	0.14%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Brucellaceae	g_Ochrobactrum	s_Unclassified_Ochrobactrum	2.71%	2.58%	0.03%	2.34%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Brucellaceae	g_Pseudochrobactrum	s_Unclassified_Pseudochrobactrum	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_Devosia	s_Unclassified_Devosia	0.03%	0.02%	0.00%	0.03%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Hyphomicrobiaceae	g_Unclassified_Hyphomicrobiaceae	s_Unclassified_Hyphomicrobiaceae	0.02%	0.02%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Methylobacteriaceae	g_Methylobacterium	s_Methylobacterium_komagatae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Methylobacteriaceae	g_Methylobacterium	s_Methylobacterium_organophilum	0.01%	0.01%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Methylobacteriaceae	g_Methylobacterium	s_Unclassified_Methylobacterium	0.07%	0.06%	0.00%	0.06%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Methylobacteriaceae	g_Unclassified_Methylobacteriaceae	s_Unclassified_Methylobacteriaceae	0.11%	0.12%	0.01%	0.10%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Methylocystaceae	g_Unclassified_Methylocystaceae	s_Unclassified_Methylocystaceae	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Phyllobacteriaceae	g_Aminobacter	s_Unclassified_Aminobacter	0.03%	0.03%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Phyllobacteriaceae	g_Aquamicrobium	s_Aquamicrobium_aerolatum	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Phyllobacteriaceae	g_Phyllobacterium	s_Unclassified_Phyllobacterium	0.02%	0.02%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Phyllobacteriaceae	g_Unclassified_Phyllobacteriaceae	s_Unclassified_Phyllobacteriaceae	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Rhizobiaceae	g_Agrobacterium	s_Unclassified_Agrobacterium	0.13%	0.15%	0.03%	0.18%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Rhizobiaceae	g_Unclassified_Rhizobiaceae	s_Unclassified_Rhizobiaceae	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Unclassified_Rhizobiales	g_Unclassified_Rhizobiales	s_Unclassified_Rhizobiales	0.10%	0.09%	0.00%	0.12%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Xanthobacteraceae	g_Labrys	s_Unclassified_Labrys	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhizobiales	f_Xanthobacteraceae	g_Xanthobacter	s_Unclassified_Xanthobacter	0.03%	0.04%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Hyphomonadaceae	g_Unclassified_Hyphomonadaceae	s_Unclassified_Hyphomonadaceae	0.00%	0.00%	0.00%	0.06%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Anaerospora	s_Unclassified_Anaerospora	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Loktanella	s_Unclassified_Loktanella	0.05%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Oceanicella	s_Oceanicella_actignis	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Octadecabacter	s_Unclassified_Octadecabacter	0.02%	0.01%	0.00%	0.16%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Paracoccus	s_Paracoccus_aminovorans	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Paracoccus	s_Unclassified_Paracoccus	0.03%	0.01%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Rhodobacter	s_Unclassified_Rhodobacter	0.06%	0.02%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Rubellimicrobium	s_Unclassified_Rubellimicrobium	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodobacterales	f_Rhodobacteraceae	g_Unclassified_Rhodobacteraceae	s_Unclassified_Rhodobacteraceae	0.04%	0.02%	0.00%	0.19%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Acetobacter	s_Unclassified_Acetobacter	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Gluconobacter	s_Unclassified_Gluconobacter	0.00%	0.00%	0.02%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Acetobacteraceae	g_Unclassified_Acetobacteraceae	s_Unclassified_Acetobacteraceae	0.00%	0.13%	0.32%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_Azospirillum	s_Azospirillum_massiliensis	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_Azospirillum	s_Unclassified_Azospirillum	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Rhodospirillaceae	g_Unclassified_Rhodospirillaceae	s_Unclassified_Rhodospirillaceae	0.07%	0.04%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rhodospirillales	f_Unclassified_Rhodospirillales	g_Unclassified_Rhodospirillales	s_Unclassified_Rhodospirillales	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_Holosporaceae	g_Unclassified_Holosporaceae	s_Unclassified_Holosporaceae	0.00%	0.88%	0.02%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_mitochondria	g_Carludovica	s_Carludovica_palmata	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_mitochondria	g_Nelumbo	s_Nelumbo_nucifera	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Rickettsiales	f_mitochondria	g_Zea	s_Zea_luxurians	0.00%	0.01%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Erythrobacteraceae	g_Unclassified_Erythrobacteraceae	s_Unclassified_Erythrobacteraceae	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Blastomonas	s_Blastomonas_natatoria	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Kaistobacter	s_Unclassified_Kaistobacter	0.00%	0.01%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Novosphingobium	s_Novosphingobium_stygium	0.02%	0.04%	0.00%	0.03%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Novosphingobium	s_Unclassified_Novosphingobium	0.01%	0.03%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Sphingobium	s_Unclassified_Sphingobium	0.02%	0.03%	0.00%	0.04%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Sphingomonas	s_Sphingomonas_azotifigens	1.34%	1.83%	0.01%	1.55%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Sphingomonas	s_Unclassified_Sphingomonas	0.12%	0.08%	0.00%	0.09%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Sphingopyxis	s_Unclassified_Sphingopyxis	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Sphingomonadaceae	g_Unclassified_Sphingomonadaceae	s_Unclassified_Sphingomonadaceae	0.12%	0.04%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Sphingomonadales	f_Unclassified_Sphingomonadales	g_Unclassified_Sphingomonadales	s_Unclassified_Sphingomonadales	0.05%	0.04%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Alphaproteobacteria	o_Unclassified_Alphaproteobacteria	f_Unclassified_Alphaproteobacteria	g_Unclassified_Alphaproteobacteria	s_Unclassified_Alphaproteobacteria	0.06%	0.03%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Alcaligenaceae	g_Achromobacter	s_Unclassified_Achromobacter	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Alcaligenaceae	g_Sutterella	s_Unclassified_Sutterella	0.00%	0.01%	0.00%	0.11%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Burkholderiaceae	g_Burkholderia	s_Unclassified_Burkholderia	14.16%	14.32%	0.10%	11.89%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Burkholderiaceae	g_Lautropia	s_Unclassified_Lautropia	0.22%	0.02%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Burkholderiaceae	g_Unclassified_Burkholderiaceae	s_Unclassified_Burkholderiaceae	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Comamonas	s_Unclassified_Comamonas	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Delftia	s_Unclassified_Delftia	0.03%	0.04%	0.00%	0.03%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Hydrogenophaga	s_Unclassified_Hydrogenophaga	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Limnohabitans	s_Unclassified_Limnohabitans	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Methylibium	s_Unclassified_Methylibium	0.01%	0.01%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Roseateles	s_Roseateles_depolymerans	0.07%	0.04%	0.00%	0.03%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Unclassified_Comamonadaceae	s_Unclassified_Comamonadaceae	0.50%	0.26%	0.00%	0.24%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Variovorax	s_Unclassified_Variovorax	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Comamonadaceae	g_Variovorax	s_Variovorax_paradoxus	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Oxalobacteraceae	g_Cupriavidus	s_Unclassified_Cupriavidus	1.34%	1.50%	0.00%	1.40%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Oxalobacteraceae	g_Herbaspirillum	s_Unclassified_Herbaspirillum	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Oxalobacteraceae	g_Janthinobacterium	s_Janthinobacterium_lividum	0.03%	0.09%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Oxalobacteraceae	g_Ralstonia	s_Unclassified_Ralstonia	0.08%	0.08%	0.00%	0.05%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Oxalobacteraceae	g_Unclassified_Oxalobacteraceae	s_Unclassified_Oxalobacteraceae	0.11%	0.11%	0.00%	0.06%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Burkholderiales	f_Unclassified_Burkholderiales	g_Unclassified_Burkholderiales	s_Unclassified_Burkholderiales	0.79%	0.75%	0.01%	0.98%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Methylophilales	f_Methylophilaceae	g_Methylotenera	s_Methylotenera_mobilis	0.03%	0.03%	0.00%	0.04%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_MND1	f_Unclassified_MND1	g_Unclassified_MND1	s_Unclassified_MND1	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Neisseriales	f_Neisseriaceae	g_Neisseria	s_Neisseria_cinerea	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Neisseriales	f_Neisseriaceae	g_Neisseria	s_Neisseria_subflava	0.16%	0.04%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Neisseriales	f_Neisseriaceae	g_Neisseria	s_Unclassified_Neisseria	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Neisseriales	f_Neisseriaceae	g_Unclassified_Neisseriaceae	s_Unclassified_Neisseriaceae	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Nitrosomonadales	f_Nitrosomonadaceae	g_Unclassified_Nitrosomonadaceae	s_Unclassified_Nitrosomonadaceae	0.04%	0.02%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Rhodocyclales	f_Rhodocyclaceae	g_Azospira	s_Unclassified_Azospira	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Rhodocyclales	f_Rhodocyclaceae	g_Dechloromonas	s_Unclassified_Dechloromonas	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Rhodocyclales	f_Rhodocyclaceae	g_Dok59	s_Unclassified_Dok59	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Rhodocyclales	f_Rhodocyclaceae	g_Thauera	s_Unclassified_Thauera	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Rhodocyclales	f_Rhodocyclaceae	g_Unclassified_Rhodocyclaceae	s_Unclassified_Rhodocyclaceae	0.06%	0.02%	0.00%	0.03%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_SC-I-84	f_Unclassified_SC-I-84	g_Unclassified_SC-I-84	s_Unclassified_SC-I-84	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Tremblayales	f_Tremblayaceae	g_Tremblaya	s_Tremblaya_phenacola	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Betaproteobacteria	o_Unclassified_Betaproteobacteria	f_Unclassified_Betaproteobacteria	g_Unclassified_Betaproteobacteria	s_Unclassified_Betaproteobacteria	0.02%	0.02%	0.00%	0.05%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Bdellovibrionales	f_Bacteriovoracaceae	g_Bacteriovorax	s_Unclassified_Bacteriovorax	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Bdellovibrionales	f_Bdellovibrionaceae	g_Bdellovibrio	s_Unclassified_Bdellovibrio	0.00%	0.00%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfarculales	f_Desulfarculaceae	g_Unclassified_Desulfarculaceae	s_Unclassified_Desulfarculaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfobacterales	f_Desulfobacteraceae	g_Desulfococcus	s_Unclassified_Desulfococcus	0.09%	0.03%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfobacterales	f_Desulfobacteraceae	g_Unclassified_Desulfobacteraceae	s_Unclassified_Desulfobacteraceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfobacterales	f_Desulfobulbaceae	g_Unclassified_Desulfobulbaceae	s_Unclassified_Desulfobulbaceae	0.30%	0.07%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfobacterales	f_Nitrospinaceae	g_Nitrospina	s_Unclassified_Nitrospina	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Bilophila	s_Unclassified_Bilophila	0.00%	0.00%	0.00%	0.03%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Desulfovibrio	s_Desulfovibrio_C21_c20	0.01%	0.02%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Desulfovibrio	s_Unclassified_Desulfovibrio	0.00%	0.00%	0.00%	0.14%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfovibrionales	f_Desulfovibrionaceae	g_Unclassified_Desulfovibrionaceae	s_Unclassified_Desulfovibrionaceae	0.01%	0.00%	0.00%	0.27%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Desulfuromonadales	f_Desulfuromonadaceae	g_Unclassified_Desulfuromonadaceae	s_Unclassified_Desulfuromonadaceae	0.10%	0.02%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_GMD14H09	f_Unclassified_GMD14H09	g_Unclassified_GMD14H09	s_Unclassified_GMD14H09	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_IndB3-24	f_Unclassified_IndB3-24	g_Unclassified_IndB3-24	s_Unclassified_IndB3-24	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_MBNT15	f_Unclassified_MBNT15	g_Unclassified_MBNT15	s_Unclassified_MBNT15	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_MIZ46	f_Unclassified_MIZ46	g_Unclassified_MIZ46	s_Unclassified_MIZ46	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Myxococcales	f_0319-6G20	g_Unclassified_0319-6G20	s_Unclassified_0319-6G20	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Myxococcales	f_Haliangiaceae	g_Unclassified_Haliangiaceae	s_Unclassified_Haliangiaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Myxococcales	f_Nannocystaceae	g_Plesiocystis	s_Unclassified_Plesiocystis	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Myxococcales	f_Unclassified_Myxococcales	g_Unclassified_Myxococcales	s_Unclassified_Myxococcales	0.08%	0.03%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_NB1-j	f_JTB38	g_Unclassified_JTB38	s_Unclassified_JTB38	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_NB1-j	f_MND4	g_Unclassified_MND4	s_Unclassified_MND4	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_NB1-j	f_NB1-i	g_Unclassified_NB1-i	s_Unclassified_NB1-i	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_NB1-j	f_Unclassified_NB1-j	g_Unclassified_NB1-j	s_Unclassified_NB1-j	0.02%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_PB19	f_Unclassified_PB19	g_Unclassified_PB19	s_Unclassified_PB19	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Sva0853	f_SAR324	g_Unclassified_SAR324	s_Unclassified_SAR324	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Syntrophobacterales	f_Syntrophaceae	g_Unclassified_Syntrophaceae	s_Unclassified_Syntrophaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Syntrophobacterales	f_Syntrophobacteraceae	g_Unclassified_Syntrophobacteraceae	s_Unclassified_Syntrophobacteraceae	0.08%	0.02%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Syntrophobacterales	f_Unclassified_Syntrophobacterales	g_Unclassified_Syntrophobacterales	s_Unclassified_Syntrophobacterales	0.04%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Deltaproteobacteria	o_Unclassified_Deltaproteobacteria	f_Unclassified_Deltaproteobacteria	g_Unclassified_Deltaproteobacteria	s_Unclassified_Deltaproteobacteria	0.04%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Epsilonproteobacteria	o_Campylobacterales	f_Campylobacteraceae	g_Arcobacter	s_Unclassified_Arcobacter	0.00%	0.00%	0.00%	0.00%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Epsilonbacteraeota	c_Campylobacteria	o_Campylobacterales	f_Sulfurovaceae	g_Sulfurovum	s_Unclassified_Sulfurovum	0.00%	0.00%	0.00%	2.73%
k_Bacteria	p_Proteobacteria	c_Epsilonproteobacteria	o_Campylobacterales	f_Helicobacteraceae	g_Unclassified_Helicobacteraceae	s_Unclassified_Helicobacteraceae	0.07%	0.01%	0.00%	6.41%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_[Marinicellales]	f_[Marinicellaceae]	g_Marinicella	s_Unclassified_Marinicella	0.00%	0.00%	0.00%	0.18%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_[Marinicellales]	f_[Marinicellaceae]	g_Unclassified_[Marinicellaceae]	s_Unclassified_[Marinicellaceae]	0.16%	0.07%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Aeromonadales	f_Aeromonadaceae	g_Unclassified_Aeromonadaceae	s_Unclassified_Aeromonadaceae	0.07%	0.03%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_[Chromatiaceae]	g_Rheinheimera	s_Unclassified_Rheinheimera	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_Alteromonadaceae	g_Alteromonas	s_Unclassified_Alteromonas	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_Alteromonadaceae	g_Cellvibrio	s_Unclassified_Cellvibrio	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_Alteromonadaceae	g_Unclassified_Alteromonadaceae	s_Unclassified_Alteromonadaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_HTCC2188	g_HTCC	s_Unclassified_HTCC	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_OM60	g_Unclassified_OM60	s_Unclassified_OM60	0.04%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Alteromonadales	f_Psychromonadaceae	g_Psychromonas	s_Unclassified_Psychromonas	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Cardiobacteriales	f_Cardiobacteriaceae	g_Cardiobacterium	s_Unclassified_Cardiobacterium	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Chromatiales	f_Chromatiaceae	g_Unclassified_Chromatiaceae	s_Unclassified_Chromatiaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Chromatiales	f_Ectothiorhodospiraceae	g_Unclassified_Ectothiorhodospiraceae	s_Unclassified_Ectothiorhodospiraceae	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Chromatiales	f_Unclassified_Chromatiales	g_Unclassified_Chromatiales	s_Unclassified_Chromatiales	0.27%	0.11%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Citrobacter	s_Unclassified_Citrobacter	0.23%	1.58%	0.95%	0.27%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_gergoviae	1.41%	2.39%	15.61%	0.93%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_hormaechei	0.29%	0.13%	0.11%	0.03%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_ludwigii	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Enterobacter_turicensis	18.09%	6.90%	5.12%	2.58%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Enterobacter	s_Unclassified_Enterobacter	0.03%	0.11%	0.59%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Erwinia	s_Unclassified_Erwinia	0.01%	0.03%	0.24%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Escherichia	s_Escherichia_blattae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Klebsiella	s_Unclassified_Klebsiella	0.01%	0.15%	0.44%	0.15%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Morganella	s_Morganella_morganii	0.06%	0.48%	0.13%	0.04%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Morganella	s_Unclassified_Morganella	0.00%	0.04%	0.02%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Pantoea	s_Pantoea_agglomerans	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Pantoea	s_Pantoea_ananatis	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Proteus	s_Unclassified_Proteus	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Providencia	s_Unclassified_Providencia	0.00%	0.02%	0.01%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Salmonella	s_Unclassified_Salmonella	0.01%	0.00%	0.03%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Serratia	s_Serratia_marcescens	0.02%	0.07%	0.13%	0.02%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Serratia	s_Serratia_ureilytica	0.00%	0.01%	0.11%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Serratia	s_Unclassified_Serratia	0.23%	0.26%	0.11%	0.40%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Trabulsiella	s_Trabulsiella_farmeri	0.00%	0.03%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Trabulsiella	s_Unclassified_Trabulsiella	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Escherichia-Shigella	s_Unclassified_Escherichia-Shigella	0.06%	0.35%	0.07%	4.20%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Unclassified_Enterobacteriaceae	s_Unclassified_Enterobacteriaceae	0.90%	2.84%	6.13%	1.57%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Enterobacteriales	f_Enterobacteriaceae	g_Xenorhabdus	s_Xenorhabdus_bovienii	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_HOC36	f_Unclassified_HOC36	g_Unclassified_HOC36	s_Unclassified_HOC36	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_HTCC2188	f_HTCC2089	g_Unclassified_HTCC2089	s_Unclassified_HTCC2089	0.03%	0.01%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Legionellales	f_Coxiellaceae	g_Aquicella	s_Unclassified_Aquicella	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Legionellales	f_Coxiellaceae	g_Rickettsiella	s_Unclassified_Rickettsiella	0.07%	0.03%	6.43%	0.06%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Legionellales	f_Unclassified_Legionellales	g_Unclassified_Legionellales	s_Unclassified_Legionellales	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Methylococcales	f_Methylomonaceae	g_Marine Methylotrophic Group 2	s_Unclassified_Marine Methylotrophic Group 2	0.00%	0.00%	0.00%	4.44%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Methylococcales	f_Unclassified_Methylococcales	g_Unclassified_Methylococcales	s_Unclassified_Methylococcales	0.00%	0.00%	0.00%	10.90%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pasteurellales	f_Pasteurellaceae	g_Aggregatibacter	s_Unclassified_Aggregatibacter	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pasteurellales	f_Pasteurellaceae	g_Gallibacterium	s_Gallibacterium_genomosp.	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pasteurellales	f_Pasteurellaceae	g_Haemophilus	s_Haemophilus_parainfluenzae	0.17%	0.03%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pasteurellales	f_Unclassified_Pasteurellales	g_Unclassified_Pasteurellales	s_Unclassified_Pasteurellales	0.20%	0.11%	0.00%	0.04%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Acinetobacter	s_Acinetobacter_guillouiae	0.01%	0.02%	0.05%	0.02%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Acinetobacter	s_Acinetobacter_johnsonii	0.01%	0.05%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Acinetobacter	s_Acinetobacter_lwoffii	0.06%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Acinetobacter	s_Acinetobacter_rhizosphaerae	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Acinetobacter	s_Unclassified_Acinetobacter	4.50%	6.94%	0.13%	0.25%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Enhydrobacter	s_Unclassified_Enhydrobacter	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Psychrobacter	s_Psychrobacter_marincola	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Psychrobacter	s_Unclassified_Psychrobacter	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Moraxellaceae	g_Unclassified_Moraxellaceae	s_Unclassified_Moraxellaceae	0.40%	0.05%	0.01%	0.00%

Table S3 (continued).

Taxonomy							Relative aboundance of taxa			
							M1	M2	M3	M4
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Pseudomonadaceae	g_Pseudomonas	s_Pseudomonas_viridiflava	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Pseudomonadaceae	g_Pseudomonas	s_Unclassified_Pseudomonas	0.11%	0.13%	0.00%	0.18%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Pseudomonadales	f_Pseudomonadaceae	g_Unclassified_Pseudomonadaceae	s_Unclassified_Pseudomonadaceae	0.03%	0.55%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiohalorhabdales	f_Unclassified_Thiohalorhabdales	g_Unclassified_Thiohalorhabdales	s_Unclassified_Thiohalorhabdales	0.01%	0.00%	0.00%	0.07%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Piscirickettsiaceae	g_Unclassified_Piscirickettsiaceae	s_Unclassified_Piscirickettsiaceae	0.62%	0.32%	0.00%	0.88%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_B46	s_Unclassified_B46	0.00%	0.00%	0.00%	7.87%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_CF-26	s_Unclassified_CF-26	0.00%	0.00%	0.00%	0.05%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_Cocleimonas	s_Unclassified_Cocleimonas	0.00%	0.00%	0.00%	2.43%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_E8	s_Unclassified_E8	0.00%	0.00%	0.00%	6.14%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_Unclassified_Thiotrichaceae	s_Unclassified_Thiotrichaceae	0.00%	0.00%	0.00%	1.16%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Thiotrichales	f_Thiotrichaceae	g_Unclassified_Thiotrichaceae	s_Unclassified_Thiotrichaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Unclassified_Gammaproteobacteria	f_Unclassified_Gammaproteobacteria	g_Unclassified_Gammaproteobacteria	s_Unclassified_Gammaproteobacteria	0.03%	0.02%	0.00%	0.06%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Vibrionales	f_Pseudoalteromonadaceae	g_Unclassified_Pseudoalteromonadaceae	s_Unclassified_Pseudoalteromonadaceae	0.03%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Vibrionales	f_Pseudoalteromonadaceae	g_Vibrio	s_Vibrio_mimicus	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Vibrionales	f_Vibrionaceae	g_Vibrio	s_Unclassified_Vibrio	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Sinobacteraceae	g_Unclassified_Sinobacteraceae	s_Unclassified_Sinobacteraceae	0.02%	0.02%	0.00%	0.02%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Xanthomonadaceae	g_Luteimonas	s_Unclassified_Luteimonas	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Xanthomonadaceae	g_Pseudoxanthomonas	s_Pseudoxanthomonas_mexicana	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Xanthomonadaceae	g_Stenotrophomonas	s_Stenotrophomonas_acidaminiphila	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Xanthomonadaceae	g_Stenotrophomonas	s_Unclassified_Stenotrophomonas	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Proteobacteria	c_Gammaproteobacteria	o_Xanthomonadales	f_Xanthomonadaceae	g_Unclassified_Xanthomonadaceae	s_Unclassified_Xanthomonadaceae	0.02%	0.02%	0.01%	0.01%
k_Bacteria	p_Proteobacteria	c_TA18	o_PHOS-HD29	f_Unclassified_PHOS-HD29	g_Unclassified_PHOS-HD29	s_Unclassified_PHOS-HD29	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Proteobacteria	c_Unclassified_Proteobacteria	o_Unclassified_Proteobacteria	f_Unclassified_Proteobacteria	g_Unclassified_Proteobacteria	s_Unclassified_Proteobacteria	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_SBR1093	c_Unclassified_SBR1093	o_Unclassified_SBR1093	f_Unclassified_SBR1093	g_Unclassified_SBR1093	s_Unclassified_SBR1093	0.04%	0.01%	0.00%	0.00%
k_Bacteria	p_SBR1093	c_VHS-B5-50	o_Unclassified_VHS-B5-50	f_Unclassified_VHS-B5-50	g_Unclassified_VHS-B5-50	s_Unclassified_VHS-B5-50	0.03%	0.01%	0.00%	0.00%
k_Bacteria	p_SR1	c_Unclassified_SR1	o_Unclassified_SR1	f_Unclassified_SR1	g_Unclassified_SR1	s_Unclassified_SR1	0.01%	0.00%	0.00%	0.01%
k_Bacteria	p_Synergistetes	c_Synergistia	o_Synergistales	f_Aminiphilaceae	g_Unclassified_Aminiphilaceae	s_Unclassified_Aminiphilaceae	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_Synergistetes	c_Synergistia	o_Synergistales	f_Dethiosulfovibrionaceae	g_Aminobacterium	s_Unclassified_Aminobacterium	0.02%	0.01%	0.00%	0.01%
k_Bacteria	p_Synergistetes	c_Synergistia	o_Synergistales	f_Dethiosulfovibrionaceae	g_TG5	s_Unclassified_TG5	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Tenericutes	c_CK-1C4-19	o_Unclassified_CK-1C4-19	f_Unclassified_CK-1C4-19	g_Unclassified_CK-1C4-19	s_Unclassified_CK-1C4-19	0.09%	0.01%	0.00%	0.00%
k_Bacteria	p_Tenericutes	c_Mollicutes	o_Acholeplasmatales	f_Acholeplasmataceae	g_Unclassified_Acholeplasmataceae	s_Unclassified_Acholeplasmataceae	0.00%	0.00%	0.01%	0.00%
k_Bacteria	p_Tenericutes	c_Mollicutes	o_Mycoplasmatales	f_Mycoplasmataceae	g_Unclassified_Mycoplasmataceae	s_Unclassified_Mycoplasmataceae	0.00%	0.02%	0.00%	0.00%
k_Bacteria	p_Tenericutes	c_Mollicutes	o_RF39	f_Unclassified_RF39	g_Unclassified_RF39	s_Unclassified_RF39	0.00%	0.00%	0.00%	0.06%
k_Bacteria	p_Thermotogae	c_Thermotogae	o_Thermotogales	f_Thermotogaceae	g_Thermotoga	s_Unclassified_Thermotoga	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_TM7	c_TM7-1	o_Unclassified_TM7-1	f_Unclassified_TM7-1	g_Unclassified_TM7-1	s_Unclassified_TM7-1	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_TM7	c_TM7-3	o_CW040	f_F16	g_Unclassified_F16	s_Unclassified_F16	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_TM7	c_TM7-3	o_CW040	f_Unclassified_CW040	g_Unclassified_CW040	s_Unclassified_CW040	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_TM7	c_TM7-3	o_EW055	f_Unclassified_EW055	g_Unclassified_EW055	s_Unclassified_EW055	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_TM7	c_TM7-3	o_Unclassified_TM7-3	f_Unclassified_TM7-3	g_Unclassified_TM7-3	s_Unclassified_TM7-3	0.03%	0.01%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_[Methylacidiphilae]	o_S-BQ2-57	f_Unclassified_S-BQ2-57	g_Unclassified_S-BQ2-57	s_Unclassified_S-BQ2-57	0.01%	0.01%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_Opitutae	o_Unclassified_Opitutae	f_Unclassified_Opitutae	g_Unclassified_Opitutae	s_Unclassified_Opitutae	0.00%	0.01%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_Verruco-5	o_LD1-PB3	f_Unclassified_LD1-PB3	g_Unclassified_LD1-PB3	s_Unclassified_LD1-PB3	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_Verruco-5	o_SS1-B-03-39	f_Unclassified_SS1-B-03-39	g_Unclassified_SS1-B-03-39	s_Unclassified_SS1-B-03-39	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_Verrucomicrobiae	o_Verrucomicrobiales	f_Verrucomicrobiaceae	g_Akkermansia	s_Akkermansia_muciniphila	0.03%	0.03%	0.00%	0.08%
k_Bacteria	p_Verrucomicrobia	c_Verrucomicrobiae	o_Verrucomicrobiales	f_Verrucomicrobiaceae	g_Persicirhabdus	s_Unclassified_Persicirhabdus	0.02%	0.00%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_Verrucomicrobiae	o_Verrucomicrobiales	f_Verrucomicrobiaceae	g_Unclassified_Verrucomicrobiaceae	s_Unclassified_Verrucomicrobiaceae	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_Verrucomicrobia	c_Verrucomicrobiae	o_Verrucomicrobiales	f_Verrucomicrobiaceae	g_Verrucomicrobium	s_Unclassified_Verrucomicrobium	0.00%	0.00%	0.00%	0.01%
k_Bacteria	p_WPS-2	c_Unclassified_WPS-2	o_Unclassified_WPS-2	f_Unclassified_WPS-2	g_Unclassified_WPS-2	s_Unclassified_WPS-2	0.01%	0.01%	0.00%	0.03%
k_Bacteria	p_WS3	c_PRR-12	o_Sediment-1	f_CV106	g_Unclassified_CV106	s_Unclassified_CV106	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_WS3	c_PRR-12	o_Sediment-1	f_Unclassified_Sediment-1	g_Unclassified_Sediment-1	s_Unclassified_Sediment-1	0.01%	0.00%	0.00%	0.00%
k_Bacteria	p_WS3	c_PRR-12	o_Unclassified_PRR-12	f_Unclassified_PRR-12	g_Unclassified_PRR-12	s_Unclassified_PRR-12	0.00%	0.00%	0.00%	0.00%
k_Bacteria	p_WS6	c_SC72	o_Unclassified_SC72	f_Unclassified_SC72	g_Unclassified_SC72	s_Unclassified_SC72	0.00%	0.00%	0.00%	0.01%
No blast hit							0.01%	0.00%	0.67%	0.01%

Table S4. Results of Welch's t-test for two group analysis.

KEGG pathways	M1 vs M2			M1 vs M3			M1 vs M4			M2 vs M3			M2 vs M4			M3 vs M4		
	Statistics*	*P*-value	corrected *P*-value	Statistics	*P*-value	corrected_ *P*-value	Statistics	*P*-value	corrected_ *P*-value	Statistics	*P*-value	corrected_ *P*-value	Statistics	*P*-value	corrected_ *P*-value	Statistics	*P*-value	corrected_ *P*-value
Membrane Transport	–0.94453	0.4406	0.6733	–8.14842	0.003215	0.007627	1.527934	0.2625	0.6143	–1.58152	0.2381	0.3234	1.800495	0.1499	0.5101	3.512305	0.06325	0.1293
Carbohydrate Metabolism	–1.30685	0.2842	0.6039	–5.44985	0.01216	0.02296	0.667818	0.542	0.6143	–1.54823	0.2473	0.3234	1.698089	0.1801	0.5101	5.463175	0.01566	0.08874
Amino Acid Metabolism	0.431302	0.7065	0.7507	13.91832	0.000776	0.004468	–1.99097	0.1561	0.6143	2.078471	0.1715	0.3234	–1.23453	0.3136	0.5923	–7.91046	0.01251	0.08874
Energy Metabolism	2.65988	0.05733	0.5225	2.881032	0.04497	0.07645	–1.20629	0.3491	0.6143	0.3891	0.7173	0.7621	–1.55304	0.2588	0.5501	–1.60178	0.2481	0.3013
Metabolism of Cofactors and Vitamins	1.608055	0.1864	0.6039	1.925934	0.1302	0.1581	–1.4112	0.2851	0.6143	0.301707	0.7779	0.7779	–1.89311	0.1848	0.5101	–1.99494	0.1697	0.2404
Nucleotide Metabolism	–0.11914	0.9143	0.9143	–2.83628	0.06777	0.1047	–0.96384	0.4334	0.6143	–1.6472	0.1855	0.3234	–0.84292	0.4667	0.6979	–0.05703	0.959	0.959
Lipid Metabolism	0.988591	0.421	0.6733	12.78182	0.001051	0.004468	0.486961	0.6627	0.7041	1.717583	0.2257	0.3234	–0.70936	0.5337	0.6979	–5.58106	0.02466	0.09096
Xenobiotics Biodegradation and Metabolism	0.429501	0.7065	0.7507	11.07169	0.002407	0.006821	–1.12909	0.3443	0.6143	2.03628	0.1767	0.3234	0.20776	0.8456	0.8985	–2.55778	0.1058	0.1634
Cell Motility	1.636944	0.1805	0.6039	2.505158	0.07787	0.1103	0.754777	0.5231	0.6143	0.857003	0.4421	0.501	–2.10675	0.1408	0.5101	–1.87261	0.1997	0.2612
Glycan Biosynthesis and Metabolism	2.017163	0.1377	0.6039	–0.30697	0.7755	0.7755	–0.75323	0.509	0.6143	–2.96654	0.04748	0.3234	–1.83566	0.1948	0.5101	–0.61889	0.5885	0.6456
Enzyme Families	1.400226	0.2418	0.6039	–0.42367	0.7068	0.7509	–0.74559	0.5086	0.6143	–2.79778	0.07362	0.3234	–1.66225	0.2101	0.5101	–0.59783	0.6076	0.6456
Metabolism of Other Amino Acids	0.771732	0.5135	0.6733	8.11775	0.003589	0.007627	0.057303	0.9587	0.9587	1.436661	0.2835	0.3442	–0.60728	0.5794	0.7036	–2.98196	0.08941	0.152
Metabolism of Terpenoids and Polyketides	0.710462	0.546	0.6733	11.60202	0.000791	0.004468	1.308009	0.29	0.6143	2.079845	0.1689	0.3234	–0.04555	0.9667	0.9667	–4.37872	0.03746	0.09096
Biosynthesis of Other Secondary Metabolites	–1.32651	0.2554	0.6039	1.782603	0.1637	0.1855	–0.99573	0.3785	0.6143	3.445132	0.03383	0.3234	0.457452	0.6719	0.7615	–3.35301	0.03122	0.09096
Transport and Catabolism	0.697115	0.5545	0.6733	10.40909	0.000498	0.004468	–1.70601	0.1664	0.6143	1.650902	0.2349	0.3234	–1.06524	0.395	0.6714	–13.3574	0.000202	0.003436
Immune System	–2.94647	0.06147	0.5225	–6.95656	0.002363	0.006821	–2.18986	0.1146	0.6143	–1.71325	0.1805	0.3234	0.703208	0.5208	0.6979	2.674791	0.06844	0.1293
Digestive System	–0.84308	0.4745	0.6733	–2.23453	0.08991	0.1176	0.88286	0.4288	0.6143	–2.1213	0.1494	0.3234	2.287704	0.1199	0.5101	3.237818	0.03557	0.09096

* "Statistics" means "T-Statistic" in the Welch's t-test for two group analysis.