

Supplementary Information

Organic fertilization co-selects genetically linked antibiotic and metal(loid) resistance genes in global soil microbiome

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Supplementary Results:

Details of the trained Random Forest classification model

The data used for training were evenly distributed across the 2 groups (NOF:109 samples; OF:109 samples), which ensured that the proportions and samples of each subgroup were consistent in both the training and test sets, which improved the representativeness of the groups. The random forest classification model was built following a two-step training. The first generated random forest classification with the default parameters acquired an error rate of 2.63%, which was used to classify the samples in the test set considering all genera. Mean decrease accuracy (MDA) which indicates the degree of decrease in the predictive accuracy of random forests, that is equal to the contribution of the genus to the classification, was used to estimate the contribution of each genus (Supplementary Table 2). Ten-fold cross-validation was executed with 10 repetitions, to eliminate the undesirable effects of unbalanced division of data in a single division, and to compensate for the limitation of insufficient training data. This approach not only reinforced the stability and reliability of the model's performance estimates but also guaranteed that every sample in the dataset has an equal chance of being included in the test set, reinforcing the representativeness of our training and testing regimes. Supplementary Figure 1 showed the relationship between the cross-validation error rate of the random forest classification model and the number of genera used for fitting. During the second training process, considering both the number of genera and the cross-validation error rate, the top 140 contributing genera (Supplementary Table 2) were selected for training the new random forest classification model using the training set, with optimal parameter adjustment using the R package "caret" (mtry = 2). The error rate of the generated new random forest classification model was 1.32%, which reduced the error rate by half compared to the previous one. Similarly, the test set was used to validate the classification model accuracy, with 31 out of the 33 NOF samples being correctly classified into NOF and all 33 OF samples being correctly classified in OF. The final random forest classification model acquired an accuracy of 0.97, recall of 0.94, and precision of 1. If setting the weights of precision and recall as 1:1, F1 score of 0.97 was obtained, indicating that the constructed random forest classification model can accurately predict the sample groupings.

Estimation of the taxonomic microbial communities and ARGs and MRGs abundances in samples with certain fertilization information and those after grouped using trained Random Forest classification model

Based on the data uploaded or corresponding article information, 109 of the 511 global agricultural soil samples were with certain information as applied with organic fertilizer, and 109 samples were without organic fertilization. The Shannon diversity and composition of microbial community, antibiotic resistance genes (ARGs), Risk ARGs, and metal resistance genes (MRGs) were firstly analyzed only on the 109 identified NOF and 109 identified OF samples, and then compared with the final classified 284 OF and 227 NOF samples by Random Forest classification model.

According to the analysis results of the identified 109 NOF and 109 OF soils, the Shannon diversity was significantly higher in NOF than in OF ($p < 0.001$, Supplementary Fig. 2a). At class level, *Actinomycetia*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, and *Bacilli* were the dominant bacteria (Supplementary Fig. 2b). Consistently, for the total agriculture soils after grouping based on the Random Forest classification model, the Shannon diversity was also significantly higher in 227 NOF than in 284 OF soils ($p < 0.001$, Fig. 1b). *Actinomycetia*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria* and *Bacilli* were the dominant bacteria at the class level in agricultural soils, accounting for 89.5% - 89.7% of the total abundances of microbes (Supplementary Fig. 2d). Slight variances in the relative abundance of these microbes between 227 NOF and 284 OF soils were revealed, i.e., *Actinomycetia* accounting for 35.7% and 31.5%, *Alphaproteobacteria* accounting for 20.9% and 18.7%, *Betaproteobacteria* accounting for 16.3% and 18.5%, *Gammaproteobacteria* accounting for 10.9% and 14.2%, and *Bacilli* accounting for 5.9% and 6.6% in NOF and OF soils, respectively (Supplementary Fig. 2d).

Regarding the abundances and diversities of ARGs, risk ARGs, and MRGs, based on the comparison results of 109 OF and 109 NOF soils with certain fertilization information, the abundance of ARGs was not significantly different in NOF and OF, while the abundance of Risk ARGs and MRGs was significantly higher in OF than in NOF (0.0076 vs. 0.0036 and 1.72 vs. 1.59 copies per cell, respectively, Supplementary Fig. 2c). A consistent trend was found in the samples after grouping using the Random Forest classification model. The overall relative abundance of ARGs was higher in 284 OF compared to 227 NOF (1.05 vs. 0.87 copies per cell) soils but with no statistically

significant differences ($p > 0.05$, Supplementary Fig. 2e). Nevertheless, the relative abundance of Risk ARGs, and MRGs was both significantly ($p < 0.001$) higher in OF than in NOF soils (0.05 vs. 0.02 and 2.32 vs. 1.46 copies per cell, respectively, Supplementary Fig. 2e). In sum, the overall microbial alpha diversity (Shannon), microbial composition, and relative abundance of ARGs, Risk ARGs, and MRGs trended consistently in NOF and OF before and after Random Forest classification.

Microbial communities in NOF and OF agricultural soils

Microbial interaction networks at the genus level in NOF and OF samples were used to identify significant associations between taxa (Supplementary Fig. 3a, b). The network of OF soils exhibited 91% more edges (2584) between nodes compared to the NOF soils (1352), although number of nodes showed little variances in the network of OF and NOF soils (443 and 413 nodes for OF and NOF, respectively, Supplementary Fig. 3c). This elevation in edge quantity significantly enhanced connection density and yielded more intricate network patterns. Various network metrics such as relative modularity (1.73 in OF and 1.11 in NOF), connectiveness (0.026 in OF and 0.016 in NOF), average clustering coefficient (0.62 in OF and 0.59 in NOF), and average degree (11.67 in OF and 6.55 in NOF; Supplementary Fig. 3c) were revealed with higher values in OF than NOF soils, indicating a heightened complexity in the interaction of microbial communities in agricultural soils with organic fertilizer application.

NMDS plot of overall taxonomic (stress = 0.13, $p = 0.001$) microbial communities showed significantly different cluttering patterns in OF and NOF soils (Supplementary Fig. 3d). NMDS plot of functional (stress = 0.08, $p = 0.001$) microbial communities also showed significantly different cluttering patterns in OF and NOF soils (Supplementary Fig. 3e). Functional genes assigned to protein metabolism were the most dominant functional category of microbes, with average abundances of 70.1 and 77.5 copies per cell in NOF and OF soils, respectively, followed by carbon metabolism (20.7 and 23.4 copies per cell for NOF and OF soils) and amino acids and derivatives (AADs, 18.2 and 23.4 for NOF and OF soils, Supplementary Fig. 3f). Among these dominant functional categories, the relative abundance of carbon metabolism, AADs, cofactors, vitamins, prosthetic groups, pigments (CVPs), miscellaneous, DNA metabolism, clustering-based subsystems (C-bs), regulation and cell signaling (RCs),

cell division and cell cycle (CDCC) was significantly ($p < 0.05$) higher in OF than NOF soils, while the functions associated with phages, prophages and transposable elements (PPTes) was significantly ($p < 0.05$) lower in OF than NOF soils (Supplementary Fig. 3f).

Variant types of ARGs in NOF and OF agricultural soils

A total of 497 ARG subtypes which belonging to 23 ARG types were detected in agricultural soils at the continental level (Supplementary Table 4) and were mostly associated with vancomycin, multidrug, and bacitracin resistance, with average abundances of 0.40, 0.30, and 0.07 copies per cell in OF soils, and 0.62, 0.12, and 0.03 copies per cell in NOF soils (Supplementary Fig. 4). Among them, 323 subtypes were shared by OF and NOF soils and were mostly assigned to beta-lactam (79 subtypes), multidrug (70 subtypes), MLS (40 subtypes), tetracycline (36 subtypes), and aminoglycoside (31 subtypes) resistance genes (Supplementary Table 4). More subtypes of ARGs were detected specifically associated with microbes in OF than NOF soils (131 vs. 46; Supplementary Table 4). According to the Wilcoxon test, the relative abundance of aminoglycoside, tetracycline, sulfonamide, chloramphenicol, and kasugamycin resistance genes significantly ($p < 0.001$) increased in OF compared to NOF soils with fold change of 2, 3, 20, 8 and 12. While the relative abundance of vancomycin significantly ($p < 0.001$) increased in NOF than OF soils with a fold change of 0.4 (Supplementary Fig. 4). Among the risk ARG types, the relative abundance of aminoglycoside (mostly comprised of *aadA*, *aph*, *aac* and *ant* genes), multidrug (*mdt* families), chloramphenicol (*cat* families), tetracycline (*tet* families), macrolide-lincosamide-streptogramin (MLS: *erm* families), and quinolone (*qnrB* gene) resistance genes' abundances showed significantly ($p < 0.001$) increased with fold change of 2, 11, 10, 6 and 13 (Supplementary Fig. 4).

Variant types of MRGs in NOF and OF agricultural soils

A total of 316 subtypes of MRGs which belonging to 19 MRG types were detected in these agricultural soils and were mostly shared in NOF and OF agricultural soils (272 MRG subtypes; Supplementary Table 5). A higher number of MRG subtypes was observed in OF than in NOF soils (39 vs. 5; Supplementary Table 5). The MRGs

detected in agricultural soils mainly belonged to multimetal resistance genes (87 subtypes), copper (Cu) resistance genes (65 subtypes), and arsenic (As) resistance genes (27 subtypes; Supplementary Table 5). In OF soils, As (abundances of 1.58 copies per cell), multimetal (abundances of 0.26 copies per cell) and chromium (Cr, abundances of 0.14 copies per cell) resistance genes were the most prominent MRG types, while As (abundances of 1.04 copies per cell), iron (Fe, abundances of 0.14 copies per cell), and multimetal (abundances of 0.11 copies per cell) resistance genes were dominated in NOF soils (Supplementary Fig. 4). According to the Wilcoxon test, the relative abundance of As (mostly comprised of *acr3* gene), multimetal, Silver (Ag), Mercury (Hg), Selenium (Se), Cadmium (Cd), Lead (Pb), Tellurium (Te), Gold (Au), Manganese (Mn) was revealed significantly ($p < 0.001$ or 0.01) increased in OF than NOF soil. Among them, the relative abundance of As resistance genes (mostly comprised of *acr3* genes) and multimetal resistance genes (mostly efflux genes) were the most increased with a fold change of 0.52 and 1.34. While the relative abundances of Cr and Cu resistance genes were also increased with fold change of 1.02 and 0.97, their differences in OF vs. NOF soils were not statistically significant (Supplementary Fig. 4).

Microbial communities with significantly differential abundances and their association with diverse ARGs and MRGs

According to DESeq2 analysis, a total of 76 genera were detected with significantly increased abundances in OF than NOF soils, while 50 genera were observed with significantly decreased abundances in OF than NOF soils ($p < 0.05$; Supplementary Fig. 6a, Supplementary Table 3). The microbes with statistically significantly higher abundances of log2FoldChange >1 in OF compared to NOF soils were mostly assigned to members of *Actinobacteria*, i.e., *Arthrobacter* (2.49% vs. 1.34%), *Phycococcus* (0.24% vs. 0.13%), *Pedococcus* (0.21% vs. 0.13%), members of *Bacteroidetes*, i.e., *Flavobacterium* (0.43% vs. 0.15%), *Chryseobacterium* (0.24% vs. 0.08%), *Pedobacter* (0.10% vs. 0.03%), members of *Firmicutes*, i.e., *Clostridium* (0.98% vs. 0.06%), and members of *Pseudomonadota*, i.e., *Stenotrophomonas* (1.26% vs. 0.64%), *Anaeromyxobacter* (0.87% vs. 0.21%), *Xanthomonas* (0.54% vs. 0.24%, Supplementary Fig. 5a). In contrast, the abundance of *Metabacillus* (0.04% vs. 0.10%, belongs to Firmicutes) and *Pseudomonadota*, mostly comprised of *Porphyrobacter* (0.07% vs.

0.16%) and *Tardibacter* (0.05% vs. 0.12%) was significantly lower ($p < 0.05$ and $\log_2\text{FoldChange} < -1$) in OF vs. NOF soils (Supplementary Fig. 6a).

Among the microbes with statistically significantly higher or lower abundances in OF vs. NOF soils (Supplementary Fig. 6a), the relative abundance of *Flavobacterium*, *Chryseobacterium*, *Pedobacter* (*Bacteroidetes* phylum), and *Clostridium* (*Firmicutes* phylum), and *Stenotrophomonas*, *Xanthomonas*, *Brevundimonas*, *Agrobacterium* (*Pseudomonadota* phylum) showed a significant ($p < 0.001$ or 0.01) positive correlation with the high abundance and diversity (richness) of the risk ARGs in OF soils (Supplementary Fig. 6b). Consistently, the relative abundance of these microbes also showed a significant ($p < 0.001$ or 0.05) positive correlation with the abundance and diversity (richness) of MRGs in OF soils, except the *Stenotrophomonas* (Supplementary Fig. 6b). The genera affiliated with *Actinobacteria* and *Pseudomonadota* (*Anaeromyxobacter*, *Ideonella*, *Thiobacillus*, *Geobacter*, *Pelobacter*, *Porphyrobacter*, and *Tardibacter*), which acquired significantly variant abundances in OF and NOF soils showed a negative correlation with the risk ARGs and/or MRGs abundance and diversity (Supplementary Fig. 6b). For the functional genes, the abundance of carbon, nitrogen, phosphorus, sulfur, and potassium metabolic genes in agricultural soils showed significantly positive correlations with risk ARGs and MRGs in both NOF and OF agricultural soils ($p < 0.05$, Supplementary Fig. 6c). The richness of ARGs was significantly positively correlated with the most of elemental metabolism genes in the OF soils, while this correlation was detected in the NOF soils only for the carbon and phosphorus metabolism genes (Supplementary Fig. 6c).

Taxonomic classification of AMCCs and their co-existent ARG and MRG subtypes

According to the taxonomic classification of AMCCs, *Pseudomonas* was the primary host where coexisting ARGs and MRGs were found, accounting for 11% and 15% of the total AMCCs in OF and NOF soils, respectively (Supplementary Fig. 7a, b). Other contributing genera included *Aeromonas*, *Arthrobacter*, *Anaeromyxobacter*, *Brevundimonas*, *Pantoea*, *Stenotrophomonas*, *Thiobacillus*, and *Xanthomonas*, which in total represented 69% and 57% of the total AMCCs in OF and NOF soils. The dominant AMCCs taxa corroboratively with the genera that acquired a significantly

increased abundance in OF soils as revealed by DESeq2 analyses (Supplementary Fig. 6a).

The average abundance of AMCCs carrying MGEs, AMCCs carrying virulence factor genes (VFGs), and AMCCs carrying both VFGs and MGEs were all detected with significantly increased abundances in OF compared to NOF soils, which is 0.0202 vs. 0.0010, 0.0120 vs. 0.0001 and 0.0050 vs. 0.0011 copies per cell, respectively (Supplementary Fig. 7c-e). In detail, the most common ARG subtypes coexisting with MRGs were *multidrug_ABC_transporter* (multidrug resistance), *multidrug_transporter* (multidrug resistance), and *rosA* (fosmidomycin resistance), each co-occurring with 18, 14, and 11 MRG subtypes respectively. The MRG subtypes that most frequently coexisted with ARGs were *acrD* (multimetal resistance) and *acn* (Fe resistance), cooccurring with 9 and 8 ARG subtypes, respectively (Fig. 2a).

Taxonomic classification and metabolism pathways of the dominant ARG-MRG-carrying MAGs

Overall, these antibiotic and metal co-resistant bacteria (AMRB) were classified into 12 class, including *Gammaproteobacteria* (48), *Alphaproteobacteria* (12), *Acidobacteriae* (12), *Actinomycetia* (7), *Nitrospirota* (4), *Thermoanaerobaculia* (3), etc, and most of them (68/90) were identified with higher abundance in OF than in NOF agricultural soils (Fig. 5a). These AMRB were mostly resistant to antibiotics including multidrug (84/95), fosmidomycin (30/95), bacitracin (26/95), MLS (9/95), aminoglycoside (7/95), beta-lactam (8/95), tetracycline (8/95), chloramphenicol (7/95), rifamycin (7/95), polymyxin (6/95) and vancomycin (5/95), and metals including Cr (94/95), As (93/95), Fe (81/95), multimetal (77/95), Cu (76/95), Zn (74/95), Se (63/95), Au(32/95) and Ag(21/95). MGEs of these AMRB were classified to the types of recombinase (92/95), transposase (88/95), ICE (82/95), AICE (40/95), IME (34/95), and VFGs of these AMRB were most associated with adherence (94/95), stress survival (84/95), immune modulation (83/95), motility (53/95), biofilm (50/95), regulation (50/95), effector delivery system (49/95), nutritional/metabolic factor (36/95), and antimicrobial activity/competitive advantage (24/95; Fig. 5a).

To further understand the function of AMRB, their elemental cycling functional genes were annotated based on the KEGG database (Supplementary Table 7). The *nirK*

gene was the most frequently occurring functional gene present in 32 AMRB, followed by *pqqC*, *phoD*, and *narG*, present in 31, 27, and 23 AMRB, respectively, and mainly involved in functional processes such as denitrification (NO_2^- to NO), inorganic P dissolution, organic P mineralization, and Nitrate reduction (Supplementary Fig. 9a). OF_MAG84 has the most diverse functional genes (12), followed by NOF_MAG31 (10) and OF_MAG76 (9), all of which are classified as *Gammaproteobacteria* (Supplementary Fig. 9b). Similarly, five AMRB (OF_MAG16, NOF_MAG7, OF_MAG76, NOF_MAG31, and OF_MAG84) belonging to *Gammaproteobacteria* present a complete sulfur-oxidation (SOX) pathway (*soxA*, *soxB*, *soxC*, *soxD*, *soxX*, *soxY*, and *soxZ*) belonging to the sulfur-oxidation bacteria (Supplementary Fig. 9a). Only 13.7% of AMRB (13/95) did not have the functional genes we selected, indicating that they do not have the functions represented by these functional genes or possibly due to the incomplete assembling of the microbial genomes. To sum, most AMRB (82/95) were associated with nitrogen (*narG*, *nirK/S*, and *nosZ*), phosphorus (*phoD* and *pqqC*), or sulfur (*aprA/B*, *dsrB*, *soxA/B/C/D/C/Y/Z*, *dmsA*, and *mddA*) cycling genes, indicating the presence of indigenous functional bacteria (Supplementary Fig. 9a), which also validated previous results showing the positive correlation of functional genes with ARGs and MRGs (Supplementary Fig. 6c).

Soil properties, metagenomic, and metatranscriptomics data profiles of 12 paddy soil samples under different As stress

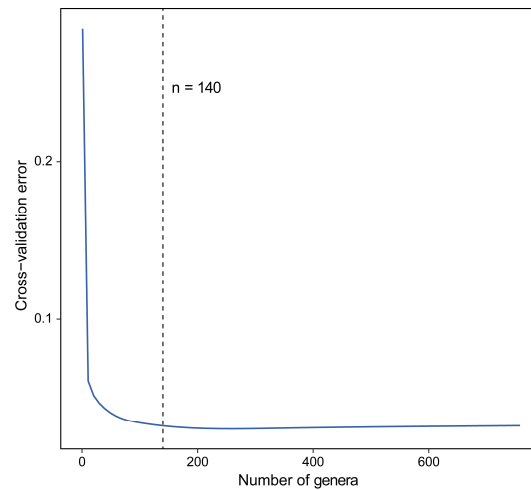
The soil properties of these 12 samples showed no significant differences, with the total carbon (TC) concentration ranged from 22.00 to 41.00 g kg⁻¹, total nitrogen (TN) concentration ranged from 1.73 to 2.41 g kg⁻¹, total phosphorus (TP) concentration ranged from 0.37 to 1.60 g kg⁻¹, and total sulfate (TS) concentration ranged from 0.19 to 0.49 g kg⁻¹. The concentration of heavy metals besides As was also analyzed with Cr concentrations ranged from 60.3 to 98.02 mg kg⁻¹, Sb concentrations ranged from 1.85 to 3.82 mg kg⁻¹, Cd concentrations ranged from 0.37 to 0.95 mg kg⁻¹, and Cu concentrations ranged from 19.42 to 42.44 mg kg⁻¹. For metagenomic datasets, 10.3 to 13.9 Gbp (12.3 Gbp, on average) of shotgun metagenomic reads and an average read length of 145 bp were acquired for each sample after trimming, and an average of 338,922 contigs and 509,273 ORFs were generated per sample. For metatranscriptomic datasets, an average of 26.7 Gbp (ranging from 24.9 to 29.8 Gbp) shotgun

metatranscriptomic reads and an average read length of 132 bp were obtained for each sample after trimming and removing of rRNA reads.

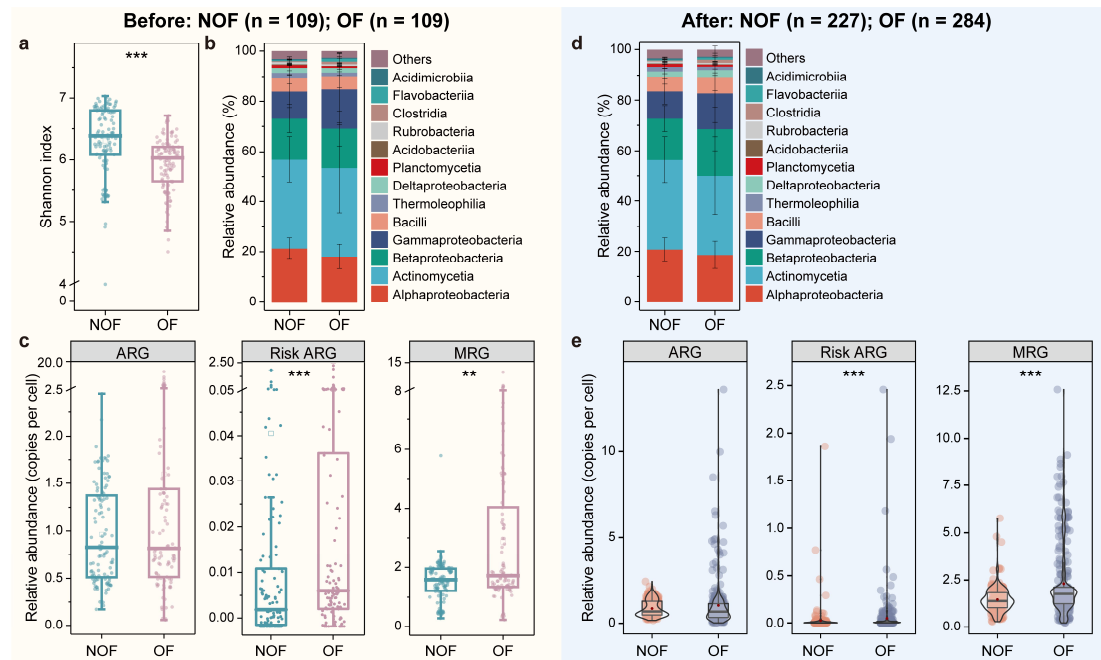
Defining the high and low risk of global threat potential of AMRB in agricultural soils

The unsupervised learning approach using k-means clustering was employed to categorize the abundance of antibiotic and metal(loid) co-resistant bacteria (AMRB) in 511 agricultural soils into six risk levels. The t-distributed Stochastic Neighbor Embedding (t-SNE) method was applied to visualize the clustering results. According to the result of t-SNE, a significant gap separates the samples into two groups, that is the low-risk group (risk levels 1, 2, and 3) and the high-risk group (risk levels 4, 5, and 6; Supplementary Fig. 10). Regarding the abundance of AMRB, the AMRB abundance in samples categorized into risk levels of 1, 2, and 3 was between $3\text{e-}4$ to $9\text{e-}3$ coverage per genome equivalent (CPG). Whereas samples classified into the risk level of 4, 5, and 6 exhibited AMRB abundance of $1\text{e-}2$ to $1\text{e-}1$ CPG. Given the clustering results and substantial disparity in AMRB abundance between these groups, we defined samples within risk levels of 1 to 3 as low risk and those with risk levels of 4 to 6 as high risk. The six risk levels therefore served as a critical indicator for differentiating between low and high risks. Upon defining the risk levels, a variety of features (such as climate data, soil properties, etc.) and machine learning algorithms were utilized to predict the microbial risk level for each point at a 0.083° resolution across global farmlands. The predicted risk levels of AMRB in different locations were used to create a map of microbial risk levels across global farmlands, where levels 1-3 were marked as 'Low Risk' areas and levels 4-6 were marked as 'High Risk' areas.

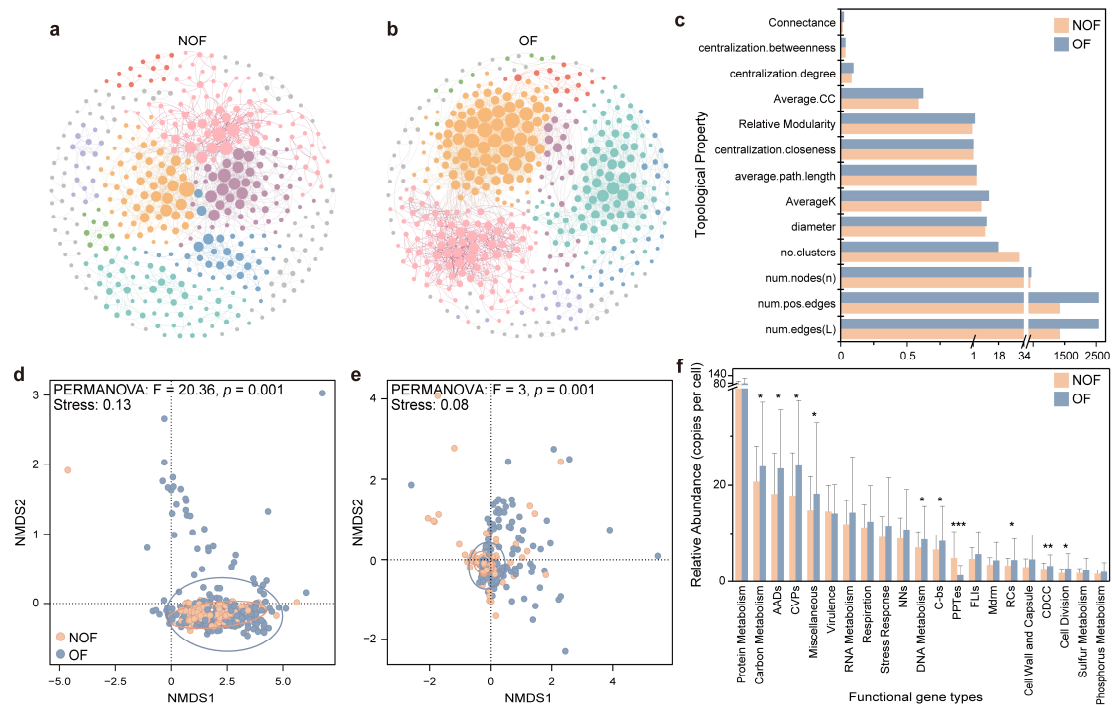
Supplementary Figures:



Supplementary Figure 1. **The relationship between Cross-validation error and the number of variables (genera) in the Random Forest (RF) classification model.** Source data were provided as a Source Data file.

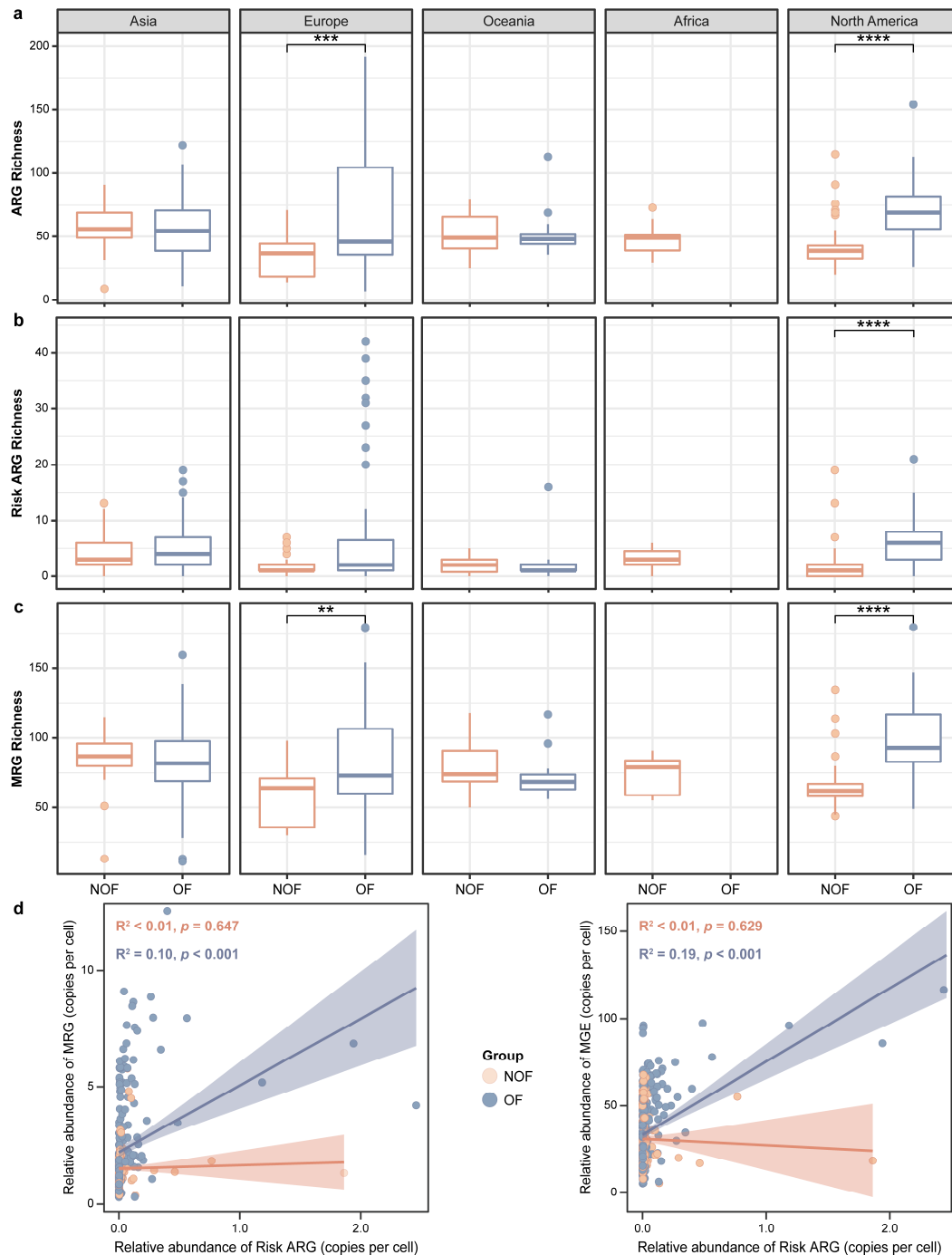


Supplementary Figure 2. **Shannon diversity and composition of microbial community and relative abundance of antibiotic resistance genes (ARGs), Risk ARGs, and metal(loid) resistance genes (MRGs) before ($n = 109$ in NOF and OF) and after ($n = 227$ in NOF and $n = 284$ in OF) grouping using the RF classification model.** **a** Shannon diversity of microbial community before grouping (Shannon diversity of microbial community after grouping in Figure 1b). **b** Microbial community compositions at the Class level before grouping. **c** Relative abundance of ARGs, Risk ARGs, and MRGs before grouping. **d** Microbial community compositions at the Class level after grouping. **e** Relative abundance of ARGs, Risk ARGs, and MRGs after grouping. The boxes indicated the 25th to 75th percentiles (with the median as a horizontal line), and the whiskers represented the maximum and minimum values except for outliers. Two-sided Wilcoxon test was used for significance analyses (** $p < 0.01$; *** $p < 0.001$). The boxes indicated the 25th to 75th percentiles (with the median as a horizontal line), and the whiskers represented the maximum and minimum values except for outliers. Each point was a sample in box plot. In Supplementary Figure 2b and 2d, each error bar corresponds to the standard deviation (SD) and data were showed as mean $\pm$ SD. Source data were provided as a Source Data file.



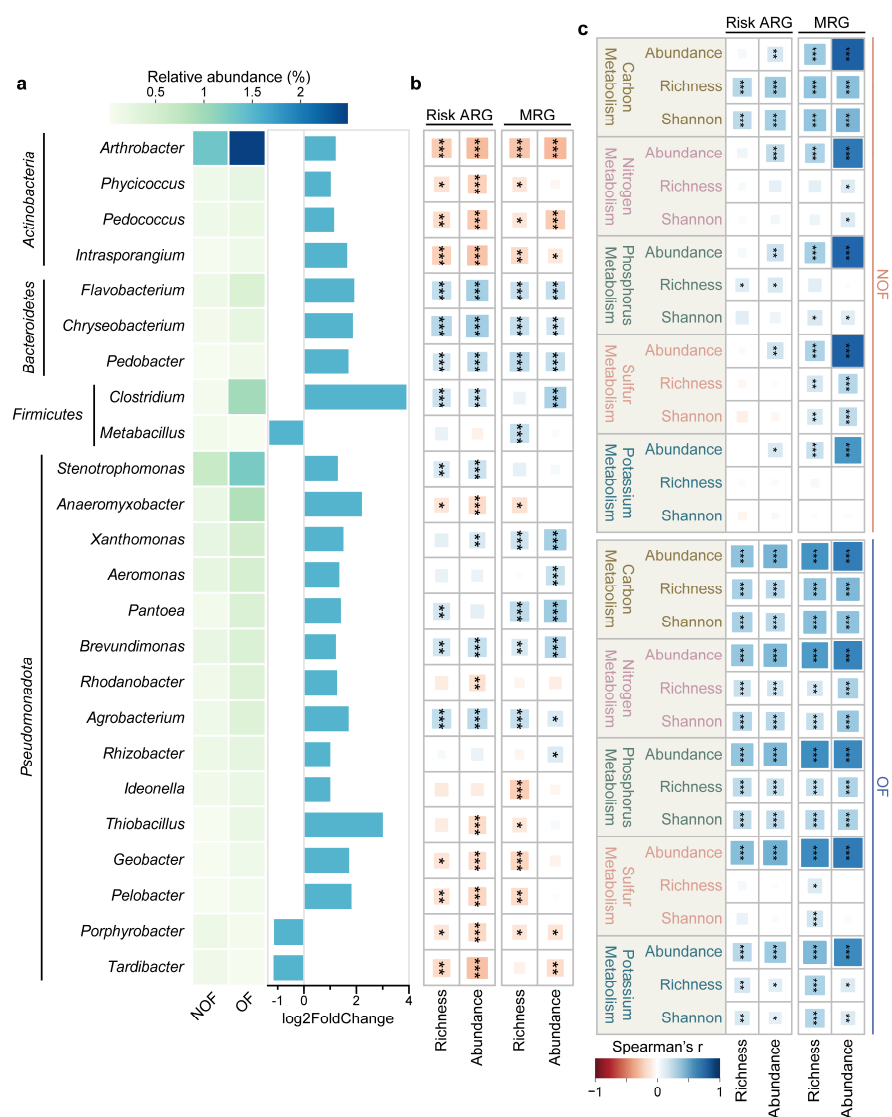
Supplementary Figure 3. **Microbial interaction networks, beta-diversity of microbial composition and functional gene composition, and relative abundance of functional gene types.** Networks of genus level based on Spearman analysis of NOF samples (**a**) and OF samples (**b**). Network colored by modularity class. In each network, node size was proportional to the number of connections (i.e., degree); edge thickness was proportional to Spearman's r . **c** Comparison of network topology of NOF and OF. **d** Beta-diversity of microbial community composition (PERMANOVA, $F = 20.36$, $p = 0.001$). **e** Beta-diversity of functional gene composition (PERMANOVA, $F = 3$, $p = 0.001$). **f** Relative abundance of functional gene types (Top 20) according to the SEED level 1 classifications (two-sides Wilcoxon test, $*p < 0.05$; $**p < 0.01$; $***p < 0.001$). Each error bar corresponds to the SD and data were showed as mean + SD. Source data were provided as a Source Data file. Average.CC: average clustering coefficient; AverageK: average degree; AADs: Amino Acids and Derivatives; CVPs: Cofactors, Vitamins, Prosthetic Groups, Pigments; NNs: Nucleosides and Nucleotides; C-bs: Clustering-based subsystems; PPTes: Phages, Prophages, Transposable elements; FLIs: Fatty Acids, Lipids, and Isoprenoids; Mdrm: Metabolite damage and its repair or mitigation; RCs: Regulation and Cell signaling; CDCC: Cell Division and Cell Cycle.

different gene types. Source data were provided as a Source Data file. MLS: macrolide-lincosamide-streptogramin.

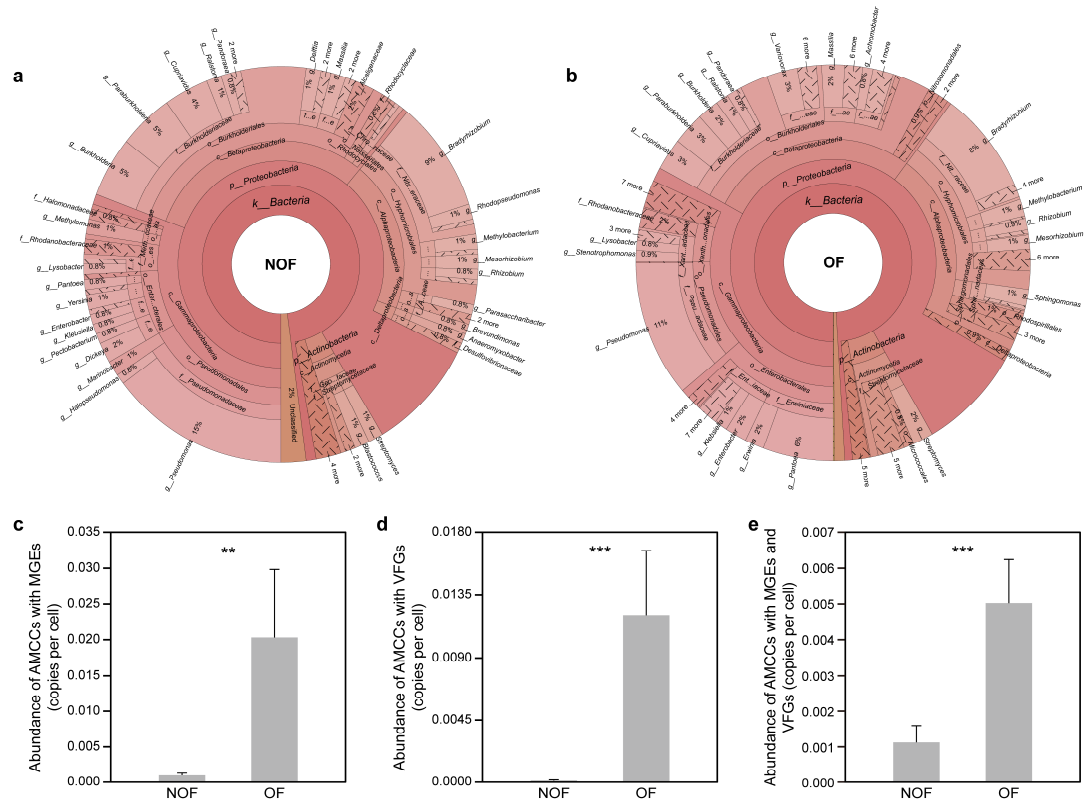


Supplementary Figure 5. **The diversity (Richness) of resistance genes on different continents.** Comparison of Richness of ARGs (a), Risk ARGs (b), and MRGs (c) on different continents between NOF and OF (two-sides Wilcoxon test, $**p < 0.01$; $***p < 0.001$; $****p < 0.0001$). The boxes indicated the 25th to 75th percentiles (with the median as a horizontal line), and the whiskers represented the maximum and minimum values except for outliers. Single points represented outliers. **d** Linear regression analysis of relative abundance between Risk ARGs and MRGs/mobile genetic elements (MGEs). Orange and blue dots represented NOF and OF samples, respectively. Source

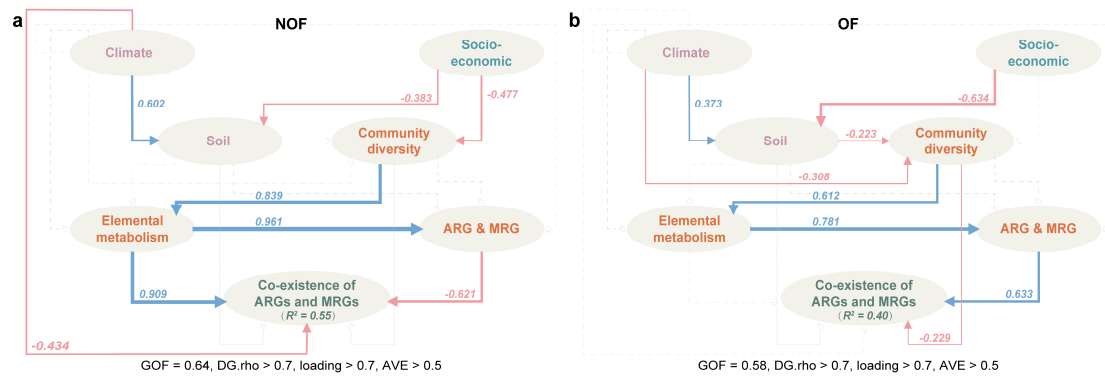
data were provided as a Source Data file. ARG: antibiotic resistance genes; MRG: metal(loid) resistance gene.



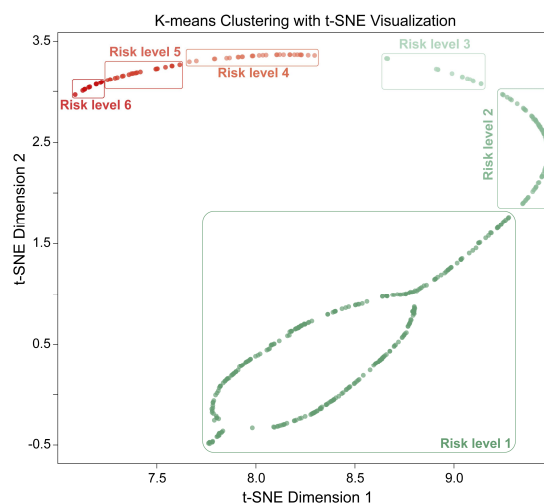
Supplementary Figure 6. **Genera with significant variation between NOF and OF and their association with Richness and relative abundance of Risk ARGs and MRGs.** **a** Genera (relative abundance > 0.1%) with significant differences in relative abundance between NOF and OF (DESeq2, $|\log_2\text{FoldChange}| \geq 1$, adjusted $p < 0.05$). **b** The Spearman correlation ($*p < 0.05$; $**p < 0.01$; $***p < 0.001$) between the relative abundance of genera and the relative abundance and diversity (Richness) of Risk ARGs and MRGs in OF samples. **c** The Spearman correlation ($*p < 0.05$; $**p < 0.01$; $***p < 0.001$) between the relative abundance of carbon (yellow), nitrogen (pink), phosphorus (green), sulfur (orange), and potassium (blue) metabolic genes and the relative abundance and diversity (Richness) of Risk ARGs and MRGs. Source data were provided as a Source Data file. ARG: antibiotic resistance gene; MRG: metal(loid) resistance gene.



Supplementary Figure 7. **Taxonomic classification and abundance of ARG-MRG-carrying contigs (AMCCs).** Taxonomic classification of AMCCs in NOF (**a**) and OF (**b**). Abundance of AMCCs with MGEs (**c**), virulence factor genes (VFGs) (**d**), and MGEs and VFGs (**e**) in NOF and OF (two-sides Wilcoxon test, ** $p < 0.01$; *** $p < 0.001$). Each error bar corresponds to the SD and data were showed as mean + SD. Source data were provided as a Source Data file. MGE: mobile genetic element.



Supplementary Figure 8. **Partial Least Square- Structural Equation Modelling (PLS-SEM) showing the direct and indirect effects of different factors on the co-existence of ARGs and MRGs for NOF (a) and OF (b) samples.** Blue, red, and gray colors indicate significantly positive, significantly negative, and no significant effects, respectively. Path coefficients and coefficients of determination (R^2) were calculated after bootstraps ($n = 100$), and all path coefficients shown were statistically significant ($p < 0.05$). Different colors represented different types of variables. Source data were provided as a Source Data file. ARG: antibiotic resistance gene; MRG: metal(loid) resistance gene; GOF: goodness of fit; DG.rho: Dillon-Goldstein's rho; AVE: average variance extracted.



Supplementary Figure 10. **Visualization of antibiotic and metal(loid) co-resistant bacteria (AMRB) abundance clusters in agricultural soil samples using t-distributed stochastic neighbor embedding (t-SNE).** Each point represents an individual soil sample, color-coded according to its assigned risk level based on the k-means method. Source data were provided as a Source Data file.

Supplementary Tables:

Supplementary Table 1. **Detailed information on global agricultural soil samples (n = 511).**

Accession Number	Sample ID	Group	Continent	Country	Longitude	Latitude
SRR13062006	NOF_110	NOF	Africa	South Africa	26.5296	-25.9946
SRR13062007	NOF_119	NOF	Africa	South Africa	26.5296	-25.9946
SRR13062008	NOF_120	NOF	Africa	South Africa	26.5296	-25.9946
SRR13062099	NOF_121	NOF	Africa	South Africa	27.33	-26.11
SRR13062098	NOF_122	NOF	Africa	South Africa	27.33	-26.11
SRR13062097	NOF_123	NOF	Africa	South Africa	27.33	-26.11
SRR5512132	OF_97	OF	Asia	China	130.2125	46.40667
SRR5512133	OF_161	OF	Asia	China	131.69722	46.74472
SRR5512134	OF_168	OF	Asia	China	120.05583	31.9375
SRR5512135	OF_178	OF	Asia	China	119.50972	30.91778
SRR5512136	OF_189	OF	Asia	China	102.74125	23.1295
SRR5512137	OF_190	OF	Asia	China	102.38253	23.21189
SRR5512138	OF_198	OF	Asia	China	101.03506	23.05222
SRR5512139	OF_204	OF	Asia	China	101.24619	24.47039
SRR5512140	OF_213	OF	Asia	China	133.46556	48.04444
SRR5512141	OF_98	OF	Asia	China	131.16583	45.28139
SRR5512142	OF_108	OF	Asia	China	114.11722	30.90472
SRR5512143	OF_119	OF	Asia	China	113.28444	30.38
SRR5512144	OF_130	OF	Asia	China	112.34306	28.79583
SRR5512145	OF_132	OF	Asia	China	113.8225	29.95
SRR5512146	OF_140	OF	Asia	China	121.24667	30.70694
SRR5512147	OF_148	OF	Asia	China	120.23528	30.63278
SRR19631180	OF_162	OF	Asia	China	109.21	27.52
SRR19631181	OF_163	OF	Asia	China	109.21	27.52

SRR19631182	OF_164	OF	Asia	China	109.21	27.52
SRR17477666	OF_165	OF	Asia	China	-	-
SRR17477667	OF_166	OF	Asia	China	-	-
SRR17477668	OF_167	OF	Asia	China	-	-
SRR17477669	NOF_140	NOF	Asia	China	-	-
SRR17477670	NOF_141	NOF	Asia	China	-	-
SRR14660885	OF_169	OF	Asia	China	-	-
SRR14660886	OF_170	OF	Asia	China	-	-
SRR14660887	NOF_142	NOF	Asia	China	-	-
SRR14660888	OF_171	OF	Asia	China	-	-
SRR14660889	OF_172	OF	Asia	China	-	-
SRR14660890	OF_173	OF	Asia	China	-	-
SRR14660891	OF_174	OF	Asia	China	-	-
SRR14660892	OF_175	OF	Asia	China	-	-
SRR14660893	OF_176	OF	Asia	China	-	-
SRR14660894	OF_177	OF	Asia	China	-	-
SRR14660895	OF_179	OF	Asia	China	-	-
SRR14660896	OF_180	OF	Asia	China	-	-
SRR14292197	OF_181	OF	Asia	China	104.06666	30.66667
SRR14292196	OF_182	OF	Asia	China	104.06666	30.66667
SRR14292189	OF_183	OF	Asia	China	104.06666	30.66667
SRR14292188	OF_184	OF	Asia	China	104.06666	30.66667
SRR14292187	OF_185	OF	Asia	China	106.71666	26.26666
SRR14292186	OF_186	OF	Asia	China	106.71666	26.26666
SRR14292185	OF_187	OF	Asia	China	106.71666	26.26666
SRR14292184	OF_188	OF	Asia	China	106.71666	26.26666
SRR13336287	NOF_18	NOF	Asia	China	108.083	34.03
SRR13336334	NOF_19	NOF	Asia	China	108.083	34.03
SRR13336326	NOF_20	NOF	Asia	China	108.083	34.03
SRR13336319	NOF_21	NOF	Asia	China	108.083	34.03

SRR13336311	NOF_22	NOF	Asia	China	108.083	34.03
SRR13336303	NOF_23	NOF	Asia	China	108.083	34.03
SRR13336296	NOF_24	NOF	Asia	China	108.083	34.03
SRR13336288	NOF_25	NOF	Asia	China	108.083	34.03
SRR11823718	NOF_143	NOF	Asia	China	86.02	44.18
SRR11823721	NOF_144	NOF	Asia	China	86.02	44.18
SRR11823722	NOF_145	NOF	Asia	China	86.02	44.18
CRR325346	OF_191	OF	Asia	China	-	-
CRR325348	OF_192	OF	Asia	China	-	-
SRR15167835	OF_193	OF	Asia	China	118.038	24.6389
SRR15167834	OF_194	OF	Asia	China	118.038	24.6389
SRR15167830	OF_195	OF	Asia	China	117.939	24.58
SRR15167829	OF_196	OF	Asia	China	117.939	24.58
SRR15167851	OF_197	OF	Asia	China	117.939	24.58
SRR13614401	NOF_146	NOF	Asia	China	116.65	37.3
SRR13614390	NOF_147	NOF	Asia	China	116.65	37.3
SRR13614402	OF_199	OF	Asia	China	116.65	37.3
SRR11450581	OF_200	OF	Asia	China	112.685873	28.171707
SRR11450582	OF_201	OF	Asia	China	112.760733	28.116708
SRR11450583	OF_202	OF	Asia	China	112.913319	28.176739
DRR012573	OF_203	OF	Asia	Japan	-	-
SRR13617630	OF_205	OF	Asia	India	94.1965	26.7248
SRR13617631	OF_206	OF	Asia	India	94.1965	26.7248
DRR160703	OF_207	OF	Asia	Japan	130.766	32.889
DRR160704	OF_208	OF	Asia	Japan	130.766	32.889
DRR160705	OF_209	OF	Asia	Japan	130.766	32.889
DRR160706	OF_210	OF	Asia	Japan	130.766	32.889
DRR160707	OF_211	OF	Asia	Japan	130.766	32.889
DRR160708	OF_212	OF	Asia	Japan	130.766	32.889
DRR160709	OF_214	OF	Asia	Japan	139.539	35.735

DRR160710	OF_215	OF	Asia	Japan	139.539	35.735
DRR160711	OF_216	OF	Asia	Japan	139.539	35.735
DRR160712	OF_217	OF	Asia	Japan	139.539	35.735
DRR160713	OF_218	OF	Asia	Japan	139.539	35.735
DRR160714	OF_219	OF	Asia	Japan	139.539	35.735
DRR160715	OF_220	OF	Asia	Japan	140.244	38.249
DRR160716	OF_221	OF	Asia	Japan	140.244	38.249
DRR160717	OF_222	OF	Asia	Japan	140.244	38.249
DRR160718	OF_223	OF	Asia	Japan	140.244	38.249
DRR160719	OF_99	OF	Asia	Japan	140.244	38.249
DRR160720	OF_100	OF	Asia	Japan	140.244	38.249
SRR2070858	OF_101	OF	Asia	Vietnam	140.244	38.249
SRR5823604	OF_224	OF	Europe	Italy	8.25	45.19
SRR5823605	OF_234	OF	Europe	Italy	8.25	45.19
SRR5823606	OF_241	OF	Europe	Italy	8.25	45.19
SRR5823607	OF_242	OF	Europe	Italy	8.25	45.19
SRR5823608	OF_250	OF	Europe	Italy	8.25	45.19
SRR5823609	OF_252	OF	Europe	Italy	8.25	45.19
SRR5823611	OF_253	OF	Europe	Italy	8.25	45.19
SRR17938967	OF_254	OF	Europe	Russian Federation	83.47	55.01
SRR17938968	OF_255	OF	Europe	Russian Federation	83.47	55.01
SRR17938975	OF_225	OF	Europe	Russian Federation	83.47	55.01
SRR17938976	OF_226	OF	Europe	Russian Federation	83.47	55.01
SRR17938977	OF_227	OF	Europe	Russian Federation	83.47	55.01
SRR17938978	OF_228	OF	Europe	Russian Federation	83.47	55.01
SRR17938979	OF_229	OF	Europe	Russian Federation	83.47	55.01
SRR17938980	OF_230	OF	Europe	Russian Federation	83.47	55.01
ERR7672969	NOF_148	NOF	Europe	The United Kingdom	-1.605268	52.205322
ERR7672970	OF_231	OF	Europe	The United Kingdom	-1.605268	52.205322
ERR7672971	OF_232	OF	Europe	The United Kingdom	-1.605268	52.205322

ERR7672972	OF_233	OF	Europe	The United Kingdom	-1.605268	52.205322
ERR3929365	OF_235	OF	Europe	Switzerland	7.233683	46.931584
ERR3943989	OF_236	OF	Europe	Switzerland	7.233683	46.931584
ERR3929366	OF_237	OF	Europe	Switzerland	7.233683	46.931584
ERR3943990	OF_238	OF	Europe	Switzerland	7.233683	46.931584
ERR3929373	OF_239	OF	Europe	Switzerland	7.233683	46.931584
ERR3943997	OF_240	OF	Europe	Switzerland	7.233683	46.931584
ERR2486618	NOF_149	NOF	Europe	Finland	21.689	60.746
ERR2486619	NOF_150	NOF	Europe	Finland	21.689	60.746
ERR2486620	NOF_151	NOF	Europe	Finland	21.689	60.746
ERR2486621	NOF_152	NOF	Europe	Finland	21.689	60.746
ERR2486622	NOF_153	NOF	Europe	Finland	21.689	60.746
ERR2486623	NOF_154	NOF	Europe	Finland	21.689	60.746
ERR2486624	NOF_155	NOF	Europe	Finland	22.64	60.559
ERR2486625	NOF_156	NOF	Europe	Finland	22.64	60.559
ERR2486626	NOF_157	NOF	Europe	Finland	22.64	60.559
ERR2486627	NOF_158	NOF	Europe	Finland	22.642	60.561
ERR2486628	NOF_159	NOF	Europe	Finland	22.642	60.561
ERR2486629	NOF_160	NOF	Europe	Finland	22.642	60.561
ERR2486630	NOF_161	NOF	Europe	Finland	22.992	60.426
ERR2486631	NOF_162	NOF	Europe	Finland	22.992	60.426
ERR2486632	NOF_163	NOF	Europe	Finland	22.992	60.426
ERR2486633	OF_243	OF	Europe	Finland	23	60.425
ERR2486634	OF_244	OF	Europe	Finland	23	60.425
ERR2486635	NOF_164	NOF	Europe	Finland	23	60.425
SRR9733659	OF_245	OF	Europe	Slovenia	15.04	46.03
SRR9733672	OF_246	OF	Europe	Slovenia	15.04	46.03
SRR9733674	OF_247	OF	Europe	Switzerland	8.01	47.3
SRR7013867	NOF_167	NOF	North America	Canada	-107.8	50.28
SRR7013889	NOF_171	NOF	North America	Canada	-107.8	50.28

SRR7013903	NOF_176	NOF	North America	Canada	-107.8	50.28
SRR7013874	NOF_182	NOF	North America	Canada	-107.8	50.28
SRR7013894	NOF_183	NOF	North America	Canada	-107.8	50.28
SRR7013900	NOF_191	NOF	North America	Canada	-107.8	50.28
SRR7013862	NOF_202	NOF	North America	Canada	-107.8	50.28
SRR7013873	NOF_208	NOF	North America	Canada	-107.8	50.28
SRR7013901	NOF_218	NOF	North America	Canada	-107.8	50.28
SRR7013893	NOF_168	NOF	North America	Canada	-107.8	50.28
SRR14458730	NOF_169	NOF	North America	The United States	-119.518373	36.597906
SRR14458731	NOF_170	NOF	North America	The United States	-119.518373	36.597906
SRR14458735	NOF_172	NOF	North America	The United States	-119.518373	36.597906
SRR14458736	NOF_173	NOF	North America	The United States	-119.518373	36.597906
SRR14458739	NOF_174	NOF	North America	The United States	-119.518373	36.597906
SRR14458740	NOF_175	NOF	North America	The United States	-119.518373	36.597906
ERR1939266	NOF_177	NOF	North America	The United States	-88.242	40.075
ERR1939268	NOF_178	NOF	North America	The United States	-88.242	40.075
ERR1939270	NOF_179	NOF	North America	The United States	-88.242	40.075
ERR1939272	NOF_180	NOF	North America	The United States	-88.242	40.075
SRR5687767	NOF_181	NOF	North America	The United States	-111.8143	41.7655
SRR5689334	OF_256	OF	North America	The United States	-83.4195	33.8834
SRR16123966	OF_257	OF	North America	The United States	-121.875957	38.545045
SRR16123968	OF_258	OF	North America	The United States	-121.871302	38.540587
SRR16123972	OF_259	OF	North America	The United States	-121.870682	38.540611
SRR16123992	OF_260	OF	North America	The United States	-121.874259	38.543123
SRR16123995	OF_261	OF	North America	The United States	-121.874896	38.543092
SRR16124002	OF_262	OF	North America	The United States	-121.876575	38.545011
SRR8987900	NOF_184	NOF	North America	Mexico	-109.55	27.22
SRR8987901	NOF_185	NOF	North America	Mexico	-109.55	27.22
SRR5678809	NOF_186	NOF	North America	The United States	-92.5	43
SRR5678810	NOF_187	NOF	North America	The United States	-92.5	43

SRR5260274	NOF_51	NOF	North America	The United States	-121.653	38.1087
SRR5260273	NOF_52	NOF	North America	The United States	-121.653	38.1087
SRR5260272	NOF_54	NOF	North America	The United States	-121.653	38.1087
SRR12823098	NOF_188	NOF	North America	The United States	-119.74	46.25
SRR12823099	NOF_189	NOF	North America	The United States	-119.74	46.25
SRR12823100	NOF_190	NOF	North America	The United States	-119.74	46.25
SRR12823102	NOF_192	NOF	North America	The United States	-119.74	46.25
SRR12823103	NOF_193	NOF	North America	The United States	-119.74	46.25
SRR12823106	NOF_194	NOF	North America	The United States	-119.74	46.25
SRR12823107	NOF_195	NOF	North America	The United States	-119.74	46.25
SRR12823109	NOF_196	NOF	North America	The United States	-119.74	46.25
SRR12823110	NOF_197	NOF	North America	The United States	-119.74	46.25
SRR12823111	NOF_198	NOF	North America	The United States	-119.74	46.25
SRR12823114	NOF_199	NOF	North America	The United States	-119.74	46.25
SRR12823117	NOF_200	NOF	North America	The United States	-119.74	46.25
SRR12823119	NOF_201	NOF	North America	The United States	-119.74	46.25
SRR6435953	OF_263	OF	North America	The United States	-79.05	35.91
SRR1926159	NOF_101	NOF	Oceania	Australia	147.178	-19.733
SRR1926199	NOF_102	NOF	Oceania	Australia	147.178	-19.733
SRR1926200	NOF_103	NOF	Oceania	Australia	147.178	-19.733
SRR1926201	NOF_104	NOF	Oceania	Australia	147.178	-19.733
SRR3591800	NOF_225	NOF	Oceania	Australia	152.379908	-25.025508
SRR3592089	OF_283	OF	Oceania	Australia	152.379908	-25.025508
SRR3592090	NOF_226	NOF	Oceania	Australia	152.379908	-25.025508
SRR3592108	OF_284	OF	Oceania	Australia	152.379908	-25.025508
ERR3029102	NOF_227	NOF	Oceania	Australia	138.6904631	-34.5376142
ERR3029103	NOF_222	NOF	Oceania	Australia	138.6904631	-34.5376142
ERR3029104	NOF_223	NOF	Oceania	Australia	138.6904631	-34.5376142
ERR3029105	NOF_224	NOF	Oceania	Australia	138.6904631	-34.5376142
SRR3601979	OF_275	OF	Oceania	Australia	152.38	-25.03

SRR3601981	OF_276	OF	Oceania	Australia	152.38	-25.03
SRR3601982	OF_277	OF	Oceania	Australia	152.38	-25.03
SRR3601984	OF_278	OF	Oceania	Australia	152.38	-25.03
SRR3601985	OF_279	OF	Oceania	Australia	152.38	-25.03
SRR3601987	OF_280	OF	Oceania	Australia	152.38	-25.03
SRR3601989	OF_281	OF	Oceania	Australia	152.38	-25.03
SRR5086369/SRR5097182	OF_282	OF	Oceania	Australia	152.38	-25.03
SRR1190384	OF_1	OF	Asia	China	111.446	28.929
SRR1190383	OF_3	OF	Asia	China	111.446	28.929
SRR1190350	OF_13	OF	Asia	China	111.446	28.929
SRR1190349	OF_19	OF	Asia	China	111.446	28.929
SRR1190336	OF_27	OF	Asia	China	120.7808	30.639
SRR1190334	OF_30	OF	Asia	China	120.7808	30.639
SRR1190316	OF_36	OF	Asia	China	116.933	28.206
SRR1190311	OF_38	OF	Asia	China	116.933	28.206
SRR1190308	OF_39	OF	Asia	China	110.0736	20.566
SRR1190306	OF_2	OF	Asia	China	110.0736	20.566
SRR11823711	NOF_1	NOF	Asia	China	86.02	44.18
SRR11823712	NOF_2	NOF	Asia	China	86.02	44.18
SRR11823713	NOF_3	NOF	Asia	China	86.02	44.18
SRR11823714	NOF_4	NOF	Asia	China	86.02	44.18
SRR11823715	NOF_5	NOF	Asia	China	86.02	44.18
SRR11823716	NOF_6	NOF	Asia	China	86.02	44.18
SRR11823717	NOF_7	NOF	Asia	China	86.02	44.18
SRR11823719	NOF_8	NOF	Asia	China	86.02	44.18
SRR11823720	NOF_9	NOF	Asia	China	86.02	44.18
SRR19174815	OF_4	OF	Asia	China	-	-
SRR19174816	OF_5	OF	Asia	China	-	-
SRR19174817	OF_6	OF	Asia	China	-	-
SRR19174818	OF_7	OF	Asia	China	-	-

SRR19174819	OF_8	OF	Asia	China	-	-
SRR19174820	OF_9	OF	Asia	China	-	-
SRR13614383	OF_10	OF	Asia	China	116.65	37.3
SRR13614385	OF_11	OF	Asia	China	116.65	37.3
SRR13614384	OF_12	OF	Asia	China	116.65	37.3
SRR13614381	NOF_10	NOF	Asia	China	116.65	37.3
SRR13614380	NOF_11	NOF	Asia	China	116.65	37.3
SRR13614382	NOF_12	NOF	Asia	China	116.65	37.3
SRR13614399	NOF_13	NOF	Asia	China	116.65	37.3
SRR13614379	NOF_14	NOF	Asia	China	116.65	37.3
SRR13614400	NOF_15	NOF	Asia	China	116.65	37.3
SRR13614397	OF_14	OF	Asia	China	116.65	37.3
SRR13614396	OF_15	OF	Asia	China	116.65	37.3
SRR13614398	OF_16	OF	Asia	China	116.65	37.3
SRR13614395	OF_17	OF	Asia	China	116.65	37.3
SRR13614394	OF_18	OF	Asia	China	116.65	37.3
SRR13614393	OF_20	OF	Asia	China	116.65	37.3
SRR13614392	OF_21	OF	Asia	China	116.65	37.3
SRR13614391	OF_22	OF	Asia	China	116.65	37.3
SRR13614389	OF_23	OF	Asia	China	116.65	37.3
SRR13614388	OF_24	OF	Asia	China	116.65	37.3
SRR13614387	OF_25	OF	Asia	China	116.65	37.3
SRR13614386	OF_26	OF	Asia	China	116.65	37.3
SRR2071948	NOF_16	NOF	Asia	Vietnam	105.727278	21.08839
SRR2071949	OF_28	OF	Asia	Vietnam	105.727361	21.088395
SRR2070862	NOF_17	NOF	Asia	Vietnam	105.727278	21.08839
SRR2070865	OF_29	OF	Asia	Vietnam	105.727361	21.088395
ERR4878502	OF_40	OF	Europe	Germany	6.1375	51.7866
ERR4878503	OF_44	OF	Europe	Germany	6.1375	51.7866
ERR4878504	OF_46	OF	Europe	Germany	6.1375	51.7866

ERR4878505	OF_53	OF	Europe	Germany	6.1375	51.7866
ERR4878506	OF_54	OF	Europe	Germany	6.1375	51.7866
ERR4878507	OF_55	OF	Europe	Germany	6.1375	51.7866
ERR4878508	OF_56	OF	Europe	Germany	6.1375	51.7866
ERR4878509	OF_57	OF	Europe	Germany	6.1375	51.7866
ERR4878510	OF_58	OF	Europe	Germany	6.1375	51.7866
ERR4878511	OF_41	OF	Europe	Germany	6.1375	51.7866
ERR4878512	OF_42	OF	Europe	Germany	6.1375	51.7866
ERR4878513	OF_43	OF	Europe	Germany	6.1375	51.7866
ERR4245117	NOF_26	NOF	Europe	Germany	11.7	51.82
ERR4245118	NOF_27	NOF	Europe	Germany	11.7	51.82
ERR4245119	NOF_28	NOF	Europe	Germany	11.7	51.82
ERR4245120	NOF_29	NOF	Europe	Germany	11.7	51.82
ERR4245121	NOF_30	NOF	Europe	Germany	11.7	51.82
ERR4245122	NOF_31	NOF	Europe	Germany	11.7	51.82
ERR4245123	NOF_32	NOF	Europe	Germany	11.7	51.82
ERR4245124	NOF_33	NOF	Europe	Germany	11.7	51.82
ERR4245125	NOF_34	NOF	Europe	Germany	11.7	51.82
ERR4245126	NOF_35	NOF	Europe	Germany	11.7	51.82
ERR4245127	NOF_36	NOF	Europe	Germany	11.7	51.82
ERR4245128	NOF_37	NOF	Europe	Germany	11.7	51.82
ERR4245129	NOF_38	NOF	Europe	Germany	11.7	51.82
ERR4245130	NOF_39	NOF	Europe	Germany	11.7	51.82
ERR4245131	NOF_40	NOF	Europe	Germany	11.7	51.82
ERR4245132	NOF_41	NOF	Europe	Germany	11.7	51.82
SRR5259830	NOF_42	NOF	North America	The United States	-121.653	38.1087
SRR5259839	NOF_53	NOF	North America	The United States	-121.653	38.1087
SRR5259939	NOF_55	NOF	North America	The United States	-121.653	38.1087
SRR5690554	NOF_43	NOF	North America	The United States	-111.8143	41.7655
SRR12823096	NOF_44	NOF	North America	The United States	-119.74	46.25

SRR12823101	NOF_45	NOF	North America	The United States	-119.74	46.25
SRR12823104	NOF_46	NOF	North America	The United States	-119.74	46.25
SRR12823108	NOF_47	NOF	North America	The United States	-119.74	46.25
SRR12823112	NOF_48	NOF	North America	The United States	-119.74	46.25
SRR12823115	NOF_49	NOF	North America	The United States	-119.74	46.25
SRR12823118	NOF_50	NOF	North America	The United States	-119.74	46.25
SRR10113573	OF_102	OF	Asia	China	120.95024	30.5907243
SRR10113582	OF_103	OF	Asia	China	120.95024	30.5907243
SRR10113588	OF_104	OF	Asia	China	120.95024	30.5907243
SRR10767026	OF_105	OF	Asia	India	85.55	20.25
SRR10767027	OF_106	OF	Asia	India	85.55	20.25
SRR10767028	OF_107	OF	Asia	India	85.55	20.25
SRR12192804	NOF_111	NOF	Africa	South Africa	26.529	-25.9945
SRR12192805	NOF_112	NOF	Africa	South Africa	26.529	-25.9945
SRR12192851	NOF_113	NOF	Africa	South Africa	27.555	-26.19778
SRR12192852	NOF_114	NOF	Africa	South Africa	27.555	-26.19778
SRR12285196	NOF_115	NOF	Africa	South Africa	25.639	-25.8
SRR12285197	NOF_116	NOF	Africa	South Africa	25.639	-25.8
SRR12288316	NOF_117	NOF	Africa	South Africa	26.8886	-26.327
SRR12288317	NOF_118	NOF	Africa	South Africa	26.8886	-26.327
SRR12376371	NOF_124	NOF	Asia	India	76.16	27.53
SRR12875365	OF_109	OF	Asia	Indonesia	106.7435	-6.8286
SRR12875366	OF_110	OF	Asia	Indonesia	106.7435	-6.8286
SRR13484447	OF_111	OF	Asia	China	112.7	28.2
SRR13484448	OF_112	OF	Asia	China	112.7	28.2
SRR13484449	OF_113	OF	Asia	China	112.7	28.2
SRR13708140	OF_114	OF	Asia	China	117.08	36.11
SRR13708141	OF_115	OF	Asia	China	117.08	36.11
SRR13708142	OF_116	OF	Asia	China	117.08	36.11
SRR13708147	OF_117	OF	Asia	China	117.08	36.11

SRR13708148	OF_118	OF	Asia	China	117.08	36.11
SRR13870169	OF_120	OF	Asia	China	113	28.21
SRR13870180	OF_121	OF	Asia	China	113	28.21
SRR13870181	OF_122	OF	Asia	China	113	28.21
SRR14292182	OF_123	OF	Asia	China	104.06666	30.66667
SRR14292183	OF_124	OF	Asia	China	104.06666	30.66667
SRR14292190	OF_125	OF	Asia	China	106.71666	26.26666
SRR14292191	OF_126	OF	Asia	China	106.71666	26.26666
SRR14292192	OF_127	OF	Asia	China	106.71666	26.26666
SRR14292193	OF_128	OF	Asia	China	106.71666	26.26666
SRR14292194	OF_129	OF	Asia	China	104.06666	30.66667
SRR14292195	OF_131	OF	Asia	China	104.06666	30.66667
SRR14301315	OF_264	OF	North America	Canada	-81.2	43.01
SRR14301317	OF_265	OF	North America	Canada	-81.2	43.01
SRR14301318	OF_266	OF	North America	Canada	-81.2	43.01
SRR14320327	NOF_125	NOF	Asia	China	118.62	37.3
SRR14320330	NOF_126	NOF	Asia	China	118.62	37.3
SRR14320331	NOF_127	NOF	Asia	China	118.62	37.3
SRR14661182	NOF_128	NOF	Asia	China	115.17	36.78
SRR14661183	NOF_129	NOF	Asia	China	115.17	36.78
SRR14661184	NOF_130	NOF	Asia	China	115.17	36.78
SRR14661185	NOF_131	NOF	Asia	China	115.17	36.78
SRR14661186	NOF_132	NOF	Asia	China	115.17	36.78
SRR14661187	NOF_133	NOF	Asia	China	115.17	36.78
SRR14661188	NOF_134	NOF	Asia	China	115.17	36.78
SRR14661189	NOF_135	NOF	Asia	China	115.17	36.78
SRR14661190	NOF_136	NOF	Asia	China	115.17	36.78
SRR15168755	OF_267	OF	North America	The United States	-104.9995	40.6529
SRR15646751	OF_133	OF	Asia	China	100.41	25.38
SRR15646754	OF_134	OF	Asia	China	100.41	25.38

SRR15646755	OF_135	OF	Asia	China	100.41	25.38
SRR15646757	OF_136	OF	Asia	China	102.93	24.67
SRR15646758	OF_137	OF	Asia	China	102.93	24.67
SRR15646759	OF_138	OF	Asia	China	102.93	24.67
SRR15910693	OF_139	OF	Asia	China	113.585	28.9266
SRR15910694	OF_141	OF	Asia	China	113.585	28.9266
SRR15910699	OF_142	OF	Asia	China	113.585	28.9266
SRR15910700	OF_143	OF	Asia	China	113.585	28.9266
SRR16106684	OF_144	OF	Asia	China	109.76373	21.50715
SRR16106685	OF_145	OF	Asia	China	109.76373	21.50715
SRR16106686	OF_146	OF	Asia	China	109.76373	21.50715
SRR17629608	OF_147	OF	Asia	India	94.33675	27.203564
SRR17938969	OF_248	OF	Europe	Russian Federation	83.47	55.01
SRR19134800	OF_31	OF	Asia	China	91.924	28.949
SRR19134801	OF_32	OF	Asia	China	91.924	28.949
SRR19134802	OF_33	OF	Asia	China	91.924	28.949
SRR19134803	OF_34	OF	Asia	China	91.924	28.949
SRR19134804	OF_35	OF	Asia	China	91.924	28.949
SRR19134805	OF_37	OF	Asia	China	91.924	28.949
SRR21169165	NOF_137	NOF	Asia	China	117.05555	24.61777
SRR21169166	NOF_138	NOF	Asia	China	117.05555	24.61777
SRR21169167	NOF_139	NOF	Asia	China	117.05555	24.61777
SRR21169168	OF_149	OF	Asia	China	117.05555	24.61777
SRR21169169	OF_150	OF	Asia	China	117.05555	24.61777
SRR21169170	OF_151	OF	Asia	China	117.05555	24.61777
SRR21169171	OF_152	OF	Asia	China	117.05555	24.61777
SRR21169172	OF_153	OF	Asia	China	117.05555	24.61777
SRR21169173	OF_154	OF	Asia	China	117.05555	24.61777
SRR21617303	OF_155	OF	Asia	China	113.58	24.55
SRR21617304	OF_156	OF	Asia	China	113.57	24.55

SRR21617313	OF_157	OF	Asia	China	113.64	24.55
SRR21617314	OF_158	OF	Asia	China	113.63	24.55
SRR21617317	OF_159	OF	Asia	China	113.52	24.55
SRR21617318	OF_160	OF	Asia	China	113.52	24.55
ERR671910	NOF_100	NOF	Oceania	Australia	142.28934	-36.67146
ERR671911	NOF_105	NOF	Oceania	Australia	142.28934	-36.67146
ERR671912	NOF_106	NOF	Oceania	Australia	142.28934	-36.67146
ERR671913	NOF_107	NOF	Oceania	Australia	142.28934	-36.67146
ERR687897	NOF_108	NOF	Oceania	Australia	142.28934	-36.67146
ERR687898	NOF_109	NOF	Oceania	Australia	142.28934	-36.67146
ERR671918	OF_94	OF	Oceania	Australia	141.97633	-35.11641
ERR671919	OF_95	OF	Oceania	Australia	141.97633	-35.11641
ERR671920	OF_96	OF	Oceania	Australia	141.97633	-35.11641
ERR671921	OF_89	OF	Oceania	Australia	141.97633	-35.11641
ERR687889	OF_90	OF	Oceania	Australia	141.97633	-35.11641
ERR687890	OF_91	OF	Oceania	Australia	141.97633	-35.11641
ERR687891	OF_92	OF	Oceania	Australia	141.97633	-35.11641
ERR687892	OF_93	OF	Oceania	Australia	141.97633	-35.11641
SRR14301321	OF_59	OF	North America	Canada	-81.2	43.01
SRR14301320	OF_60	OF	North America	Canada	-81.2	43.01
SRR14301319	OF_61	OF	North America	Canada	-81.2	43.01
SRR14301300	OF_62	OF	North America	Canada	-81.2	43.01
SRR14301316	OF_63	OF	North America	Canada	-81.2	43.01
SRR14301308	OF_64	OF	North America	Canada	-81.2	43.01
SRR14301304	OF_65	OF	North America	Canada	-81.2	43.01
SRR14301299	OF_66	OF	North America	Canada	-81.2	43.01
SRR14301298	OF_67	OF	North America	Canada	-81.2	43.01
SRR14301324	OF_68	OF	North America	Canada	-81.2	43.01
SRR14301323	OF_69	OF	North America	Canada	-81.2	43.01
SRR14301322	OF_70	OF	North America	Canada	-81.2	43.01

SRR14301301	OF_71	OF	North America	Canada	-81.2	43.01
SRR14301307	OF_72	OF	North America	Canada	-81.2	43.01
SRR14301306	OF_73	OF	North America	Canada	-81.2	43.01
SRR14301305	OF_74	OF	North America	Canada	-81.2	43.01
SRR14301303	OF_75	OF	North America	Canada	-81.2	43.01
SRR14301302	OF_76	OF	North America	Canada	-81.2	43.01
SRR17938970	OF_45	OF	Europe	Russian Federation	83.47	55.01
SRR17938971	OF_47	OF	Europe	Russian Federation	83.47	55.01
SRR17938972	OF_48	OF	Europe	Russian Federation	83.47	55.01
SRR17938973	OF_49	OF	Europe	Russian Federation	83.47	55.01
SRR17938974	OF_50	OF	Europe	Russian Federation	83.47	55.01
SRR17938981	OF_51	OF	Europe	Russian Federation	83.47	55.01
SRR17938982	OF_52	OF	Europe	Russian Federation	83.47	55.01
SRR7013883	NOF_60	NOF	North America	Canada	-107.8	50.28
SRR7013888	NOF_61	NOF	North America	Canada	-107.8	50.28
SRR7013866	NOF_62	NOF	North America	Canada	-107.8	50.28
SRR7013886	NOF_63	NOF	North America	Canada	-107.8	50.28
SRR7013881	NOF_64	NOF	North America	Canada	-107.8	50.28
SRR7013905	NOF_65	NOF	North America	Canada	-107.8	50.28
SRR7013890	NOF_66	NOF	North America	Canada	-107.8	50.28
SRR7013880	NOF_67	NOF	North America	Canada	-107.8	50.28
SRR7013868	NOF_68	NOF	North America	Canada	-107.8	50.28
SRR7013897	NOF_69	NOF	North America	Canada	-107.8	50.28
SRR7013870	NOF_70	NOF	North America	Canada	-107.8	50.28
SRR7013902	NOF_71	NOF	North America	Canada	-107.8	50.28
SRR7013882	NOF_72	NOF	North America	Canada	-107.8	50.28
SRR7013904	NOF_73	NOF	North America	Canada	-107.8	50.28
SRR7013872	NOF_74	NOF	North America	Canada	-107.8	50.28
SRR7013858	NOF_75	NOF	North America	Canada	-107.8	50.28
SRR7013876	NOF_76	NOF	North America	Canada	-107.8	50.28

SRR7013864	NOF_77	NOF	North America	Canada	-107.8	50.28
SRR7013895	NOF_78	NOF	North America	Canada	-107.8	50.28
SRR7013861	NOF_79	NOF	North America	Canada	-107.8	50.28
SRR7013896	NOF_80	NOF	North America	Canada	-107.8	50.28
SRR7013877	NOF_81	NOF	North America	Canada	-107.8	50.28
SRR7013906	NOF_82	NOF	North America	Canada	-107.8	50.28
SRR7013907	NOF_83	NOF	North America	Canada	-107.8	50.28
SRR7013879	NOF_84	NOF	North America	Canada	-107.8	50.28
SRR7013860	NOF_85	NOF	North America	Canada	-107.8	50.28
SRR7013859	NOF_86	NOF	North America	Canada	-107.8	50.28
SRR7013863	NOF_87	NOF	North America	Canada	-107.8	50.28
SRR7013871	NOF_88	NOF	North America	Canada	-107.8	50.28
SRR7013891	NOF_89	NOF	North America	Canada	-107.8	50.28
SRR7013899	NOF_90	NOF	North America	Canada	-107.8	50.28
SRR7013898	NOF_91	NOF	North America	Canada	-107.8	50.28
SRR7013869	NOF_92	NOF	North America	Canada	-107.8	50.28
SRR7013875	NOF_93	NOF	North America	Canada	-107.8	50.28
SRR7013878	NOF_94	NOF	North America	Canada	-107.8	50.28
SRR7013887	NOF_95	NOF	North America	Canada	-107.8	50.28
SRR7013885	NOF_96	NOF	North America	Canada	-107.8	50.28
SRR7013884	NOF_97	NOF	North America	Canada	-107.8	50.28
SRR7013865	NOF_98	NOF	North America	Canada	-107.8	50.28
SRR7013892	NOF_99	NOF	North America	Canada	-107.8	50.28
SRR16123970	OF_269	OF	North America	The United States	-121.871302	38.540587
SRR16123974	OF_270	OF	North America	The United States	-121.870682	38.540611
SRR16123980	OF_271	OF	North America	The United States	-121.875957	38.545045
SRR16123993	OF_272	OF	North America	The United States	-121.874259	38.543123
SRR16123997	OF_273	OF	North America	The United States	-121.874896	38.543092
SRR16124003	OF_274	OF	North America	The United States	-121.876575	38.545011
SRR16123964	OF_77	OF	North America	The United States	-121.876549	38.544366

SRR16123976	OF_78	OF	North America	The United States	-121.871718	38.541886
SRR16123977	OF_79	OF	North America	The United States	-121.871718	38.541886
SRR16123979	OF_80	OF	North America	The United States	-121.871537	38.541894
SRR16123982	OF_81	OF	North America	The United States	-121.871537	38.541894
SRR16123984	OF_82	OF	North America	The United States	-121.875162	38.541763
SRR16123986	OF_83	OF	North America	The United States	-121.875162	38.541763
SRR16123988	OF_84	OF	North America	The United States	-121.874985	38.541811
SRR16123989	OF_85	OF	North America	The United States	-121.874985	38.541811
SRR16123999	OF_86	OF	North America	The United States	-121.876379	38.544363
SRR16124000	OF_87	OF	North America	The United States	-121.876379	38.544363
SRR16123962	OF_88	OF	North America	The United States	-121.876549	38.544366
ERR7672977	NOF_165	NOF	Europe	The United Kingdom	-1.605268	52.205322
ERR7672978	OF_249	OF	Europe	The United Kingdom	-1.605268	52.205322
ERR7672979	NOF_166	NOF	Europe	The United Kingdom	-1.605268	52.205322
ERR7672980	OF_251	OF	Europe	The United Kingdom	-1.605268	52.205322
ERR1939165	NOF_56	NOF	North America	The United States	-88.242	40.075
ERR1939167	NOF_57	NOF	North America	The United States	-88.242	40.075
ERR1939169	NOF_58	NOF	North America	The United States	-88.242	40.075
ERR1939171	NOF_59	NOF	North America	The United States	-88.242	40.075
SRR14458715	NOF_203	NOF	North America	The United States	-119.518373	36.597906
SRR14458716	NOF_204	NOF	North America	The United States	-119.518373	36.597906
SRR14458717	NOF_205	NOF	North America	The United States	-119.518373	36.597906
SRR14458718	NOF_206	NOF	North America	The United States	-119.518373	36.597906
SRR14458719	NOF_207	NOF	North America	The United States	-119.518373	36.597906
SRR14458720	NOF_209	NOF	North America	The United States	-119.518373	36.597906
SRR14458721	NOF_210	NOF	North America	The United States	-119.518373	36.597906
SRR14458723	NOF_211	NOF	North America	The United States	-119.518373	36.597906
SRR14458724	NOF_212	NOF	North America	The United States	-119.518373	36.597906
SRR14458725	NOF_213	NOF	North America	The United States	-119.518373	36.597906
SRR14458726	NOF_214	NOF	North America	The United States	-119.518373	36.597906

SRR14458727	NOF_215	NOF	North America	The United States	-119.518373	36.597906
SRR14458728	NOF_216	NOF	North America	The United States	-119.518373	36.597906
SRR14458729	OF_268	OF	North America	The United States	-119.518373	36.597906
SRR14458734	NOF_217	NOF	North America	The United States	-119.518373	36.597906
SRR14458737	NOF_219	NOF	North America	The United States	-119.518373	36.597906
SRR14458738	NOF_220	NOF	North America	The United States	-119.518373	36.597906
SRR14458732	NOF_221	NOF	North America	The United States	-119.518373	36.597906

Supplementary Table 2. **Importance ranking of genera for NOF and OF classification according to the Random Forest classification model.**

Genus	MeanDecreaseAccuracy	MeanDecreaseGini
<i>Cytobacillus</i>	5.066867544	1.415330112
<i>Frigoriglobus</i>	4.890445257	0.787378366
<i>Botrimarina</i>	4.836414521	1.014917978
<i>Limnoglobus</i>	4.595851102	1.043591914
<i>Legionella</i>	4.593898245	0.952147181
<i>Humisphaera</i>	4.505362369	0.885653464
<i>Tardibacter</i>	4.460508291	1.02608585
<i>Erythrobacter</i>	4.409716891	0.872883261
<i>Paroceanicella</i>	4.335528804	0.739380581
<i>Pseudonocardia</i>	4.314292146	1.017012886
<i>Phycisphaera</i>	4.240033749	0.761341249
<i>Georhizobium</i>	4.215222055	0.979211849
<i>Geodermatophilus</i>	4.119103953	0.791115613
<i>Tsuneonella</i>	4.015584372	0.546703437
<i>Gemmata</i>	3.950867919	0.607687137
<i>Metabacillus</i>	3.926153273	0.593344291
<i>Porphyrobacter</i>	3.886633534	0.549197982
<i>Microlunatus</i>	3.876847101	0.665632553
<i>Chloracidobacterium</i>	3.869053433	0.725044684
<i>Rubrobacter</i>	3.866363016	0.682881481
<i>Parasphingopyxis</i>	3.84075223	0.72604298
<i>Actinomarinicola</i>	3.721008816	0.450252244
<i>Leptolyngbya</i>	3.675330779	0.559725351
<i>Methyloceanibacter</i>	3.648938924	0.511003426
<i>Mycolicibacterium</i>	3.589843659	0.388344315
<i>Rhodobacter</i>	3.587719137	0.513085153
<i>Flavisolibacter</i>	3.520549325	0.21797956
<i>Qipengyuania</i>	3.506472244	0.71673119
<i>Rhizorhabdus</i>	3.502458935	0.347610667
<i>Blastomonas</i>	3.477613725	0.456274848
<i>Croceicoccus</i>	3.408799584	0.983806467
<i>Telmatocola</i>	3.404109363	0.469101031
<i>Croceibacterium</i>	3.391429194	0.278802985
<i>Urbifossiella</i>	3.382824052	0.268269968
<i>Nakamurella</i>	3.313687884	0.295764718
<i>Sphingosinithalassobacter</i>	3.273581755	0.609337339
<i>Aquicella</i>	3.271683731	0.386325427
<i>Sediminicoccus</i>	3.271163626	0.482490443
<i>Methylocaldum</i>	3.21895609	0.281245386

<i>Roseovarius</i>	3.199271239	0.451843016
<i>Altererythrobacter</i>	3.186750658	0.223087094
<i>Thermomicrobium</i>	3.176467714	0.359137368
<i>Staphylococcus</i>	3.156983045	0.464616084
<i>Candidatus Nitrosocosmicus</i>	3.134323148	0.275988023
<i>Steroidobacter</i>	3.128676296	0.146328974
<i>Allokutzneria</i>	3.125011024	0.47651838
<i>Modestobacter</i>	3.074776883	0.302662564
<i>Brevibacillus</i>	3.066305353	0.373649711
<i>Saccharomonospora</i>	3.004238425	0.33331072
<i>Scytonema</i>	2.978689367	0.36478388
<i>Aminobacter</i>	2.969158275	0.229182799
<i>Elioraea</i>	2.960996743	0.259780778
<i>Rufibacter</i>	2.945837218	0.185560682
<i>Nitrosopumilus</i>	2.938480107	0.177234025
<i>Roseococcus</i>	2.92952983	0.349751117
<i>Skermanella</i>	2.922373365	0.231787337
<i>Miniimonas</i>	2.866097742	0.187656363
<i>Nitrosospira</i>	2.844531789	0.13884895
<i>Lysobacter</i>	2.841708185	0.213187487
<i>Rothia</i>	2.787965094	0.376669159
<i>Planctomyces</i>	2.765937532	0.111583225
<i>Salipiger</i>	2.756197065	0.274220545
<i>Streptomyces</i>	2.74340013	0.229857676
<i>Arenimonas</i>	2.735066073	0.203465434
<i>Arthrobacter</i>	2.731617012	0.141671228
<i>Virgibacillus</i>	2.717773333	0.163720998
<i>Micropruina</i>	2.706452776	0.412212538
<i>Pelagerythrobacter</i>	2.691217533	0.389295883
<i>Terricaulis</i>	2.683362802	0.068775911
<i>Indioceanicola</i>	2.678795948	0.234517471
<i>Chondromyces</i>	2.658176877	0.268159765
<i>Jiangella</i>	2.655129817	0.142957907
<i>Serratia</i>	2.654944477	0.179125126
<i>Paludibaculum</i>	2.652048599	0.14245373
<i>Luteimonas</i>	2.649026446	0.150537885
<i>Lacibacter</i>	2.628624848	0.121730761
<i>Fimbriimonas</i>	2.618517614	0.108197901
<i>Noviherbaspirillum</i>	2.618395741	0.098981363
<i>Pigmentiphaga</i>	2.593828352	0.186087969
<i>Rhodoferax</i>	2.590115555	0.392259288
<i>Citromicrobium</i>	2.565023723	0.169183819
<i>Catellatospora</i>	2.547483378	0.138196427
<i>Diaminobutyricimonas</i>	2.537845859	0.112716147

<i>Blastococcus</i>	2.517531793	0.3299565
<i>Auraticoccus</i>	2.509051986	0.140726083
<i>Pikeienuela</i>	2.50636933	0.258899778
<i>Roseomonas</i>	2.506016547	0.18575959
<i>Methylobacterium</i>	2.505188022	0.220306642
<i>Microvirga</i>	2.499111863	0.085403529
<i>Phyllobacterium</i>	2.487522396	0.246789724
<i>Gordonia</i>	2.478773569	0.220444439
<i>Plantibacter</i>	2.473373587	0.177634543
<i>Neobacillus</i>	2.470665478	0.097363463
<i>Miltoncostaea</i>	2.465410131	0.08497456
<i>Desulfobulbus</i>	2.464876229	0.078698851
<i>Methyloligella</i>	2.434025189	0.100852735
<i>Diaphorobacter</i>	2.433714599	0.09791283
<i>Iamia</i>	2.423464043	0.189513376
<i>Methanosarcina</i>	2.421210423	0.152879328
<i>Methylomicrobium</i>	2.419886828	0.122554804
<i>Aquihabitans</i>	2.417577314	0.112477712
<i>Hoeflea</i>	2.389606619	0.199704427
<i>Labrys</i>	2.381986611	0.069373609
<i>Sphingobacterium</i>	2.372205523	0.175640383
<i>Pelagibacterium</i>	2.363599341	0.069204358
<i>Anaeromyxobacter</i>	2.354029031	0.175317908
<i>Nocardia</i>	2.344558502	0.071041382
<i>Candidatus Saccharimonas</i>	2.343947844	0.143911185
<i>Celeribacter</i>	2.336584082	0.074508421
<i>Gemmatimonas</i>	2.334210553	0.098195783
<i>Pseudorhodoplanes</i>	2.332999399	0.190118151
<i>Thermobacillus</i>	2.32723436	0.178639584
<i>Rhodovulum</i>	2.321129525	0.13625852
<i>Intrasporangium</i>	2.317532595	0.172815841
<i>Methylococcus</i>	2.307981981	0.071231734
<i>Denitratisoma</i>	2.299201648	0.151988311
<i>Sphingosinicella</i>	2.297637046	0.230885327
<i>Komagataeibacter</i>	2.290114978	0.194640305
<i>Rhizobium</i>	2.287677481	0.191115754
<i>Egibacter</i>	2.279939763	0.239490946
<i>Deinococcus</i>	2.278594227	0.137558221
<i>Thermomonas</i>	2.276050459	0.09589974
<i>Novosphingopyxis</i>	2.270894582	0.198443378
<i>Geobacillus</i>	2.244578038	0.270879281
<i>Marinobacterium</i>	2.239510899	0.224451717
<i>Thermus</i>	2.236041731	0.24233961
<i>Thalassospira</i>	2.235250796	0.095504445

<i>Enterobacter</i>	2.231044111	0.130176828
<i>Sandaracinobacter</i>	2.223921305	0.245870367
<i>Youhaiella</i>	2.220175915	0.073330935
<i>Brevirhabdus</i>	2.214006528	0.126139057
<i>Sulfuricaulis</i>	2.212941456	0.068824739
<i>Aquibium</i>	2.212016632	0.04481868
<i>Bacillus</i>	2.181914441	0.169864235
<i>Rhodothermus</i>	2.178878961	0.167483537
<i>Actinotalea</i>	2.17007412	0.033482969
<i>Epidermidibacterium</i>	2.167909112	0.103874162
<i>Cobetia</i>	2.165035021	0.228929069
<i>Nonomuraea</i>	2.160661841	0.054772474
<i>Pseudocnuella</i>	2.160151872	0.031400955
<i>Nitrososphaera</i>	2.157951642	0.154598968
<i>Shewanella</i>	2.152610658	0.224502363
<i>Allospingosinicella</i>	2.146550575	0.107411994
<i>Marinithermus</i>	2.144393767	0.174932497
<i>Symbiobacterium</i>	2.140050792	0.175561281
<i>Isosphaera</i>	2.136075831	0.163074464
<i>Usitatibacter</i>	2.131061981	0.075807347
<i>Gloeobacter</i>	2.130842786	0.143214586
<i>Geobacter</i>	2.130616452	0.134777958
<i>Thiodictyon</i>	2.130434498	0.063675275
<i>Mucisphaera</i>	2.12945747	0.074739563
<i>Azospirillum</i>	2.125354357	0.216594467
<i>Kaistia</i>	2.12212946	0.139453264
<i>Chloroflexus</i>	2.12150208	0.204519095
<i>Caulobacter</i>	2.120468135	0.144398586
<i>Vogesella</i>	2.115028411	0.111882637
<i>Halomarina</i>	2.112035329	0.109499427
<i>Spirosoma</i>	2.105359383	0.077063554
<i>Candidatus Bipolaricaulis</i>	2.099597757	0.078266273
<i>Melaminivora</i>	2.093550187	0.106657087
<i>Labilithrix</i>	2.088820762	0.04859369
<i>Cellulosimicrobium</i>	2.082728511	0.070468496
<i>Novosphingobium</i>	2.076924829	0.103957656
<i>Aeoliella</i>	2.072720937	0.286318304
<i>Niveispirillum</i>	2.064920249	0.036417167
<i>Singulisphaera</i>	2.062459158	0.088245772
<i>Paraconexibacter</i>	2.057895173	0.106315417
<i>Devosia</i>	2.052534697	0.074305933
<i>Stieleria</i>	2.051905753	0.126904268
<i>Mycolicibacter</i>	2.049815514	0.117548634
<i>Mesorhizobium</i>	2.046090272	0.12767898

<i>Haloterrigena</i>	2.041053479	0.078902842
<i>Archangium</i>	2.040702293	0.093977661
<i>Proteus</i>	2.040371261	0.124007065
<i>Tessaracoccus</i>	2.036228077	0.201507202
<i>Dactylosporangium</i>	2.028925067	0.118579019
<i>Anatilimnocola</i>	2.025763701	0.072969363
<i>Stella</i>	2.024558157	0.034203044
<i>Solidesulfovibrio</i>	2.023755125	0.147167331
<i>Sphingopyxis</i>	2.022816434	0.160780348
<i>Nitrosomonas</i>	2.019416862	0.158333214
<i>Sorangium</i>	2.016124159	0.066444878
<i>Brevilactibacter</i>	2.013232934	0.068722615
<i>Roseivivax</i>	2.011789164	0.041442184
<i>Thermococcus</i>	2.008504009	0.127164851
<i>Pulveribacter</i>	2.007736877	0.032013309
<i>Paludisphaera</i>	1.988416421	0.03309013
<i>Chryseoglobus</i>	1.987173377	0.062739417
<i>Roseiflexus</i>	1.986631249	0.067066029
<i>Pseudobacter</i>	1.985252596	0.154758664
<i>Propioniciclava</i>	1.980922282	0.088971313
<i>Polymorphum</i>	1.980679013	0.19259483
<i>Nitrosococcus</i>	1.978142094	0.102966751
<i>Pseudactinotalea</i>	1.978094234	0.048539405
<i>Polymorphobacter</i>	1.975916717	0.086562921
<i>Ralstonia</i>	1.974129135	0.130810861
<i>Rhodoplanes</i>	1.970040172	0.100302063
<i>Methylogaea</i>	1.966060783	0.059622446
<i>Hypericibacter</i>	1.961130328	0.126068798
<i>Cereibacter</i>	1.961123164	0.155062435
<i>Microterricola</i>	1.957310165	0.066763633
<i>Anaerolinea</i>	1.953853331	0.106255503
<i>Gimesia</i>	1.953794733	0.124215828
<i>Alicyclobacillus</i>	1.952734475	0.112106237
<i>Calothrix</i>	1.941938236	0.096219066
<i>Candidatus Viadribacter</i>	1.941525914	0.156811817
<i>Jeongeupia</i>	1.94132814	0.031822195
<i>Duganella</i>	1.939672065	0.064958757
<i>Phytohabitans</i>	1.936789416	0.073475638
<i>Desulfosarcina</i>	1.929916369	0.082250602
<i>Haliangium</i>	1.929623334	0.072047822
<i>Candidatus Nitrotoga</i>	1.918857684	0.064532747
<i>Caldilinea</i>	1.915844442	0.057446283
<i>Hyphomicrobium</i>	1.910480321	0.035196622
<i>Micrococcus</i>	1.906293748	0.204453502

<i>Lichenicola</i>	1.906198803	0.055613284
<i>Lichenihabitans</i>	1.904491321	0.047696918
<i>Phaeobacter</i>	1.903485525	0.036580032
<i>Clavibacter</i>	1.899125272	0.099596331
<i>Aureimonas</i>	1.895842333	0.041564018
<i>Synechococcus</i>	1.894258119	0.084465393
<i>Conexibacter</i>	1.894033861	0.194207288
<i>Pannonibacter</i>	1.890678182	0.064414456
<i>Rhizobacter</i>	1.886258286	0.072289302
<i>Yinghuangia</i>	1.879994766	0.022449131
<i>Nisaea</i>	1.879133281	0.070728393
<i>Cellvibrio</i>	1.878822012	0.048996414
<i>Sphingorhabdus</i>	1.872371738	0.147865833
<i>Ramlibacter</i>	1.86925932	0.131554435
<i>Cystobacter</i>	1.865345863	0.074565384
<i>Thauera</i>	1.865014028	0.146301162
<i>Paraurantiacibacter</i>	1.863041063	0.111094425
<i>Agrococcus</i>	1.857227838	0.05184665
<i>Acidipropionibacterium</i>	1.854295316	0.034454577
<i>Paralcaligenes</i>	1.853748884	0.119084257
<i>Filomicrobium</i>	1.851404863	0.086836517
<i>Streptococcus</i>	1.849893401	0.094582449
<i>Allochromatium</i>	1.841753082	0.038480709
<i>Xanthomonas</i>	1.837203782	0.052724497
<i>Luteipulveratus</i>	1.832962967	0.059144517
<i>Nitrospira</i>	1.832903516	0.067120924
<i>Halobaculum</i>	1.831821994	0.036623559
<i>Agrobacterium</i>	1.829822542	0.048581141
<i>Ereboglobus</i>	1.828744104	0.160046376
<i>Treponema</i>	1.825898656	0.151164949
<i>Simplicispira</i>	1.823945608	0.055637321
<i>Oceanithermus</i>	1.823167637	0.023847102
<i>Xylophilus</i>	1.822231592	0.060337374
<i>Salaquimonas</i>	1.820631831	0.02450915
<i>Luteitalea</i>	1.817095575	0.066898971
<i>Clostridium</i>	1.811873985	0.042137025
<i>Tautonia</i>	1.810815954	0.093137944
<i>Meiothermus</i>	1.80971986	0.12296613
<i>Variibacter</i>	1.809359358	0.077936064
<i>Herbaspirillum</i>	1.800269617	0.067435755
<i>Variovorax</i>	1.793237326	0.027109356
<i>Luteimicrobium</i>	1.791378292	0.080349374
<i>Thioalkalivibrio</i>	1.791330994	0.118197204
<i>Halorubrum</i>	1.7911438	0.056241185

<i>Methanoculleus</i>	1.791035019	0.125651176
<i>Acidothermus</i>	1.789385653	0.115507049
<i>Ruegeria</i>	1.781032516	0.080894539
<i>Pseudarthrobacter</i>	1.773048204	0.066002377
<i>Serpentinimonas</i>	1.771871692	0.08677057
<i>Isoptericola</i>	1.769485003	0.059138796
<i>Flavihumibacter</i>	1.767674753	0.061345883
<i>Ferribacterium</i>	1.766333119	0.077786535
<i>Gemmobacter</i>	1.76157675	0.137378316
<i>Agromyces</i>	1.757015016	0.067743824
<i>Methylobacterium</i>	1.753527993	0.083626824
<i>Actinoplanes</i>	1.742552012	0.086999049
<i>Dietzia</i>	1.738927385	0.064139058
<i>Pararhodospirillum</i>	1.736408014	0.011261905
<i>Pyxidicoccus</i>	1.734708743	0.02092954
<i>Acidovorax</i>	1.734037314	0.031092407
<i>Azoarcus</i>	1.731719061	0.066981153
<i>Kosakonia</i>	1.730692602	0.035018984
<i>Bdellovibrio</i>	1.729077713	0.052451026
<i>Luteolibacter</i>	1.728171292	0.064841974
<i>Thermobifida</i>	1.726730459	0.083197436
<i>Verminephrobacter</i>	1.726321895	0.061482997
<i>Aquabacterium</i>	1.72613893	0.075074973
<i>Spiractinospora</i>	1.7255349	0.089434818
<i>Cryobacterium</i>	1.7232239	0.040931459
<i>Maoricimonas</i>	1.722890271	0.031378862
<i>Rhodanobacter</i>	1.720801714	0.053584523
<i>Collinsella</i>	1.720186204	0.044125044
<i>Marisediminicola</i>	1.71896457	0.053469042
<i>Tumebacillus</i>	1.715324229	0.157314027
<i>Bradyrhizobium</i>	1.707979826	0.116078118
<i>Alienimonas</i>	1.704600554	0.037256509
<i>Cnuibacter</i>	1.703623509	0.074971719
<i>Saccharothrix</i>	1.702585132	0.048357073
<i>Leucobacter</i>	1.69453049	0.052043881
<i>Candidatus Symbiobacter</i>	1.687519517	0.032815046
<i>Oryzomicrobium</i>	1.687376758	0.029186809
<i>Polaromonas</i>	1.68666936	0.068568913
<i>Mycobacterium</i>	1.68599605	0.112476125
<i>Dermacoccus</i>	1.684710906	0.036620294
<i>Tomitella</i>	1.682052277	0.020636508
<i>Massilia</i>	1.681578083	0.15999241
<i>Mycolicibacillus</i>	1.678218373	0.026131279
<i>Microcella</i>	1.676428949	0.045423132

<i>Acetobacter</i>	1.674017155	0.159121365
<i>Olsenella</i>	1.671039821	0.053563664
<i>Shinella</i>	1.670995319	0.054804876
<i>Tepidimonas</i>	1.669927267	0.017911308
<i>Sandaracinus</i>	1.668106844	0.036482836
<i>Pontibacter</i>	1.666687145	0.06354487
<i>Achromobacter</i>	1.664236583	0.029656533
<i>Martelella</i>	1.664115364	0.059244003
<i>Granulicella</i>	1.662126823	0.030612236
<i>Starkeya</i>	1.661792636	0.08503726
<i>Thermomonospora</i>	1.649509319	0.101951188
<i>Paraoerskovia</i>	1.64936784	0.075490298
<i>Bythopirellula</i>	1.647024004	0.032181796
<i>Pelobacter</i>	1.639577439	0.03222551
<i>Acidisarcina</i>	1.635741057	0.073697344
<i>Pseudolysobacter</i>	1.633875861	0.053694493
<i>Bordetella</i>	1.632410277	0.026095238
<i>Phototrophicus</i>	1.632319694	0.029558914
<i>Pseudosulfitobacter</i>	1.630149591	0.030700443
<i>Ktedonosporobacter</i>	1.629365222	0.028472727
<i>Undibacterium</i>	1.628071164	0.079154508
<i>Salinibacterium</i>	1.62760138	0.018130265
<i>Citri fermentans</i>	1.62541838	0.061471721
<i>Sphaerotilus</i>	1.619986848	0.05711865
<i>Ancylobacter</i>	1.61683864	0.040925977
<i>Peribacillus</i>	1.614946273	0.076548262
<i>Bosea</i>	1.614677685	0.045954936
<i>Thioflavicoccus</i>	1.613323226	0.078003978
<i>Paenarthrobacter</i>	1.6129802	0.060884533
<i>Desulfarculus</i>	1.61279146	0.045403764
<i>Acidithiobacillus</i>	1.610387171	0.089026463
<i>Caulifigura</i>	1.610058873	0.080728171
<i>Paucibacter</i>	1.607881237	0.045541524
<i>Janthinobacterium</i>	1.604887252	0.033219974
<i>Ectothiorhodospira</i>	1.604785734	0.03311413
<i>Chthonomonas</i>	1.604192198	0.047646039
<i>Phycicoccus</i>	1.595894426	0.027040855
<i>Cupriavidus</i>	1.595686532	0.08259166
<i>Ferrigenium</i>	1.593012571	0.124233053
<i>Frigoribacterium</i>	1.588213855	0.130977021
<i>Persicimonas</i>	1.588040669	0.023935007
<i>Terriglobus</i>	1.583796134	0.052061823
<i>Pseudogulbenkiania</i>	1.580668145	0.069323464
<i>Sanguibacter</i>	1.580576821	0.037618605

<i>Ottowia</i>	1.580065401	0.039302052
<i>Gryllotalpicola</i>	1.572805379	0.029794571
<i>Azotobacter</i>	1.571456873	0.088945404
<i>Neisseria</i>	1.570981255	0.073769294
<i>Desulfomicrobium</i>	1.555949312	0.04307518
<i>Curtobacterium</i>	1.55110576	0.082953536
<i>Halorhodospira</i>	1.540802785	0.13343771
<i>Parolsenella</i>	1.540773934	0.058037775
<i>Immundisolibacter</i>	1.535234144	0.035082159
<i>Acidimicrobium</i>	1.533820252	0.052377185
<i>Frankia</i>	1.527734242	0.075901781
<i>Haematobacter</i>	1.521886661	0.049432072
<i>Chlorobaculum</i>	1.520561491	0.039823877
<i>Roseitalea</i>	1.520091408	0.047479278
<i>Hankyongella</i>	1.517896535	0.016153257
<i>Baekduia</i>	1.513979777	0.04774087
<i>Aquisphaera</i>	1.510935522	0.133810713
<i>Hyphomonas</i>	1.508768664	0.023266071
<i>Thioclava</i>	1.508258437	0.043787688
<i>Eggerthella</i>	1.507896479	0.041679102
<i>Ferrovibrio</i>	1.505298819	0.036851495
<i>Rosistilla</i>	1.50076082	0.074031555
<i>Selenomonas</i>	1.495867774	0.087555556
<i>Capnocytophaga</i>	1.486011242	0.158540485
<i>Dickeya</i>	1.485812682	0.138479237
<i>Sphingomonas</i>	1.474194356	0.103468578
<i>Prevotella</i>	1.471500033	0.051249339
<i>Tuwongella</i>	1.457221504	0.093478842
<i>Methylomagma</i>	1.454329345	0.023894574
<i>Corynebacterium</i>	1.445775024	0.080471026
<i>Jatrophihabitans</i>	1.442012986	0.086617453
<i>Pelolinea</i>	1.440181164	0.044087475
<i>Sideroxydans</i>	1.424106874	0.06058358
<i>Nitrogeniibacter</i>	1.42329841	0.040580161
<i>Sinorhizobium</i>	1.421648548	0.03344691
<i>Burkholderia</i>	1.417578666	0.032273848
<i>Chryseolinea</i>	1.417050503	0.038065354
<i>Haloplanus</i>	1.417050503	0.025078521
<i>Granulibacter</i>	1.417050503	0.014229963
<i>Spiribacter</i>	1.416994796	0.007580201
<i>Lacunisphaera</i>	1.416815398	0.059163103
<i>Halovivax</i>	1.416815398	0.018478095
<i>Gephyromycinifex</i>	1.416806612	0.029067268
<i>Halopseudomonas</i>	1.416806612	0.027164423

<i>Edaphobacter</i>	1.416806612	0.007466667
<i>Symmachiella</i>	1.416511938	0.018010256
<i>Delftia</i>	1.416491629	0.050490079
<i>Phenylobacterium</i>	1.416233777	0.026210826
<i>Falsirhodobacter</i>	1.416205397	0.013708244
<i>Dinoroseobacter</i>	1.416175512	0.02938271
<i>Catenulispora</i>	1.416175512	0.012707692
<i>Alkalihalobacillus</i>	1.416075693	0.038072593
<i>Phnomibacter</i>	1.415837373	0.011266443
<i>Sagittula</i>	1.415214853	0.00875174
<i>Phreatobacter</i>	1.415084048	0.027661594
<i>Nocardiopsis</i>	1.415084048	0.014121569
<i>Mucilaginibacter</i>	1.415084048	0.009841444
<i>Aquabacter</i>	1.414938758	0.010320582
<i>Polynucleobacter</i>	1.414938758	0.008728029
<i>Defluviicoccus</i>	1.414568388	0.026653594
<i>Collimonas</i>	1.414125725	0.036141683
<i>Roseateles</i>	1.41356023	0.018582888
<i>Raineyella</i>	1.413213502	0.020410928
<i>Ahniella</i>	1.413016187	0.09601982
<i>Hoyosella</i>	1.412859872	0.013340468
<i>Silicimonas</i>	1.412559373	0.006705835
<i>Stappia</i>	1.412136112	0.032870773
<i>Aerosticca</i>	1.411793262	0.00977381
<i>Acidobacterium</i>	1.410951664	0.106794892
<i>Bremerella</i>	1.406243202	0.021136296
<i>Lacipirellula</i>	1.406017395	0.068230192
<i>Cohnella</i>	1.40568924	0.048105001
<i>Marmoricola</i>	1.405410236	0.035695003
<i>Tepidiforma</i>	1.405100663	0.014709273
<i>Gluconobacter</i>	1.402384878	0.050027168
<i>Dyadobacter</i>	1.401907936	0.033901407
<i>Psychrobacillus</i>	1.400273435	0.134201798
<i>Sterolibacterium</i>	1.398135697	0.120753505
<i>Pelagovum</i>	1.397213773	0.039570215
<i>Dokdonella</i>	1.397110485	0.04011241
<i>Salinibacter</i>	1.392905865	0.034403485
<i>Marichromatium</i>	1.392032268	0.02753354
<i>Tardiphaga</i>	1.388742182	0.046080213
<i>Dechloromonas</i>	1.386975702	0.069409459
<i>Salinisphaera</i>	1.384393921	0.043886356
<i>Asticcacaulis</i>	1.380555181	0.042771229
<i>Fulvivirga</i>	1.379432432	0.031793222
<i>Thiocapsa</i>	1.37715085	0.034944538

<i>Demequina</i>	1.376466103	0.09550918
<i>Yangia</i>	1.374578563	0.044534244
<i>Curvibacter</i>	1.368040394	0.035753059
<i>Marinobacter</i>	1.36232155	0.057186061
<i>Ideonella</i>	1.360347783	0.012952381
<i>Sporosarcina</i>	1.357730837	0.105851358
<i>Rhodospirillum</i>	1.354050258	0.092876838
<i>Sulfurifustis</i>	1.353290406	0.015241918
<i>Rhodopseudomonas</i>	1.34740485	0.007820463
<i>Quatrionicoccus</i>	1.347228355	0.068260607
<i>Corallococcus</i>	1.347173593	0.014075817
<i>Chitinolyticbacter</i>	1.347120692	0.010603674
<i>Nitrospirillum</i>	1.34406228	0.027220482
<i>Microbacterium</i>	1.341949555	0.051525881
<i>Aquisalimonas</i>	1.340862477	0.020976492
<i>Sideroxyarcus</i>	1.339758218	0.028965821
<i>Candidatus Promineofilum</i>	1.339376819	0.10287474
<i>Afipia</i>	1.338805363	0.032211765
<i>Tsukamurella</i>	1.336245685	0.091713813
<i>Paracoccus</i>	1.334009152	0.063425466
<i>Methylocella</i>	1.331422542	0.050480226
<i>Anoxybacillus</i>	1.331196937	0.047556408
<i>Mycetohabitans</i>	1.330963147	0.01448505
<i>Crenobacter</i>	1.327466668	0.02190095
<i>Melittangium</i>	1.327069782	0.076560943
<i>Amycolatopsis</i>	1.326497378	0.023688889
<i>Brevibacterium</i>	1.323854186	0.109983912
<i>Alistipes</i>	1.319094732	0.047165271
<i>Aeromicrobium</i>	1.317051599	0.102991997
<i>Desulfuromonas</i>	1.316945747	0.069075778
<i>Parvibaculum</i>	1.316945747	0.018789651
<i>Micromonospora</i>	1.314286069	0.052201278
<i>Runella</i>	1.313391379	0.038628571
<i>Niabella</i>	1.313281884	0.038584141
<i>Friedmanniella</i>	1.307166499	0.02174733
<i>Roseibium</i>	1.305424598	0.020344912
<i>Sulfuriferula</i>	1.303663422	0.074058928
<i>Mameliella</i>	1.300530356	0.022401805
<i>Alloacidobacterium</i>	1.292697001	0.03543424
<i>Georgenia</i>	1.287190525	0.046308653
<i>Bacteroides</i>	1.287190525	0.042884738
<i>Pirellulimonas</i>	1.281088152	0.130677858
<i>Actinomadura</i>	1.27994566	0.015269846
<i>Actinokineospora</i>	1.276598073	0.007134426

<i>Austwickia</i>	1.275549417	0.033671874
<i>Polaribacter</i>	1.273423649	0.034287558
<i>Blastochloris</i>	1.270648817	0.021182429
<i>Arachnia</i>	1.270444292	0.010746032
<i>Geomonas</i>	1.262628285	0.052174444
<i>Algoriphagus</i>	1.259906152	0.018102857
<i>Allosaccharopolyspora</i>	1.256313447	0.044266651
<i>Terrihabitans</i>	1.254049344	0.067752481
<i>Chryseobacterium</i>	1.251782545	0.053215986
<i>Ilumatobacter</i>	1.249925817	0.049451879
<i>Ruficoccus</i>	1.248580611	0.041802377
<i>Thiobacillus</i>	1.247109264	0.073019499
<i>Inhella</i>	1.243241783	0.066634616
<i>Gluconacetobacter</i>	1.241264168	0.09810631
<i>Sphaerobacter</i>	1.234643622	0.070848628
<i>Truepera</i>	1.226783691	0.110705085
<i>Roseobacter</i>	1.225377559	0.058030075
<i>Methylomonas</i>	1.22110651	0.036421443
<i>Desulfovibrio</i>	1.220774308	0.043108295
<i>Citrobacter</i>	1.220016326	0.055060938
<i>Stigmatella</i>	1.217464725	0.058447582
<i>Thermaerobacter</i>	1.206958526	0.110945257
<i>Niastella</i>	1.195880425	0.019541667
<i>Mycobacteroides</i>	1.194067355	0.030750725
<i>Nostoc</i>	1.18892511	0.056307387
<i>Protaetiibacter</i>	1.18773909	0.120596886
<i>Methylibium</i>	1.186905304	0.02266372
<i>Cellulomonas</i>	1.185922851	0.09516558
<i>Mycetocola</i>	1.184517246	0.022293333
<i>Actinopolymorpha</i>	1.170420228	0.030914734
<i>Oceanidesulfovibrio</i>	1.164829447	0.018875277
<i>Frateuria</i>	1.162940684	0.016299766
<i>Syntrophobacter</i>	1.162639657	0.063281455
<i>Aurantimonas</i>	1.161992499	0.00841232
<i>Pimelobacter</i>	1.159691983	0.017574883
<i>Salinicola</i>	1.159073033	0.027870236
<i>Pedococcus</i>	1.157643033	0.046017648
<i>Adhaeribacter</i>	1.157192782	0.035916985
<i>Polymorphospora</i>	1.156622311	0.034971167
<i>Pyruvatibacter</i>	1.150033496	0.017514058
<i>Adhaeritor</i>	1.114119733	0.025068853
<i>Xanthobacter</i>	1.103984197	0.056308407
<i>Segniliparus</i>	1.102115207	0.0434062
<i>Kaustia</i>	1.100802143	0.015389831

<i>Paenibacillus</i>	1.098682065	0.044317728
<i>Sulfuritortus</i>	1.098482844	0.065507838
<i>Occultella</i>	1.088928225	0.047489647
<i>Aromatoleum</i>	1.064619593	0.035179832
<i>Nordella</i>	1.051760126	0.095132759
<i>Roseimaritima</i>	1.047217216	0.047972275
<i>Rhodocytophaga</i>	1.046355508	0.05035057
<i>Leifsonia</i>	1.045491109	0.077409281
<i>Sphingobium</i>	1.039276534	0.073414407
<i>Oscillatoria</i>	1.014463868	0.061951678
<i>Roseimicrobium</i>	1.014433201	0.109561858
<i>Actinomyces</i>	1.001001503	0.072453188
<i>Sulfuritalea</i>	1.001001503	0.05498131
<i>Nibricoccus</i>	1.001001503	0.051770936
<i>Opitutus</i>	1.001001503	0.049989947
<i>Bifidobacterium</i>	1.001001503	0.049542044
<i>Edwardsiella</i>	1.001001503	0.048710957
<i>Acuticoccus</i>	1.001001503	0.046322373
<i>Brachybacterium</i>	1.001001503	0.039655083
<i>Kitasatospora</i>	1.001001503	0.036936035
<i>Kutzneria</i>	1.001001503	0.034302875
<i>Polyangium</i>	1.001001503	0.033846422
<i>Ornithinimicrobium</i>	1.001001503	0.033432975
<i>Orrella</i>	1.001001503	0.03204127
<i>Sulfitobacter</i>	1.001001503	0.029312821
<i>Comamonas</i>	1.001001503	0.028723618
<i>Rhodovastum</i>	1.001001503	0.02848749
<i>Halomonas</i>	1.001001503	0.027370439
<i>Citricoccus</i>	1.001001503	0.027242424
<i>Tetrasphaera</i>	1.001001503	0.026320346
<i>Schaalia</i>	1.001001503	0.025967805
<i>Actinopolyspora</i>	1.001001503	0.024513043
<i>Halobacterium</i>	1.001001503	0.023789899
<i>Sulfurivermis</i>	1.001001503	0.023625397
<i>Syntrophotalea</i>	1.001001503	0.022956522
<i>Nitrobacter</i>	1.001001503	0.022841119
<i>Exiguobacterium</i>	1.001001503	0.021977408
<i>Lignipirellula</i>	1.001001503	0.021833117
<i>Fibrella</i>	1.001001503	0.021223817
<i>Tabrizicola</i>	1.001001503	0.020228448
<i>Hyphobacterium</i>	1.001001503	0.019455649
<i>Herbiconiux</i>	1.001001503	0.018658421
<i>Fronidhabitans</i>	1.001001503	0.018609091
<i>Caballeronia</i>	1.001001503	0.018238095

<i>Humibacter</i>	1.001001503	0.017889474
<i>Actinoalloteichus</i>	1.001001503	0.01764
<i>Panacibacter</i>	1.001001503	0.017570691
<i>Hydrogenibacillus</i>	1.001001503	0.016806723
<i>Pseudomonas</i>	1.001001503	0.016
<i>Actinosynnema</i>	1.001001503	0.015652174
<i>Castellaniella</i>	1.001001503	0.015268376
<i>Dehalogenimonas</i>	1.001001503	0.01524097
<i>Pandoraea</i>	1.001001503	0.014540476
<i>Verrucomicrobium</i>	1.001001503	0.013592689
<i>Hartmannibacter</i>	1.001001503	0.0135
<i>Pectobacterium</i>	1.001001503	0.013333333
<i>Aquisediminimonas</i>	1.001001503	0.013212121
<i>Halorussus</i>	1.001001503	0.012467532
<i>Thiomonas</i>	1.001001503	0.011166276
<i>Natronomonas</i>	1.001001503	0.010804466
<i>Filimonas</i>	1.001001503	0.010689177
<i>Erwinia</i>	1.001001503	0.010616357
<i>Frigidibacter</i>	1.001001503	0.010178437
<i>Paraburkholderia</i>	1.001001503	0.010169697
<i>Fuscovulum</i>	1.001001503	0.00974026
<i>Acidihalobacter</i>	1.001001503	0.008927273
<i>Verrucosispora</i>	1.001001503	0.008213904
<i>Haloprofundus</i>	1.001001503	0.008126984
<i>Ponticoccus</i>	1.001001503	0.007822134
<i>Salinispora</i>	1.001001503	0.00734864
<i>Myxococcus</i>	1.001001503	0.007314286
<i>Oleiharenicola</i>	1.001001503	0.007272727
<i>Acidiphilium</i>	1.001001503	0.007254658
<i>Candidatus Koribacter</i>	1.001001503	0.007058824
<i>Agreia</i>	1.001001503	0.007
<i>Natronosporangium</i>	1.001001503	0.006878788
<i>Schlegelella</i>	1.001001503	0.006666667
<i>Gemmatirosa</i>	1.001001503	0.006612613
<i>Pirellula</i>	1.001001503	0.005940299
<i>Acidiferrobacter</i>	1.001001503	0.003935484
<i>Kytococcus</i>	1.001001503	0.003914894
<i>Ferruginibacter</i>	1.001001503	0.003789474
<i>Neotabrizicola</i>	1.001001503	0.003777778
<i>Vulгатibacter</i>	1.001001503	0.003756803
<i>Leptothrix</i>	1.001001503	0.003751773
<i>Flagellatimonas</i>	1.001001503	0.00374026
<i>Vibrio</i>	1.001001503	0.003666667
<i>Alkalilimnicola</i>	1.001001503	0.0036

<i>Kineococcus</i>	1.001001503	0.0032
<i>Halosimplex</i>	1.001001503	0.003
<i>Methyloversatilis</i>	1.001001503	0.002666667
<i>Paludibacterium</i>	1.001001503	0.002666667
<i>Streptosporangium</i>	1.001001503	0.001935484
<i>Alcaligenes</i>	1.001001503	0.001173333
<i>Aeromonas</i>	1.001001503	0.000609524
<i>Couchioplanes</i>	0.986369954	0.044935948
<i>Rathayibacter</i>	0.967997221	0.085100419
<i>Cyanobium</i>	0.959282214	0.062283057
<i>Raoultella</i>	0.953195867	0.100508869
<i>Salmonella</i>	0.943867551	0.03701356
<i>Pseudolabrys</i>	0.94349889	0.040010693
<i>Rhodococcus</i>	0.93593174	0.046938011
<i>Glutamicibacter</i>	0.931846756	0.05627241
<i>Pseudoalteromonas</i>	0.915674681	0.071994753
<i>Niallia</i>	0.902318224	0.107019479
<i>Lentzea</i>	0.857319242	0.06609926
<i>Thiocystis</i>	0.848311476	0.025841026
<i>Kocuria</i>	0.847330501	0.029142022
<i>Alloactinosynnema</i>	0.829038739	0.02977902
<i>Kibdelosporangium</i>	0.82171306	0.033015306
<i>Thiohalobacter</i>	0.817139863	0.064577584
<i>Hylemonella</i>	0.812056449	0.031355996
<i>Neorhizobium</i>	0.800712977	0.056142866
<i>Labrenzia</i>	0.797141636	0.017222816
<i>Saccharibacillus</i>	0.793183832	0.020731228
<i>Chitinimonas</i>	0.784947734	0.037973355
<i>Cutibacterium</i>	0.78082395	0.080972458
<i>Solitalea</i>	0.760940591	0.011612236
<i>Limnohabitans</i>	0.738194679	0.042546224
<i>Methylosinus</i>	0.707226768	0.029585193
<i>Prauserella</i>	0.68128777	0.04462864
<i>Leclercia</i>	0.643440934	0.018388094
<i>Azospira</i>	0.626040904	0.024439385
<i>Sulfidibacter</i>	0.616321145	0.059719825
<i>Chitinophaga</i>	0.600828586	0.045042931
<i>Luteibacter</i>	0.577733856	0.038450182
<i>Paraflavitalea</i>	0.536174862	0.018359544
<i>Brevundimonas</i>	0.510411603	0.070452739
<i>Alicyclophilus</i>	0.46498502	0.057781232
<i>Serinicoccus</i>	0.447303065	0.013
<i>Solimonas</i>	0.389623401	0.029951487
<i>Mitsuaria</i>	0.378975795	0.027421724

<i>Niveibacterium</i>	0.37779147	0.066116425
<i>Actinocatenispora</i>	0.376053754	0.010547726
<i>Thermobispora</i>	0.355538515	0.049500793
<i>Klebsiella</i>	0.318386358	0.021181406
<i>Sinomonas</i>	0.289921705	0.032185281
<i>Escherichia</i>	0.253526357	0.017488057
<i>Wenzhouxiangella</i>	0.231708268	0.008716667
<i>Chelatococcus</i>	0.166267862	0.0211679
<i>Alcanivorax</i>	0.136080775	0.07056645
<i>Allobranchiibius</i>	0.102582044	0.016907359
<i>Methylocystis</i>	0.097301772	0.029871403
<i>Hymenobacter</i>	0.025708742	0.075940767
<i>Hydrogenophaga</i>	0.012086856	0.039167411
<i>Pengzhenrongella</i>	0.012086856	0.028231461
<i>Bradymonas</i>	0	0.069484269
<i>Microvirgula</i>	0	0.059712028
<i>Marinicauda</i>	0	0.02725873
<i>Stutzerimonas</i>	0	0.023513043
<i>Faecalibacterium</i>	0	0.0232
<i>Saccharopolyspora</i>	0	0.020644855
<i>Stenotrophomonas</i>	0	0.016143247
<i>Oricola</i>	0	0.014861598
<i>Skermania</i>	0	0.01302381
<i>Pedobacter</i>	0	0.012885714
<i>Subtercola</i>	0	0.010784416
<i>Mumia</i>	0	0.010181818
<i>Pseudodesulfovibrio</i>	0	0.008545455
<i>Aquitalea</i>	0	0.007555556
<i>Egicoccus</i>	0	0.006545455
<i>Cronobacter</i>	0	0.006035714
<i>Limnochorda</i>	0	0.005333333
<i>Chromobacterium</i>	0	0.003777778
<i>Plantactinospira</i>	0	0.003671186
<i>Acidibrevibacterium</i>	0	0.003636364
<i>Stackebrandtia</i>	0	0.003555556
<i>Pontivivens</i>	0	0.0035
<i>Yersinia</i>	0	0.0034279
<i>Flaviflexus</i>	0	0.0032
<i>Pukyongiella</i>	0	0.003
<i>Dyella</i>	0	0.002937705
<i>Janibacter</i>	0	0.002666667
<i>Pseudorhizobium</i>	0	0.002666667
<i>Ruania</i>	0	0.002
<i>Oerskovia</i>	0	0.001827817

<i>Brucella</i>	0	0
<i>Yimella</i>	0	0
<i>Nitratireductor</i>	0	0
<i>Methyacidimicrobium</i>	0	0
<i>Glaciihabitans</i>	0	0
<i>Leptospira</i>	0	0
<i>Nocardioides</i>	0	0
<i>Beutenbergia</i>	0	0
<i>Akkermansia</i>	0	0
<i>Pusillimonas</i>	0	0
<i>Methylovirgula</i>	0	0
<i>Vitreoscilla</i>	0	0
<i>Casimicrobium</i>	0	0
<i>Magnetospirillum</i>	0	0
<i>Propionibacterium</i>	0	0
<i>Microbulbifer</i>	0	0
<i>Leisingera</i>	0	0
<i>Lautropia</i>	0	0
<i>Kiritimatiella</i>	0	0
<i>Halotalea</i>	0	0
<i>Rhodomicrobium</i>	0	0
<i>Kribbella</i>	0	0
<i>Ensifer</i>	0	0
<i>Breoghanian</i>	-0.013216374	0.013333333
<i>Arsenicococcus</i>	-0.038208092	0.011466667
<i>Priestia</i>	-0.046342855	0.019282407
<i>Aquicola</i>	-0.051392117	0.020990218
<i>Lysinibacillus</i>	-0.052697306	0.056772558
<i>Kinneretia</i>	-0.12146625	0.057352328
<i>Tistrella</i>	-0.158498849	0.030205025
<i>Candidatus Xiphinematobacter</i>	-0.24029854	0.045376852
<i>Pseudoxanthomonas</i>	-0.316984736	0.069951963
<i>Sulfurimicrobium</i>	-0.42594132	0.028749747
<i>Acinetobacter</i>	-0.438066394	0.011597576
<i>Natrinema</i>	-0.492863431	0.009328671
<i>Streptacidiphilus</i>	-0.566066968	0.008555556
<i>Sulfuricella</i>	-0.584462562	0.018765161
<i>Gulosibacter</i>	-0.786043763	0.018973372
<i>Geotalea</i>	-0.802403273	0.026171394
<i>Rhodocaloribacter</i>	-0.870245725	0.026555555
<i>Sutterella</i>	-0.883605848	0.051944849
<i>Guyaparkeria</i>	-1.001001503	0.058890634
<i>Rubrivivax</i>	-1.001001503	0.020978738
<i>Campylobacter</i>	-1.001001503	0.0166

<i>Planctopirus</i>	-1.001001503	0.014985185
<i>Paradevosia</i>	-1.001001503	0.0145869
<i>Ketogulonicigenium</i>	-1.001001503	0.010737116
<i>Xylanimonas</i>	-1.001001503	0.009246422
<i>Pantoea</i>	-1.001001503	0.008564706
<i>Ciceribacter</i>	-1.001001503	0.007684706
<i>Streptomonospora</i>	-1.001001503	0.007662959
<i>Arachidicoccus</i>	-1.001001503	0.007644411
<i>Beijerinckia</i>	-1.001001503	0.007578198
<i>Azorhizobium</i>	-1.001001503	0.006933333
<i>Aurantiacibacter</i>	-1.001001503	0.004770833
<i>Flavobacterium</i>	-1.138741801	0.021191101
<i>Caenibius</i>	-1.172355223	0.043534658
<i>Planococcus</i>	-1.349551596	0.056045705
<i>Euzebya</i>	-1.737084657	0.012925253

Supplementary Table 3. Detailed information of DESeq2 analysis.

Genus	baseMean	log2FoldChange	lfcSE	stat	pvalue	padj	NOF	OF
<i>Sphingobium</i>	45149.66	0.3058	0.0824	3.7129	0.000204893	0.000559088	1.000%	1.065%
<i>Massilia</i>	34500.61	0.9118	0.1077	8.4672	2.51349E-17	3.84673E-16	0.578%	0.877%
<i>Methylibium</i>	4939.03	0.6060	0.0867	6.9890	2.76825E-12	2.47735E-11	0.096%	0.125%
<i>Flavobacterium</i>	13075.03	1.9187	0.1620	11.8464	2.24758E-32	1.31858E-30	0.152%	0.427%
<i>Kocuria</i>	4597.19	-0.5043	0.1360	-3.7078	0.000209045	0.000567483	0.130%	0.068%
<i>Metabacillus</i>	3111.81	-1.3106	0.2206	-5.9422	2.81273E-09	1.66867E-08	0.103%	0.036%
<i>Rhodoplanes</i>	11165.57	0.2448	0.0927	2.6394	0.008306367	0.015497391	0.256%	0.262%
<i>Caulobacter</i>	11825.98	0.5817	0.0827	7.0325	2.0283E-12	1.86251E-11	0.238%	0.287%
<i>Aquicola</i>	8017.30	0.6112	0.0843	7.2467	4.26898E-13	4.25287E-12	0.153%	0.202%
<i>Aromatoleum</i>	4958.29	0.4560	0.1013	4.5039	6.673E-06	2.35675E-05	0.102%	0.120%
<i>Shinella</i>	15384.78	0.3062	0.0732	4.1812	2.89996E-05	9.56987E-05	0.330%	0.397%
<i>Aeromonas</i>	18330.35	1.3437	0.1324	10.1486	3.36129E-24	9.85978E-23	0.248%	0.472%
<i>Porphyrobacter</i>	4717.25	-1.1332	0.1369	-8.2766	1.26692E-16	1.80793E-15	0.156%	0.064%
<i>Paenibacillus</i>	111453.68	0.4130	0.1612	2.5622	0.010400562	0.018871122	2.323%	2.501%
<i>Azoarcus</i>	6094.54	0.5629	0.1037	5.4254	5.78364E-08	2.80162E-07	0.117%	0.151%
<i>Burkholderia</i>	26465.24	0.2115	0.0919	2.3011	0.021386739	0.035848248	0.611%	0.554%
<i>Microthlax</i>	4883.11	-0.7202	0.1090	-6.6087	3.87642E-11	3.00992E-10	0.150%	0.074%
<i>Hydrogenophaga</i>	49148.82	0.5220	0.0971	5.3748	7.66856E-08	3.64775E-07	0.967%	1.194%
<i>Bosea</i>	7018.12	0.2659	0.0704	3.7768	0.000158855	0.000443785	0.155%	0.152%
<i>Brevundimonas</i>	15208.72	1.2208	0.1135	10.7535	5.70807E-27	2.23249E-25	0.220%	0.413%
<i>Microbacterium</i>	35155.08	0.3029	0.0932	3.2505	0.00115219	0.002624842	0.736%	0.749%
<i>Xanthomonas</i>	19411.09	1.5039	0.1346	11.1744	5.4401E-29	2.49771E-27	0.237%	0.538%
<i>Pandoraea</i>	5312.91	0.3770	0.1000	3.7697	0.000163443	0.0004542	0.113%	0.124%

<i>Frateuria</i>	3194.21	0.6186	0.1569	3.9437	8.02219E-05	0.000242735	0.063%	0.114%
<i>Microvirga</i>	14465.57	-0.4920	0.1383	-3.5574	0.000374526	0.00095072	0.404%	0.234%
<i>Roseomonas</i>	9931.39	-0.1989	0.0830	-2.3947	0.016636058	0.028894207	0.256%	0.188%
<i>Nonomuraea</i>	9174.50	-0.3291	0.0969	-3.3971	0.000680979	0.001638072	0.245%	0.170%
<i>Clostridium</i>	21935.51	3.9038	0.2158	18.0917	3.70381E-73	3.91122E-70	0.060%	0.975%
<i>Skermanella</i>	35511.74	-0.4684	0.1387	-3.3766	0.000733782	0.001753108	0.966%	0.610%
<i>Priestia</i>	22139.12	0.8262	0.1461	5.6542	1.56552E-08	8.52161E-08	0.363%	0.559%
<i>Azospirillum</i>	5948.28	-0.3160	0.0673	-4.6936	2.68435E-06	9.94622E-06	0.164%	0.112%
<i>Kutzneria</i>	3976.10	-0.3869	0.1393	-2.7778	0.005472782	0.010702328	0.116%	0.069%
<i>Phytohabitans</i>	4140.73	-0.8702	0.1145	-7.5979	3.01089E-14	3.41882E-13	0.130%	0.059%
<i>Arthrobacter</i>	97940.02	1.2113	0.1251	9.6848	3.49757E-22	9.23359E-21	1.343%	2.489%
<i>Tetrasphaera</i>	3585.74	0.9865	0.1161	8.4992	1.90947E-17	2.96529E-16	0.057%	0.120%
<i>Tessaracoccus</i>	3686.68	-0.4852	0.0874	-5.5500	2.85633E-08	1.46422E-07	0.106%	0.063%
<i>Sphaerotilus</i>	18331.14	0.8222	0.1054	7.7975	6.31236E-15	7.66189E-14	0.315%	0.485%
<i>Sphingomonas</i>	87829.49	-0.4329	0.0711	-6.0925	1.1119E-09	7.07328E-09	2.581%	1.588%
<i>Sinorhizobium</i>	9716.76	-0.6251	0.1245	-5.0194	5.18265E-07	2.12952E-06	0.282%	0.139%
<i>Brevibacterium</i>	4456.89	-0.5699	0.1083	-5.2632	1.41558E-07	6.36105E-07	0.132%	0.067%
<i>Planctomyces</i>	5023.63	-0.1858	0.0762	-2.4372	0.014800924	0.02584372	0.132%	0.094%
<i>Marinobacter</i>	508.51	-0.2994	0.1189	-2.5172	0.01183014	0.021149226	0.111%	0.013%
<i>Geodermatophilus</i>	27510.81	0.3407	0.1700	2.0039	0.045075679	0.070894199	0.519%	0.504%
<i>Gordonia</i>	6743.81	-0.6970	0.0859	-8.1103	5.04764E-16	6.83373E-15	0.210%	0.102%
<i>Acidovorax</i>	39367.73	0.7695	0.0885	8.6966	3.42064E-18	5.82613E-17	0.696%	1.018%
<i>Ramlibacter</i>	8406.04	0.2221	0.0807	2.7527	0.005910592	0.01145245	0.189%	0.191%
<i>Sinomonas</i>	1473.65	0.8386	0.1713	4.8963	9.76582E-07	3.86244E-06	0.026%	0.160%
<i>Saccharopolyspora</i>	4816.71	0.2367	0.1146	2.0655	0.038875881	0.061919955	0.106%	0.096%
<i>Rubrivivax</i>	4402.09	0.9185	0.0980	9.3770	6.78482E-21	1.52442E-19	0.074%	0.117%

<i>Tardibacter</i>	3458.28	-1.1498	0.1280	-8.9822	2.65456E-19	5.00574E-18	0.123%	0.048%
<i>Pedococcus</i>	8585.26	1.1494	0.1324	8.6828	3.86058E-18	6.27195E-17	0.128%	0.211%
<i>Castellaniella</i>	3456.80	0.5161	0.1539	3.3532	0.00079897	0.001887499	0.066%	0.114%
<i>Pseudonocardia</i>	33453.56	-0.5876	0.0985	-5.9677	2.40688E-09	1.46917E-08	0.976%	0.536%
<i>Enterobacter</i>	18836.91	0.4815	0.1519	3.1697	0.001525827	0.003399311	0.385%	0.530%
<i>Rubrobacter</i>	7631.71	-0.8966	0.1679	-5.3385	9.37416E-08	4.38014E-07	0.219%	0.091%
<i>Phycococcus</i>	8714.73	1.0224	0.1269	8.0545	7.97803E-16	1.0531E-14	0.133%	0.237%
<i>Paenarthrobacter</i>	8115.11	0.6955	0.1280	5.4334	5.53038E-08	2.71631E-07	0.144%	0.180%
<i>Methylobacterium</i>	13473.59	-0.2673	0.0854	-3.1311	0.001741525	0.003776817	0.364%	0.262%
<i>Pedobacter</i>	2263.09	1.6965	0.1815	9.3443	9.24831E-21	2.03463E-19	0.026%	0.120%
<i>Rhodoferax</i>	25462.70	0.4863	0.0945	5.1453	2.67034E-07	1.16044E-06	0.516%	0.639%
<i>Mycolicibacterium</i>	48592.65	0.4611	0.0719	6.4126	1.43025E-10	1.0069E-09	0.969%	1.149%
<i>Anaeromyxobacter</i>	26620.72	2.2065	0.1610	13.7040	9.60214E-43	1.26748E-40	0.206%	0.868%
<i>Pannonibacter</i>	3974.26	-0.2794	0.1409	-1.9834	0.047318265	0.073808106	0.101%	0.074%
<i>Hypericibacter</i>	4829.24	0.6983	0.1286	5.4303	5.62456E-08	2.73711E-07	0.086%	0.129%
<i>Ideonella</i>	7391.27	1.0026	0.1208	8.3020	1.02413E-16	1.48148E-15	0.118%	0.200%
<i>Nocardiosis</i>	2675.91	0.3065	0.1318	2.3248	0.020082188	0.033930864	0.057%	0.174%
<i>Pseudarthrobacter</i>	24649.40	0.6912	0.1467	4.7109	2.46584E-06	9.26665E-06	0.424%	0.506%
<i>Pelobacter</i>	3387.15	1.8131	0.2325	7.7983	6.27241E-15	7.66189E-14	0.033%	0.101%
<i>Iamia</i>	4691.21	-0.2226	0.0945	-2.3562	0.018465455	0.031501648	0.119%	0.092%
<i>Chryseobacterium</i>	7391.22	1.8611	0.1618	11.4989	1.33665E-30	6.72142E-29	0.079%	0.243%
<i>Pantoea</i>	5025.65	1.4065	0.1877	7.4933	6.71678E-14	7.23767E-13	0.088%	0.414%
<i>Actinoplanes</i>	25716.51	-0.4707	0.1026	-4.5895	4.44337E-06	1.60692E-05	0.745%	0.432%
<i>Epidermidibacterium</i>	4683.41	-0.6229	0.1572	-3.9621	7.43082E-05	0.000228109	0.142%	0.077%
<i>Stenotrophomonas</i>	47820.47	1.2907	0.1101	11.7182	1.02781E-31	5.71249E-30	0.642%	1.264%
<i>Gemmata</i>	4659.15	-0.4620	0.0869	-5.3142	1.07151E-07	4.9628E-07	0.133%	0.076%

<i>Delftia</i>	19573.52	0.7224	0.0933	7.7448	9.57185E-15	1.1231E-13	0.352%	0.460%
<i>Caballeronia</i>	8166.58	-0.3535	0.1382	-2.5585	0.010512708	0.019041885	0.235%	0.156%
<i>Agrobacterium</i>	12199.97	1.7041	0.1407	12.1099	9.36117E-34	6.59027E-32	0.133%	0.375%
<i>Phenylobacterium</i>	13651.31	0.4202	0.0805	5.2176	1.8127E-07	8.0429E-07	0.289%	0.330%
<i>Croceicoccus</i>	5028.20	-0.5607	0.0979	-5.7258	1.02948E-08	5.69179E-08	0.151%	0.086%
<i>Geobacter</i>	4231.02	1.7232	0.1598	10.7843	4.08191E-27	1.7242E-25	0.043%	0.130%
<i>Methylobacterium</i>	4616.36	-0.2413	0.0779	-3.0974	0.001952198	0.00416469	0.120%	0.085%
<i>Lysobacter</i>	42313.51	0.3633	0.1111	3.2699	0.001075844	0.002459072	0.880%	0.959%
<i>Pseudomonas</i>	157997.61	0.9935	0.1038	9.5736	1.03226E-21	2.59645E-20	2.558%	3.803%
<i>Devosia</i>	8350.53	0.5774	0.1182	4.8855	1.03177E-06	4.06549E-06	0.143%	0.199%
<i>Gemmatirosa</i>	15979.79	-0.8511	0.1130	-7.5311	5.03218E-14	5.5354E-13	0.528%	0.241%
<i>Stutzerimonas</i>	6418.68	0.2572	0.1256	2.0471	0.040653109	0.064458984	0.146%	0.134%
<i>Rhizorhabdus</i>	13711.20	-0.5676	0.0728	-7.7982	6.28084E-15	7.66189E-14	0.422%	0.250%
<i>Nocardia</i>	10620.74	-0.2824	0.0793	-3.5600	0.000370903	0.000943791	0.285%	0.189%
<i>Thauera</i>	24445.50	0.4228	0.1226	3.4496	0.000561417	0.001378736	0.474%	0.580%
<i>Erythrobacter</i>	4423.17	-0.5465	0.0834	-6.5487	5.80323E-11	4.40878E-10	0.133%	0.075%
<i>Sphingopyxis</i>	19731.57	0.3293	0.1006	3.2728	0.001064741	0.002444276	0.423%	0.472%
<i>Schlegelella</i>	4665.87	0.3146	0.0813	3.8708	0.000108492	0.000319129	0.102%	0.109%
<i>Cellulomonas</i>	18810.77	-0.3748	0.0875	-4.2823	1.84948E-05	6.23978E-05	0.513%	0.322%
<i>Pimelobacter</i>	4338.60	-0.2397	0.0859	-2.7909	0.005255521	0.010296532	0.114%	0.084%
<i>Peribacillus</i>	5950.49	-0.3181	0.1550	-2.0519	0.040182127	0.063808009	0.146%	0.107%
<i>Intrasporangium</i>	4650.98	1.6474	0.1323	12.4498	1.40223E-35	1.13904E-33	0.052%	0.129%
<i>Alicyclophila</i>	12868.80	0.3895	0.1067	3.6514	0.000260804	0.000686806	0.264%	0.304%
<i>Archangium</i>	11519.64	-0.3923	0.1055	-3.7188	0.000200141	0.000547537	0.314%	0.211%
<i>Luteitalea</i>	12936.70	-0.4206	0.0791	-5.3144	1.07027E-07	4.9628E-07	0.370%	0.244%
<i>Enterococcus</i>	1291.15	-0.7286	0.2702	-2.6961	0.007015291	0.013300084	0.116%	0.038%

<i>Rhodanobacter</i>	8253.21	1.2614	0.1625	7.7628	8.30574E-15	9.85489E-14	0.117%	0.384%
<i>Bacillus</i>	97284.91	0.8658	0.1329	6.5169	7.1762E-11	5.33666E-10	1.562%	2.314%
<i>Pseudolabrys</i>	11257.42	0.7262	0.1185	6.1282	8.88683E-10	5.7929E-09	0.207%	0.299%
<i>Aerosticca</i>	8915.19	0.5452	0.1716	3.1764	0.001491183	0.003329153	0.178%	0.223%
<i>Cupriavidus</i>	47104.94	0.2989	0.0895	3.3382	0.00084311	0.001969743	1.056%	1.163%
<i>Corynebacterium</i>	13986.61	0.3612	0.1302	2.7741	0.005536223	0.010786442	0.286%	0.290%
<i>Azospira</i>	7596.65	0.9930	0.1253	7.9277	2.2317E-15	2.90948E-14	0.118%	0.205%
<i>Bradyrhizobium</i>	221665.82	0.2821	0.0734	3.8439	0.000121109	0.00034943	4.983%	5.297%
<i>Aureimonas</i>	3592.14	-0.3495	0.0705	-4.9539	7.27449E-07	2.94324E-06	0.101%	0.068%
<i>Luteimonas</i>	5912.93	0.6267	0.1053	5.9514	2.65853E-09	1.59512E-08	0.121%	0.242%
<i>Thermomonas</i>	5961.61	0.7059	0.1133	6.2298	4.66978E-10	3.20214E-09	0.108%	0.146%
<i>Couchioplanes</i>	5809.01	-0.4893	0.1272	-3.8476	0.000119299	0.000345149	0.167%	0.094%
<i>Denitratisoma</i>	4456.29	0.5931	0.1467	4.0431	5.27566E-05	0.000165314	0.084%	0.111%
<i>Kinneretia</i>	4631.25	0.2925	0.0632	4.6307	3.64475E-06	1.32719E-05	0.103%	0.107%
<i>Catellatospora</i>	6848.84	-0.3191	0.1101	-2.8983	0.003751366	0.007502732	0.177%	0.121%
<i>Jiangella</i>	3828.67	-0.7132	0.1092	-6.5323	6.47629E-11	4.88497E-10	0.115%	0.057%
<i>Rhizobacter</i>	9373.16	1.0036	0.0932	10.7725	4.64184E-27	1.8853E-25	0.152%	0.258%
<i>Nakamurella</i>	4434.27	0.8634	0.1109	7.7850	6.97264E-15	8.36716E-14	0.077%	0.125%
<i>Lentzea</i>	16303.79	0.3911	0.1479	2.6443	0.008185298	0.015298539	0.334%	0.350%
<i>Cellulosimicrobium</i>	9875.42	0.4032	0.1368	2.9467	0.003212356	0.006561408	0.197%	0.244%
<i>Rhodopseudomonas</i>	5379.70	0.2511	0.0728	3.4487	0.000563193	0.001379887	0.123%	0.123%
<i>Comamonas</i>	37871.20	0.8449	0.1171	7.2158	5.36066E-13	5.24153E-12	0.644%	1.025%
<i>Thiobacillus</i>	5415.20	3.0047	0.2057	14.6051	2.60787E-48	9.17971E-46	0.032%	0.190%
<i>Corallococcus</i>	4443.94	-0.1372	0.0680	-2.0177	0.043623271	0.068858258	0.114%	0.089%
<i>Mycobacterium</i>	44795.37	0.6571	0.0783	8.3967	4.59271E-17	6.83085E-16	0.825%	1.159%

Supplementary Table 4. **Shared and specific ARG subtypes in NOF and OF.**

Uniq ARG subtypes of NOF	Shared ARG subtypes	Uniq ARG subtypes of OF
<i>beta-lactam__blaZ</i>	<i>aminoglycoside__aac(2')-I</i>	<i>aminoglycoside__aac(3)-IX</i>
<i>beta-lactam__CARB-6</i>	<i>aminoglycoside__aac(3)-I</i>	<i>aminoglycoside__aac(3)-VI</i>
<i>beta-lactam__class D beta-lactamase</i>	<i>aminoglycoside__aac(3)-II</i>	<i>aminoglycoside__ant(3'')-Ih-aac(6')-IId</i>
<i>beta-lactam__CMY-100</i>	<i>aminoglycoside__aac(3)-IIIa</i>	<i>aminoglycoside__aph(2'')-Ie</i>
<i>beta-lactam__CTX-M-131</i>	<i>aminoglycoside__aac(3)-IV</i>	<i>aminoglycoside__aph(2'')-IV</i>
<i>beta-lactam__CTX-M-68</i>	<i>aminoglycoside__aac(3)-VII</i>	<i>aminoglycoside__rmtB</i>
<i>beta-lactam__IMP-27</i>	<i>aminoglycoside__aac(3)-VIII</i>	<i>aminoglycoside__streptomycin_resistance_protein</i>
<i>beta-lactam__IMP-4</i>	<i>aminoglycoside__aac(3)-X</i>	<i>aminoglycoside__tunicamycin_resistance_protein</i>
<i>beta-lactam__IND-15</i>	<i>aminoglycoside__aac(6')-3I</i>	<i>beta-lactam__ACT-13</i>
<i>beta-lactam__IND-7</i>	<i>aminoglycoside__aac(6')-I</i>	<i>beta-lactam__ACT-14</i>
<i>beta-lactam__LRA-8</i>	<i>aminoglycoside__aac(6')-II</i>	<i>beta-lactam__ACT-19</i>
<i>beta-lactam__OKP-A</i>	<i>aminoglycoside__aad(6)</i>	<i>beta-lactam__ACT-20</i>
<i>beta-lactam__OXA-117</i>	<i>aminoglycoside__aad(9)</i>	<i>beta-lactam__ACT-21</i>
<i>beta-lactam__OXA-20</i>	<i>aminoglycoside__aadA</i>	<i>beta-lactam__ACT-23</i>
<i>beta-lactam__OXA-214</i>	<i>aminoglycoside__aadB</i>	<i>beta-lactam__blaI</i>
<i>beta-lactam__OXA-230</i>	<i>aminoglycoside__aadD</i>	<i>beta-lactam__CARB-8</i>
<i>beta-lactam__OXA-82</i>	<i>aminoglycoside__aadE</i>	<i>beta-lactam__CfxA3</i>
<i>beta-lactam__OXA-94</i>	<i>aminoglycoside__aadK</i>	<i>beta-lactam__class B beta-lactamase</i>
<i>beta-lactam__TEM-112</i>	<i>aminoglycoside__ant(2'')-I</i>	<i>beta-lactam__CMY-40</i>
<i>beta-lactam__TEM-120</i>	<i>aminoglycoside__ant(4')-Ia</i>	<i>beta-lactam__CMY-44</i>
<i>beta-lactam__TEM-125</i>	<i>aminoglycoside__ant(9)-I</i>	<i>beta-lactam__CMY-61</i>
<i>beta-lactam__TEM-127</i>	<i>aminoglycoside__aph(2'')-II</i>	<i>beta-lactam__CMY-78</i>
<i>beta-lactam__TEM-128</i>	<i>aminoglycoside__aph(2'')-III</i>	<i>beta-lactam__CMY-9</i>
<i>beta-lactam__TEM-130</i>	<i>aminoglycoside__aph(3')-I</i>	<i>beta-lactam__CTX-M</i>
<i>beta-lactam__TEM-136</i>	<i>aminoglycoside__aph(3'')-I</i>	<i>beta-lactam__DHA-6</i>
<i>beta-lactam__TEM-141</i>	<i>aminoglycoside__aph(3')-IIb</i>	<i>beta-lactam__fmtC</i>

<i>beta-lactam__TEM-145</i>	<i>aminoglycoside__aph(3''')-III</i>	<i>beta-lactam__FONA-6</i>
<i>beta-lactam__TEM-147</i>	<i>aminoglycoside__aph(4)-I</i>	<i>beta-lactam__FOX-1</i>
<i>beta-lactam__TEM-148</i>	<i>aminoglycoside__aph(6)-I</i>	<i>beta-lactam__FOX-5</i>
<i>beta-lactam__TEM-156</i>	<i>aminoglycoside__streptothricin_acetyltransferase</i>	<i>beta-lactam__FOX-9</i>
<i>beta-lactam__TEM-159</i>	<i>aminoglycoside__viomycin_phosphotransferase</i>	<i>beta-lactam__IMP-15</i>
<i>beta-lactam__TEM-162</i>	<i>bacitracin__bacA</i>	<i>beta-lactam__IMP-16</i>
<i>beta-lactam__TEM-166</i>	<i>bacitracin__bcrA</i>	<i>beta-lactam__IMP-22</i>
<i>beta-lactam__TEM-169</i>	<i>beta-lactam__ACT-16</i>	<i>beta-lactam__IMP-31</i>
<i>beta-lactam__TEM-182</i>	<i>beta-lactam__AER-1</i>	<i>beta-lactam__IMP-32</i>
<i>beta-lactam__TEM-183</i>	<i>beta-lactam__ampC</i>	<i>beta-lactam__IMP-44</i>
<i>beta-lactam__TEM-193</i>	<i>beta-lactam__blaR1</i>	<i>beta-lactam__IND-4</i>
<i>beta-lactam__TEM-208</i>	<i>beta-lactam__CARB-12</i>	<i>beta-lactam__LEN-1</i>
<i>beta-lactam__TEM-54</i>	<i>beta-lactam__CfxA2</i>	<i>beta-lactam__LEN-15</i>
<i>beta-lactam__TEM-67</i>	<i>beta-lactam__CGB-1</i>	<i>beta-lactam__LEN-17</i>
<i>beta-lactam__TEM-83</i>	<i>beta-lactam__class A beta-lactamase</i>	<i>beta-lactam__LEN-21</i>
<i>beta-lactam__TEM-90</i>	<i>beta-lactam__class C beta-lactamase</i>	<i>beta-lactam__LEN-5</i>
<i>beta-lactam__TEM-95</i>	<i>beta-lactam__CMY-1</i>	<i>beta-lactam__mecA</i>
<i>beta-lactam__TEM-96</i>	<i>beta-lactam__CMY-19</i>	<i>beta-lactam__mecR1</i>
<i>trimethoprim__dfrA22</i>	<i>beta-lactam__CMY-98</i>	<i>beta-lactam__MIR-2</i>
<i>unclassified__patB</i>	<i>beta-lactam__FEZ-1</i>	<i>beta-lactam__MOX-1</i>
	<i>beta-lactam__GOB-1</i>	<i>beta-lactam__MOX-5</i>
	<i>beta-lactam__IMP-11</i>	<i>beta-lactam__MOX-6</i>
	<i>beta-lactam__IMP-13</i>	<i>beta-lactam__MOX-7</i>
	<i>beta-lactam__IMP-33</i>	<i>beta-lactam__MUS-1</i>
	<i>beta-lactam__IMP-7</i>	<i>beta-lactam__OCH-8</i>
	<i>beta-lactam__IMP-8</i>	<i>beta-lactam__OXA-1</i>
	<i>beta-lactam__IND-1</i>	<i>beta-lactam__OXA-11</i>
	<i>beta-lactam__IND-14</i>	<i>beta-lactam__OXA-118</i>

*beta-lactam*__IND-3
*beta-lactam*__IND-5
*beta-lactam*__IND-8
*beta-lactam*__IND-9
*beta-lactam*__JOHN-1
*beta-lactam*__KHM-1
*beta-lactam*__LRA-1
*beta-lactam*__LRA-12
*beta-lactam*__LRA-13
*beta-lactam*__LRA-17
*beta-lactam*__LRA-19
*beta-lactam*__LRA-2
*beta-lactam*__LRA-3
*beta-lactam*__LRA-5
*beta-lactam*__LRA-9
*beta-lactam*__*mecI*
*beta-lactam*__metallo-beta-lactamase
*beta-lactam*__MOX-4
*beta-lactam*__OXA-10
*beta-lactam*__OXA-114
*beta-lactam*__OXA-129
*beta-lactam*__OXA-205
*beta-lactam*__OXA-209
*beta-lactam*__OXA-211
*beta-lactam*__OXA-22
*beta-lactam*__OXA-236
*beta-lactam*__OXA-278
*beta-lactam*__OXA-29
*beta-lactam*__OXA-333
*beta-lactam*__OXA-334

*beta-lactam*__OXA-119
*beta-lactam*__OXA-12
*beta-lactam*__OXA-142
*beta-lactam*__OXA-145
*beta-lactam*__OXA-161
*beta-lactam*__OXA-18
*beta-lactam*__OXA-2
*beta-lactam*__OXA-21
*beta-lactam*__OXA-212
*beta-lactam*__OXA-213
*beta-lactam*__OXA-237
*beta-lactam*__OXA-243
*beta-lactam*__OXA-258
*beta-lactam*__OXA-3
*beta-lactam*__OXA-309
*beta-lactam*__OXA-324
*beta-lactam*__OXA-325
*beta-lactam*__OXA-327
*beta-lactam*__OXA-349
*beta-lactam*__OXA-350
*beta-lactam*__OXA-352
*beta-lactam*__OXA-354
*beta-lactam*__OXA-358
*beta-lactam*__OXA-359
*beta-lactam*__OXA-361
*beta-lactam*__OXA-4
*beta-lactam*__OXA-56
*beta-lactam*__OXA-62
*beta-lactam*__OXA-7
*beta-lactam*__OXA-96

beta-lactam__OXA-335
beta-lactam__OXA-34
beta-lactam__OXA-36
beta-lactam__OXA-5
beta-lactam__OXA-50
beta-lactam__OXA-53
beta-lactam__OXA-58
beta-lactam__OXA-60
beta-lactam__OXA-9
beta-lactam__PBP-1A
beta-lactam__PBP-1B
beta-lactam__penA
beta-lactam__PSE-1
beta-lactam__SHV-1
beta-lactam__SHV-53
beta-lactam__SMB-1
beta-lactam__TEM-1

beta-lactam__TEM-102

beta-lactam__TEM-117

beta-lactam__TEM-124
beta-lactam__TEM-157
beta-lactam__TEM-171
beta-lactam__TEM-178
beta-lactam__TEM-187
beta-lactam__TEM-197
beta-lactam__TEM-30
beta-lactam__TEM-89
beta-lactam__THIN-B

beta-lactam__OXY-1
beta-lactam__OXY-2
beta-lactam__OXY-5
beta-lactam__PER-2
beta-lactam__PER-3
beta-lactam__RTG-4
beta-lactam__SHV
beta-lactam__SHV-105
beta-lactam__SHV-112
beta-lactam__SHV-12
beta-lactam__SHV-39
beta-lactam__SHV-6
beta-lactam__TEM-186
beta-lactam__VEB-1
bleomycin__bleomycin_resistance_protein
chloramphenicol__catD
chloramphenicol__catS
chloramphenicol__chloramphenicol_and_florfenicol
resistance_gene
chloramphenicol__chloramphenicol_and_florfenicol_ex
porter
MLS__lmrP
MLS__msrC
MLS__vatE
MLS__vgbA
multidrug__mtrE
multidrug__qacA
multidrug__qacG
polymyxin__mcr-1.5
polymyxin__mcr-3

bleomycin__bleO
carbomycin__carA
chloramphenicol__cat
chloramphenicol__catA
chloramphenicol__catB
chloramphenicol__catQ
chloramphenicol__cmlA
chloramphenicol__cmrA
chloramphenicol__floR
fosfomycin__fosA
fosfomycin__fosB
fosfomycin__fosX
fosmidomycin__rosA
fosmidomycin__rosB
fusidic-acid__fusH

kasugamycin__ksgA
MLS__ereA
MLS__erm(31)
MLS__erm(33)
MLS__erm(35)
MLS__erm(36)
MLS__erm(38)
MLS__erm(39)
MLS__erm(TR)
MLS__ermA
MLS__ermB
MLS__ermC
MLS__ermE
MLS__ermF

puromycin__puromycin_resistance_protein
quinolone__qnrB
quinolone__qnrS
spectinomycin__spcN
sulfonamide__sul3
tetracycline__tet34
tetracycline__tetD
tetracycline__tetE
tetracycline__tetJ
trimethoprim__dfrA12
trimethoprim__dfrA13
trimethoprim__dfrA16
trimethoprim__dfrA17
unclassified__16S_rRNA_methylase
unclassified__antibiotic resistance rRNA adenine methyltransferase
unclassified__EvgA
unclassified__tmrB
vancomycin__vanC
vancomycin__vanT

MLS__ermG
MLS__ermO
MLS__ermT
MLS__ermX
MLS__lmrA
MLS__lmrB
MLS__lnuA
MLS__lnuB
MLS__lsa
MLS__macA
MLS__macB
MLS__mefA
MLS__mgtA
MLS__mphA
MLS__mphB
MLS__mphC
MLS__msrA
MLS__oleB
MLS__oleD
MLS__srmB
MLS__tlcC
MLS__vatA
MLS__vatB
MLS__vatG
MLS__vgaA
MLS__vgaD
MLS__vgaE
multidrug__abeS
multidrug__acrA
multidrug__acrB

multidrug__adeA
multidrug__adeB
multidrug__adeC
multidrug__adeJ
multidrug__adeK
multidrug__amrB
multidrug__bcr
multidrug__bpeE
multidrug__bpeF
multidrug__ceoB
multidrug__cmeB
multidrug__emrA
multidrug__emrB
multidrug__EmrB-QacA
multidrug__emrD
multidrug__emrE
multidrug__emrK
multidrug__major_facilitator_superfamily_transporter
multidrug__mdfA
multidrug__mdtA
multidrug__mdtB
multidrug__mdtC
multidrug__mdtD
multidrug__mdtE
multidrug__mdtF
multidrug__mdtG
multidrug__mdtH
multidrug__mdtK
multidrug__mdtL
multidrug__mdtM

multidrug__mdtN
multidrug__mdtO
multidrug__mdtP
multidrug__mepA
multidrug__mexA
multidrug__mexB
multidrug__mexC
multidrug__mexD
multidrug__mexE
multidrug__mexF
multidrug__mexG
multidrug__mexI
multidrug__mexT
multidrug__mexW
multidrug__mexY
multidrug__multidrug_ABC_transporter
multidrug__multidrug_transporter
multidrug__norA
multidrug__opcM
multidrug__opmD
multidrug__oprA
multidrug__oprC
multidrug__oprJ
multidrug__oprM
multidrug__oprN
multidrug__pmrA
multidrug__qacB
multidrug__qacEdelta1
multidrug__sdeY
multidrug__smeB

multidrug__smeC
multidrug__smeD
multidrug__smeE
multidrug__smeF
multidrug__TolC
multidrug__ykkC
multidrug__ykkD
polymyxin__arnA
polymyxin__icr-Mo
polymyxin__mcr-5
quinolone__abaQ
quinolone__mfpA
quinolone__norB
quinolone__qepA
rifamycin__arr
rifamycin__rifampin_monooxygenase
sulfonamide__sul1
sulfonamide__sul2
sulfonamide__sul4
tetracenomycin_C__tcmA
tetracycline__otrA
tetracycline__tcr3
tetracycline__tet31
tetracycline__tet32
tetracycline__tet35
tetracycline__tet36
tetracycline__tet39
tetracycline__tet40
tetracycline__tet41
tetracycline__tet43

tetracycline__tet44
tetracycline__tetA
tetracycline__tetB
tetracycline__tetC
tetracycline__tetG
tetracycline__tetH
tetracycline__tetK
tetracycline__tetL
tetracycline__tetM
tetracycline__tetO
tetracycline__tetP
tetracycline__tetQ
tetracycline__tetR
tetracycline__tetracycline_resistance_protein
tetracycline__tetS
tetracycline__tetT
tetracycline__tetV
tetracycline__tetW
tetracycline__tetX
tetracycline__tetX1
tetracycline__tetX2
tetracycline__tetX3
tetracycline__tetX4
tetracycline__tetX5
tetracycline__tetY
tetracycline__tetZ
trimethoprim__dfrA1
trimethoprim__dfrA14
trimethoprim__dfrA15
trimethoprim__dfrA20

trimethoprim__dfrA5
trimethoprim__dfrB1
trimethoprim__dfrB2
trimethoprim__dfrB3
trimethoprim__dfrB6
unclassified__ArlR
unclassified__cAMP-regulatory_protein
unclassified__cob(I)alamin_adenolsyltransferase
unclassified__cpxR
unclassified__EvgA
unclassified__gadX
unclassified__H-NS
unclassified__LuxR
unclassified__rpsD
unclassified__sdiA
unclassified__tsnR
vancomycin__vanA
vancomycin__vanB
vancomycin__vanD
vancomycin__vanE
vancomycin__vanG
vancomycin__vanH
vancomycin__vanM
vancomycin__vanR
vancomycin__vanS
vancomycin__vanW
vancomycin__vanX
vancomycin__vanY
vancomycin__vanZ

Supplementary Table 5. **Shared and specific MRG subtypes in NOF and OF.**

Uniq MRG subtypes of NOF	Shared MRG subtypes	Uniq MRG subtypes of OF
<i>Copper(Cu)__CopH</i>	<i>Mercury(Hg)__merD</i>	<i>Lead(Pb)__pbrD</i>
<i>multimetal__cnrH</i>	<i>multimetal__fecE</i>	<i>Copper(Cu)__cueP</i>
<i>Iron(Fe)__pmrB</i>	<i>multimetal__golT</i>	<i>Mercury(Hg)__merB1</i>
<i>Zinc(Zn)__zraP</i>	<i>Arsenic(As)__aioA</i>	<i>Cadmium(Cd)__frnE</i>
<i>Copper(Cu)__copV</i>	<i>multimetal__kmtR</i>	<i>Tungsten(W)__tupB</i>
	<i>multimetal__dsbA</i>	<i>multimetal__fptA</i>
	<i>Copper(Cu)__corR</i>	<i>Mercury(Hg)__merB2</i>
	<i>Copper(Cu)__pcoD</i>	<i>multimetal__nccB</i>
	<i>Gold(Au)__gesB</i>	<i>Lead(Pb)__pbrB/pbrC</i>
	<i>Zinc(Zn)__soxS</i>	<i>Mercury(Hg)__merH</i>
	<i>Zinc(Zn)__znuB/yebI</i>	<i>Mercury(Hg)__merB3</i>
	<i>multimetal__fieF/yiip</i>	<i>multimetal__irlS</i>
	<i>multimetal__yfeC</i>	<i>multimetal__trgB</i>
	<i>Arsenic(As)__arsC</i>	<i>Nickel(Ni)__nirD</i>
	<i>Selenium(Se)__sodB</i>	<i>multimetal__fbpB</i>
	<i>Copper(Cu)__mmco</i>	<i>Tellurium(Te)__terW</i>
	<i>Nickel(Ni)__nirC</i>	<i>Silver(Ag)__silE</i>
	<i>Chromium(Cr)__srpC</i>	<i>multimetal__cnrR/cnrX</i>
	<i>multimetal__troB</i>	<i>Iron(Fe)__pmrC</i>
	<i>Tellurium(Te)__tehB</i>	<i>Copper(Cu)__ycnK</i>
	<i>Copper(Cu)__cuiD</i>	<i>Tellurium(Te)__terZ</i>
	<i>Copper(Cu)__cutE/lnt</i>	<i>multimetal__fecD</i>
	<i>Manganese(Mn)__mntP/yebN</i>	<i>Arsenic(As)__aioE</i>

multimetal__modE
multimetal__dmeF
Tellurium(Te)__terE
Nickel(Ni)__nikC
Zinc(Zn)__mdtB
Chromium(Cr)__chrC
multimetal__zupT/ygiE
Mercury(Hg)__merP
Copper(Cu)__CopC
multimetal__czcA
Cadmium(Cd)__yodD
multimetal__actA
Copper(Cu)__cusS
multimetal__cnrA
Arsenic(As)__pstB
Copper(Cu)__copS
multimetal__ctpC
Nickel(Ni)__nikR
Arsenic(As)__aioX/aoxX
multimetal__nmtR
Chromium(Cr)__chrR
Copper(Cu)__CusC
multimetal__cusC/ylcB
multimetal__czcD
Iron(Fe)__pmrA
Iron(Fe)__acn

Zinc(Zn)__zneB/hmxB
Copper(Cu)__copY/tcrY
Chromium(Cr)__chrI
Zinc(Zn)__smtB/ziaR
Tungsten(W)__tupC
multimetal__nccH
multimetal__cztB
Nickel(Ni)__hupE
Gold(Au)__gesC
multimetal__smtA
multimetal__pgpA/ltpgpA
Copper(Cu)__copZ
multimetal__nccC
Tellurium(Te)__trgA
Copper(Cu)__tcrZ
multimetal__cznA

Tellurium(Te) __klaB/telA/kilB
Arsenic(As) __arsR
Lead(Pb) __pbrA
multimetal __mgtA
Arsenic(As) __arsR4
Arsenic(As) __arsM
multimetal __pitA
Copper(Cu) __csoR
Iron(Fe) __dpr/dps
multimetal __modB
Zinc(Zn) __zitB/ybgR
Iron(Fe) __fetA/ybbL
Nickel(Ni) __nrsS
multimetal __corC
Arsenic(As) __arsH
multimetal __cueA
Copper(Cu) __pcoA
Copper(Cu) __Cop_restriction_enzyme
multimetal __rcnB/yohN
Copper(Cu) __cutA
multimetal __sitB
Copper(Cu) __actP
multimetal __czcP
Mercury(Hg) __merA
Copper(Cu) __copL
multimetal __nrsD/nreB

Silver(Ag)__silS
Copper(Cu)__yfmP
Tellurium(Te)__terB
Arsenic(As)__acr3
Copper(Cu)__CopF
Iron(Fe)__ybtP
Chromium(Cr)__chrA
Nickel(Ni)__nikA
Nickel(Ni)__hoxN
Copper(Cu)__copB
Arsenic(As)__pstS
Cadmium(Cd)__yjaA
multimetal__ctpD
Copper(Cu)__tcrY
multimetal__acrD
Copper(Cu)__copG
Copper(Cu)__CopA
multimetal__czcC
Copper(Cu)__ctpV
Nickel(Ni)__nirA
Lead(Pb)__pbrR
Iron(Fe)__bfrA
Aluminium(Al)__ALU1-P
multimetal__cztA
multimetal__arsA
multimetal__yfeA

Iron(Fe)__dpsA
Copper(Cu)__cueR
multimetal__corD
Copper(Cu)__dsbC
multimetal__nia
Chromium(Cr)__oscA
Nickel(Ni)__hupE2
Copper(Cu)__pcoR
multimetal__zinT/yodA
Mercury(Hg)__merR
Copper(Cu)__CueO
multimetal__nczA
Copper(Cu)__tcrB
Silver(Ag)__silB
Arsenic(As)__arrB
Cadmium(Cd)__ygiW
Nickel(Ni)__ncrB
multimetal__corA
multimetal__perO
Arsenic(As)__arsP
Copper(Cu)__cutC
Chromium(Cr)__chrB1
Silver(Ag)__silF
Copper(Cu)__pcoC
Arsenic(As)__arsD
multimetal__yfeD

Arsenic(As)__aioR/aoxR
Copper(Cu)__comR/ycfQ
Nickel(Ni)__nikD
Copper(Cu)__CusA
Iron(Fe)__furA
multimetal__baeS
Copper(Cu)__cusB
multimetal__actR
multimetal__cmtR
Copper(Cu)__ycnJ
Nickel(Ni)__ncrY
multimetal__czcR
Copper(Cu)__CopD
Gold(Au)__golS
multimetal__zipB
Tellurium(Te)__terD
Arsenic(As)__arsR1
multimetal__rcnR/yohL
multimetal__mrdH
Silver(Ag)__silC
Aluminium(Al)__G2alt
multimetal__glpF
Vanadium(V)__mexI
multimetal__zntA/yhhO
Copper(Cu)__hmrR
multimetal__sitD

Arsenic(As)__arsC2
multimetal__cadC
Iron(Fe)__ideR
Copper(Cu)__corS
Mercury(Hg)__merF
multimetal__dsbB
Tellurium(Te)__tehA
Zinc(Zn)__zntR/yhdM
Copper(Cu)__cueR/ybbI
multimetal__robA
multimetal__troA
Copper(Cu)__pcoE
Nickel(Ni)__hupN
Selenium(Se)__sodA
Chromium(Cr)__ruvB
multimetal__nreB
multimetal__mntH/yfeP
multimetal__czcB
Cadmium(Cd)__ychH
Zinc(Zn)__zraR/hydH
Cadmium(Cd)__yhcn
Mercury(Hg)__merE
multimetal__cmeB
Zinc(Zn)__mdtA
Tungsten(W)__tupA
Cobalt(Co)__nhfF

Copper(Cu)__copM
Mercury(Hg)__merT-P
Copper(Cu)__Cop-unnamed
Copper(Cu)__Cop_inner_membrane
Mercury(Hg)__merT
Copper(Cu)__copR
multimetal__mreA
Arsenic(As)__pstA
multimetal__fbpC
Copper(Cu)__cinA
Copper(Cu)__CopB-like
Chromium(Cr)__nfsA
Zinc(Zn)__ziaA
multimetal__rcnA/yohM
multimetal__sitA
Arsenic(As)__arsR2
Cadmium(Cd)__cadR
multimetal__cusF/cusX
Arsenic(As)__arsI
Copper(Cu)__pcoB
multimetal__yieF
Nickel(Ni)__nrsR
multimetal__nccA
multimetal__modA
Lead(Pb)__pbrT
Mercury(Hg)__merG

multimetal__cadX
Cobalt(Co)__corT/coaT
Nickel(Ni)__ncrC
Arsenic(As)__arsC1
Silver(Ag)__silR
Mercury(Hg)__merB
Copper(Cu)__mctB
multimetal__cnrT
multimetal__czcE
Copper(Cu)__cutF/nlpE
Mercury(Hg)__merR2
multimetal__mntR
Zinc(Zn)__mdtC
Nickel(Ni)__nikB
Arsenic(As)__arsR3
Chromium(Cr)__chrB
Arsenic(As)__aioS/aoxS
Arsenic(As)__arsB
multimetal__yfeB
Copper(Cu)__bhsA/ycfR/comC
multimetal__dmeR
Copper(Cu)__copJ
Copper(Cu)__CusF
Zinc(Zn)__ziaR
Copper(Cu)__Cop_response_transcription_regulator
Copper(Cu)__pcoS

multimetal__yqjH
Chromium(Cr)__recG
Arsenic(As)__arsT
Nickel(Ni)__nrsA
Copper(Cu)__tcrA
Silver(Ag)__silA
multimetal__cusR/ylcA
multimetal__irlR
Copper(Cu)__cutO
multimetal__cusA/ybdE
multimetal__corR/coaR
Nickel(Ni)__nikE
Zinc(Zn)__znuC/yebM
Copper(Cu)__Cop_sensor_histidine_kinase
Iron(Fe)__ybtQ
Nickel(Ni)__ncrA
Tellurium(Te)__terC
Arsenic(As)__arrA
Arsenic(As)__aioA/aoxB
Chromium(Cr)__chrA1
multimetal__sitC
multimetal__cadD
multimetal__fpvA
multimetal__modC
Zinc(Zn)__zur/yjbK
multimetal__corB

Mercury(Hg) __merR1
multimetal __zraS/hydG
Zinc(Zn) __znuA/yebL
Copper(Cu) __yfmO
Chromium(Cr) __chrF
Copper(Cu) __ricR
Copper(Cu) __ctpG
multimetal __czcS
Iron(Fe) __fetB/ybbM
multimetal __actS
Arsenic(As) __pstC
multimetal __baeR
multimetal __mntA/ytgA
Arsenic(As) __arsC3
Silver(Ag) __silP

Supplementary Table 6. **The taxonomic novelty of the MAGs.**

MAGs ID	Domain	Phylum	Class	Order	Family	Genus	Species	Subspecies	Dataset
OF_MAG90	0.97	0.886	0.753	0.42	0.151	0.099	0.000171	0	0
OF_MAG62	0.861	0.476	0.0597	0.0392	0.00938	0.0152	5.72E-05	0	0
OF_MAG61	0.968	0.88	0.739	0.392	0.143	0.0871	0.000171	0	0
NOF_MAG24	0.991	0.967	0.928	0.753	0.515	0.265	0.000457	0	0
NOF_MAG18	0.933	0.748	0.455	0.141	0.0294	0.0221	0.000171	0	0
NOF_MAG15	0.975	0.907	0.798	0.509	0.184	0.125	0.000229	0	0
OF_MAG50	0.934	0.752	0.463	0.146	0.0312	0.0225	0.000171	0	0
OF_MAG88	0.977	0.911	0.807	0.526	0.195	0.132	0.000343	0	0
OF_MAG87	0.99	0.964	0.921	0.728	0.475	0.246	0.000457	0	0
OF_MAG85	0.904	0.636	0.249	0.0702	0.0144	0.0184	0.000114	0	0
OF_MAG84	0.994	0.978	0.952	0.832	0.683	0.405	0.0008	0	0
NOF_MAG27	0.829	0.359	0.0111	0.00439	0.0043	0.00794	0	0	0
NOF_MAG25	0.876	0.531	0.109	0.0488	0.0111	0.0167	5.72E-05	0	0
OF_MAG77	0.992	0.969	0.932	0.768	0.542	0.282	0.000514	0	0
OF_MAG78	0.979	0.919	0.825	0.552	0.216	0.148	0.000343	0	0
OF_MAG59	0.994	0.976	0.949	0.82	0.655	0.382	0.0008	0	0
OF_MAG56	0.876	0.531	0.109	0.0488	0.0111	0.0167	5.72E-05	0	0
OF_MAG72	0.979	0.919	0.825	0.552	0.216	0.148	0.000343	0	0
OF_MAG48	0.963	0.859	0.693	0.325	0.125	0.0682	0.000171	0	0
OF_MAG44	0.985	0.942	0.873	0.637	0.328	0.204	0.000343	0	0
NOF_MAG3	0.99	0.962	0.917	0.716	0.457	0.24	0.000457	0	0
NOF_MAG7	0.992	0.971	0.938	0.785	0.578	0.311	0.000514	0	0
NOF_MAG6	0.999	0.997	0.993	0.975	0.942	0.873	0.00269	0.000182	0

NOF_MAG9	0.993	0.972	0.94	0.792	0.593	0.325	0.000514	0	0
NOF_MAG10	0.988	0.954	0.9	0.682	0.405	0.227	0.0004	0	0
OF_MAG39	0.994	0.976	0.948	0.817	0.649	0.376	0.0008	0	0
OF_MAG36	0.99	0.963	0.919	0.724	0.469	0.244	0.000457	0	0
OF_MAG35	0.981	0.928	0.844	0.58	0.248	0.169	0.000343	0	0
OF_MAG34	0.973	0.897	0.777	0.468	0.166	0.113	0.000171	0	0
OF_MAG32	0.983	0.937	0.862	0.614	0.293	0.191	0.000343	0	0
OF_MAG31	0.841	0.401	0.0172	0.0121	0.00528	0.00864	0	0	0
OF_MAG30	0.986	0.946	0.883	0.66	0.365	0.218	0.0004	0	0
OF_MAG28	0.998	0.993	0.985	0.947	0.879	0.748	0.00252	0.000182	0
OF_MAG23	0.996	0.984	0.965	0.877	0.775	0.524	0.0016	0	0
OF_MAG22	0.995	0.98	0.957	0.848	0.718	0.441	0.00131	0	0
OF_MAG17	0.843	0.41	0.02	0.0154	0.00573	0.00938	0	0	0
OF_MAG10	0.982	0.933	0.854	0.599	0.271	0.18	0.000343	0	0
OF_MAG7	0.976	0.91	0.804	0.52	0.191	0.13	0.000286	0	0
OF_MAG2	0.846	0.419	0.0245	0.0197	0.00619	0.0102	5.72E-05	0	0
NOF_MAG31	0.975	0.906	0.796	0.503	0.181	0.123	0.000229	0	0
OF_MAG95	0.97	0.888	0.758	0.429	0.153	0.102	0.000171	0	0
OF_MAG94	0.916	0.684	0.332	0.0908	0.0169	0.0197	0.000171	0	0
OF_MAG93	0.852	0.442	0.0363	0.0284	0.00734	0.0121	5.72E-05	0	0
OF_MAG92	0.999	0.997	0.994	0.98	0.954	0.892	0.00269	0.000182	0
OF_MAG91	1	0.999	0.997	0.989	0.973	0.93	0.00509	0.000182	0
OF_MAG89	1	0.999	0.998	0.993	0.984	0.956	0.0477	0.00182	0.000206
OF_MAG70	0.997	0.988	0.974	0.909	0.831	0.641	0.002	0	0
OF_MAG64	0.91	0.662	0.292	0.0792	0.0155	0.0192	0.000171	0	0
OF_MAG65	0.847	0.423	0.0262	0.0213	0.00639	0.0105	5.72E-05	0	0

OF_MAG63	0.975	0.905	0.793	0.498	0.178	0.12	0.000171	0	0
NOF_MAG22	0.959	0.844	0.661	0.288	0.111	0.0607	0.000171	0	0
NOF_MAG20	0.995	0.98	0.957	0.849	0.72	0.444	0.00131	0	0
NOF_MAG19	0.965	0.868	0.713	0.35	0.132	0.0739	0.000171	0	0
NOF_MAG17	0.906	0.645	0.264	0.0729	0.0148	0.0187	0.000114	0	0
OF_MAG58	0.997	0.989	0.977	0.917	0.841	0.664	0.002	0	0
OF_MAG57	1	0.998	0.996	0.987	0.969	0.92	0.00292	0.000182	0
OF_MAG55	0.985	0.942	0.873	0.637	0.328	0.204	0.000343	0	0
OF_MAG54	1	0.999	0.997	0.99	0.976	0.935	0.0064	0.000182	0
OF_MAG53	0.998	0.993	0.985	0.948	0.88	0.75	0.00252	0.000182	0
OF_MAG51	0.996	0.987	0.971	0.899	0.812	0.599	0.00177	0	0
OF_MAG83	0.863	0.484	0.0663	0.0412	0.00973	0.0157	5.72E-05	0	0
OF_MAG81	0.969	0.882	0.744	0.402	0.145	0.0911	0.000171	0	0
NOF_MAG26	0.854	0.448	0.0398	0.0305	0.00769	0.0126	5.72E-05	0	0
OF_MAG76	0.967	0.876	0.729	0.375	0.138	0.0809	0.000171	0	0
OF_MAG75	0.999	0.996	0.992	0.97	0.93	0.852	0.00257	0.000182	0
OF_MAG74	0.974	0.9	0.784	0.48	0.17	0.116	0.000171	0	0
OF_MAG71	0.977	0.913	0.81	0.531	0.198	0.135	0.000343	0	0
OF_MAG73	0.924	0.712	0.384	0.107	0.0198	0.0205	0.000171	0	0
OF_MAG49	1	0.999	0.998	0.993	0.985	0.959	0.0827	0.0107	0.00103
NOF_MAG11	0.973	0.897	0.777	0.468	0.166	0.113	0.000171	0	0
OF_MAG43	1	0.999	0.998	0.994	0.985	0.959	0.0898	0.014	0.00124
OF_MAG42	0.999	0.995	0.99	0.963	0.914	0.82	0.00252	0.000182	0
NOF_MAG8	0.995	0.982	0.961	0.862	0.748	0.479	0.00149	0	0
NOF_MAG4	0.986	0.946	0.883	0.66	0.365	0.218	0.0004	0	0
NOF_MAG5	0.998	0.993	0.985	0.948	0.88	0.75	0.00252	0.000182	0

OF_MAG40	0.998	0.994	0.987	0.953	0.891	0.768	0.00252	0.000182	0
OF_MAG37	0.998	0.993	0.986	0.95	0.886	0.757	0.00252	0.000182	0
OF_MAG33	0.997	0.988	0.974	0.908	0.829	0.636	0.00194	0	0
OF_MAG29	0.998	0.993	0.985	0.949	0.883	0.754	0.00252	0.000182	0
OF_MAG27	0.996	0.987	0.971	0.899	0.812	0.599	0.00177	0	0
OF_MAG26	0.998	0.993	0.985	0.948	0.88	0.75	0.00252	0.000182	0
OF_MAG25	0.985	0.944	0.877	0.648	0.346	0.211	0.0004	0	0
OF_MAG24	0.998	0.994	0.987	0.955	0.895	0.775	0.00252	0.000182	0
OF_MAG21	0.996	0.985	0.968	0.887	0.791	0.556	0.00171	0	0
OF_MAG19	1	0.999	0.997	0.99	0.976	0.937	0.00857	0.000182	0
OF_MAG20	0.995	0.981	0.958	0.851	0.725	0.449	0.00131	0	0
OF_MAG18	0.991	0.966	0.926	0.746	0.503	0.258	0.000457	0	0
OF_MAG16	0.974	0.903	0.79	0.492	0.175	0.119	0.000171	0	0
OF_MAG14	0.997	0.987	0.972	0.9	0.814	0.605	0.00177	0	0
OF_MAG8	0.994	0.977	0.951	0.826	0.671	0.395	0.0008	0	0
OF_MAG6	0.995	0.983	0.962	0.867	0.757	0.493	0.00154	0	0
OF_MAG4	0.995	0.98	0.957	0.849	0.72	0.444	0.00131	0	0
NOF_MAG1	0.999	0.998	0.996	0.984	0.963	0.906	0.00269	0.000182	0
OF_MAG12	0.993	0.972	0.94	0.792	0.593	0.325	0.000514	0	0
OF_MAG47	0.993	0.973	0.942	0.799	0.61	0.341	0.000514	0	0

Supplementary Table 7. **Detailed information of elemental cycling functional genes.**

KO number	Gene ID	Description	Gene type
K00370	<i>narG</i>	nitrate reductase / nitrite oxidoreductase, alpha subunit [EC:1.7.5.1 1.7.99.-]	N-related gene
K00368	<i>nirK</i>	nitrite reductase (NO-forming) [EC:1.7.2.1]	N-related gene
K15864	<i>nirS</i>	nitrite reductase (NO-forming) / hydroxylamine reductase [EC:1.7.2.1 1.7.99.1]	N-related gene
K00376	<i>nosZ</i>	nitrous-oxide reductase [EC:1.7.2.4]	N-related gene
K01113	<i>phoD</i>	alkaline phosphatase D [EC:3.1.3.1]	P-related gene
K06137	<i>pqqC</i>	pyrroloquinoline-quinone synthase [EC:1.3.3.11]	P-related gene
K00394	<i>aprA</i>	adenylylsulfate reductase, subunit A [EC:1.8.99.2]	S-related gene
K00395	<i>aprB</i>	adenylylsulfate reductase, subunit B [EC:1.8.99.2]	S-related gene
K11181	<i>dsrB</i>	dissimilatory sulfite reductase beta subunit [EC:1.8.99.5]	S-related gene
K17222	<i>soxA</i>	L-cysteine S-thiosulfotransferase [EC:2.8.5.2]	S-related gene
K17224	<i>soxB</i>	S-sulfosulfanyl-L-cysteine sulfohydrolase [EC:3.1.6.20]	S-related gene
K17225	<i>soxC</i>	sulfane dehydrogenase subunit SoxC	S-related gene
K22622	<i>soxD</i>	S-disulfanyl-L-cysteine oxidoreductase SoxD [EC:1.8.2.6]	S-related gene
K17223	<i>soxX</i>	L-cysteine S-thiosulfotransferase [EC:2.8.5.2]	S-related gene
K17226	<i>soxY</i>	sulfur-oxidizing protein SoxY	S-related gene
K17227	<i>soxZ</i>	sulfur-oxidizing protein SoxZ	S-related gene
K07306	<i>dmsA</i>	anaerobic dimethyl sulfoxide reductase subunit A [EC:1.8.5.3]	S-related gene
K21310	<i>mddA</i>	methanethiol S-methyltransferase [EC:2.1.1.334]	S-related gene
K02588	<i>nifH</i>	nitrogenase iron protein NifH	N-related gene
K22357	<i>amoA</i>	alkene monooxygenase alpha subunit [EC:1.14.13.69]	N-related gene
KO4561	<i>norB</i>	nitric oxide reductase subunit B [EC:1.7.2.5]	N-related gene
K10944	<i>pmoA-amoA</i>	methane/ammonia monooxygenase subunit A [EC:1.14.18.3 1.14.99.39]	C-related gene
K00399	<i>mcrA</i>	methyl-coenzyme M reductase alpha subunit [EC:2.8.4.1]	C-related gene

K16157	<i>mmoX</i>	methane monooxygenase component A alpha chain [EC:1.14.13.25]	C-related gene
K11180	<i>dsrA</i>	dissimilatory sulfite reductase alpha subunit [EC:1.8.99.5]	S-related gene
K17486	<i>dmdA</i>	dimethylsulfoniopropionate demethylase [EC:2.1.1.269]	S-related gene

Supplementary Table 8. **Detailed information on variables in SEM.**

Latent Variable	Observable Variable	Units
Climate	mean annual temperature	°C
	annual precipitation	mm
Fertilizer type	Fertilizer type	
	Total nitrogen	g/kg
Soil	Organic carbon density	kg/m ³
	Soil organic carbon	g/kg
	pH	
Community diversity	Shannon index	
	Richness index	
Elements metabolism	Abundance of Carbon Metabolism	copies/cell
	Abundance of Nitrogen Metabolism	copies/cell
	Abundance of Phosphorus Metabolism	copies/cell
	Abundance of Sulfur Metabolism	copies/cell
	Abundance of Potassium Metabolism	copies/cell
ARG & MRG	ARG abundance	copies/cell
	MRG abundance	copies/cell
Co-existence of ARGs and MRGs	Abundance of ARG-MRG-carrying contigs	copies/cell