

A faecal metabolite signature of impaired fasting glucose: results from two independent population-based cohorts

Ana Nogal^{1*}, Francesca Tettamanzi^{1,2*}, Qiuling Dong³, Panayiotis Louca¹, Alessia Visconti¹, Colette Christiansen^{1,4}, Taylor Breuninger⁵, Jakob Linseisen^{5,6,7}, Harald Grallert^{3,8}, Nina Wawro^{3a,5}, Francesco Asnicar⁹, Kari Wong¹⁰, Andrei-Florin Baleanu¹, Gregory A. Michelotti¹⁰, Nicola Segata⁹, Mario Falchi¹, Annette Peters^{3a,8,11}, Paul W. Franks^{12,13}, Vincenzo Bagnardi¹⁴, Tim D Spector¹, Jordana T Bell¹, Christian Gieger^{3,8}, Ana M Valdes^{15‡}, Cristina Menni^{1‡}

Authors' affiliations:

¹ Department of Twin Research, King's College London, St Thomas' Hospital Campus, London SE1 7EH.

² Humanitas Clinical and Research Centre – IRCCS - Via Manzoni 56, 20089 Rozzano (Milan), Italy.

³ Institute of Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health (GmbH), Research Unit of Molecular Epidemiology, Ingolstädter Landstr. 1, 85764 Neuherberg, Germany.

^{3a} Institute of Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health (GmbH), Ingolstädter Landstr. 1, 85764 Neuherberg, Germany.

⁴ School of Mathematics and Statistics, The Open University, Milton Keynes, United Kingdom.

⁵ Epidemiology, University Hospital Augsburg, University of Augsburg, Stenglinstr. 2, 86156 Augsburg, Germany.

⁶ ZIEL-Institute for Food & Health, Technische Universität München, Weihenstephaner Berg 3, 85354 Freising, Germany.

⁷ Institute for Medical Information Processing, Biometry, and Epidemiology, Medical Faculty, Ludwig-Maximilian University Munich, Marchioninistr. 15, 81377, Munich, Germany.

⁸ German Center for Diabetes Research (DZD), Ingolstädter Landstraße 1, 85764 Neuherberg, Germany.

⁹ Department CIBIO, University of Trento, Trento, Italy.

¹⁰ Metabolon, Research Triangle Park, Morrisville, NC, USA.

¹¹ Munich Heart Alliance, German Center for Cardiovascular Research (DZHK e.V., Partner-Site Munich), Munich, Germany.

¹² Lund University Diabetes Center, Lund University, Malmö, Sweden.

¹³ Department of Clinical Sciences, Lund University, Malmö, Sweden.

¹⁴ Department of Statistics and Quantitative Methods, University of Milan-Bicocca, Milan, Italy.

¹⁵ Academic Rheumatology Clinical Sciences Building, Nottingham City Hospital, University of Nottingham, United Kingdom.

*Equal contribution

‡ **Corresponding authors:** Cristina Menni, PhD & Ana M. Valdes, PhD

Department of Twin Research, King's College London, St Thomas' Hospital Campus, 4th Floor South Wing Block D, Westminster Bridge Road, London SE1 7EH, UK. Phone: +44 (0) 207 188 7188 (ext. 52594); email: cristina.menni@kcl.ac.uk

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Abstract

Prediabetes is a metabolic condition associated with gut microbiome composition, though mechanisms remain elusive. We searched for faecal metabolites, a readout of gut microbiome function, associated with impaired fasting glucose (IFG) in 142 individuals with IFG and 1105 healthy individuals from TwinsUK. We used the KORA cohort (318 IFG individuals, 689 healthy individuals) to replicate our findings. We linearly combined 8 IFG-positively associated metabolites (1-methylxanthine, nicotinate, glucuronate, uridine, cholesterol, serine, caffeine and protoporphyrin IX) into an IFG-metabolite score, which was significantly associated with higher odds ratios for IFG (TwinsUK: OR[95%CI]=3.9[3.02-5.02], $p<0.0001$, KORA: OR[95%CI]=1.3[1.16-1.52], $p<0.0001$) and incident type-2 diabetes (T2D) (TwinsUK: HR[95%CI]=4[1.97-8], $p=0.0002$). Although these are host-produced metabolites, we found that the gut microbiome is strongly associated with their faecal levels (AUC>70%). Abundances of *Faecalibacillus intestinalis*, *Dorea formicigenerans*, *Ruminococcus torques* and *Dorea sp. AF24_7LB* were positively associated with IFG, and such associations were partially mediated by 1-methylxanthine and nicotinate (VAF mean(SD)=14.4%(5.1), $p<0.05$). Our results suggest that gut microbiome is linked to prediabetes not only via the production of microbial metabolites but also by affecting intestinal absorption/excretion of host-produced metabolites and xenobiotics, which are correlated with the risk of IFG. Faecal metabolites enable modelling of another mechanism of gut microbiome effect on prediabetes and T2D onset.

Keywords: impaired fasting glucose, prediabetes, faecal metabolomics, gut microbiome, type-2 diabetes

Article highlights

- **Gap:** Prediabetes is a metabolic condition associated with gut microbiome composition, though mechanisms remain elusive.
- **Question:** Is there a faecal metabolite signature of impaired fasting glucose (IFG)? What are the underlying mechanisms of action?
- **Findings:** We identified a faecal metabolite signature of IFG associated with prevalent IFG in two independent cohorts and incident type-2 diabetes in a sub-analysis. Although the signature consists of metabolites of non-microbial origin, it is strongly correlated with gut microbiome composition.
- **Meaning:** Faecal metabolites enable modelling of another mechanism of gut microbiome effect on prediabetes by affecting intestinal absorption or excretion of host compounds and xenobiotics.

Introduction

Type-2 diabetes (T2D) is a leading cause of mortality and morbidity (1) affecting more than 536.6 million people (10.5% of the total population) worldwide (2), thus representing a huge public health burden (1). The causation of T2D is multifactorial, influenced by host genetics and environmental factors, including diet, obesity, inactivity and smoking, and the interaction between these factors (3). Furthermore, its onset is gradual, with people progressing through a state of prediabetes (4) and is defined as impaired levels of fasting glucose (IFG), and/or glucose intolerance (IGT), and/or elevated haemoglobin A1c (HbA1c) (5).

Over the past decade, T2D and prediabetes have been linked by us and others (6-8) to changes in the gut microbiota, and we have recently demonstrated that T2D development is preceded by an alteration in gut microbiota composition (7). A critical challenge in human microbiome research, however, is to characterise and quantify metabolic activity across the full microbial ecosystem (9). The gut microbiome is highly variable and different bacterial types may have similar metabolic effects on the host. Microbial metabolites are now widely seen as key mediators of the effects of gut microbiome composition on human physiology (10). Faecal metabolites provide a functional readout of the gut microbiome (11; 12) and are a novel tool to explore links between gut microbiome composition and activity, host phenotypes, and heritable complex traits, thus improving our understanding of the impact that the gut microbiome can have on its host (11). As the gut microbiome is modifiable with nutritional and lifestyle interventions (13), it is of utmost importance to identify alterations in the faecal metabolites abundances, which reflect metabolic activity perturbations of the human gut microbial ecosystem that might lead to T2D onset.

In the first faecal metabolomics study of prediabetes to date, we aim to identify a faecal metabolite signature of this condition in two independent cohorts to shed light on mechanisms of action underlying T2D onset/development. Addressing this challenge also has long-term implications for future studies into therapies and lifestyle interventions that alter microbial metabolic activity to improve human health.

Methods

A flowchart of the study design with the main results is presented in **Figure 1**.

Discovery cohort

We analysed data from 1247 non-related individuals from TwinsUK (14) for whom concurrent non-targeted faecal metabolomic profiling (526 metabolites at fasting) and glucose/diabetic information were available (cross-sectional design). Concurrent metagenome sequencing (as a measure of the gut microbiome composition) was also available for a subset of 342 individuals. Subjects were classified into three groups following the American Diabetes Association (ADA) criteria based on isolated fasting glucose levels (15) at the time of initial sampling and at subsequent visits (on average 3.5 visits (SD=2.0), 4.6 (SD=2.7) years apart): individuals with T2D (fasting glucose ≥ 7 mmol/L or physician's letter confirming diabetes diagnosis), individuals with IFG (>5.5 mmol/L fasting glucose <7 mmol/L, not on diabetic medication), and subjects without IFG and T2D (>3.9 mmol/L fasting glucose ≤ 5.5 mmol/L) (see **Table 1**). We refer to 'healthy individuals' to indicate individuals without IFG and/or T2D. Only one twin per twin pair was included in the analyses to eliminate potential bias through correlated error, which might inflate effect estimates.

In a small sub-analysis, we included individuals with incident T2D (average follow-up time =2.1 (SD=1.3) years) and an independent subset of healthy individuals that remained healthy during follow-up.

All twins provided informed written consent and the study was approved by St. Thomas' Hospital Research Ethics Committee (REC Ref: EC04/015).

Replication cohort

The Cooperative Health Research in the Region of Augsburg (KORA) study is a population-based cohort study. The KORA FF4 study (2013–2014) is the second follow-up of KORA S4 (1999–2001). The 1007 samples included in the study were collected in the morning between 8:00 A.M. and 10:30 A.M. after at least 8 h of fasting. Metabolon - Untargeted LC/MS-based techniques were applied to measure the metabolites in the KORA cohort (a different version of the platform used in TwinsUK). Healthy individuals and IFG individuals were assigned based on the same criteria as in TwinsUK (described in the above section and in **Table 1**).

Faecal metabolomics profiling

Metabolomics profiling was conducted using ultrahigh-performance liquid chromatography-tandem mass spectrometry (LC/MS/MS) by the metabolomics provider Metabolon Inc. (Morrisville, USA) on faecal samples from participants in the TwinsUK and KORA cohorts (**Supplementary Text**). The metabolomic dataset measured by Metabolon includes 526 known metabolites for TwinsUK belonging to the following broad categories – amino-acids, peptides, carbohydrates, energy intermediates, lipids, nucleotides, cofactors and vitamins, and xenobiotics, of which 357 were also measured in KORA. These include metabolites of established microbial origin (16). A complete list of the included metabolites with their super-

pathways, sub-pathways, KEGG and HMDB identifiers are reported in **Supplementary Table**

1. We imputed to the day minimum metabolites with less than 20% missing.

Metagenomic assessment

Gut microbiota composition was generated from faecal shotgun metagenomes for a subset of the discovery cohort. DNA extraction, library preparation and sequencing were conducted as detailed in Visconti et al. (2019) (11). For details see the **Supplementary Text**. Of note, gut microbiota composition is described by Species-level Genome Bins (SGB), which is the best proxy to define microbial species (17).

Statistical analysis

Statistical analyses were conducted using R 4.2.2.

To identify a faecal metabolite signature of prediabetes, we ran logistic regressions adjusting for age, BMI, sex, and multiple testing using the Benjamini and Hochberg method (18) (FDR<0.05). We then checked whether the metabolites significantly associated with IFG in the discovery set were also replicated in KORA (p-value<0.1). We used a less stringent threshold for KORA because of the Winner's Curse (the effect sizes of the most strongly associated variables within a cohort-specific analysis are inflated) (19). Results were meta-analysed using inverse variance random effect meta-analysis. We then created the IFG-metabolite score by linearly combining the replicated metabolites along with covariates. To assess the performance of the score in predicting prevalent IFG and incident T2D, we calculated the area under the curve (AUC) values obtained using 5-fold cross-validation (caret package implemented in R (20)). Finally, logistic and Cox regressions were used to investigate the association between the IFG score (Z-scaled) and prevalent IFG risk and incident T2D risk, respectively.

Given the strong association between faecal metabolites and gut microbiome composition (12), we investigated to what extent the gut microbiota composition was associated with each of the replicated metabolites using Random Forest regressors and classifiers with compositional data and 5-fold cross-validation. The performance was calculated using the average of the obtained Spearman's correlations (between the observed metabolite levels and the levels predicted by the model - denoted as *rho*) over the 5 folds used as a test set for the regressors, and the average of the obtained AUC values over the testing folds for the classifiers. For details see **Supplementary File**.

We further investigated the associations between their top 100 bacterial features and IFG by running logistic regression models adjusting for covariates and multiple testing species (FDR<0.05). Specifically, we included all the faecal metabolites that could be predicted by the gut microbiome with an AUC>70% and we then focussed on those that had an outstanding prediction performance (AUC>90%).

Finally, we used formal mediation analysis as implemented in the R package 'mediation' with 1000 nonparametric bootstrap samples (21) to test the mediation effects of the metabolites on the total effect of the gut bacteria on IFG. The mediation model was used to quantify both the direct effect of these gut bacterial species on IFG and the indirect (mediated) effects mentioned above while controlling for age, BMI and sex. The variance accounted for (VAF) score, which represents the ratio of indirect-to-total effect and determines the proportion of the variance explained by the mediation process, was used to determine the significance of the mediation effect.

Data and resource availability

TwinsUK data are available upon request on the department website (<https://twinsuk.ac.uk/resources-for-researchers/our-data/>). All other data sets generated and/or analysed in this study are available from the corresponding author upon request.

Results

We included 1247 unrelated individuals from the TwinsUK cohort who had faecal metabolite measures along with glucose/diabetic and prediabetic information. Of these, 142 individuals had IFG (mean fasting glucose 5.9 mmol/L (SD=0.4)) and 1105 were healthy individuals (mean fasting glucose 4.5 mmol/L (SD=0.3)). Descriptive characteristics of the discovery and replication populations are included in **Table 1**.

Faecal metabolites associated cross-sectionally to IFG

In TwinsUK, out of the 526 known faecal metabolites analysed, the faecal abundances of 26 compounds were associated with IFG after adjusting for age, BMI, sex and multiple testing (FDR<0.05) (**Figure 2**). Identified metabolites were mainly amino acids (n=7) and lipids (n=7), but also included xenobiotics (n=4), cofactors and vitamins (n=3), nucleotides (n=2), carbohydrates (n=2) and one energy-related metabolite (**Figure 2**). All significant metabolites, but 3-hydroxyoleate, octadecanedioate (C18-DC), azelate (C9-DC), gamma-tocotrienol and enterolactone, were positively associated with IFG (**Figure 2**). Out of the 26, 18 metabolites were also measured in KORA (**Supplementary Table 1**), and 8 metabolites were replicated (p-value<0.1) (**Figure 3**). These were the lipid cholesterol (sterol metabolism), the carbohydrate glucuronate (aminosugar metabolism), the cofactors/vitamins nicotinate

(nicotinate and nicotinamide metabolism) and protoporphyrin IX (haemoglobin and porphyrin metabolism), the xenobiotics caffeine and 1-methylxanthine (both involved in the xanthine metabolism), the amino acid serine (glycine, serine and threonine metabolism), and the nucleotide uridine (pyrimidine metabolism). The correlation matrices for the 8 faecal metabolites in TwinsUK and KORA are depicted in **Supplementary Figure 1**. We combined the results from both cohorts using inverse variance random effect meta-analysis (**Figure 3**).

IFG-metabolite score and predictive power

We then generated the IFG-metabolite score using TwinsUK individuals:

$$\begin{aligned} \text{IFG-metabolite score} = & -8.79 + 0.07 \times \text{glucuronate} + 0.25 \times \text{protoporphyrin IX} + 0.09 \times \text{1-} \\ & \text{methylxanthine} + 0.14 \times \text{cholesterol} + 0.04 \times \text{serine} + 0.07 \times \text{uridine} + 0.04 \times \text{nicotinate} + \\ & 0.17 \times \text{caffeine} + 0.07 \times \text{age} + 0.1 \times \text{BMI} - 0.6 \times \text{sex (female=1)} \end{aligned}$$

The IFG-metabolite score was associated with an increased risk of IFG in TwinsUK (OR[95%CI]=3.9[3.02-5.02], $p < 0.0001$) and in KORA (OR[95%CI]=1.3[1.16-1.52], $p < 0.0001$). The association remained significant when further adjusting for clinical covariates (i.e. systolic and diastolic blood pressure, circulating levels of high-density lipoprotein (HDL), total cholesterol and triglycerides, alternative health eating index (aHEI – not available in KORA), activity levels and smoking status – see **Table 1**) in both cohorts (TwinsUK: OR[95%CI]= 3.4[2.65-4.49], $p < 0.0001$; KORA: OR[95%CI]=1.2[1.06-1.41], $p = 0.008$). Finally, in TwinsUK the IFG-metabolite score accurately predicted prevalent IFG with an AUC of 79.8%[95% CI=76.3-83.3] in 5-fold stratified cross-validation and outperformed the model including only covariates (AUC=77.2%[95% CI=73.6-81]) by 2.6%[Δ 95% CI=2.7-2.1]. In KORA, the IFG-metabolite score (top vs lowest decile) could satisfactory predict prevalent IFG (AUC=65.4[95%CI=57.9-73]).

Sub-analysis: incident T2D

In a small independent sample from TwinsUK (descriptive characteristics are shown in **Table 1**) consisting of 17 healthy individuals (different from the healthy subjects of the IFG dataset) and 10 individuals with incident T2D (follow-up time between faecal metabolite measurements and incident events: mean=2.1 (SD=1.3) years), the IFG-metabolite score was also predictive of an increased risk of incident T2D (HR[95%CI]=4[1.97-8], $p=0.0002$) in TwinsUK after further adjusting for baseline circulating glucose levels. It also accurately predicted incident T2D (AUC[95% CI]=83.3%[74.4-92.2]), while a model using baseline circulating glucose levels as predictor presented a lower prediction power (AUC[95% CI]=72.4%[51.8-92.9]).

Gut microbiome – faecal metabolites association

We further evaluated the extent to which the gut microbiota was associated with the faecal abundances of the 8 replicated metabolites using the AUC obtained by the Random Forest classifiers and the Spearman's correlations (denoted as ρ) between the real abundances and predicted values by the Random Forest regressors. We included a subset of 342 individuals from TwinsUK with concurrent gut microbiota composition assessed by shotgun metagenomics and faecal metabolites measurements. Descriptive characteristics of this subset are shown in **Supplementary Table 2**.

The gut microbiome composition was strongly associated with the replicated metabolites with performance metric values ranging from AUC[95% CI]=70.7%[69.1-72.4] and ρ [95% CI]=0.24[0.23-0.25] for caffeine to AUC[95% CI]=91.4%[90.8-91.9] and ρ [95% CI]=0.62[0.62-0.62] for 1-methylxanthine (**Figure 4A** and **Supplementary Table 3**). Protoporphyrin IX was the only metabolite presenting a moderate association (AUC[95% CI]=64.8%[63.9-65.6]; $\rho=0.25$ [95%CI=0.24-0.26] (**Figure 4A**).

We then investigated whether the abundances from their top 100 bacterial features based on the Random Forest models were also significantly associated with IFG (**Supplementary Table 4**). We focussed on the faecal metabolites that presented the strongest associations with the gut microbiome composition (AUC>90% - outstanding prediction performance) (1-methylxanthine and nicotinate). We identified 4 characterised gut bacterial species for 1-methylxanthine and nicotinate, of which 3 overlapping (overlapping: *D. formicigenerans*, *R. torques* and *F. intestinalis*; 1-methylxanthine only: *D. sp. AF24 7LB*; nicotinate only: *D. sp. AF36 15AT*), that were positively associated with IFG after adjusting for age, BMI and sex (FDR<0.05) (**Supplementary Table 4**). We, therefore, performed a formal mediation analysis adjusting for age, BMI, and sex to determine whether 1-methylxanthine and/or nicotinate mediated the associations between these species and IFG. The analysis revealed that 1-methylxanthine acted as a potential mediator in the positive associations of *D. sp. AF24 7LB* (VAF=10.3%, p-value=0.03) and *R. torques* (VAF=9.7%, p-value=0.04) with IFG, while nicotinate acted as a potential mediator in the positive associations of *F. intestinalis* (VAF=22.3%, p-value=0.002), *D. formicigenerans* (VAF=15.8%, p-value=0.002) and *R. torques* (VAF=14.1%, p-value=0.03) with IFG (**Figure 4B**). We further run mediation analyses for the metabolites that could be predicted by the gut microbiome with an AUC>70%. As reported in the **Supplementary Figure 2**, uridine, serine, cholesterol and caffeine were also mediators in the associations between different species (e.g., *Dorea* species and *A. hallii*) and IFG. Models were not further adjusted for other comorbidities (e.g., systolic and diastolic blood pressure, circulating levels of HDL, total cholesterol and triglycerides, aHEI, activity levels and smoking status) as these were not significantly associated with the identified bacterial species, nor the metabolites making up the score (**Supplementary Table 5**).

Discussion

Here we identify for the first time a faecal metabolite signature of IFG, which is associated with prevalent IFG in two independent cohorts and in a small sub-analysis, also predictive of incident T2D. The faecal metabolites making up the score are not microbial-derived metabolites but are “host metabolites” (e.g., xenobiotics, cofactors, and vitamins). However, the gut microbiome can accurately predict their faecal abundances (AUC>70%). It is well known that the gut microbiome composition can affect diseases via several mechanisms (22). Circulating microbial metabolites have been reported by us and others to be reflective of gut microbiome diversity and composition (6-8) and predictive of prevalent and incident T2D (7). Taken together, this suggests that the gut microbiome can influence T2D, not only by producing metabolites that enter the bloodstream (7) but also by regulating the absorption or excretion of host-produced compounds, thereby influencing IFG and T2D risk. This hypothesis is further supported by the results of our mediation analysis, showing that metabolites making up the score act as partial mediators on the significant associations between several gut microbial species, (e.g., *Faecalibacillus intestinalis*, *Dorea formicigenerans*, *Ruminococcus torques* and *Dorea sp. AF24_7LB*) and IFG.

Studies have shown that gut microbiome composition differs between prediabetic/diabetic individuals and healthy subjects (6; 7), with compositional shifts correlated with synthesis profile changes of gut bacteria-derived metabolites, including short-chain fatty acids, indolepropionic acid and trimethylamine (7; 22). These “microbial” metabolites enter into the bloodstream and reach different tissues, where they can influence glucose homeostasis and insulin resistance by activating or inhibiting signalling pathways (22). Nevertheless, in this study, the identified signature of prediabetes consists of 8 metabolites of non-bacterial origin. Serine is a non-essential amino acid mainly obtained by intrinsic synthesis (23). Glucuronate

is a sugar acid derived from glucose and involved in the detoxification of xenobiotic compounds (24). Protoporphyrin IX is a cofactor ubiquitously present in the human body as a heme precursor (25). Nicotinate, also known as vitamin B3 and niacin, is a water-soluble vitamin that can be produced by the human body from tryptophan (26). Cholesterol is an essential lipid of eukaryotic cell membranes and is also a precursor of bile acids and steroid hormones, which is mainly produced by the liver (27). Uridine is a necessary pyrimidine nucleotide for RNA synthesis produced by several reversible reactions (e.g., de-phosphorylation of uridine monophosphate, de-amination of a cytidine or combination of uracil and ribose 1-phosphate) (28). Caffeine and 1-methylxanthine are xenobiotics involved in the caffeine metabolism pathway (29).

Strikingly, we find that the gut microbiome is strongly associated with faecal levels of these metabolites suggesting that the gut microbiome influences the absorption or excretion of compounds involved in various metabolic pathways (e.g., cholesterol, uridine and glucuronate) and xenobiotics (e.g., caffeine and its derivatives), among others, and such levels of absorption or excretion are directly related to IFG. Our findings lead us to speculate that prediabetic individuals present gut microbiome composition perturbations, which likewise, influence the absorption or excretion of the identified compounds. This is further supported by the mediation analyses which suggest that the associations between specific gut microbial species, including *Faecalibacillus intestinalis*, *Dorea formicigenerans*, *Ruminococcus torques* and *Dorea sp. AF24_7LB*, and IFG are mainly reflecting the effect of the gut microbiome in the absorption or excretion of the found compounds.

Under normal conditions, the small intestine can break down, emulsify and absorb most nutrients, including fats, simple carbohydrates and proteins (30). For instance, <5g/day of fat are not absorbed and reach the colon (30). Nonetheless, the absorption capability of the gut can be limited depending on the gut microbiome composition (31). A study conducted by Basolo

and colleagues demonstrated that changes in participants' gut microbiome composition, due to diet or antibiotic use, impaired nutrient absorption (31). Several mechanisms might explain how gut microbiome composition might influence absorption, and thus, the disease onset (32-34). For instance, the gut microbiome can affect the gut barrier, which consists of a collection of physical and chemical structures that protects the host from pathogenic invasions and harmful stimuli (32). This can be provoked by the presence of pathogen-associated molecular patterns (PAMPs), such as lipopolysaccharides (LPS), in the cell walls of some gram-negative bacteria, which play an important role in intestinal absorption, blood glucose and inflammation (33). Moreover, changes in the permeability of the gut barrier can be caused by an unbalanced increase in bacteria able to degrade mucin (the main component of mucus, which covers the epithelial surfaces of the gastrointestinal tract) (32). Indeed, in this study, we identify that prediabetic individuals present larger abundances compared to healthy individuals of the mucin-degraders *Dorea formicigenerans* (35) and *Ruminococcus torques* (36), which have been previously associated with lower nutrient absorption (36). Finally, some gut microbes can also reduce absorption in the jejunum by altering the expression of intestinal transporters of different types of compounds (34).

Another possible explanation for our findings could be a reduction of specific beneficial bacteria able to utilize these compounds, thus resulting in increased excretion (27; 37). In the case of cholesterol, bacterial members of the genera *Bifidobacterium*, *Lactobacillus* and *Peptostreptococcus* are needed to convert cholesterol into coprostanol (27). Likewise, an inefficient cholesterol-coprostanol conversion is linked to cardiometabolic diseases (27). For glucuronate, most of it is not absorbed by the small intestine, however, under normal conditions, the amounts that make it to the colon are then efficiently utilized by *Bifidobacterium* (37).

This work has several strengths. Our study benefits from a large, accurately phenotyped discovery cohort, with metabolomic profiling and gut microbiome composition. We were also able to replicate our findings in a large independent cohort, thus strengthening our findings. Finally, a machine learning algorithm was applied to investigate the prediction of the gut microbiota to the levels of the found 8 metabolites, allowing us to simultaneously integrate all the species in the models.

We also note some study limitations. First, the cross-sectional nature of the data used for our primary analysis does not allow us to determine the temporal link between IFG and the identified faecal metabolites. Second, HbA1c, postprandial glucose to derive impaired glucose tolerance (IGT), which more closely resembles the T2D state (38), and a clinician's diagnosis were not available in the discovery cohort. Thus, in this study, the division of categories is derived from IFG. Third, for the sub-analysis looking at incident T2D, the sample size was limited and we were unable to seek independent replication as, to the best of our knowledge, there are no other cohorts in the world that have measured this faecal metabolome panel and incident T2D. Future studies with larger sample size are therefore needed to test the robustness of the IFG metabolite score to predict incident T2D. Fourth, there was not a full overlap between metabolites measured in the discovery and validation datasets, which might cause the loss of metabolites of interest to study. Fifth, the included study groups were unbalanced in terms of age and sex. Hence, although we adjusted all analyses for them and other important clinical variates, the confidence of the results is lowered. In addition, gut microbiota composition data was only available for a subset from the discovery set, and therefore, we could not replicate the mediation analysis in KORA. Furthermore, the Spearman's correlations between the predicted (from gut microbiome composition) and actual metabolites' levels were modest. Indeed, Random Forest models were trained based on microbial features extracted from metagenomic data, which for procedural and technical reasons, does not retrieve all

species present in a microbiome sample. Finally, this study does not include measures of permeability markers, which would contribute to a better understanding of the role of intestinal permeability in the absorption or excretion of the identified compounds.

In conclusion, we are proposing a novel mechanism of how gut microbiome composition affects prediabetes and consequently the onset of T2D. The gut microbiome is linked to prediabetes not only by microbial-derived metabolites but also by affecting intestinal absorption or excretion of metabolites of non-microbial origin, which are correlated with the risk of IFG and incident type-2 diabetes. Henceforth, to better understand the onset of T2D, the effect of the gut microbiome in the excretion or/and absorption of host-produced compounds and xenobiotics also needs to be also considered.

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Author's contributions

C.M. and T.D.S. conceived and designed the experiments. Q.D., P.L., A.V., C.C., T.B., J.L., H.G., N.W., F.A., K.W., A.F.B., G.A.M, N.S., M.F., A.P., P.W.F., V.B., T.D.S, J.T.B. and C.G. contributed reagents/materials/analysis tools. A.N., F.T., Q.D., A.V, C.C., F.A., H.G. and C.G. curated the data. A.N., F.T., Q.D. and C.M. performed the formal analyses. A.N., A.M.V. and C.M. wrote the manuscript. All the authors revised the manuscript.

Dr. Cristina Menni is the guarantor of this work, had full access to all the data, and takes full responsibility for the integrity of data and the accuracy of data analysis.

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Disclosures

T.D.S. is a co-founder and shareholder of Zoe Ltd. A.M.V., P.W.F., F.A., and N.S. are consultants to Zoe Ltd. K.W. and G.A.M. are employees of Metabolon Inc. No other potential conflicts of interest relevant to this article were reported.

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Table 1. Descriptive characteristics of the study populations.

	Discovery cohort: TwinsUK						Replication cohort: KORA		
	Prevalent IFG (n=1247)			Incident T2D (n=27)			Prevalent IFG (n=1007)		
	<i>Healthy individuals</i>	<i>IFG individuals</i>	<i>Differences between groups (p-value)</i>	<i>Healthy individuals</i>	<i>T2D individuals</i>	<i>Differences between groups (p-value)</i>	<i>Healthy individuals</i>	<i>IFG individuals</i>	<i>Differences between groups (p-value)</i>
ADA definition (15), fasting glucose, mmol/L	≤5.5	>5.5 & <7	-	≤5.5	≥7	-	≤5.5	>5.5 & <7	-
N	1105	142	-	17	10	-	689	318	-
Females, %	88.8	79	0.003	94.1	90	1	58.1	35.5	
Age, yrs	56.6 (14.9)	67.1 (10)	<0.0001	66.5 (6.6)	65 (7.7)	0.7	55.2 (10.9)	59.8 (10.8)	<0.0001
BMI, kg/m²	25.2 (4.6)	28.5 (5.1)	<0.0001	25.3 (3.3)	35.1 (6.7)	0.0004	26.1 (4.1)	28.4 (4.5)	<0.0001
Circulating fasting glucose, mmol/L	4.5 (0.3)	5.9 (0.4)	<0.0001	3.8 (0.3)	4.6 (1.5)	0.06	5.1 (0.3)	5.9 (0.3)	<0.0001

SBP, mmHg	125 (13.6)	134 (17)	<0.0001	132 (21.5)	133 (9.5)	0.8	114.5 (15.9)	123.1 (15.3)	<0.0001
DBP, mmHg	74.7 (8.1)	77.9 (10.3)	<0.0001	73.8 (11.9)	81.7 (8.1)	0.05	72.3 (8.9)	76 (9.7)	<0.0001
Circulating HDL, mmol/L	1.8 (1.2)	1.6 (1)	0.003	1.7 (0.4)	1.3 (0.2)	0.004	1.8 (0.5)	1.6 (0.5)	<0.0001
Circulating total cholesterol, mmol/L	4.1 (0.5)	4.1 (0.7)	0.73	4.7 (1.2)	3.6 (0.8)	0.02	5.6 (1)	5.7 (1)	0.008
Circulating triglycerides, mmol/L	1 (1)	1.6 (2.7)	0.0003	1 (0.3)	1.3 (0.4)	0.01	1.2 (0.7)	1.4 (0.9)	<0.0001
aHEI	70.5 (6.4)	70.1 (6.5)	0.49	72.8 (9.9)	71.4 (6.2)	0.68	NA	NA	NA
Current Smoker	No: 1060 Yes: 45	No: 139 Yes: 3	0.36	No: 17	No: 10	-	No: 346 Yes: 343	No: 139 Yes: 179	0.9
Activity levels	Low: 100 Moderate: 802 High: 203	Low: 13 Moderate: 102 High: 27	0.98	Low: 3 Moderate: 11 High: 3	Low: 2 Moderate: 5 High: 3	0.71	Inactive: 225 Active: 464	Inactive: 133 Active: 185	0.006

'Healthy individuals' refers to individuals with no IFG or T2D. Continuous variables are presented as mean and standard deviation. Measures are shown at baseline. There was no overlap between the healthy subjects from the IFG and incident T2D datasets. The p-value from a Wilcoxon test/t.test (continuous variable) or chi-squared test (categorical variable) was calculated to check whether differences between the different

subject groups for the described parameters existed. *Abbreviations:* ADA, American Diabetes Association; aHEI, alternative health eating index; BMI, body mass index; DBP, diastolic blood pressure; HDL, high-density lipoprotein; IFG, impaired fasting glucose; KORA, Cooperative Health Research in the Region of Augsburg; NA, not available; SBP, systolic blood pressure; T2D, type-2 diabetes; yrs, years

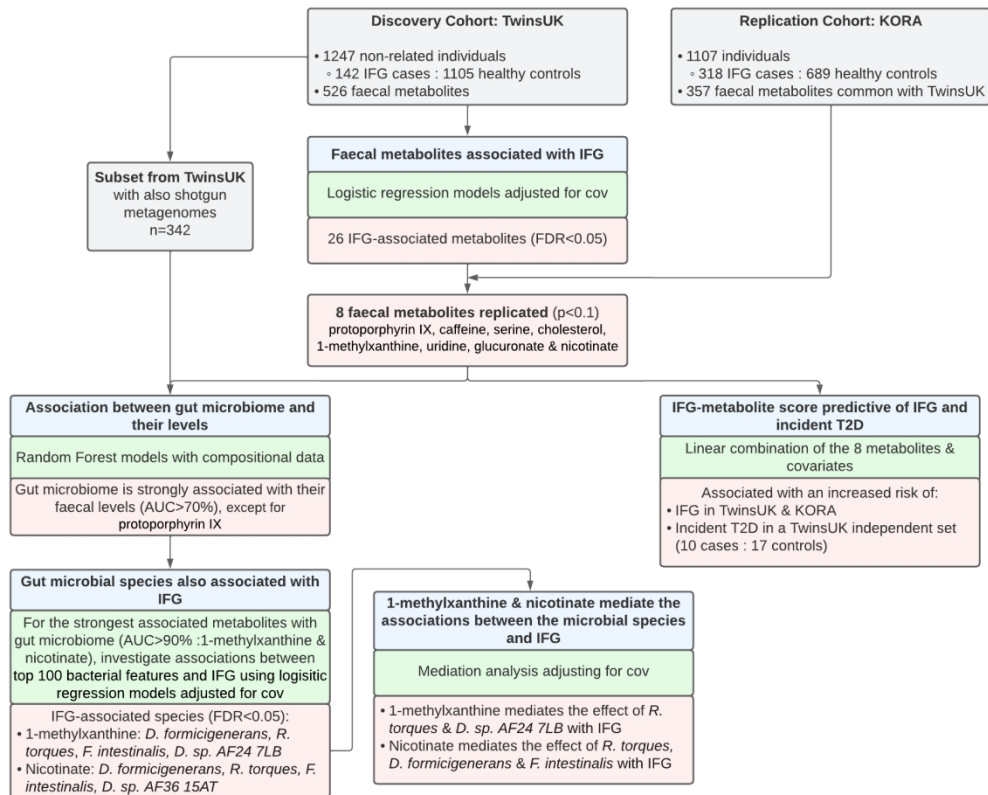
Figure legends

Figure 1. Flowchart of the study design with the main results. Data, aims, methods and results are shown in grey, blue, green, and pink squares, respectively. Mediation analyses were also performed for the metabolites making up the score that were predicted by the gut microbiome composition with an AUC>70%. *Abbreviations:* Cov, covariates (age, BMI and sex); FDR, false discovery rate; IFG, impaired fasting glucose; T2D, type-2 diabetes.

Figure 2. Faecal metabolites significantly associated with IFG in 1247 individuals from TwinsUK after adjusting for baseline age and BMI, sex, and multiple testing (FDR<0.05). Bars represent OR. Base labels illustrate subpathways. *Abbreviations:* met., metabolism.

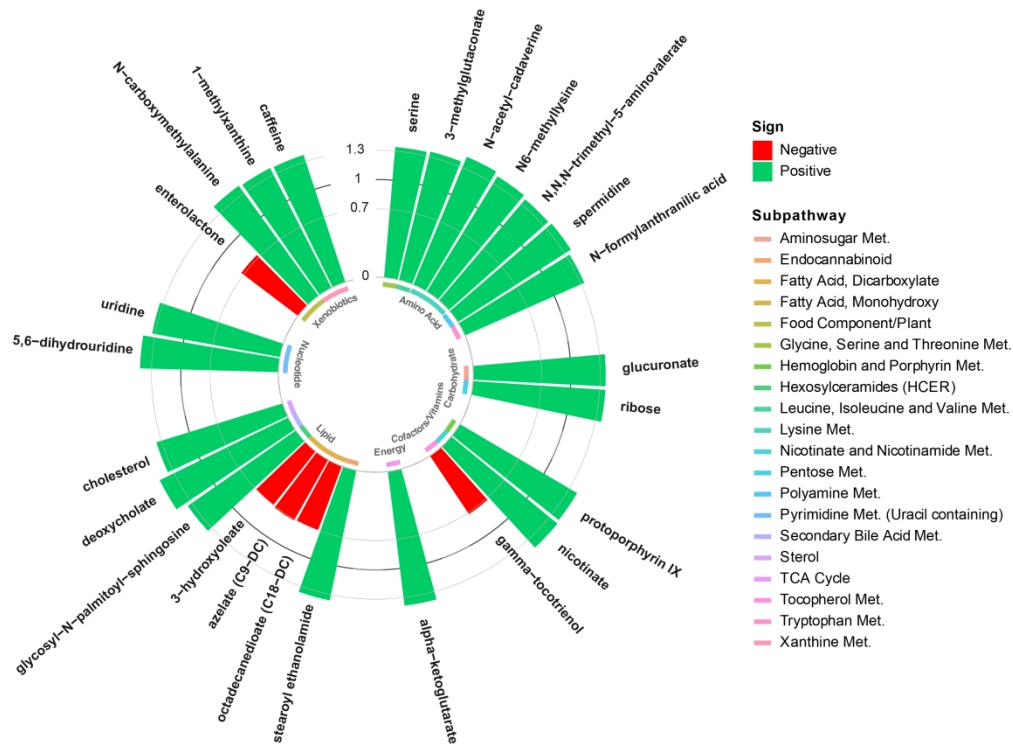
Figure 3. Faecal metabolites significantly associated with IFG after adjusting for age, BMI and sex in TwinsUK (FDR<0.05), KORA (p-value<0.1) and in the overall cohort (applying inverse variance random effect meta-analysis). The odds ratio (OR) and 95% confidence interval are indicated.

Figure 4. Associations of the gut microbiota with the 8 faecal replicated metabolites and impaired fasting glucose (IFG) in 342 TwinsUK participants. (A) Influence of the gut microbiota composition in the faecal abundances of the 8 replicated metabolites estimated by Random Forest regressors (Spearman's correlations between the real value of each metabolite and the value predicted) and classifiers (AUC). Red and blue bars represent the mean AUC and Spearman's correlations with the respective 95% confidence intervals across 5 folds, respectively. (B) Mediation analyses of the associations between characterised gut bacterial species and IFG. Models were adjusted for age, BMI, and sex. Path coefficients are shown beside each path, and indirect effects and variance accounted for (VAF) score are indicated below each mediator (left: nicotinate, right: 1-methylxanthine). Only metabolites with a predictive power of AUC>90% in '(A)' are shown.



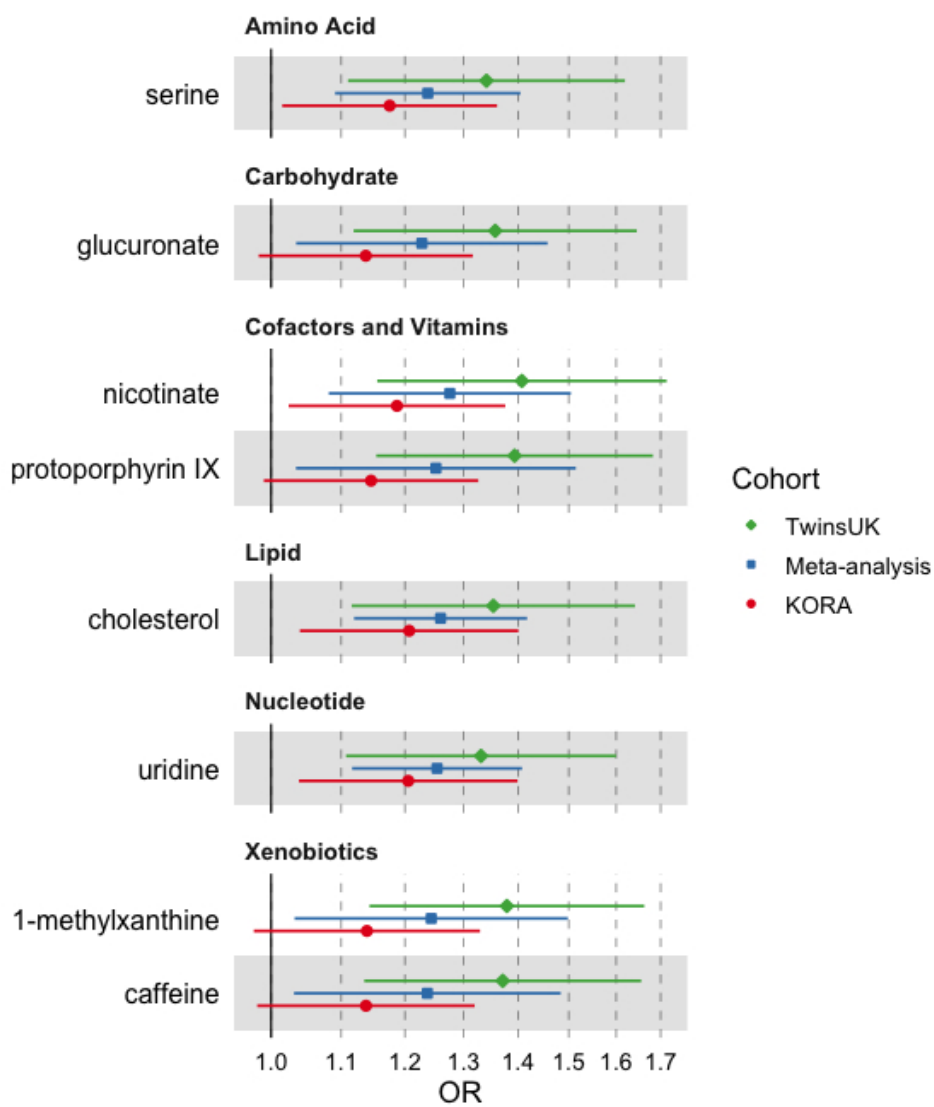
Flowchart of the study design with the main results. Data, aims, methods and results are shown in grey, blue, green, and pink squares, respectively. Mediation analyses were also performed for the metabolites making up the score that were predicted by the gut microbiome composition with an AUC>70%. Abbreviations: Cov, covariates (age, BMI and sex); FDR, false discovery rate; IFG, impaired fasting glucose; T2D, type-2 diabetes.

732x594mm (63 x 63 DPI)



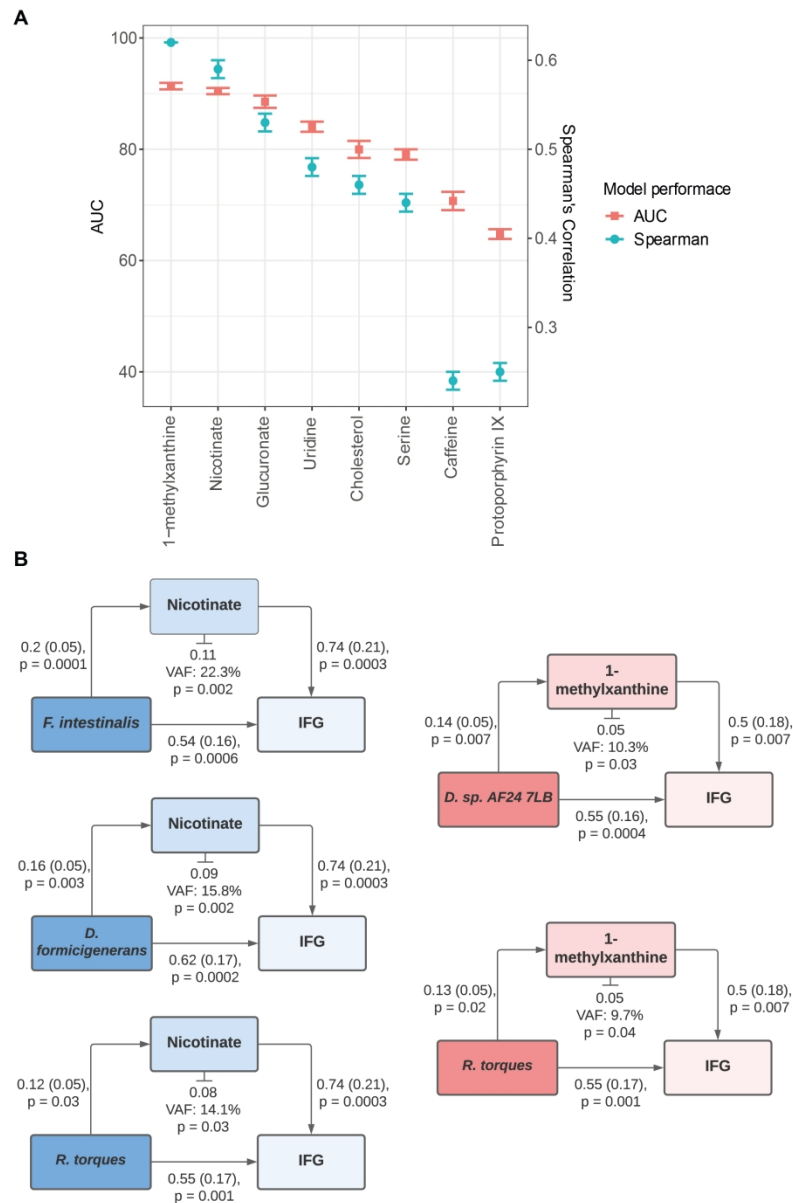
Faecal metabolites significantly associated with IFG in 1247 individuals from TwinsUK after adjusting for baseline age and BMI, sex, and multiple testing (FDR<0.05). Bars represent OR. Base labels illustrate subpathways. Abbreviations: met., metabolism.

729x538mm (118 x 118 DPI)



Faecal metabolites significantly associated with IFG after adjusting for age, BMI and sex in TwinsUK (FDR<0.05), KORA (p-value<0.1) and in the overall cohort (applying inverse variance random effect meta-analysis). The odds ratio (OR) and 95% confidence interval are indicated.

206x234mm (72 x 72 DPI)



Associations of the gut microbiota with the 8 faecal replicated metabolites and IFG in 342 TwinsUK participants. (A) Influence of the gut microbiota composition in the faecal abundances of the 8 replicated metabolites estimated by Random Forest regressors (Spearman's correlations between the real value of each metabolite and the value predicted) and classifiers (AUC). Red and blue bars represent the mean AUC and Spearman's correlations with the respective 95% confidence intervals across 5 folds, respectively. (B) Mediation analyses of the associations between characterised gut bacterial species and IFG. Models were adjusted for age, BMI, and sex. Path coefficients are shown beside each path, and indirect effects and variance accounted for (VAF) score are indicated below each mediator (left: nicotinate, right: 1-methylxanthine). Only metabolites with a predictive power of AUC>90% in '(A)' are shown.

520x744mm (118 x 118 DPI)

A faecal metabolite signature of impaired fasting glucose: results from two independent population-based cohorts

Ana Nogal^{1*}, Francesca Tettamanzi^{1,2*}, Qiuling Dong³, Panayiotis Louca¹, Alessia Visconti¹, Colette Christiansen¹, Taylor Breuninger⁴, Jakob Linseisen^{4,5,6}, Harald Grallert^{3,7}, Nina Wawro^{3a,4}, Francesco Asnicar⁸, Kari Wong⁹, Andrei-Florin Baleanu¹, Gregory A. Michelotti⁹, Nicola Segata⁸, Mario Falchi¹, Annette Peters^{3a,7,10}, Paul W. Franks^{11,12}, Vincenzo Bagnardi¹³, Tim D Spector¹, Jordana T Bell¹, Christian Gieger^{3,7}, Ana M Valdes¹⁴, Cristina Menni¹

Supplementary material

Metabolomics profiling

Metabolite concentrations were measured from faecal samples by Metabolon Inc. (Durham, USA) using an untargeted LC-MS platform. All samples were maintained at -80°C until processing. As a means of quality control, several recovery standards were added prior to the first step in the extraction process. Briefly, to remove protein, dissociate small molecules bound to proteins or trapped within the precipitated protein matrix, and to recover chemically diverse metabolites, proteins were precipitated in methanol and vigorously shaken for 2 minutes (Glen Mills GenoGrinder 2000), then centrifuged. The resulting extract was divided into five fractions; both aliquots (i) and (ii) were analysed using acidic positive ion conditions and chromatographically optimised for hydrophilic and hydrophobic compounds respectively, aliquot (iii) was analysed using a basic negative ion optimised conditions using a dedicated separate dedicated C18 column, aliquot (iv) was analysed using negative ionisation following

elution from a hydrophilic interaction liquid chromatography column, while aliquot (v) was reserved as a back-up.

Several controls were analysed in concert with experimental samples. (i) a pooled sample generated from a small volume of each experimental sample of interest served as a technical replicate throughout the platform run; (ii) extracted water samples served as process blanks; (iii) and a cocktail of standards, known not to interfere with measurements, spiked into every analysed sample facilitated instrument performance monitoring and aided chromatographic alignment. Instrument variability was determined by calculating the median relative standard deviation (RSD) for the standards that were added to each sample prior to injection into the mass spectrometers. Overall process variability was determined by calculating the median RSD for all endogenous metabolites (i.e., non-instrument standards) present in 100% or more of the pooled technical replicate samples. Experimental samples and controls were randomised across the platform run.

Compound identification

Metabolites were identified by comparison of the ion features in the experimental samples to a reference library of chemical standard entries that included retention time/index, molecular weight (m/z), and MS spectra. Identification of known chemical entities is based on comparison across all 3 features to metabolomic library entries of purified standards. More than 3300 commercially available purified standard compounds have been acquired and registered into the library, while additional mass spectral entries have been created for structurally unnamed biochemicals, which have been identified by virtue of their recurrent nature (both chromatographic and mass

spectral). These compounds have the potential to be identified by future acquisition of a matching purified standard or by classical structural analysis.

Metabolite quantification and normalisation

Peaks were quantified using area-under-the-curve. Raw area counts for each metabolite in each sample were normalised to correct for variation resulting from instrument inter-day tuning differences by the median value for each run-day, therefore, setting the medians to 1.0 for each run. This preserved variation between samples but allowed metabolites of widely different raw peak areas to be compared on a similar graphical scale.

Metagenomic assessment in TwinsUK

Faecal sample collection

Participants collected stool samples at home in pre-labelled kits (containing 2 x 25ml tube or 1 x 25ml tube and 1 x 10ml Zymo buffer), which were posted to them before their clinic visit date and brought with them to the visit. In the laboratory, samples were homogenised, aliquoted into 4 bijoux tubes, and stored at -80°C , within 2 hours of receipt.

DNA extraction, library preparation, and sequencing

To isolate genomic DNA from faecal material, bijoux tubes were removed from the freezer and grounded with glass beads and 5-6ml distilled water (Spex Grinder, 10 seconds, 800 strokes per minute). The supernatant was centrifuged and further

grounded (5 minutes, 1000 strokes per minute) before 200-300µl of the sample was mixed with 10µl PK solution and 720µl of Lysis/Bind Master Mix). Proteins were degraded by the binding solution and subsequently extracted by KingFisher Flex robot. DNA was washed in 2 steps using washing solutions and eluted in MagMax Core Elution Buffer in 100µl. Library preparation and sequencing was performed by GenomeScan.

Metagenome quality control and preprocessing

Sequenced metagenomes were processed using the YAMP pipeline (v. 0.9.5.3). Briefly, identical reads were removed. Reads were filtered to remove adapters, known artefacts, phix174, and then quality trimmed (PhRED quality score < 10). Reads that became too short after trimming (N < 60 bp) were discarded. We retained singleton reads (i.e., reads whose mate has been discarded) to retain as much information as possible. Contaminant reads belonging to the host genome were removed (build: GRCh37), and low-quality samples (i.e., samples with <10M reads after QC) were discarded.

Microbiome taxonomic profiling

The metagenomic analysis was conducted following the general guidelines and based on the bioBakery computational environment. High resolution taxonomic profiling of the metagenomes was performed using MetaPhlAn 4.beta.2 with the January 2021 database and default parameters.

Statistical analysis

We run random forest regression (1000 trees and a third of features number as number of variables randomly sampled as candidates at each split) and classification models (1000 trees and square root of features number as number of variables randomly sampled as candidates at each split) with compositional data using 5-folds cross-validation. Before running the models, gut microbiota variables with variance zero or near to zero were excluded using the `nearZeroVar` function implemented in R in the `caret` package (the included/excluded SGBs are shown in **Supplementary Table 6**). For the classifiers, the continuous response was converted into two classes based on the top and bottom quartiles. The features were ranked based on the node purity.

Super-pathway

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Peptide
Amino Acid
Xenobiotics
Amino Acid
Xenobiotics
Lipid
Lipid
Carbohydrate
Partially Characterized Molecules
Amino Acid
Lipid
Amino Acid
Carbohydrate
Lipid
Lipid
Xenobiotics
Amino Acid
Xenobiotics
Lipid
Amino Acid
Xenobiotics
Carbohydrate
Carbohydrate
Carbohydrate
Peptide
Carbohydrate
Carbohydrate
Carbohydrate
Xenobiotics
Amino Acid
Amino Acid
Amino Acid
Lipid
Carbohydrate

Carbohydrate
Xenobiotics
Amino Acid
Energy
Lipid
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Lipid
Cofactors and Vitamins
Lipid
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Xenobiotics
Xenobiotics
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Cofactors and Vitamins
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Cofactors and Vitamins

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Cofactors and Vitamins
Cofactors and Vitamins
Cofactors and Vitamins
Lipid
Lipid
Nucleotide
Lipid
Amino Acid
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Amino Acid
Lipid
Xenobiotics
Amino Acid
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Nucleotide
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Xenobiotics
Carbohydrate
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Xenobiotics
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Xenobiotics
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Cofactors and Vitamins
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Amino Acid

Xenobiotics
Amino Acid
Lipid
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Amino Acid
Amino Acid
Amino Acid
Amino Acid
Xenobiotics
Amino Acid
Xenobiotics
Amino Acid
Lipid
Partially Characterized Molecules
Partially Characterized Molecules
Xenobiotics
Peptide
Amino Acid
Amino Acid
Peptide
Amino Acid

Sub-pathway

Glutamate Metabolism
Tryptophan Metabolism
Pyrimidine Metabolism, Uracil containing
Methionine, Cysteine, SAM and Taurine Metabolism
Glutamate Metabolism
Glycine, Serine and Threonine Metabolism
Histidine Metabolism
Leucine, Isoleucine and Valine Metabolism
Sterol
Phenylalanine Metabolism
Fatty Acid, Dicarboxylate
Alanine and Aspartate Metabolism
Polyamine Metabolism
Alanine and Aspartate Metabolism
Creatine Metabolism
Pyrimidine Metabolism, Cytidine containing
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism
TCA Cycle
Mevalonate Metabolism
Pentose Metabolism
Phenylalanine Metabolism
Ketone Bodies
Purine Metabolism, Adenine containing
Purine Metabolism, Adenine containing
Phenylalanine Metabolism
Biotin Metabolism
Xanthine Metabolism
Pyrimidine Metabolism, Cytidine containing
Pentose Metabolism
Food Component/Plant
Nicotinate and Nicotinamide Metabolism
Food Component/Plant
Pyrimidine Metabolism, Orotate containing
Pyrimidine Metabolism, Thymine containing
Pyrimidine Metabolism, Uracil containing
Pyrimidine Metabolism, Uracil containing
Histidine Metabolism
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Secondary Bile Acid Metabolism
Long Chain Saturated Fatty Acid
Long Chain Saturated Fatty Acid
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Inositol Metabolism
Leucine, Isoleucine and Valine Metabolism

Alanine and Aspartate Metabolism
Sterol
Glycine, Serine and Threonine Metabolism
Tyrosine Metabolism
Lysine Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism
TCA Cycle
Long Chain Saturated Fatty Acid
Long Chain Saturated Fatty Acid
Long Chain Saturated Fatty Acid
Long Chain Saturated Fatty Acid
Polyamine Metabolism
Purine Metabolism, Guanine containing
Pyrimidine Metabolism, Uracil containing
Phenylalanine Metabolism
Tryptophan Metabolism
TCA Cycle
Lysine Metabolism
Pentose Metabolism
Secondary Bile Acid Metabolism
Urea cycle; Arginine and Proline Metabolism
Glutathione Metabolism
Lysine Metabolism
Nicotinate and Nicotinamide Metabolism
Pyrimidine Metabolism, Orotate containing
Pantothenate and CoA Metabolism
Sphingolipid Synthesis
Tryptophan Metabolism
Drug - Topical Agents
Purine Metabolism, Adenine containing
Long Chain Monounsaturated Fatty Acid
Purine Metabolism, Adenine containing
Polyamine Metabolism
Tocopherol Metabolism
TCA Cycle
Pyrimidine Metabolism, Thymine containing
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism
Purine Metabolism, Guanine containing
Histidine Metabolism
Alanine and Aspartate Metabolism
Leucine, Isoleucine and Valine Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism
Leucine, Isoleucine and Valine Metabolism
Pyrimidine Metabolism, Orotate containing
Tyrosine Metabolism
Purine Metabolism, (Hypo)Xanthine/Inosine containing

Urea cycle; Arginine and Proline Metabolism
Medium Chain Fatty Acid
TCA Cycle
Medium Chain Fatty Acid
Medium Chain Fatty Acid
Glycine, Serine and Threonine Metabolism
Leucine, Isoleucine and Valine Metabolism
Vitamin B6 Metabolism
Tyrosine Metabolism
Riboflavin Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism
Urea cycle; Arginine and Proline Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism
Urea cycle; Arginine and Proline Metabolism
Hemoglobin and Porphyrin Metabolism
Vitamin B6 Metabolism
Pyrimidine Metabolism, Thymine containing
Tryptophan Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Glycine, Serine and Threonine Metabolism
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Pyrimidine Metabolism, Uracil containing
Tryptophan Metabolism
Glycine, Serine and Threonine Metabolism
Thiamine Metabolism
Tryptophan Metabolism
Lysine Metabolism
Phenylalanine Metabolism
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Glycerolipid Metabolism
Bacterial/Fungal
Purine Metabolism, (Hypo)Xanthine/Inosine containing
Lysine Metabolism
Aminosugar Metabolism
Carnitine Metabolism
Phospholipid Metabolism
Pentose Metabolism
Glycogen Metabolism
Aminosugar Metabolism
Food Component/Plant
Leucine, Isoleucine and Valine Metabolism
Histidine Metabolism
Guanidino and Acetamido Metabolism
Lysine Metabolism
Histidine Metabolism

Glutamate Metabolism
TCA Cycle
Fatty Acid, Dicarboxylate
Leucine, Isoleucine and Valine Metabolism
Histidine Metabolism
Benzoate Metabolism
Leucine, Isoleucine and Valine Metabolism
Pentose Metabolism
Benzoate Metabolism
Fatty Acid Synthesis
Pyrimidine Metabolism, Cytidine containing
Phospholipid Metabolism
Benzoate Metabolism
Sphingosines
Sphingolipid Synthesis
Lysine Metabolism
Tyrosine Metabolism
Benzoate Metabolism
Lysine Metabolism
Food Component/Plant
Tryptophan Metabolism
Aminosugar Metabolism
Dipeptide
Fatty Acid, Dicarboxylate
Gamma-glutamyl Amino Acid
Methionine, Cysteine, SAM and Taurine Metabolism
Xanthine Metabolism
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Primary Bile Acid Metabolism
Secondary Bile Acid Metabolism
Fatty Acid, Dicarboxylate
Chemical
Leucine, Isoleucine and Valine Metabolism
Food Component/Plant
Benzoate Metabolism
Fatty Acid, Dicarboxylate
Food Component/Plant
Fatty Acid, Monohydroxy
Food Component/Plant
Monoacylglycerol
Leucine, Isoleucine and Valine Metabolism
Pyrimidine Metabolism, Uracil containing
Purine Metabolism, Adenine containing
Phenylalanine Metabolism
Leucine, Isoleucine and Valine Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism

Food Component/Plant
Alanine and Aspartate Metabolism
Food Component/Plant
Fatty Acid, Branched
Primary Bile Acid Metabolism
Sterol
Monoacylglycerol
Tryptophan Metabolism
Food Component/Plant
Thiamine Metabolism
Creatine Metabolism
Fructose, Mannose and Galactose Metabolism
Food Component/Plant
Pentose Metabolism
Ascorbate and Aldarate Metabolism
Dipeptide
Glutamate Metabolism
Vitamin B6 Metabolism
Glutamate Metabolism
Fatty Acid Metabolism (also BCAA Metabolism)
Secondary Bile Acid Metabolism
Secondary Bile Acid Metabolism
Fatty Acid Metabolism (also BCAA Metabolism)
Fatty Acid, Monohydroxy
Tyrosine Metabolism
Urea cycle; Arginine and Proline Metabolism
Primary Bile Acid Metabolism
Histidine Metabolism
Histidine Metabolism
Purine Metabolism, Guanine containing
Aminosugar Metabolism
Fatty Acid, Dicarboxylate
Tyrosine Metabolism
Xanthine Metabolism
Fatty Acid, Dicarboxylate
Nicotinate and Nicotinamide Metabolism
Tryptophan Metabolism
Food Component/Plant
Fatty Acid, Monohydroxy
Medium Chain Fatty Acid
Medium Chain Fatty Acid
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Monoacylglycerol
Urea cycle; Arginine and Proline Metabolism
Nicotinate and Nicotinamide Metabolism
Tocopherol Metabolism

Gamma-glutamyl Amino Acid
Pyrimidine Metabolism, Uracil containing
Short Chain Fatty Acid
Benzoate Metabolism
Long Chain Monounsaturated Fatty Acid
Nicotinate and Nicotinamide Metabolism
Glutamate Metabolism
Long Chain Monounsaturated Fatty Acid
Gamma-glutamyl Amino Acid
Food Component/Plant
Alanine and Aspartate Metabolism
Glutamate Metabolism
Histidine Metabolism
Phenylalanine Metabolism
Urea cycle; Arginine and Proline Metabolism
Lysophospholipid
Lysophospholipid
Tryptophan Metabolism
Leucine, Isoleucine and Valine Metabolism
Medium Chain Fatty Acid
Sterol
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Secondary Bile Acid Metabolism
Urea cycle; Arginine and Proline Metabolism
Sphingolipid Synthesis
Food Component/Plant
Urea cycle; Arginine and Proline Metabolism
Xanthine Metabolism
Phospholipid Metabolism
Dipeptide
Xanthine Metabolism
Xanthine Metabolism
Xanthine Metabolism
Xanthine Metabolism
Gamma-glutamyl Amino Acid
Leucine, Isoleucine and Valine Metabolism
Purine Metabolism, Guanine containing
Pyrimidine Metabolism, Uracil containing
Sterol
Leucine, Isoleucine and Valine Metabolism
Aminosugar Metabolism
Food Component/Plant
Lysophospholipid
Benzoate Metabolism
Glutathione Metabolism
Food Component/Plant

Chemical
Fatty Acid, Dicarboxylate
Fatty Acid, Monohydroxy
Fatty Acid, Dicarboxylate
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Food Component/Plant
Benzoate Metabolism
Benzoate Metabolism
Dipeptide
Advanced Glycation End-product
Leucine, Isoleucine and Valine Metabolism
Carnitine Metabolism
Fatty Acid, Dicarboxylate
Lysine Metabolism
Lysine Metabolism
Fatty Acid, Dicarboxylate
Food Component/Plant
Urea cycle; Arginine and Proline Metabolism
TCA Cycle
Gamma-glutamyl Amino Acid
Alanine and Aspartate Metabolism
Purine and Pyrimidine Metabolism
Glycine, Serine and Threonine Metabolism
Dipeptide
Urea cycle; Arginine and Proline Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism
Phospholipid Metabolism
Polyamine Metabolism
Tocopherol Metabolism
Tocopherol Metabolism
Sphingomyelins
Fatty Acid, Monohydroxy
Endocannabinoid
Food Component/Plant
Tryptophan Metabolism
Sterol
Endocannabinoid
Food Component/Plant
Food Component/Plant
Fatty Acid, Branched
Endocannabinoid
Nicotinate and Nicotinamide Metabolism
Drug - Other
Fatty Acid, Branched
Hemoglobin and Porphyrin Metabolism
Mevalonate Metabolism

Benzoate Metabolism
Food Component/Plant
Food Component/Plant
Dipeptide
Glutamate Metabolism
Dipeptide
Dipeptide
Hemoglobin and Porphyrin Metabolism
Hemoglobin and Porphyrin Metabolism
Phospholipid Metabolism
Histidine Metabolism
Chemical
Histidine Metabolism
Dipeptide
Food Component/Plant
Food Component/Plant
Short Chain Fatty Acid
Chemical
Dipeptide
Histidine Metabolism
Dipeptide
Dipeptide
Tyrosine Metabolism
Dipeptide
Oxidative Phosphorylation
Fatty Acid, Dicarboxylate
Lysophospholipid
Aminosugar Metabolism
Phosphatidylcholine (PC)
Fatty Acid, Monohydroxy
Biotin Metabolism
Fatty Acid, Dicarboxylate
Phenylalanine Metabolism
Pterin Metabolism
Food Component/Plant
Fatty Acid, Dicarboxylate
Lysine Metabolism
Urea cycle; Arginine and Proline Metabolism
Polyamine Metabolism
Food Component/Plant
Tryptophan Metabolism
Tyrosine Metabolism
Food Component/Plant
Food Component/Plant
Histidine Metabolism
Methionine, Cysteine, SAM and Taurine Metabolism

Lysine Metabolism
Tryptophan Metabolism
Fatty Acid, Amino
Hemoglobin and Porphyrin Metabolism
Gamma-glutamyl Amino Acid
Glycerolipid Metabolism
Leucine, Isoleucine and Valine Metabolism
Phenylalanine Metabolism
Leucine, Isoleucine and Valine Metabolism
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)
Glycogen Metabolism
Gamma-glutamyl Amino Acid
Methionine, Cysteine, SAM and Taurine Metabolism
Chemical
Methionine, Cysteine, SAM and Taurine Metabolism
Chemical
Lysophospholipid
Sterol
Fructose, Mannose and Galactose Metabolism
Partially Characterized Molecules
Lysine Metabolism
Secondary Bile Acid Metabolism
Leucine, Isoleucine and Valine Metabolism
Aminosugar Metabolism
Diacylglycerol
Diacylglycerol
Chemical
Methionine, Cysteine, SAM and Taurine Metabolism
Bacterial/Fungal
Fatty Acid, Monohydroxy
Guanidino and Acetamido Metabolism
Food Component/Plant
Aminosugar Metabolism
Glycolysis, Gluconeogenesis, and Pyruvate Metabolism
Fructose, Mannose and Galactose Metabolism
Dipeptide
Fructose, Mannose and Galactose Metabolism
Pentose Metabolism
Pentose Metabolism
Food Component/Plant
Tyrosine Metabolism
Urea cycle; Arginine and Proline Metabolism
Lysine Metabolism
Glycerolipid Metabolism
Pentose Metabolism

Glycolysis, Gluconeogenesis, and Pyruvate Metabolism
Food Component/Plant
Glutathione Metabolism
TCA Cycle
Long Chain Monounsaturated Fatty Acid
Fatty Acid, Dicarboxylate
Phospholipid Metabolism
Dihydrosphingomyelins
Phosphatidylcholine (PC)
Phosphatidylcholine (PC)
Tocopherol Metabolism
Phosphatidylcholine (PC)
Dihydroceramides
Endocannabinoid
Hexosylceramides (HCER)
Bacterial/Fungal
Bacterial/Fungal
Fatty Acid, Dicarboxylate
Fatty Acid, Dicarboxylate
Galactosyl Glycerolipids
Galactosyl Glycerolipids
Glutamate Metabolism
Diacylglycerol
Diacylglycerol
Diacylglycerol
Diacylglycerol
Gamma-glutamyl Amino Acid
Urea cycle; Arginine and Proline Metabolism
Fatty Acid Hydroxyl Fatty Acid
Food Component/Plant
Phospholipid Metabolism
Sphingolipid Synthesis
Sphingosines
Sphingosines
Ceramides
Urea cycle; Arginine and Proline Metabolism
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)
Fatty Acid Metabolism (Acyl Carnitine, Long Chain Saturated)
Endocannabinoid
Endocannabinoid
Sphingolipid Synthesis
Thiamine Metabolism
Secondary Bile Acid Metabolism
Secondary Bile Acid Metabolism
Vitamin A Metabolism

Sphingosines
Vitamin A Metabolism
Vitamin A Metabolism
Vitamin A Metabolism
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Long Chain Polyunsaturated Fatty Acid (n3 and n6)
Pyrimidine Metabolism, Uracil containing
Fatty Acid, Monohydroxy
Lysine Metabolism
Ceramides
Phenylalanine Metabolism
Leucine, Isoleucine and Valine Metabolism
Secondary Bile Acid Metabolism
Bacterial/Fungal
Polyamine Metabolism
Fatty Acid, Monohydroxy
Fatty Acid, Monohydroxy
Pyrimidine Metabolism, Uracil containing
Fatty Acid, Monohydroxy
Food Component/Plant
Pentose Metabolism
Fatty Acid, Dicarboxylate
Fatty Acid, Dicarboxylate
Fatty Acid, Dicarboxylate
Fatty Acid, Dicarboxylate
Polyamine Metabolism
Galactosyl Glycerolipids
Galactosyl Glycerolipids
Lysine Metabolism
Urea cycle; Arginine and Proline Metabolism
Lysine Metabolism
Lysine Metabolism
Food Component/Plant
Histidine Metabolism
Urea cycle; Arginine and Proline Metabolism
Fatty Acid, Dihydroxy
Fatty Acid, Dihydroxy
Fatty Acid, Dihydroxy
Sphingolipid Synthesis
Drug - Topical Agents
Sterol
Pantothenate and CoA Metabolism
Fatty Acid, Dihydroxy
Secondary Bile Acid Metabolism
Secondary Bile Acid Metabolism
Alanine and Aspartate Metabolism

Food Component/Plant
Tryptophan Metabolism
Fatty Acid, Dicarboxylate
Fatty Acid, Dicarboxylate
Phenylalanine Metabolism
Phenylalanine Metabolism
Leucine, Isoleucine and Valine Metabolism
Leucine, Isoleucine and Valine Metabolism
Food Component/Plant
Methionine, Cysteine, SAM and Taurine Metabolism
Chemical
Polyamine Metabolism
Sterol
Partially Characterized Molecules
Partially Characterized Molecules
Chemical
Polypeptide
Tryptophan Metabolism
Lysine Metabolism
Modified Peptides
Histidine Metabolism

Metabolite

glutamine
tryptophan
beta-alanine
cystine
glutamate
glycine
histidine
leucine
cholesterol
phenylalanine
glutarate (C5-DC)
aspartate
spermidine
asparagine
creatinine
cytidine
lactate
alpha-ketoglutarate
3-hydroxy-3-methylglutarate
2-deoxyribose
4-hydroxyphenylacetate
3-hydroxybutyrate (BHBA)
adenine
adenosine
phenylpyruvate
biotin
caffeine
cytosine
arabinose
gluconate
nicotinamide
phytanate
dihydroorotate
thymine
uracil
uridine
trans-urocanate
linoleate (18:2n6)
allantoin
deoxycholate
arachidate (20:0)
margarate (17:0)
inosine
myo-inositol
isoleucine

alanine
lanosterol
threonine
tyrosine
lysine
methionine
malate
palmitate (16:0)
nonadecanoate (19:0)
stearate (18:0)
myristate (14:0)
putrescine
2'-deoxyguanosine
2'-deoxyuridine
3-hydroxyphenylacetate
kynurenate
succinate
pipercolate
ribose
lithocholate
ornithine
5-oxoproline
N6,N6,N6-trimethyllysine
nicotinate
orotate
pantothenate
phytosphingosine
picolinate
salicylate
1-methyladenine
erucate (22:1n9)
2'-deoxyadenosine
4-acetamidobutanoate
alpha-tocopherol
citrate
3-aminoisobutyrate
glycerate
guanosine
histamine
N-acetylalanine
N-acetylleucine
N-acetylmethionine
N-acetylvaline
N-carbamoylaspartate
tyramine
urate

arginine
caprate (10:0)
fumarate
heptanoate (7:0)
laurate (12:0)
serine
valine
pyridoxal
4-hydroxyphenylpyruvate
riboflavin (Vitamin B2)
cysteine
proline
taurine
citrulline
biliverdin
pyridoxamine
thymidine
serotonin
N-formylmethionine
hypoxanthine
betaine
xanthine
3-ureidopropionate
anthranilate
dimethylglycine
thiamin (Vitamin B1)
tryptamine
2-aminoadipate
phenethylamine
2'-deoxyinosine
glycerol
diaminopimelate
xanthosine
cadaverine
glucuronate
carnitine
choline
xylose
maltose
fucose
2-isopropylmalate
3-methyl-2-oxovalerate
3-methylhistidine
4-guanidinobutanoate
5-hydroxylysine
imidazole lactate

N-acetylglutamate
tricarballylate
suberate (C8-DC)
methylsuccinate
anserine
3-phenylpropionate (hydrocinnamate)
ethylmalonate
ribitol
benzoate
malonate
2'-deoxycytidine
glycerophosphorylcholine (GPC)
p-hydroxybenzaldehyde
sphingosine
sphinganine
N6-formyllysine
gentisate
3,4-dihydroxybenzoate
5-aminovalerate
quinate
indolelactate
N-acetylmuramate
glycylvaline
azelate (C9-DC)
gamma-glutamylleucine
methionine sulfoxide
theophylline
eicosapentaenoate (EPA; 20:5n3)
glycocholate
glycodeoxycholate
maleate
diethanolamine
2,3-dimethylsuccinate
galacturonate
4-hydroxybenzoate
adipate (C6-DC)
saccharin
3-hydroxymyristate
caffeate
1-oleoylglycerol (18:1)
4-methyl-2-oxopentanoate
4-ureidobutyrate
N6-dimethylallyladenine
phenyllactate (PLA)
alpha-hydroxyisocaproate
cysteine s-sulfate

levulinate (4-oxovalerate)
N-acetylaspartate (NAA)
theanine
isocaproate (i6:0)
cholate
beta-sitosterol
1-linoleoylglycerol (18:2)
indoleacetate
harmane
5-(2-Hydroxyethyl)-4-methylthiazole
creatine
galactonate
erythrose
ribonate
threonate
threonylphenylalanine
N-methylglutamate
pyridoxate
2-pyrrolidinone
butyrylglycine
dehydrolithocholate
7-ketodeoxycholate
propionylglycine
5-hydroxyhexanoate
3-(4-hydroxyphenyl)lactate
trans-4-hydroxyproline
glycochenodeoxycholate
4-imidazoleacetate
1-methyl-4-imidazoleacetate
guanine
N-acetylneuraminate
dodecanedioate (C12-DC)
N-acetyltyrosine
1,3-dimethylurate
sebacate (C10-DC)
trigonelline (N'-methylnicotinate)
indolepropionate
daidzein
3-hydroxylaurate
caproate (6:0)
caprylate (8:0)
docosapentaenoate (n3 DPA; 22:5n3)
2-linoleoylglycerol (18:2)
N-alpha-acetylornithine
nicotinamide riboside
delta-tocopherol

gamma-glutamylphenylalanine
pseudouridine
valerate (5:0)
p-cresol
palmitoleate (16:1n7)
nicotinate ribonucleoside
glutamate, gamma-methyl ester
eicosenoate (20:1)
gamma-glutamyl-epsilon-lysine
piperine
N-acetylasparagine
N-acetylglutamine
N-acetylhistidine
N-acetylphenylalanine
N-acetylarginine
1-palmitoyl-GPC (16:0)
1-stearoyl-GPC (18:0)
indole
N-acetylisoleucine
5-dodecenoate (12:1n7)
campesterol
linolenate [alpha or gamma; (18:3n3 or 6)]
hyocholate
methylurea
3-ketosphinganine
stachydrine
N-acetylproline
1-methylxanthine
choline phosphate
glycylleucine
3,7-dimethylurate
1,7-dimethylurate
1,3,7-trimethylurate
5-acetylamino-6-amino-3-methyluracil
gamma-glutamylisoleucine*
isovalerylglycine
7-methylguanine
5-methyluridine (ribothymidine)
cholesterol sulfate
isobutyrylglycine
N-acetyl-beta-glucosaminylamine
ferulate
1-palmitoyl-GPE (16:0)
3-(3-hydroxyphenyl)propionate
cysteinylglycine
vanillate

ectoine
tetradecanedioate (C14-DC)
2-hydroxypalmitate
hexadecanedioate (C16-DC)
dihomo-linolenate (20:3n3 or n6)
pheophorbide A
2,4,6-trihydroxybenzoate
p-cresol sulfate
glycylisoleucine
N6-carboxymethyllysine
2-hydroxy-3-methylvalerate
deoxycarnitine
3-methyladipate
N2-acetyllysine
N6-acetyllysine
octadecanedioate (C18-DC)
4-hydroxycinnamate
dimethylarginine (SDMA + ADMA)
succinylcarnitine (C4-DC)
gamma-glutamylalanine
N-methylalanine
methylphosphate
N-acetylserine
alanylleucine
N-methylproline
cysteine sulfinic acid
glycerophosphoethanolamine
N-acetylputrescine
gamma-tocotrienol
alpha-tocotrienol
palmitoyl sphingomyelin (d18:1/16:0)
13-HODE + 9-HODE
oleoyl ethanolamide
2-aminophenol
indole-3-carboxylate
4-cholesten-3-one
palmitoyl ethanolamide
piperidine
2,3-dihydroxyisovalerate
(16 or 17)-methylstearate (a19:0 or i19:0)
stearoyl ethanolamide
maleamate
N-carbamoylglutamate
(14 or 15)-methylpalmitate (a17:0 or i17:0)
protoporphyrin IX
mevalonate

3-(4-hydroxyphenyl)propionate
enterolactone
solanidine
valylleucine
carboxyethyl-GABA
isoleucylglycine
leucylglycine
D-urobilin
L-urobilin
trimethylamine N-oxide
cis-urocanate
2-oxo-1-pyrrolidinepropionate
hydantoin-5-propionate
valylglycine
2-oxindole-3-acetate
dihydroferulate
butyrate/isobutyrate (4:0)
diglycerol
prolylglycine
imidazole propionate
phenylalanylglycine
phenylalanylalanine
tyrosol
valylglutamine
phosphate
undecanedioate (C11-DC)
1-stearoyl-GPE (18:0)
erythronate*
1-palmitoyl-2-linoleoyl-GPC (16:0/18:2)
2-hydroxydecanoate
biocytin
dimethylmalonic acid
N-methylphenylalanine
pterin
nicotianamine
tridecanedioate (C13-DC)
6-oxopiperidine-2-carboxylate
N-delta-acetylmethionine
acisoga
indolin-2-one
tryptophol
o-Tyrosine
2-piperidinone
1-methyl-beta-carboline-3-carboxylic acid
formiminoglutamate
N-propionylmethionine

N-acetyl-cadaverine
N-formylanthranilic acid
2-aminoheptanoate
bilirubin (Z,Z)
gamma-glutamylvaline
glycerol 3-phosphate
3-methyl-2-oxobutyrate
valerylphenylalanine
isovalerate (i5:0)
docosahexaenoate (DHA; 22:6n3)
palmitoylcarnitine (C16)
maltotriose
gamma-glutamylmethionine
methionine sulfone
O-sulfo-L-tyrosine
N-acetylmethionine sulfoxide
1,3-propanediol
1-palmitoyl-GPG (16:0)*
coprostanol
mannitol/sorbitol
glutamine_degradant*
fructosyllysine
6-oxolithocholate
alpha-hydroxyisovalerate
N-acetylglucosamine/N-acetylgalactosamine
oleoyl-linoleoyl-glycerol (18:1/18:2) [1]
oleoyl-linoleoyl-glycerol (18:1/18:2) [2]
sulfate*
3-sulfo-L-alanine
N-methylpiperolate
10-hydroxystearate
1-methylguanidine
2-keto-3-deoxy-gluconate
N-acetylglucosaminylasparagine
glucose
mannose
leucylglutamine*
fructose
arabonate/xylonate
ribulose/xylulose
pyrraline
N-formylphenylalanine
N-acetylcitrulline
N2,N6-diacetyllysine
glycerophosphoglycerol
arabitol/xylitol

pyruvate
 sitostanol
 2-hydroxybutyrate/2-hydroxyisobutyrate
 2-methylcitrate/homocitrate
 oleate/vaccenate (18:1)
 2-hydroxyglutarate
 glycerophosphoinositol*
 palmitoyl dihydrosphingomyelin (d18:0/16:0)*
 1-oleoyl-2-linoleoyl-GPC (18:1/18:2)*
 1-palmitoyl-2-oleoyl-GPC (16:0/18:1)
 gamma-tocopherol/beta-tocopherol
 1,2-dilinoleoyl-GPC (18:2/18:2)
 N-palmitoyl-sphinganine (d18:0/16:0)
 linoleoyl ethanolamide
 glycosyl-N-palmitoyl-sphingosine (d18:1/16:0)
 glutamyl-meso-diaminopimelate
 2-acetamidobutanoate
 3-methylglutarate/2-methylglutarate
 3-carboxyadipate
 1-palmitoyl-2-linoleoyl-digalactosylglycerol (16:0/18:2)*
 1,2-dilinoleoyl-galactosylglycerol (18:2/18:2)*
 butyrylglutamine/isobutyrylglutamine
 linoleoyl-linolenoyl-glycerol (18:2/18:3) [1]*
 linoleoyl-linolenoyl-glycerol (18:2/18:3) [2]*
 linoleoyl-linoleoyl-glycerol (18:2/18:2) [1]*
 linoleoyl-linoleoyl-glycerol (18:2/18:2) [2]*
 gamma-glutamyl-alpha-lysine
 2-oxoarginine*
 LAHSA (18:2/OH-18:0)*
 deoxymugineic acid
 glycerophosphoserine*
 sphingadienine
 heptadecasphingosine (d17:1)
 hexadecasphingosine (d16:1)*
 ceramide (d18:1/14:0, d16:1/16:0)*
 argininate*
 arachidoylcarnitine (C20)*
 behenoylcarnitine (C22)*
 lignoceroylcarnitine (C24)*
 behenoyl ethanolamide (22:0)*
 lignoceroyl ethanolamide (24:0)*
 hexadecasphinganine (d16:0)*
 hydroxymethylpyrimidine
 ursocholate
 isoursodeoxycholate
 beta-cryptoxanthin

eicosanoylsphingosine (d20:1)*
carotene diol (1)
carotene diol (2)
carotene diol (3)
hexadecatrienoate (16:3n3)
hexadecadienoate (16:2n6)
2'-O-methyluridine
2-hydroxybehenate
N,N,N-trimethyl-5-aminovalerate
N-(2-hydroxypalmitoyl)-sphingosine (d18:1/16:0(2OH))
phenylacetate
3-methylglutaconate
isohydroxycholelate
Urolithin A
(N(1) + N(8))-acetylspermidine
2-hydroxylignocerate*
2-hydroxyarachidate*
5,6-dihydrouridine
3-hydroxyoleate*
pheophytin A
lyxonate
octadecenedioate (C18:1-DC)
heptenedioate (C7:1-DC)*
3-carboxy-4-methyl-5-pentyl-2-furanpropionate (3-CMPFP)**
3-hydroxyadipate
diacetylspermidine*
1-palmitoyl-galactosylglycerol (16:0)*
2-palmitoyl-galactosylglycerol (16:0)*
N,N-dimethyl-5-aminovalerate
3-amino-2-piperidone
N6-methyllysine
N6,N6-dimethyllysine
3-formylindole
1-methyl-5-imidazoleacetate
N,N,N-trimethyl-alanylproline betaine (TMAP)
2S,3R-dihydroxybutyrate
2,4-dihydroxybutyrate
3,4-dihydroxybutyrate
dehydrophytosphingosine*
2,6-dihydroxybenzoic acid
stigmastadienone
pantoate
2R,3R-dihydroxybutyrate
12-ketolithocholate
3-dehydrodeoxycholelate
N,N-dimethylalanine

N-carboxymethylalanine
5-hydroxypicolinic acid
branched chain 14:0 dicarboxylic acid**
2-hydroxysebacate
N-butyryl-phenylalanine
N-isobutyryl-phenylalanine
N-butyryl-leucine
N-butyryl-isoleucine
3-indoleglyoxylic acid
2-hydroxy-4-(methylthio)butanoic acid
dibutyl sulfosuccinate
N-carbamoylputrescine
25-hydroxycholesterol sulfate
bilirubin degradation product, C₁₆H₁₈N₂O₅ (1)**
bilirubin degradation product, C₁₆H₁₈N₂O₅ (3)**
diethyl phosphate
val-val-ala
oxindolylalanine
N-butyryl-lysine
N,N-dimethyl-pro-pro
1-methyl-5-imidazolelactate

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	yes
	yes
C00059	yes
C00506	yes
	yes
C03195	yes
C02294	yes
C00204	no
C04540	yes
C00031	yes
C00159,C02209,C00936	yes
	yes
C00095	yes
C00502,C05411	no
	no
C21013	yes
	yes
C15532,C02851	yes
	no
C03274	yes
C00379,C00542,C01904	no

C00022	no
C19644	yes
C21297,C05984	yes
C01251	no
C21944,C08367,C01712,C00712	no
C02630	yes
	yes
	yes
	no
C13875	no
C14152,C02483	yes
	no
	yes
	no
	yes
	no
	yes
	yes
	yes
	yes
	yes
	no
	yes
	yes
	yes
	yes
	yes
C03771	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
	yes
C13915	yes
C01279	no
C17644	yes
C17662	yes
C08591	yes

	yes
	yes
	yes
	yes
	yes
	yes
	no
	no
	yes
	yes
C07086	no
	no
	no
	no
C01029,C00612	no
C17873	no
	no
	no
C05797	no
	no
	no
	no
	no
C03413	no
	no
	no
	no
	no
C02728	no
C05545	no
C08493	no
	no
	no
	no
	no
	no
	no
	no
	no
	no
	no
	no
	no
	no
C00522	no
	no
	no
	no
	no
	no

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	Total	Healthy individuals	IFG individuals	Differences between groups (p-value)
N	342	297	45	-
Females, %	83.9	86.2	68.9	0.006
Age, yrs	56 (16.6)	54.3 (16.8)	67.4 (9.3)	<0.0001
BMI, kg/m²	25.6 (5)	25 (4.6)	29.4 (6.1)	<0.0001
Fasting glucose, mmol/L	4.7 (0.5)	4.5 (0.2)	5.8 (0.3)	<0.0001
SBP, mmHg	126.7 (13.7)	126 (12.6)	134 (17.7)	0.002
DBP, mmHg	74.2 (7.5)	73.8 (6.8)	76.9 (10.8)	0.07
Circulating total cholesterol, mmol/L	4.1 (0.5)	4.1 (0.5)	4 (0.7)	0.25
Circulating HDL, mmol/L	1.87 (1.3)	1.91 (1.3)	1.6 (0.8)	0.15
Circulating triglycerides, mmol/L	0.94 (1.1)	0.91 (1.1)	1.11 (1)	0.03
aHEI	70.6 (5.7)	70.6 (5.6)	70.8 (6.3)	0.88
Current Smoker	No: 331 Yes: 11	No: 286 Yes: 11	No: 45	0.39
Activity level	Low: 25 Moderate: 259 High: 58	Low: 22 Moderate: 225 High: 50	Low: 3 Moderate: 34 High: 8	0.98

Metabolite name	AUC (%) [95% CI]	Spearman's rho [95% CI]
Protoporphyrin IX	64.8 [63.9,65.6]	0.25 [0.24,0.26]
Caffeine	70.7 [69.1,72.4]	0.24 [0.23,0.25]
Serine	79.1 [78.1,80]	0.44 [0.43,0.45]
Cholesterol	80 [78.4,81.5]	0.46 [0.45,0.47]
Uridine	84.1 [83.1,85]	0.48 [0.47,0.49]
Glucuronate	88.6 [87.4,89.7]	0.53 [0.52,0.54]
Nicotinate	90.5 [89.9,91]	0.59 [0.58,0.6]
1-methylxanthine	91.4 [90.8,91.9]	0.62 [0.62,0.62]

bacteria

k_Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Streptococcaceae|g__Streptococcus|s__Strepto
 k_Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Streptococcaceae|g__Streptococcus|s__Strepto
 k_Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Streptococcaceae|g__Streptococcus|s__Strepto
 k_Bacteria|p__Firmicutes|c__CFGB3047|o__OFGB3047|f__FGB3047|g__GGB9557|s__GGB9557_SGB14966
 k_Bacteria|p__Firmicutes|c__CFGB9612|o__OFGB9612|f__FGB9612|g__GGB45495|s__GGB45495_SGB631
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Candidatu
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Candidatu
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_
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 k_Archaea|p__Euryarchaeota|c__Methanobacteria|o__Methanobacteriales|f__Methanobacteriaceae|g__M
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Christensenellaceae|g__Christensenellaceae_u
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Christensenellaceae|g__Christensenellaceae_u
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Christensenellaceae|g__Christensenellaceae_u
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Clostridiaceae|g__Clostridiaceae_unclassified|s
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Clostridiaceae|g__Clostridiaceae_unclassified|s
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Clostridiaceae|g__Clostridium|s__Clostridium_
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Clostridiaceae|g__Clostridium|s__Clostridium_
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Clostridiales_unclassified|g__Clostridiales_uncl
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Clostridiales_unclassified|g__Lawsonibacter|s_
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Eubacteriaceae|g__Eubacterium|s__Eubacteriu
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Blautia|s__Blautia_faecis|
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Blautia|s__Blautia_massili
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Blautia|s__Blautia_obeun
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 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Blautia|s__Blautia_SGB48
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Blautia|s__Blautia_wexler
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Coproccoccus|s__Coprocco
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_formicig
 k_Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_longicat

k__Bacteria|p__Firmicutes|c__Bacilli|o__Bacillales|f__Bacillales_unclassified|g__Gemella|s__Gemella_sangi

estimate	SE	p_val	n	fdr	g_Random	prevalence
0.31	0.14	0.035	342	0.201	88	57.02%
0.28	0.16	0.079	342	0.264	96	77.78%
0.29	0.16	0.063	342	0.264	25	45.61%
0.17	0.17	0.325	342	0.608	53	46.78%
-0.3	0.27	0.258	342	0.526	54	31.29%
0.4	0.16	0.016	342	0.154	13	59.36%
-0.24	0.22	0.28	342	0.56	77	19.30%
0.38	0.16	0.015	342	0.154	72	66.96%
-0.49	0.23	0.032	342	0.198	7	55.56%
-0.02	0.18	0.927	342	0.983	65	86.26%
-0.07	0.19	0.711	342	0.857	95	48.54%
-0.16	0.19	0.396	342	0.648	76	59.36%
-0.1	0.18	0.575	342	0.777	27	61.11%
-0.08	0.22	0.708	342	0.857	14	67.25%
-0.1	0.22	0.657	342	0.816	18	43.86%
0.29	0.17	0.092	342	0.282	80	91.23%
-0.38	0.24	0.109	342	0.302	100	24.27%
-0.12	0.2	0.531	342	0.769	91	55.26%
0.05	0.17	0.778	342	0.892	3	63.74%
-0.43	0.22	0.058	342	0.262	50	47.95%
-0.01	0.17	0.958	342	0.988	32	50.88%
0.16	0.15	0.301	342	0.579	74	49.71%
-0.34	0.23	0.136	342	0.341	85	52.05%
-0.67	0.29	0.02	342	0.157	36	35.09%
-0.17	0.19	0.373	342	0.648	84	72.51%
-0.25	0.19	0.184	342	0.417	33	51.46%
0.11	0.18	0.539	342	0.769	56	50.00%
0.28	0.16	0.082	342	0.264	20	73.68%
0.24	0.15	0.111	342	0.302	67	26.61%
0.59	0.17	0.001	342	0.015	30	95.32%
0.11	0.18	0.557	342	0.769	40	49.42%
0.11	0.19	0.561	342	0.769	8	78.95%
0.28	0.16	0.08	342	0.264	9	61.40%
-0.05	0.19	0.785	342	0.892	44	43.57%
0.12	0.17	0.468	342	0.714	47	57.02%
-0.01	0.2	0.944	342	0.983	78	19.01%
0.06	0.18	0.733	342	0.873	15	83.33%
-0.17	0.24	0.472	342	0.714	19	45.03%
-0.24	0.25	0.328	342	0.608	41	56.43%
0.22	0.16	0.172	342	0.399	52	73.39%
0.25	0.16	0.132	342	0.339	63	99.42%
0.38	0.17	0.024	342	0.16	58	92.98%
0.13	0.17	0.443	342	0.692	51	53.22%
0.31	0.17	0.073	342	0.264	69	97.08%
0.04	0.17	0.829	342	0.921	97	86.26%
0.37	0.16	0.02	342	0.157	23	99.42%
0.23	0.17	0.189	342	0.42	60	85.67%
0.62	0.17	0	342	0.015	82	96.20%
0.29	0.16	0.08	342	0.264	48	89.18%

0.47	0.16	0.004	342	0.056	90	68.42%
0.56	0.16	0.001	342	0.015	70	93.27%
0.1	0.18	0.603	342	0.784	71	50.00%
0.06	0.17	0.744	342	0.874	10	78.07%
0.14	0.17	0.402	342	0.649	92	71.93%
0.4	0.17	0.017	342	0.154	11	97.08%
0.28	0.18	0.118	342	0.309	34	70.47%
0.03	0.22	0.892	342	0.965	98	24.27%
0.47	0.17	0.005	342	0.058	31	96.78%
0.24	0.17	0.161	342	0.384	99	91.23%
-0.18	0.21	0.388	342	0.648	73	67.54%
0.1	0.15	0.523	342	0.769	5	61.99%
0.11	0.19	0.553	342	0.769	17	66.08%
0.14	0.18	0.44	342	0.692	49	86.84%
0.34	0.18	0.066	342	0.264	61	86.26%
-0.17	0.19	0.377	342	0.648	21	77.49%
-0.4	0.24	0.093	342	0.282	66	56.14%
0.4	0.18	0.024	342	0.16	75	83.04%
0.55	0.17	0.001	342	0.02	59	84.80%
-0.2	0.19	0.294	342	0.577	45	77.78%
0	0.16	0.998	342	0.998	24	71.64%
0.04	0.17	0.799	342	0.898	26	85.96%
-0.16	0.19	0.395	342	0.648	86	75.73%
0.26	0.18	0.143	342	0.348	12	92.11%
-0.06	0.19	0.752	342	0.874	79	75.15%
0.12	0.17	0.496	342	0.74	55	90.94%
-0.32	0.2	0.112	342	0.302	16	92.69%
0.21	0.18	0.233	342	0.486	4	88.30%
-0.03	0.19	0.863	342	0.949	42	85.67%
-0.53	0.26	0.038	342	0.202	2	94.74%
-0.24	0.2	0.223	342	0.485	28	82.16%
0.36	0.19	0.058	342	0.262	64	39.47%
-0.43	0.24	0.077	342	0.264	57	43.27%
-0.55	0.32	0.08	342	0.264	38	53.22%
-0.53	0.45	0.233	342	0.486	43	25.15%
0.02	0.19	0.897	342	0.965	35	85.67%
-0.8	0.26	0.002	342	0.038	39	43.57%
0.01	0.18	0.938	342	0.983	87	93.86%
-0.77	0.37	0.036	342	0.201	37	31.58%
0.08	0.17	0.661	342	0.816	1	98.25%
0	0.18	0.992	342	0.998	89	61.99%
0.54	0.16	0.001	342	0.015	22	83.33%
0.07	0.16	0.65	342	0.816	6	89.18%
-0.43	0.26	0.101	342	0.297	29	77.19%
0.16	0.17	0.349	342	0.635	94	56.43%
0	0.17	0.997	342	0.998	81	95.91%
-0.16	0.19	0.382	342	0.648	68	78.95%
0.09	0.19	0.639	342	0.816	46	67.54%
-0.09	0.17	0.591	342	0.784	83	57.02%
-0.11	0.22	0.603	342	0.784	62	40.35%

0.29 0.15 0.05 342 0.251 93 44.15%

bacteria

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
k_Bacteria|p_Firmicutes|c_CFGB3035|o_OFGB3035|f_FGB3035|g_GGB9524|s_GGB9524_SGB14924
k_Bacteria|p_Firmicutes|c_CFGB40382|o_OFGB40382|f_FGB40382|g_GGB45491|s_GGB45491_SGE
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB2980|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9176|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9342|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9347|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9522|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9787|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenellaceae_u
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenellaceae_u
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Intestinimonas|s_
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Lawsonibacter|s_
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Massilistercora|s_
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Anaerostipes|s_Anaeros
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_caecir
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_faecis|
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_SGB48
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_sp_MS
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_wexler
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Coprococcus|s_Coproco
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Coprococcus|s_Coproco
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_formicig
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_longicat
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_sp_AF24
k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Faecalicatena|s_Faecalic

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Fusicatenibacter|s_Fusic
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_M
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_M
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_Ru
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_Ru
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_Ru
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Roseburia|s_Roseburia_i
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Agathobaculum|s_Agat
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaeromassilibacillus|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaerotruncus|s_Anae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Candidatus_Cibiobacter|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Flavonifractor|s_Flavor
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9602|s_GGB9602_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9633|s_GGB9633_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9635|s_GGB9635_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9646|s_GGB9646_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9677|s_GGB9677_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9694|s_GGB9694_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9699|s_GGB9699_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9705|s_GGB9705_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9730|s_GGB9730_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Massilimalia|s_Massili
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Neobittarella|s_Neobit
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruthenibacterium|s_Ru
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Faecalibacill
 k_Bacteria|p_Firmicutes|c_Firmicutes_unclassified|o_Firmicutes_unclassified|f_Firmicutes_unclassifie
 k_Bacteria|p_Firmicutes|c_Firmicutes_unclassified|o_Firmicutes_unclassified|f_Firmicutes_unclassifie
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Adlercreutzia|s_
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthella|s_I
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_I
 k_Bacteria|p_Verrucomicrobia|c_Verrucomicrobiae|o_Verrucomicrobiales|f_Akkermansiaceae|g_Akl
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_GGB45432|s_G
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_

k__Bacteria|p__Bacteroidetes|c__Bacteroidia|o__Bacteroidales|f__Rikenellaceae|g__Alistipes|s__Alistipes_

estimate	SE	p_val	n	fdr	ing_RandomFo	prev
0.31	0.14	0.035	342	0.151	44	57.02%
0.29	0.16	0.063	342	0.216	38	45.61%
-0.93	0.31	0.002	342	0.04	35	50.29%
0.21	0.15	0.184	342	0.411	22	39.47%
0.4	0.16	0.016	342	0.13	69	59.36%
0.28	0.16	0.085	342	0.259	73	58.48%
-0.27	0.21	0.206	342	0.426	40	22.22%
-0.79	0.29	0.008	342	0.07	94	36.84%
-0.49	0.23	0.032	342	0.151	6	55.56%
-0.02	0.18	0.927	342	0.966	30	86.26%
-0.16	0.19	0.396	342	0.599	93	59.36%
-0.1	0.18	0.575	342	0.747	25	61.11%
-0.16	0.18	0.365	342	0.588	15	42.11%
-0.08	0.22	0.708	342	0.843	3	67.25%
-0.1	0.22	0.657	342	0.815	24	43.86%
-0.06	0.16	0.728	342	0.857	42	42.11%
0.29	0.17	0.092	342	0.269	51	91.23%
-0.58	0.25	0.021	342	0.13	78	31.29%
-0.18	0.2	0.376	342	0.588	57	52.63%
-0.12	0.2	0.531	342	0.718	95	55.26%
0.05	0.17	0.778	342	0.864	5	63.74%
-0.43	0.22	0.058	342	0.205	2	47.95%
-0.01	0.17	0.958	342	0.988	10	50.88%
0.14	0.18	0.43	342	0.623	58	61.70%
-0.68	0.34	0.043	342	0.161	64	23.98%
-0.34	0.23	0.136	342	0.35	4	52.05%
-0.67	0.29	0.02	342	0.13	14	35.09%
-0.17	0.19	0.373	342	0.588	1	72.51%
-0.25	0.19	0.184	342	0.411	54	51.46%
0.28	0.16	0.082	342	0.256	28	73.68%
0.24	0.15	0.111	342	0.301	43	26.61%
0.59	0.17	0.001	342	0.015	65	95.32%
-0.03	0.18	0.851	342	0.915	98	87.13%
0.02	0.15	0.88	342	0.937	67	12.87%
-0.17	0.24	0.472	342	0.664	12	45.03%
-0.24	0.25	0.328	342	0.576	27	56.43%
-0.11	0.19	0.565	342	0.747	33	36.55%
0.2	0.17	0.249	342	0.469	53	99.42%
-0.08	0.19	0.669	342	0.815	96	28.95%
0.25	0.16	0.132	342	0.348	80	99.42%
0.04	0.17	0.829	342	0.901	17	86.26%
0.33	0.16	0.038	342	0.151	90	60.23%
0.37	0.16	0.02	342	0.13	11	99.42%
0.23	0.17	0.189	342	0.411	76	85.67%
0.37	0.17	0.032	342	0.151	99	90.06%
0.63	0.17	0	342	0.015	77	96.20%
0.47	0.16	0.004	342	0.056	87	68.42%
0.55	0.16	0	342	0.015	48	76.32%
0.06	0.17	0.744	342	0.863	61	78.07%

0.4	0.17	0.017	342	0.13	13	97.08%
0.47	0.17	0.005	342	0.058	60	96.78%
0.14	0.18	0.44	342	0.628	81	86.84%
-0.17	0.19	0.377	342	0.588	8	77.49%
0.4	0.18	0.024	342	0.133	82	83.04%
0.18	0.16	0.265	342	0.491	46	34.21%
-0.21	0.23	0.361	342	0.588	86	50.88%
0.25	0.16	0.111	342	0.301	37	53.51%
0.55	0.17	0.001	342	0.02	55	84.80%
0	0.16	0.998	342	0.998	70	71.64%
0.26	0.18	0.143	342	0.35	20	92.11%
-0.06	0.19	0.752	342	0.863	74	75.15%
-0.17	0.2	0.381	342	0.588	89	47.08%
0.12	0.17	0.496	342	0.689	39	90.94%
0.21	0.18	0.233	342	0.456	47	88.30%
-0.53	0.26	0.038	342	0.151	62	94.74%
-0.24	0.2	0.223	342	0.446	56	82.16%
0.13	0.16	0.417	342	0.614	75	75.15%
-0.27	0.2	0.189	342	0.411	23	64.04%
-0.13	0.2	0.526	342	0.718	92	40.94%
-0.66	0.24	0.007	342	0.067	19	53.80%
-0.22	0.19	0.248	342	0.469	34	47.08%
-0.43	0.24	0.077	342	0.256	84	43.27%
-0.55	0.32	0.08	342	0.256	7	53.22%
0.02	0.19	0.897	342	0.944	18	85.67%
-0.73	0.27	0.006	342	0.066	100	52.34%
0.15	0.18	0.412	342	0.614	97	77.19%
0.22	0.17	0.193	342	0.411	66	61.99%
0.35	0.16	0.031	342	0.151	59	36.84%
-0.09	0.22	0.676	342	0.815	68	63.45%
-0.77	0.37	0.036	342	0.151	16	31.58%
0.05	0.18	0.76	342	0.863	32	63.74%
-0.3	0.2	0.143	342	0.35	9	68.71%
-0.28	0.22	0.209	342	0.426	26	54.68%
-0.45	0.22	0.039	342	0.151	21	63.74%
-0.18	0.19	0.342	342	0.588	85	63.74%
0.08	0.17	0.661	342	0.815	45	98.25%
0.54	0.16	0.001	342	0.015	29	83.33%
0.07	0.16	0.65	342	0.815	49	89.18%
-0.72	0.32	0.022	342	0.13	31	35.67%
-0.11	0.2	0.568	342	0.747	63	90.35%
0.05	0.18	0.768	342	0.863	88	88.30%
-0.43	0.26	0.101	342	0.289	71	77.19%
0	0.18	0.994	342	0.998	83	58.77%
0.04	0.19	0.819	342	0.9	79	84.80%
0	0.17	0.997	342	0.998	91	95.91%
-0.16	0.19	0.382	342	0.588	41	78.95%
0.09	0.19	0.639	342	0.815	36	67.54%
-0.33	0.24	0.173	342	0.411	72	81.58%
-0.19	0.19	0.318	342	0.568	50	85.38%

-0.2 0.19 0.296 342 0.539 52 77.19%

k__Bacteria|p__Firmicutes|c__Bacilli|o__Bacillales|f__Bacillales_unclassified|g__Gemella|s__Gemella_sangi

estimate	SE	p_val	n	fdr	ing_RandomFo	prev
0.31	0.14	0.035	342	0.204	57	57.02%
0.09	0.13	0.507	342	0.799	52	92.40%
0.23	0.14	0.104	342	0.319	83	96.78%
0.29	0.16	0.063	342	0.284	33	45.61%
-0.93	0.31	0.002	342	0.048	49	50.29%
-0.3	0.27	0.258	342	0.537	64	31.29%
0.4	0.16	0.016	342	0.16	44	59.36%
-0.24	0.22	0.28	342	0.56	48	19.30%
0.05	0.17	0.791	342	0.898	68	48.83%
-0.49	0.23	0.032	342	0.198	3	55.56%
-0.02	0.18	0.927	342	0.986	67	86.26%
-0.16	0.19	0.396	342	0.682	28	59.36%
-0.1	0.18	0.575	342	0.799	6	61.11%
-0.08	0.22	0.708	342	0.885	4	67.25%
-0.1	0.22	0.657	342	0.846	9	43.86%
-0.06	0.16	0.728	342	0.894	75	42.11%
0.12	0.17	0.478	342	0.784	58	68.13%
-0.38	0.24	0.109	342	0.319	20	24.27%
-0.12	0.2	0.531	342	0.799	55	55.26%
0.05	0.17	0.778	342	0.898	2	63.74%
-0.43	0.22	0.058	342	0.274	15	47.95%
-0.01	0.17	0.958	342	0.998	29	50.88%
-0.68	0.34	0.043	342	0.228	77	23.98%
-0.34	0.23	0.136	342	0.369	35	52.05%
-0.67	0.29	0.02	342	0.16	23	35.09%
-0.17	0.19	0.373	342	0.672	98	72.51%
-0.25	0.19	0.184	342	0.437	22	51.46%
0.11	0.18	0.539	342	0.799	66	50.00%
0.28	0.16	0.082	342	0.303	81	73.68%
0.24	0.15	0.111	342	0.319	70	26.61%
0.59	0.17	0.001	342	0.015	25	95.32%
0.11	0.19	0.561	342	0.799	31	78.95%
-0.03	0.18	0.851	342	0.937	71	87.13%
-0.48	0.3	0.111	342	0.319	36	34.21%
0.05	0.19	0.79	342	0.898	97	84.21%
-0.11	0.19	0.553	342	0.799	80	72.81%
0.28	0.16	0.08	342	0.303	1	61.40%
-0.05	0.19	0.785	342	0.898	45	43.57%
0.06	0.18	0.733	342	0.894	32	83.33%
-0.04	0.19	0.853	342	0.937	84	53.80%
-0.17	0.24	0.472	342	0.784	11	45.03%
-0.24	0.25	0.328	342	0.62	17	56.43%
0.22	0.16	0.172	342	0.423	38	73.39%
0.6	0.17	0.001	342	0.015	95	94.74%
0.2	0.17	0.249	342	0.529	46	99.42%
0.38	0.17	0.024	342	0.16	60	92.98%
-0.51	0.3	0.095	342	0.319	42	48.25%
0.37	0.16	0.02	342	0.16	19	99.42%
0.23	0.17	0.189	342	0.439	51	85.67%

0.63	0.17	0	342	0.015	54	96.20%
0.29	0.16	0.08	342	0.303	85	89.18%
0.47	0.16	0.004	342	0.066	82	68.42%
0.06	0.17	0.744	342	0.895	8	78.07%
0.4	0.17	0.017	342	0.16	12	97.08%
0.47	0.17	0.005	342	0.067	14	96.78%
0.24	0.17	0.161	342	0.414	92	91.23%
-0.18	0.21	0.388	342	0.681	91	67.54%
0.1	0.15	0.523	342	0.799	10	61.99%
0.11	0.19	0.553	342	0.799	41	66.08%
0.14	0.18	0.44	342	0.745	24	86.84%
-0.17	0.19	0.377	342	0.672	26	77.49%
-0.4	0.24	0.093	342	0.319	87	56.14%
0.4	0.18	0.024	342	0.16	94	83.04%
0.18	0.16	0.265	342	0.541	90	34.21%
0.26	0.17	0.125	342	0.347	93	81.87%
-0.2	0.19	0.294	342	0.577	65	77.78%
0	0.16	0.998	342	0.998	27	71.64%
0.04	0.17	0.799	342	0.898	86	85.96%
0.14	0.16	0.362	342	0.67	89	63.74%
0.26	0.18	0.143	342	0.376	5	92.11%
-0.06	0.19	0.752	342	0.895	50	75.15%
0.12	0.17	0.496	342	0.799	40	90.94%
-0.32	0.2	0.112	342	0.319	37	92.69%
0.21	0.18	0.233	342	0.506	7	88.30%
-0.03	0.19	0.863	342	0.938	69	85.67%
-0.53	0.26	0.038	342	0.213	21	94.74%
-0.24	0.2	0.223	342	0.496	47	82.16%
0.07	0.17	0.668	342	0.846	79	75.44%
-0.66	0.24	0.007	342	0.084	39	53.80%
-0.43	0.24	0.077	342	0.303	63	43.27%
-0.55	0.32	0.08	342	0.303	13	53.22%
0.02	0.19	0.897	342	0.965	16	85.67%
0.11	0.18	0.547	342	0.799	88	82.46%
0.01	0.18	0.938	342	0.987	99	93.86%
0.08	0.17	0.661	342	0.846	18	98.25%
0.54	0.16	0.001	342	0.015	62	83.33%
0.07	0.16	0.65	342	0.846	34	89.18%
-0.72	0.32	0.022	342	0.16	72	35.67%
-0.11	0.2	0.568	342	0.799	56	90.35%
-0.43	0.26	0.101	342	0.319	30	77.19%
0	0.18	0.994	342	0.998	76	58.77%
0.2	0.16	0.196	342	0.445	100	47.08%
0	0.18	0.983	342	0.998	73	86.84%
0	0.17	0.997	342	0.998	53	95.91%
0.09	0.19	0.639	342	0.846	43	67.54%
-0.09	0.17	0.591	342	0.809	59	57.02%
-0.33	0.24	0.173	342	0.423	74	81.58%
-0.19	0.19	0.318	342	0.611	96	85.38%
-0.11	0.22	0.603	342	0.815	61	40.35%

0.29 0.15 0.05 342 0.251 78 44.15%

bacteria

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_CFB3047|o_OFGB3047|f_FGB3047|g_GGB9557|s_GGB9557_SGB14966
 k_Bacteria|p_Firmicutes|c_CFB9612|o_OFGB9612|f_FGB9612|g_GGB45495|s_GGB45495_SGB631
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Archaea|p_Euryarchaeota|c_Methanobacteria|o_Methanobacteriales|f_Methanobacteriaceae|g_M
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB2980|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9342|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9347|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9522|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9787|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenellaceae_u
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridiaceae_unclassified|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridiaceae_unclassified|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Micrococcales|f_Micrococcaceae|g_Rothia|s_Roth
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Clostridiales_uncl
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacteriaceae_unclassified
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacterium|s_Eubacteriu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacterium|s_Eubacteriu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Anaerostipes|s_Anaeros
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_SGB48
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_wexler
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Coproccoccus|s_Coprocco
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Coproccoccus|s_Coprocco
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_formicig
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_longicat
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_longicat
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_sp_AF36
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Faecalicatena|s_Faecalic
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Fusicatenibacter|s_Fusic
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3571|s_GGB3571_S
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lacrimispora|s_Lacrimispor
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_M
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_Ru
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_Ru
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Roseburia|s_Roseburia_i
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Roseburia|s_Roseburia_i
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_Intestinibacter|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_Romboutsia|s_Ro
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Agathobaculum|s_Agat
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaeromassilibacillus|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Bittarella|s_Bittarella_r
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Candidatus_Cibiobacter|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9633|s_GGB9633_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9694|s_GGB9694_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9694|s_GGB9694_
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Collinsella|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9730|s_GGB9730_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Phocaea|s_Phocaea_mas
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruthenibacterium|s_Ru
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Faecalibacill
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Holdmania
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Solobacteriu
 k_Bacteria|p_Firmicutes|c_Firmicutes_unclassified|o_Firmicutes_unclassified|f_Firmicutes_unclassifie
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Acidaminococcales|f_Acidaminococcaceae|g_Phascalarc
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Veillonella|s_Veillone
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Adlercreutzia|s_
 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_F
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_I
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_GGB45432|s_C
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillales_unclassified|g_Gemella|s_Gemella_sangr

k__Bacteria|p__Actinobacteria|c__Actinobacteria|o__Bifidobacteriales|f__Bifidobacteriaceae|g__Bifidobact

estimate	SE	p_val	n	fdr	ranking_RandomForest	prev
0.27	0.14	0.049	342	0.21	18	45.32%
0.31	0.14	0.035	342	0.174	13	57.02%
0.14	0.13	0.266	342	0.516	85	39.47%
0.29	0.16	0.063	342	0.24	6	45.61%
0.17	0.17	0.325	342	0.58	97	46.78%
-0.3	0.27	0.258	342	0.516	47	31.29%
0.4	0.16	0.016	342	0.141	36	59.36%
0.38	0.16	0.015	342	0.141	53	66.96%
-0.49	0.23	0.032	342	0.174	15	55.56%
-0.02	0.18	0.927	342	0.986	69	86.26%
0.28	0.16	0.083	342	0.267	87	41.52%
-0.1	0.18	0.575	342	0.767	9	61.11%
-0.08	0.22	0.708	342	0.873	5	67.25%
-0.1	0.22	0.657	342	0.827	19	43.86%
-0.06	0.16	0.728	342	0.873	39	42.11%
0.29	0.17	0.092	342	0.286	92	91.23%
0.05	0.17	0.778	342	0.894	2	63.74%
-0.43	0.22	0.058	342	0.23	44	47.95%
-0.01	0.17	0.958	342	0.991	25	50.88%
0.14	0.18	0.43	342	0.661	76	61.70%
-0.34	0.23	0.136	342	0.369	3	52.05%
-0.67	0.29	0.02	342	0.146	55	35.09%
-0.17	0.19	0.373	342	0.626	88	72.51%
-0.25	0.19	0.184	342	0.459	40	51.46%
0.28	0.16	0.082	342	0.267	32	73.68%
0.59	0.17	0.001	342	0.015	27	95.32%
0.43	0.15	0.004	342	0.056	49	56.43%
0.28	0.16	0.08	342	0.267	12	61.40%
0.12	0.17	0.468	342	0.698	68	57.02%
0.31	0.15	0.034	342	0.174	91	27.19%
0.06	0.18	0.733	342	0.873	65	83.33%
-0.18	0.22	0.413	342	0.646	42	41.52%
0.22	0.16	0.172	342	0.44	89	73.39%
0.2	0.18	0.268	342	0.516	84	67.54%
0.2	0.17	0.249	342	0.516	43	99.42%
0.04	0.17	0.829	342	0.901	82	86.26%
0.37	0.16	0.02	342	0.146	8	99.42%
0.23	0.17	0.189	342	0.461	58	85.67%
0.37	0.17	0.032	342	0.174	35	90.06%
0.63	0.17	0	342	0.015	46	96.20%
0.29	0.16	0.08	342	0.267	21	89.18%
0.47	0.16	0.004	342	0.056	59	68.42%
0.56	0.16	0.001	342	0.015	38	93.27%
0.06	0.17	0.744	342	0.874	22	78.07%
0.4	0.17	0.017	342	0.141	77	97.08%
0.28	0.18	0.118	342	0.336	80	70.47%
0.47	0.17	0.005	342	0.058	29	96.78%
-0.18	0.21	0.388	342	0.626	37	67.54%
0.1	0.15	0.523	342	0.751	11	61.99%

0.14	0.18	0.44	342	0.666	52	86.84%
-0.17	0.19	0.377	342	0.626	33	77.49%
0.33	0.16	0.038	342	0.174	31	78.36%
0.18	0.16	0.265	342	0.516	34	34.21%
0.55	0.17	0.001	342	0.02	41	84.80%
0.26	0.17	0.125	342	0.347	99	81.87%
0	0.16	0.998	342	0.998	28	71.64%
0.04	0.17	0.799	342	0.898	24	85.96%
-0.1	0.17	0.553	342	0.757	94	49.71%
0.01	0.17	0.962	342	0.991	62	86.55%
0.26	0.18	0.143	342	0.376	16	92.11%
-0.06	0.19	0.752	342	0.874	83	75.15%
0.06	0.17	0.717	342	0.873	90	86.84%
0.12	0.17	0.496	342	0.729	14	90.94%
-0.32	0.2	0.112	342	0.328	66	92.69%
0.21	0.18	0.233	342	0.516	61	88.30%
-0.53	0.26	0.038	342	0.174	23	94.74%
-0.24	0.2	0.223	342	0.516	72	82.16%
-0.13	0.2	0.526	342	0.751	71	40.94%
-0.55	0.32	0.08	342	0.267	4	53.22%
-0.53	0.45	0.233	342	0.516	50	25.15%
0.11	0.18	0.547	342	0.757	100	82.46%
0.15	0.18	0.412	342	0.646	79	77.19%
0.19	0.17	0.286	342	0.539	81	40.64%
0.01	0.18	0.938	342	0.987	86	93.86%
-0.77	0.37	0.036	342	0.174	54	31.58%
0.05	0.18	0.789	342	0.896	98	60.23%
-0.49	0.23	0.03	342	0.174	95	58.48%
0.08	0.17	0.661	342	0.827	30	98.25%
0.54	0.16	0.001	342	0.015	57	83.33%
0.38	0.15	0.014	342	0.141	26	50.58%
0.15	0.16	0.336	342	0.587	73	48.25%
0.07	0.16	0.65	342	0.827	10	89.18%
-0.25	0.22	0.244	342	0.516	75	43.27%
0.02	0.14	0.867	342	0.932	17	41.52%
-0.11	0.2	0.568	342	0.767	96	90.35%
0.04	0.18	0.829	342	0.901	64	80.99%
-0.43	0.26	0.101	342	0.306	7	77.19%
0.04	0.19	0.819	342	0.901	48	84.80%
0.1	0.17	0.552	342	0.757	67	79.53%
0	0.18	0.983	342	0.998	74	86.84%
0.09	0.17	0.609	342	0.791	63	74.85%
0	0.17	0.997	342	0.998	78	95.91%
-0.2	0.21	0.34	342	0.587	45	60.82%
0.19	0.17	0.264	342	0.516	60	32.75%
-0.2	0.19	0.296	342	0.539	70	77.19%
0.15	0.17	0.385	342	0.626	20	71.64%
-0.11	0.22	0.603	342	0.791	1	40.35%
-0.22	0.21	0.296	342	0.539	56	88.01%
0.29	0.15	0.05	342	0.21	93	44.15%

-0.36 0.31 0.249 342 0.516 51 26.02%

bacteria	estimate	SE	p_val	n	fdr	ing_RandomFr
k__Bacteria p	0.31	0.14	0.035	342	0.165	35
k__Bacteria p	0.23	0.14	0.104	342	0.305	30
k__Bacteria p	0.28	0.16	0.079	342	0.273	62
k__Bacteria p	0.29	0.16	0.063	342	0.261	7
k__Bacteria p	-0.93	0.31	0.002	342	0.04	47
k__Bacteria p	-0.08	0.17	0.626	342	0.773	39
k__Bacteria p	-0.3	0.27	0.258	342	0.477	50
k__Bacteria p	0.4	0.16	0.016	342	0.121	41
k__Bacteria p	0.38	0.16	0.015	342	0.121	100
k__Bacteria p	-0.43	0.26	0.092	342	0.288	88
k__Bacteria p	-0.49	0.23	0.032	342	0.161	66
k__Bacteria p	-0.02	0.18	0.927	342	0.95	18
k__Bacteria p	-0.16	0.19	0.396	342	0.582	22
k__Bacteria p	-0.1	0.18	0.575	342	0.747	27
k__Bacteria p	-0.16	0.18	0.365	342	0.57	56
k__Bacteria p	-0.08	0.22	0.708	342	0.824	25
k__Bacteria p	-0.06	0.18	0.748	342	0.84	74
k__Bacteria p	0.29	0.17	0.092	342	0.288	97
k__Bacteria p	0.05	0.17	0.778	342	0.845	44
k__Bacteria p	-0.39	0.25	0.117	342	0.316	4
k__Bacteria p	-0.34	0.23	0.136	342	0.35	1
k__Bacteria p	-0.67	0.29	0.02	342	0.128	96
k__Bacteria p	-0.17	0.19	0.373	342	0.57	95
k__Bacteria p	-0.25	0.19	0.184	342	0.4	87
k__Bacteria p	0.11	0.18	0.539	342	0.743	54
k__Bacteria p	0.28	0.16	0.082	342	0.273	21
k__Bacteria p	-0.3	0.21	0.149	342	0.355	52
k__Bacteria p	0.59	0.17	0.001	342	0.015	63
k__Bacteria p	0.43	0.15	0.004	342	0.052	82
k__Bacteria p	0.11	0.18	0.557	342	0.743	83
k__Bacteria p	-0.11	0.19	0.553	342	0.743	73
k__Bacteria p	0.28	0.16	0.08	342	0.273	37
k__Bacteria p	0.06	0.18	0.733	342	0.84	68
k__Bacteria p	-0.19	0.19	0.313	342	0.535	38
k__Bacteria p	-0.24	0.25	0.328	342	0.538	28
k__Bacteria p	0.2	0.18	0.268	342	0.479	60
k__Bacteria p	0.6	0.17	0.001	342	0.015	59
k__Bacteria p	0.2	0.17	0.249	342	0.469	34
k__Bacteria p	-0.08	0.19	0.669	342	0.795	16
k__Bacteria p	0.38	0.17	0.024	342	0.141	72
k__Bacteria p	0.04	0.17	0.829	342	0.873	31
k__Bacteria p	0.42	0.17	0.014	342	0.121	71
k__Bacteria p	0.37	0.16	0.02	342	0.128	3
k__Bacteria p	0.23	0.17	0.189	342	0.4	26
k__Bacteria p	0.37	0.17	0.032	342	0.161	90
k__Bacteria p	0.29	0.16	0.08	342	0.273	75
k__Bacteria p	0.56	0.16	0.001	342	0.015	67
k__Bacteria p	0.06	0.17	0.744	342	0.84	92
k__Bacteria p	0.4	0.17	0.017	342	0.121	42

k__Bacteria p	-0.11	0.21	0.607	342	0.765	53
k__Bacteria p	0.47	0.17	0.005	342	0.058	77
k__Bacteria p	0.24	0.17	0.161	342	0.375	79
k__Bacteria p	0.34	0.18	0.066	342	0.266	40
k__Bacteria p	0.13	0.17	0.445	342	0.636	51
k__Bacteria p	-0.17	0.19	0.377	342	0.57	2
k__Bacteria p	0.18	0.16	0.265	342	0.479	89
k__Bacteria p	-0.21	0.23	0.361	342	0.57	49
k__Bacteria p	0.25	0.16	0.111	342	0.31	14
k__Bacteria p	0.55	0.17	0.001	342	0.02	23
k__Bacteria p	0.26	0.17	0.125	342	0.328	46
k__Bacteria p	0	0.16	0.998	342	0.998	65
k__Bacteria p	0.26	0.18	0.143	342	0.35	57
k__Bacteria p	0.12	0.17	0.496	342	0.698	93
k__Bacteria p	-0.32	0.2	0.112	342	0.31	81
k__Bacteria p	0.21	0.18	0.233	342	0.447	11
k__Bacteria p	-0.53	0.26	0.038	342	0.171	98
k__Bacteria p	-0.24	0.2	0.223	342	0.437	64
k__Bacteria p	0.13	0.16	0.417	342	0.605	55
k__Bacteria p	0.08	0.17	0.644	342	0.786	61
k__Bacteria p	-0.27	0.2	0.189	342	0.4	80
k__Bacteria p	0.07	0.17	0.668	342	0.795	48
k__Bacteria p	-0.66	0.24	0.007	342	0.067	70
k__Bacteria p	-0.55	0.32	0.08	342	0.273	19
k__Bacteria p	0.02	0.19	0.897	342	0.935	5
k__Bacteria p	-0.73	0.27	0.006	342	0.066	69
k__Bacteria p	0.11	0.18	0.547	342	0.743	91
k__Bacteria p	0.22	0.17	0.193	342	0.4	33
k__Bacteria p	-0.09	0.22	0.676	342	0.795	9
k__Bacteria p	0.05	0.18	0.76	342	0.844	36
k__Bacteria p	-0.3	0.2	0.143	342	0.35	32
k__Bacteria p	0.05	0.18	0.789	342	0.848	76
k__Bacteria p	0.2	0.15	0.188	342	0.4	99
k__Bacteria p	-0.28	0.22	0.209	342	0.418	29
k__Bacteria p	-0.49	0.23	0.03	342	0.161	12
k__Bacteria p	-0.45	0.22	0.039	342	0.171	20
k__Bacteria p	-0.18	0.19	0.342	342	0.552	10
k__Bacteria p	0.54	0.16	0.001	342	0.015	13
k__Bacteria p	-0.11	0.2	0.568	342	0.747	78
k__Bacteria p	0.05	0.18	0.768	342	0.844	6
k__Bacteria p	-0.43	0.26	0.101	342	0.305	94
k__Bacteria p	0.04	0.19	0.819	342	0.872	15
k__Bacteria p	0.2	0.16	0.196	342	0.4	85
k__Bacteria p	0	0.17	0.997	342	0.998	86
k__Bacteria p	0.09	0.18	0.612	342	0.765	58
k__Bacteria p	-0.16	0.19	0.382	342	0.57	17
k__Bacteria p	-0.1	0.19	0.604	342	0.765	43
k__Bacteria p	-0.19	0.19	0.318	342	0.535	24
k__Bacteria p	-0.2	0.19	0.296	342	0.52	8
k__Bacteria p	-0.02	0.18	0.931	342	0.95	84

k__Bacteria p	-0.19	0.19	0.321	342	0.535	45
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prev

- 57.02%
- 96.78%
- 77.78%
- 45.61%
- 50.29%
- 51.75%
- 31.29%
- 59.36%
- 66.96%
- 22.22%
- 55.56%
- 86.26%
- 59.36%
- 61.11%
- 42.11%
- 67.25%
- 33.92%
- 91.23%
- 63.74%
- 35.67%
- 52.05%
- 35.09%
- 72.51%
- 51.46%
- 50.00%
- 73.68%
- 28.95%
- 95.32%
- 56.43%
- 49.42%
- 72.81%
- 61.40%
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- 86.26%
- 92.40%
- 99.42%
- 85.67%
- 90.06%
- 89.18%
- 93.27%
- 78.07%
- 97.08%

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84.80%
47.08%
95.91%
81.58%
78.95%
73.10%
85.38%
77.19%
85.67%

34.50%

bacteria	estimate	SE	p_val	n	fd	ing_RandomFr
k__Bacteria p	0.31	0.14	0.035	342	0.192	19
k__Bacteria p	0.09	0.13	0.507	342	0.793	40
k__Bacteria p	0.23	0.14	0.104	342	0.345	32
k__Bacteria p	0.28	0.16	0.079	342	0.303	20
k__Bacteria p	0.29	0.16	0.063	342	0.272	1
k__Bacteria p	0.54	0.16	0.001	342	0.014	34
k__Bacteria p	-0.3	0.27	0.258	342	0.559	8
k__Bacteria p	0.4	0.16	0.016	342	0.141	53
k__Bacteria p	-0.49	0.23	0.032	342	0.186	5
k__Bacteria p	-0.02	0.18	0.927	342	0.977	59
k__Bacteria p	-0.16	0.19	0.396	342	0.67	66
k__Bacteria p	-0.1	0.18	0.575	342	0.81	4
k__Bacteria p	-0.08	0.22	0.708	342	0.883	12
k__Bacteria p	-0.1	0.22	0.657	342	0.87	10
k__Bacteria p	-0.06	0.18	0.748	342	0.883	67
k__Bacteria p	0.29	0.17	0.092	342	0.327	51
k__Bacteria p	0.05	0.17	0.778	342	0.884	2
k__Archaea p	-0.43	0.22	0.058	342	0.262	6
k__Bacteria p	-0.39	0.25	0.117	342	0.354	83
k__Bacteria p	-0.01	0.17	0.958	342	0.981	7
k__Bacteria p	-0.34	0.23	0.136	342	0.371	3
k__Bacteria p	-0.67	0.29	0.02	342	0.146	21
k__Bacteria p	-0.17	0.19	0.373	342	0.67	35
k__Bacteria p	0.09	0.16	0.565	342	0.81	16
k__Bacteria p	0.15	0.16	0.338	342	0.637	24
k__Bacteria p	-0.3	0.22	0.181	342	0.42	77
k__Bacteria p	0.11	0.18	0.539	342	0.81	31
k__Bacteria p	0.28	0.16	0.082	342	0.303	13
k__Bacteria p	0.59	0.17	0.001	342	0.012	62
k__Bacteria p	0.11	0.19	0.561	342	0.81	18
k__Bacteria p	0.05	0.19	0.79	342	0.888	95
k__Bacteria p	0.28	0.16	0.08	342	0.303	15
k__Bacteria p	0.06	0.18	0.733	342	0.883	37
k__Bacteria p	-0.19	0.19	0.313	342	0.618	25
k__Bacteria p	-0.17	0.24	0.472	342	0.773	46
k__Bacteria p	0.22	0.16	0.172	342	0.413	14
k__Bacteria p	0.2	0.18	0.268	342	0.559	64
k__Bacteria p	0.25	0.16	0.132	342	0.371	88
k__Bacteria p	0.04	0.17	0.829	342	0.901	65
k__Bacteria p	0.37	0.16	0.02	342	0.146	23
k__Bacteria p	0.63	0.17	0	342	0.012	71
k__Bacteria p	0.47	0.16	0.004	342	0.049	33
k__Bacteria p	0.55	0.16	0	342	0.012	39
k__Bacteria p	0.56	0.16	0.001	342	0.012	92
k__Bacteria p	0.1	0.18	0.603	342	0.823	100
k__Bacteria p	0.06	0.17	0.744	342	0.883	29
k__Bacteria p	0.4	0.17	0.017	342	0.141	9
k__Bacteria p	0.47	0.17	0.005	342	0.052	26
k__Bacteria p	0.24	0.17	0.161	342	0.403	68

k__Bacteria p	0.1	0.15	0.523	342	0.804	44
k__Bacteria p	-0.17	0.19	0.377	342	0.67	58
k__Bacteria p	0.33	0.16	0.038	342	0.192	82
k__Bacteria p	0.18	0.16	0.265	342	0.559	94
k__Bacteria p	0.25	0.16	0.111	342	0.349	91
k__Bacteria p	0.55	0.17	0.001	342	0.014	22
k__Bacteria p	0.26	0.17	0.125	342	0.367	41
k__Bacteria p	0	0.16	0.998	342	0.998	72
k__Bacteria p	0.04	0.17	0.799	342	0.888	55
k__Bacteria p	-0.16	0.19	0.395	342	0.67	80
k__Bacteria p	0.01	0.17	0.962	342	0.981	81
k__Bacteria p	0.26	0.18	0.143	342	0.371	48
k__Bacteria p	-0.06	0.19	0.752	342	0.883	99
k__Bacteria p	-0.17	0.2	0.381	342	0.67	36
k__Bacteria p	0.06	0.17	0.717	342	0.883	78
k__Bacteria p	0.12	0.17	0.496	342	0.787	63
k__Bacteria p	-0.32	0.2	0.112	342	0.349	27
k__Bacteria p	0.21	0.18	0.233	342	0.517	28
k__Bacteria p	-0.53	0.26	0.038	342	0.192	38
k__Bacteria p	-0.66	0.24	0.007	342	0.067	97
k__Bacteria p	-0.55	0.32	0.08	342	0.303	17
k__Bacteria p	0.02	0.19	0.897	342	0.965	90
k__Bacteria p	0.11	0.18	0.547	342	0.81	89
k__Bacteria p	0.15	0.18	0.412	342	0.687	57
k__Bacteria p	0.22	0.17	0.193	342	0.439	50
k__Bacteria p	0.35	0.16	0.031	342	0.186	93
k__Bacteria p	0.01	0.18	0.938	342	0.977	75
k__Bacteria p	-0.09	0.22	0.676	342	0.878	11
k__Bacteria p	0.05	0.18	0.76	342	0.883	84
k__Bacteria p	-0.3	0.2	0.143	342	0.371	60
k__Bacteria p	0.08	0.17	0.661	342	0.87	43
k__Bacteria p	0.54	0.16	0.001	342	0.012	49
k__Bacteria p	-0.11	0.2	0.568	342	0.81	79
k__Bacteria p	0.05	0.18	0.768	342	0.883	54
k__Bacteria p	-0.43	0.26	0.101	342	0.345	56
k__Bacteria p	0.25	0.17	0.145	342	0.371	76
k__Bacteria p	0.04	0.19	0.819	342	0.9	30
k__Bacteria p	-0.65	0.29	0.024	342	0.159	61
k__Bacteria p	-0.15	0.22	0.487	342	0.785	85
k__Bacteria p	0.09	0.17	0.609	342	0.823	86
k__Bacteria p	0	0.17	0.997	342	0.998	73
k__Bacteria p	0.05	0.18	0.757	342	0.883	98
k__Bacteria p	-0.1	0.19	0.604	342	0.823	74
k__Bacteria p	-0.07	0.19	0.701	342	0.883	45
k__Bacteria p	-0.33	0.24	0.173	342	0.413	87
k__Bacteria p	-0.19	0.19	0.318	342	0.618	47
k__Bacteria p	-0.02	0.18	0.931	342	0.977	69
k__Bacteria p	-0.21	0.2	0.3	342	0.612	52
k__Bacteria p	0.15	0.17	0.385	342	0.67	70
k__Bacteria p	0.29	0.15	0.05	342	0.239	42

k__Bacteria p	-0.19	0.19	0.321	342	0.618	96
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prev

- 57.02%
- 92.40%
- 96.78%
- 77.78%
- 45.61%
- 68.42%
- 31.29%
- 59.36%
- 55.56%
- 86.26%
- 59.36%
- 61.11%
- 67.25%
- 43.86%
- 33.92%
- 91.23%
- 63.74%
- 47.95%
- 35.67%
- 50.88%
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- 25.73%
- 44.15%
- 23.98%
- 50.00%
- 73.68%
- 95.32%
- 78.95%
- 84.21%
- 61.40%
- 83.33%
- 54.39%
- 45.03%
- 73.39%
- 67.54%
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- 86.26%
- 99.42%
- 96.20%
- 68.42%
- 76.32%
- 93.27%
- 50.00%
- 78.07%
- 97.08%
- 96.78%
- 91.23%

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49.12%
81.58%
85.38%
85.67%
16.37%
71.64%
44.15%

34.50%

bacteria	estimate	SE	p_val	n	fdr	ing_RandomFr
k__Bacteria p	0.31	0.14	0.035	342	0.174	11
k__Bacteria p	0.09	0.13	0.507	342	0.74	61
k__Bacteria p	0.23	0.14	0.104	342	0.32	21
k__Bacteria p	0.28	0.16	0.079	342	0.294	94
k__Bacteria p	0.1	0.16	0.526	342	0.751	73
k__Bacteria p	-0.93	0.31	0.002	342	0.04	47
k__Bacteria p	-0.15	0.2	0.453	342	0.708	100
k__Bacteria p	0.38	0.16	0.015	342	0.15	5
k__Bacteria p	-0.49	0.23	0.032	342	0.174	9
k__Bacteria p	0.29	0.16	0.069	342	0.276	59
k__Bacteria p	-0.02	0.18	0.927	342	0.966	13
k__Bacteria p	0.12	0.18	0.511	342	0.74	80
k__Bacteria p	-0.15	0.18	0.407	342	0.656	63
k__Bacteria p	-0.16	0.18	0.365	342	0.642	33
k__Bacteria p	-0.06	0.18	0.748	342	0.849	12
k__Bacteria p	-0.06	0.16	0.728	342	0.842	57
k__Bacteria p	0.29	0.17	0.092	342	0.32	19
k__Bacteria p	-0.58	0.25	0.021	342	0.15	49
k__Bacteria p	-0.18	0.2	0.376	342	0.642	90
k__Bacteria p	-0.38	0.24	0.109	342	0.32	20
k__Bacteria p	0.05	0.17	0.778	342	0.864	28
k__Archaea p	-0.43	0.22	0.058	342	0.25	2
k__Bacteria p	-0.34	0.23	0.136	342	0.35	38
k__Bacteria p	-0.17	0.19	0.373	342	0.642	1
k__Bacteria p	-0.25	0.19	0.184	342	0.421	70
k__Bacteria p	0.09	0.16	0.565	342	0.758	91
k__Bacteria p	0.59	0.17	0.001	342	0.012	54
k__Bacteria p	0.43	0.15	0.004	342	0.052	97
k__Bacteria p	-0.03	0.18	0.851	342	0.915	40
k__Bacteria p	0.06	0.18	0.733	342	0.842	74
k__Bacteria p	0.28	0.17	0.105	342	0.32	42
k__Bacteria p	-0.28	0.22	0.199	342	0.433	79
k__Bacteria p	-0.17	0.24	0.472	342	0.725	84
k__Bacteria p	0.6	0.17	0.001	342	0.012	93
k__Bacteria p	0.2	0.17	0.249	342	0.497	6
k__Bacteria p	-0.08	0.19	0.669	342	0.811	88
k__Bacteria p	0.25	0.16	0.132	342	0.348	41
k__Bacteria p	0.38	0.17	0.024	342	0.15	92
k__Bacteria p	0.31	0.17	0.073	342	0.281	55
k__Bacteria p	0.04	0.17	0.829	342	0.901	26
k__Bacteria p	0.42	0.18	0.022	342	0.15	72
k__Bacteria p	-0.51	0.3	0.095	342	0.32	65
k__Bacteria p	0.33	0.16	0.038	342	0.174	46
k__Bacteria p	0.06	0.16	0.682	342	0.811	68
k__Bacteria p	0.37	0.16	0.02	342	0.15	8
k__Bacteria p	0.23	0.17	0.189	342	0.421	89
k__Bacteria p	0.37	0.17	0.032	342	0.174	29
k__Bacteria p	0.63	0.17	0	342	0.012	25
k__Bacteria p	0.56	0.16	0.001	342	0.012	36

k__Bacteria p	0.4	0.17	0.017	342	0.15	10
k__Bacteria p	0.47	0.17	0.005	342	0.058	52
k__Bacteria p	0.24	0.17	0.161	342	0.393	48
k__Bacteria p	0.16	0.15	0.302	342	0.56	37
k__Bacteria p	0.1	0.18	0.582	342	0.766	81
k__Bacteria p	0.11	0.19	0.553	342	0.757	66
k__Bacteria p	0.4	0.18	0.024	342	0.15	31
k__Bacteria p	0.25	0.16	0.111	342	0.32	15
k__Bacteria p	0.26	0.17	0.125	342	0.337	96
k__Bacteria p	-0.2	0.19	0.294	342	0.559	53
k__Bacteria p	-0.02	0.17	0.912	342	0.96	23
k__Bacteria p	-0.16	0.19	0.395	342	0.647	50
k__Bacteria p	-0.1	0.17	0.553	342	0.757	83
k__Bacteria p	0.01	0.17	0.962	342	0.981	4
k__Bacteria p	0.26	0.18	0.143	342	0.357	7
k__Bacteria p	0.06	0.17	0.717	342	0.842	14
k__Bacteria p	0.12	0.17	0.496	342	0.74	56
k__Bacteria p	-0.38	0.23	0.1	342	0.32	35
k__Bacteria p	0.21	0.18	0.233	342	0.475	30
k__Bacteria p	-0.03	0.19	0.863	342	0.918	82
k__Bacteria p	-0.53	0.26	0.038	342	0.174	32
k__Bacteria p	-0.24	0.2	0.223	342	0.465	16
k__Bacteria p	0.13	0.16	0.417	342	0.662	3
k__Bacteria p	0.08	0.17	0.644	342	0.805	24
k__Bacteria p	0.28	0.14	0.037	342	0.174	60
k__Bacteria p	-0.27	0.2	0.189	342	0.421	22
k__Bacteria p	-0.33	0.21	0.115	342	0.32	17
k__Bacteria p	0.11	0.18	0.547	342	0.757	64
k__Bacteria p	0.01	0.18	0.938	342	0.967	75
k__Bacteria p	-0.09	0.22	0.676	342	0.811	99
k__Bacteria p	-0.28	0.22	0.209	342	0.444	18
k__Bacteria p	0.08	0.17	0.661	342	0.811	45
k__Bacteria p	0.54	0.16	0.001	342	0.012	69
k__Bacteria p	-0.72	0.32	0.022	342	0.15	76
k__Bacteria p	0.24	0.15	0.115	342	0.32	44
k__Bacteria p	-0.11	0.2	0.568	342	0.758	78
k__Bacteria p	0.05	0.18	0.768	342	0.863	87
k__Bacteria p	0.04	0.19	0.819	342	0.9	58
k__Bacteria p	0	0.18	0.983	342	0.992	67
k__Bacteria p	0.28	0.15	0.069	342	0.276	98
k__Bacteria p	-0.15	0.22	0.487	342	0.738	39
k__Bacteria p	0.09	0.17	0.609	342	0.785	86
k__Bacteria p	0	0.17	0.997	342	0.997	95
k__Bacteria p	0.09	0.18	0.612	342	0.785	43
k__Bacteria p	-0.28	0.2	0.17	342	0.405	85
k__Bacteria p	-0.16	0.19	0.382	342	0.642	34
k__Bacteria p	0.09	0.19	0.639	342	0.805	51
k__Bacteria p	-0.19	0.19	0.318	342	0.578	62
k__Bacteria p	-0.2	0.19	0.296	342	0.559	27
k__Bacteria p	0.15	0.17	0.385	342	0.642	77

k__Bacteria p	-0.22	0.21	0.296	342	0.559	71
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prev

- 57.02%
- 92.40%
- 96.78%
- 77.78%
- 83.92%
- 50.29%
- 54.97%
- 66.96%
- 55.56%
- 63.74%
- 86.26%
- 73.10%
- 54.97%
- 42.11%
- 33.92%
- 42.11%
- 91.23%
- 31.29%
- 52.63%
- 24.27%
- 63.74%
- 47.95%
- 52.05%
- 72.51%
- 51.46%
- 25.73%
- 95.32%
- 56.43%
- 87.13%
- 83.33%
- 51.17%
- 58.77%
- 45.03%
- 94.74%
- 99.42%
- 28.95%
- 99.42%
- 92.98%
- 97.08%
- 86.26%
- 77.19%
- 48.25%
- 60.23%
- 59.36%
- 99.42%
- 85.67%
- 90.06%
- 96.20%
- 93.27%

97.08%
96.78%
91.23%
37.43%
44.74%
66.08%
83.04%
53.51%
81.87%
77.78%
85.96%
75.73%
49.71%
86.55%
92.11%
86.84%
90.94%
62.57%
88.30%
85.67%
94.74%
82.16%
75.15%
89.47%
59.65%
64.04%
68.42%
82.46%
93.86%
63.45%
54.68%
98.25%
83.33%
35.67%
34.21%
90.35%
88.30%
84.80%
86.84%
39.47%
75.15%
74.85%
95.91%
81.58%
85.38%
78.95%
67.54%
85.38%
77.19%
71.64%

88.01%

Comorbidities	rho	p-value	fdr	n	prevalence
aHEI	-0.037	0.498	0.929	342	94.74%
DBP	0.028	0.610	0.929	342	94.74%
SBP	-0.046	0.401	0.929	342	94.74%
HDL	-0.015	0.780	0.929	342	94.74%
Total cholesterol	-0.006	0.906	0.929	342	94.74%
Triglycerides	-0.005	0.929	0.929	342	94.74%
aHEI	-0.108	0.045	0.273	342	96.20%
DBP	-0.048	0.375	0.658	342	96.20%
SBP	-0.084	0.120	0.359	342	96.20%
HDL	0.006	0.906	0.906	342	96.20%
Total cholesterol	-0.042	0.439	0.658	342	96.20%
Triglycerides	-0.018	0.745	0.894	342	96.20%
aHEI	0.012	0.823	0.915	342	68.42%
DBP	0.006	0.915	0.915	342	68.42%
SBP	-0.009	0.863	0.915	342	68.42%
HDL	-0.006	0.905	0.915	342	68.42%
Total cholesterol	-0.091	0.091	0.548	342	68.42%
Triglycerides	-0.054	0.320	0.915	342	68.42%
aHEI	-0.113	0.037	0.222	342	76.32%
DBP	0.028	0.605	0.907	342	76.32%
SBP	0.032	0.561	0.907	342	76.32%
HDL	0.000	0.999	0.999	342	76.32%
Total cholesterol	-0.036	0.510	0.907	342	76.32%
Triglycerides	-0.004	0.942	0.999	342	76.32%
aHEI	-0.038	0.478	0.759	342	93.27%
DBP	0.093	0.087	0.262	342	93.27%
SBP	0.096	0.075	0.262	342	93.27%
HDL	-0.017	0.758	0.768	342	93.27%
Total cholesterol	-0.016	0.768	0.768	342	93.27%
Triglycerides	0.036	0.506	0.759	342	93.27%
aHEI	-0.089	0.101	0.608	342	84.80%
DBP	0.040	0.466	0.855	342	84.80%
SBP	0.012	0.819	0.983	342	84.80%
HDL	0.001	0.983	0.983	342	84.80%
Total cholesterol	0.035	0.523	0.855	342	84.80%
Triglycerides	-0.031	0.570	0.855	342	84.80%
aHEI	-0.010	0.848	0.931	342	83.33%
DBP	0.046	0.400	0.800	342	83.33%
SBP	-0.048	0.374	0.800	342	83.33%
HDL	0.061	0.261	0.800	342	83.33%
Total cholesterol	0.005	0.931	0.931	342	83.33%
Triglycerides	-0.015	0.783	0.931	342	83.33%

Bacteria

k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Anaerobutyricum|s__Ana
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_formicig
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_longicat
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_sp_AF24
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_sp_AF36
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Lachnospiraceae_unclassif
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Mediterraneibacter|s__Ru
k__Bacteria|p__Firmicutes|c__Erysipelotrichia|o__Erysipelotrichales|f__Erysipelotrichaceae|g__Faecalibacill
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Anaerobutyricum|s__Ana
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_formicig
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_longicat
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_sp_AF24
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Dorea|s__Dorea_sp_AF36
k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridiales|f__Lachnospiraceae|g__Mediterraneibacter|s__Ru
k__Bacteria|p__Firmicutes|c__Erysipelotrichia|o__Erysipelotrichales|f__Erysipelotrichaceae|g__Faecalibacill

Comorbidities	p-value	fdr	n	prevalence
Current smoker	0.128	0.256	342	94.74%
Current smoker	0.246	0.262	342	96.20%
Current smoker	0.042	0.083	342	68.42%
Current smoker	0.476	0.830	342	76.32%
Current smoker	0.451	0.451	342	93.27%
Current smoker	0.912	0.912	342	96.78%
Current smoker	0.689	0.849	342	84.80%
Current smoker	0.486	0.546	342	83.33%
Sports	0.913	0.913	342	94.74%
Sports	0.262	0.262	342	96.20%
Sports	0.750	0.750	342	68.42%
Sports	0.830	0.830	342	76.32%
Sports	0.331	0.451	342	93.27%
Sports	0.849	0.849	342	84.80%
Sports	0.546	0.546	342	83.33%

Metabolite	Comorbidities	rho	p-value	fdr	n
Caffeine	aHEI	-0.035	0.521	0.626	342
Caffeine	DBP	-0.041	0.447	0.626	342
Caffeine	SBP	0.028	0.600	0.626	342
Caffeine	HDL	0.036	0.504	0.626	342
Caffeine	Total cholester	-0.036	0.51	0.626	342
Caffeine	Triglycerides	-0.026	0.626	0.626	342
Nicotinate	aHEI	-0.062	0.252	0.755	342
Nicotinate	DBP	0.014	0.802	0.809	342
Nicotinate	SBP	0.014	0.790	0.809	342
Nicotinate	HDL	-0.013	0.809	0.809	342
Nicotinate	Total cholester	-0.015	0.785	0.809	342
Nicotinate	Triglycerides	0.072	0.182	0.755	342
Uridine	aHEI	-0.077	0.154	0.308	342
Uridine	DBP	0.057	0.297	0.329	342
Uridine	SBP	0.098	0.070	0.308	342
Uridine	HDL	-0.053	0.329	0.329	342
Uridine	Total cholester	-0.057	0.30	0.329	342
Uridine	Triglycerides	0.079	0.143	0.308	342
Serine	aHEI	-0.045	0.404	0.791	342
Serine	DBP	-0.011	0.836	0.836	342
Serine	SBP	0.033	0.543	0.791	342
Serine	HDL	-0.024	0.659	0.791	342
Serine	Total cholester	-0.054	0.316	0.791	342
Serine	Triglycerides	0.043	0.427	0.791	342
Cholesterol	aHEI	-0.103	0.057	0.341	342
Cholesterol	DBP	0.034	0.531	0.825	342
Cholesterol	SBP	-0.019	0.726	0.825	342
Cholesterol	HDL	0.014	0.796	0.825	342
Cholesterol	Total cholester	0.037	0.494	0.825	342
Cholesterol	Triglycerides	0.012	0.825	0.825	342
1-methylxantf	aHEI	-0.068	0.207	0.622	342
1-methylxantf	DBP	-0.052	0.337	0.675	342
1-methylxantf	SBP	-0.028	0.604	0.818	342
1-methylxantf	HDL	-0.003	0.960	0.960	342
1-methylxantf	Total cholester	0.022	0.682	0.818	342
1-methylxantf	Triglycerides	0.084	0.121	0.622	342
Protoporphyr	aHEI	0.057	0.294	0.469	342
Protoporphyr	DBP	0.133	0.014	0.081	342
Protoporphyr	SBP	0.097	0.074	0.223	342
Protoporphyr	HDL	0.039	0.469	0.469	342
Protoporphyr	Total cholester	0.052	0.336	0.469	342
Protoporphyr	Triglycerides	0.041	0.453	0.469	342
Glucuronate	aHEI	-0.039	0.468	0.608	342
Glucuronate	DBP	0.032	0.560	0.608	342
Glucuronate	SBP	0.028	0.608	0.608	342
Glucuronate	HDL	-0.118	0.030	0.089	342
Glucuronate	Total cholester	-0.119	0.028	0.089	342
Glucuronate	Triglycerides	0.079	0.147	0.295	342

Metabolite	Comorbidities	p-value
Caffeine	Current smoker	0.110
Nicotinate	Current smoker	0.262
Uridine	Current smoker	0.602
Serine	Current smoker	0.299
Cholesterol	Current smoker	0.220
1-methylxanthine	Current smoker	0.422
protoporphyrin IX	Current smoker	0.662
Glucuronate	Current smoker	0.122
Caffeine	Sports	0.395
Nicotinate	Sports	0.000
Uridine	Sports	0.064
Serine	Sports	0.018
Cholesterol	Sports	0.440
1-methylxanthine	Sports	0.017
protoporphyrin IX	Sports	0.056
Glucuronate	Sports	0.003

fdr	n
0.219	342
0.262	342
0.602	342
0.299	342
0.440	342
0.422	342
0.662	342
0.122	342
0.395	342
0.001	342
0.128	342
0.035	342
0.440	342
0.034	342
0.112	342
0.007	342

Bacteria name

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Anaerostipes|s_Anaeros
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_faecis|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_wexler
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruthenibacterium|s_Ru
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_obeur
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Fusicatenibacter|s_Fusic
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_formicig
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridiaceae_unclassified|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Anaerobutyricum|s_Ana
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_sp_AF36
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_massili
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_SGB48
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Agathobaculum|s_Agat
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Candidatus_Cibiobacter|
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Adlercreutzia|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Coprococcus|s_Coproco
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Gemmiger|s_Gemmige
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_longicat
 k_Bacteria|p_Firmicutes|c_Firmicutes_unclassified|o_Firmicutes_unclassified|f_Firmicutes_unclassifie
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthella|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Bittarella|s_Bittarella_r
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_Romboutsia|s_Ro
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_SGB48
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Tannerellaceae|g_Parabacteroides|s_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_GGB45432|s_C
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_Ru

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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
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k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Clostridiales_uncl
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassified|s
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnoclostridium|s_Clo
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Coprococcus|s_Coprococ
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Lactococcus|s_Lactococ
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_sp_AF:
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Solobacteriu
 k_Archaea|p_Euryarchaeota|c_Methanobacteria|o_Methanobacteriales|f_Methanobacteriaceae|g_M
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Gordonibacter|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospira|s_Lachnosp
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaerotruncus|s_Anaer
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9646|s_GGB9646_
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Turicibacter
 k_Bacteria|p_Firmicutes|c_CFGB3047|o_OFGB3047|f_FGB3047|g_GGB9557|s_GGB9557_SGB14966
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 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Dialister|s_Dialister_i
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Butyricoccus|s_Butyricoc
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Saccharibacteria_unclassified|o_Candidatus_S
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Anaerotignum|s_Anaero
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Corynebacteriales|f_Corynebacteriaceae|g_Coryneb
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_GGB3034|s
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinobac
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Catenibacillus|s_Catenib
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Intestinimonas|s
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillales_unclassified|g_Gemella|s_Gemella_sangi
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenella|s_Chri
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
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k_Bacteria|p_Firmicutes|c_Negativicutes|o_Acidaminococcales|f_Acidaminococcaceae|g_Phascalarc
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Massilioclostridium|s_Mas
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_M
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_GGB4456|s_GGB4
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Parasutter
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
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 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Mediterraneibacter|s_M
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Enterocloster|s_Enterocl
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 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Sutterella|
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Trueperelli

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenella|s_Christensenella
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Senegalimariproductus|s_Senegalimariproductus
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 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_Desulfovibrio|s_Desulfovibrio
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae|s_Eggerthellaceae
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Sellimonas|s_Sellimonas
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 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyces|s_Actinomyces
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidales_unclassified|g_Phocaecium|s_Phocaecium

k_Bacteria|p_Firmicutes|c_CFGB9612|o_OFGB9612|f_FGB9612|g_GGB45495|s_GGB45495_SGB631
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Lancefieldella|s_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB4585|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Firmicutes|c_Firmicutes_unclassified|o_Firmicutes_unclassified|f_Firmicutes_unclassifie
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacterium|s_Eubacteriu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3433|s_GGB3433_S
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9512|s_GGB9512_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridiaceae_unclassified|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_caecir
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9642|s_GGB9642_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcus|s_Rumir
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Harryflintia|s_Harryflin
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_GGB3478|s_GGB3478_SGB
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Micrococcales|f_Micrococcaceae|g_Rothia|s_Roth
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9590|s_GGB9590_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Clostridiales_uncl
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Micrococcales|f_Micrococcaceae|g_Rothia|s_Roth
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Olsenella|s_Ol
 k_Bacteria|p_Bacteroidetes|c_CFGB602|o_OFGB602|f_FGB602|g_GGB1420|s_GGB1420_SGB1957|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Oscillospiraceae|g_Oscillospiraceae_unclassifi
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9615|s_GGB9615_

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacterium|s_Eubacteriu
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Massilimicro
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenellaceae_u
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Barnesiellaceae|g_Coproacter|s_Cop
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Veillonella|s_Veillon
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Pauljensen
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_GGB33516|s_GGB33516_
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 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Erysipelotric
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Odoribacteraceae|g_Butyricimonas|s_
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 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_G
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaerotruncus|s_Anaer
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lactobacillus|s_Lactobacil
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Neglecta|s_Neglecta_ti
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Tannerellaceae|g_Parabacteroides|s_

k_Bacteria|p_Firmicutes|c_CFGB24517|o_OFGB24517|f_FGB24517|g_GGB45620|s_GGB45620_SGE
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Christensenellaceae|g_Christensenellaceae_u
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Faecalibacterium|s_Fae
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Coproba
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Prevotellaceae|g_Paraprevotella|s_Pa
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaerotruncus|s_Anaer
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Sutterella|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB3277|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcus|s_Rumir
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco
 k_Bacteria|p_Firmicutes|c_CFGB3048|o_OFGB3048|f_FGB3048|g_GGB9561|s_GGB9561_SGB14972
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9631|s_GGB9631_
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Gordonibacter|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9618|s_GGB9618_
 k_Bacteria|p_Proteobacteria|c_Alphaproteobacteria|o_Alphaproteobacteria_unclassified|f_Alphaprot
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 k_Bacteria|p_Proteobacteria|c_Alphaproteobacteria|o_Alphaproteobacteria_unclassified|f_Alphaprot
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Oxalobacteraceae|g_GGB66
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Propionibacteriales|f_Propionibacteriaceae|g_Propi

k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Raoultibacter|s
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Enterocloster|s_Enterocl
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 k_Bacteria|p_Proteobacteria|c_Alphaproteobacteria|o_Rhizobiales|f_Phyllobacteriaceae|g_GGB3817|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Negativibacillus|s_Nega
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Pseudoruminococcus|s_
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Veillonella|s_Veillon
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Dielma|s_
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Raoultibacter|s
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 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Micrococcales|f_Kytococcaceae|g_Kytococcus|s_k
 k_Bacteria|p_Firmicutes|c_CFGB2801|o_OFGB2801|f_FGB2801|g_GGB8965|s_GGB8965_SGB13825|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Pseudoflavonifractor|s_
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Erysipelotric
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Longicatena
 k_Bacteria|p_Proteobacteria|c_Alphaproteobacteria|o_Alphaproteobacteria_unclassified|f_Alphaprot
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9774|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9501|s_GGB9501_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcus|s_Rumir
 k_Bacteria|p_Bacteroidetes|c_Flavobacteriia|o_Flavobacteriales|f_Flavobacteriales_unclassified|g_G
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9350|
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 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Aeromonadales|f_Aeromonadaceae|g_GGI|
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Alloscardoc|
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Carnobacteriaceae|g_Granulicatella|s_Granul|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lacrimispora|s_Lacrimisp|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_produc|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Enterocloster|s_Enterocl|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla|
 k_Bacteria|p_Firmicutes|c_CFBG1218|o_OFGB1218|f_FGB1218|g_GGB2983|s_GGB2983_SGB3965|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_GGB9568|s_GGB9568_SGB|
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Enorma|s_|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_|
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 k_Bacteria|p_Verrucomicrobia|c_Verrucomicrobiae|o_Verrucomicrobiales|f_Akkermansiaceae|g_Akl|
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_GGB1681|s_GGB168|
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_|

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9610|s_GGB9610
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 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Acidaminococcales|f_Acidaminococcaceae|g_Phascalarc
 k_Bacteria|p_Synergistetes|c_Synergistia|o_Synergistales|f_Synergistaceae|g_Cloacibacillus|s_Cloa
 k_Eukaryota|p_Ascomycota|c_Saccharomycetes|o_Saccharomycetales|f_Saccharomycetaceae|g_Sac
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 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Tissierellaceae|g_Urmitella|s_Urmitella_tin

k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinomyc
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3569|s_GGB3569_S
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Limosilactobacillus|s_Limc

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
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 k_Bacteria|p_Firmicutes|c_CFGB20074|o_OFGB20074|f_FGB20074|g_GGB48169|s_GGB48169_SGE
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Leuconostoc|s_Leucono
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Leuconostoc|s_Leucono
 k_Bacteria|p_Firmicutes|c_CFGB14246|o_OFGB14246|f_FGB14246|g_GGB38987|s_GGB38987_SGE
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Lawsonibacter|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Cuneatibacter|s_Cuneati
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptococcaceae|g_Peptococcaceae_unclassifi
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9618|s_GGB9618_
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_(
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4676|s_GGB46
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Latilactobacillus|s_Latilact
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_CFGB1424|o_OFGB1424|f_FGB1424|g_GGB3490|s_GGB3490_SGB4664|
 k_Bacteria|p_Firmicutes|c_CFGB16911|o_OFGB16911|f_FGB16911|g_GGB49418|s_GGB49418_SGE
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB4569|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnoclostridium|s_Lac
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB3189|s_GGB3189_
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Merdibacter
 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_(
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Olsenella|s_Ol
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Subdoligranulum|s_Suk
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 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_
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 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Mesosutte
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Parascardi
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Olsenella|s_Ol
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco
 k_Bacteria|p_Firmicutes|c_CFGB12541|o_OFGB12541|f_FGB12541|g_GGB35551|s_GGB35551_SGE
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Angelakisella|s_Angelal
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Flavonifractor|s_Flavon
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9620|s_GGB9620_
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 k_Bacteria|p_Tenericutes|c_Mollicutes|o_Acholeplasmatales|f_Acholeplasmatales_unclassified|g_Ac
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Olsenella|s_Ol
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Rikenellaceae_unclass
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Verrucomicrobia|c_Opitutae|o_Opitutales|f_Opitutales_unclassified|g_Opitutales_uncl
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Olsenella|s_Ol
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Collinsella|s
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Slackia|s_Slack
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Collinsella|s
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae
 k_Bacteria|p_Bacteria_unclassified|c_Bacteria_unclassified|o_Bacteria_unclassified|f_Bacteria_unclas
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillales_unclassified|g_Gemella|s_Gemella_haen
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lactiplantibacillus|s_Lactip
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9603|s_GGB9603_
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 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Saccharibacteria_unclassified|o_Candidatus_S
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4651|s_GGB46
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco
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k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3678|s_GGB3678_S
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 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Massilicoli|s
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Enterorhabdus|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Roseburia|s_Roseburia_!
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9593|s_GGB9593_
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriia_unclassified|f_Coriobacteriia_unclassif
 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_C
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9595|s_GGB9595_
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 k_Bacteria|p_Lentisphaerae|c_Lentisphaeria|o_Lentisphaeria_unclassified|f_Lentisphaeria_unclassifie
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Oxalobacteraceae|g_Oxalob
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Varibaculu
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Odoribacteraceae|g_Butyricimonas|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9636|s_GGB9636_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Clostridiales_uncl
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 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriia_unclassified|f_Coriobacteriia_unclassif
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Leuconostoc|s_Leucono
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Weissella|s_Weissella_c
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidales_unclassified|g_Phocaeicc
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Porphyrmonadaceae|g_Sanguibacterc
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_GGB1680|s_GGB168

k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Ligilactobacillus|s_Ligilact
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Dorea|s_Dorea_phocaeae
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Bifidobact
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4711|s_GGB47
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Ligilactobacillus|s_Ligilact
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_CFGB2897|o_OFGB2897|f_FGB2897|g_GGB9209|s_GGB9209_SGB14148

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 k_Archaea|p_Candidatus_Thermoplasmatota|c_Thermoplasmatota|o_Methanomassiliicoccales|f_Metha
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Senegalima
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriales_unclassified|g_C
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 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Sutterella|
 k_Bacteria|p_Synergistetes|c_Synergistia|o_Synergistales|f_Synergistaceae|g_Cloacibacillus|s_Cloa
 k_Archaea|p_Euryarchaeota|c_Methanobacteria|o_Methanobacteriales|f_Methanobacteriaceae|g_M
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Micrococcales|f_Microbacteriaceae|g_Microbacteri
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_GGB9423|s_GC
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroidaceae_uncl
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Alistipes|s_Alistipes_
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Staphylococcaceae|g_Staphylococcus|s_Staphylococ
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lactobacillus|s_Lactobacil
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
 k_Bacteria|p_Firmicutes|c_CFGB3606|o_OFGB3606|f_FGB3606|g_GGB42689|s_GGB42689_SGB598
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Candidatu

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_Clostridia_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_Family_XIII_Incertae_Sedis|g_Mc
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9455|s_GGB9455_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9634|s_GGB9634_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9710|s_GGB9710_
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Amedibacte
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Parvimonas|s_Parvimc
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Propionibacteriales|f_Propionibacteriaceae|g_Aracl
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae_
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae_
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroidaceae_uncl
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Prevotellaceae|g_Paraprevotella|s_Pa
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_Rikenellaceae_unclass
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4661|s_GGB46
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4700|s_GGB47
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Limosilactobacillus|s_Limc
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Leuconostoc|s_Leucono
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Weissella|s_Weissella_c
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Lactococcus|s_Lactococc
 k_Bacteria|p_Firmicutes|c_CFGB3048|o_OFGB3048|f_FGB3048|g_GGB9560|s_GGB9560_SGB69175
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_Peptostreptococcus
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Subdoligranulum|s_Suk
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Erysipelotric
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_GGB4266|s_GGB4266
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Sutterella|
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_I

k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Tannerellaceae|g_Parabacteroides|s__
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_
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 k_Bacteria|p_Spirochaetes|c_Spirochaetia|o_Brachyspirales|f_Brachyspiraceae|g_Brachyspira|s_Br
 k_Bacteria|p_Verrucomicrobia|c_Verrucomicrobiae|o_Verrucomicrobiales|f_Akkermansiaceae|g_Akk
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Gardnerel
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Lancefieldella|s_
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Odoribacteraceae|g_Odoribacter|s_O
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Porphyrmonadaceae|g_Porphyrmon
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_GGB1632|s_GGB163

k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Tannerellaceae|g_GGB1407|s_GGB14
 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_C
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9635|s_GGB9635_
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Atopobium|s_
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Bacteroides|s_Bact
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 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_C
 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Nanoperiomorbia|o_Candidatus_Nanoperiom
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Staphylococcaceae|g_Staphylococcus|s_Staphyloc
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4667|s_GGB46

k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4739|s_GGB47
 k_Bacteria|p_Firmicutes|c_CFGB12855|o_OFGB12855|f_FGB12855|g_GGB36331|s_GGB36331_SGE
 k_Bacteria|p_Firmicutes|c_CFGB1456|o_OFGB1456|f_FGB1456|g_GGB3654|s_GGB3654_SGB4965|
 k_Bacteria|p_Firmicutes|c_CFGB25373|o_OFGB25373|f_FGB25373|g_GGB45597|s_GGB45597_SGE
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Clostridiales_uncl
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Intestinimonas|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_argi|t_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Blautia|s_Blautia_hanser
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Stomatobaculum|s_Ston
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Oscillospiraceae|g_Oscillospiraceae_unclassifi
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptococcaceae|g_Peptococcaceae_unclassifi
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Agathobaculum|s_Agat
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Drancourtella|s_Dranc
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9457|s_GGB9457_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9635|s_GGB9635_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9694|s_GGB9694_
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_GGB4263|s_GGB426:
 k_Bacteria|p_Fusobacteria|c_Fusobacteriia|o_Fusobacteriales|f_Fusobacteriaceae|g_Fusobacterium|
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Oxalobacteraceae|g_GGB66
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Oxalobacteraceae|g_Oxalob
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_I
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Hafniaceae|g_Hafnia|s_
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Pseudomonadales|f_Pseudomonadaceae|g_
 k_Bacteria|p_Verrucomicrobia|c_CFGB2164|o_OFGB2164|f_FGB2164|g_GGB6132|s_GGB6132_SGE
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 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Schaalia|s_
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Corynebacteriales|f_Lawsonellaceae|g_Lawsonella|
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_GGB25442|s_C
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Parolsenella|s_

k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Collinsella|s
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Eggerthellaceae
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Gordonibacter|s
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Odoribacteraceae|g_GGB1332|s_GGB
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_GGB1631|s_GGB163
 k_Bacteria|p_Bacteroidetes|c_CFBG540|o_OFGB540|f_FGB540|g_GGB1110|s_GGB1110_SGB1424|
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3606|s_GGB3606_S
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Ruminococcaceae_uncla
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k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_Turicimon:
 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacterales|f_Morganellaceae|g_Prof
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Micrococcales|f_Micrococcaceae|g_Rothia|s_Roth
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Collinsella|s
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 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_C
 k_Bacteria|p_Candidatus_Saccharibacteria|c_CFGB4355|o_OFGB4355|f_FGB4355|g_GGB12788|s_C
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Carnobacteriaceae|g_Granulicatella|s_Granul
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Lactococcus|s_Lactococ
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Streptococcus|s_Strepto
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridia_unclassified|f_Clostridia_unclassified|g_GGB9270|
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiaceae|g_Clostridium|s_Clostridium_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacterium|s_Eubacteriu

k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3523|s_GGB3523_S
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptococcaceae|g_Peptococcaceae_unclassifi
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_GGB9668|s_GGB9668_
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 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Selenomonadales|f_Selenomonadaceae|g_Mitsuokella|s
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 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Finegoldia|s_Finegoldi
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Lentisphaerae|c_Lentisphaeria|o_Lentisphaeria_unclassified|f_Lentisphaeria_unclassifie
 k_Bacteria|p_Lentisphaerae|c_Lentisphaeria|o_Lentisphaeria_unclassified|f_Lentisphaeria_unclassifie
 k_Bacteria|p_Proteobacteria|c_Deltaproteobacteria|o_Desulfovibrionales|f_Desulfovibrionaceae|g_
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Enterobacteriaceae|g_
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacteriales|f_Hafniaceae|g_Hafnia|s
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Pasteurellales|f_Pasteurellaceae|g_Haemo
 k_Bacteria|p_Verrucomicrobia|c_Opitutae|o_Puniceicoccales|f_Puniceicoccaceae|g_Puniceicoccaceae
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Trueperelli
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Scardovia|
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Corynebacteriales|f_Corynebacteriaceae|g_Coryneb
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Propionibacteriales|f_Propionibacteriaceae|g_Acidi
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Propionibacteriales|f_Propionibacteriaceae|g_Aracl
 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Collinsella|s
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Coriobacteriaceae|g_Enorma|s_
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Eggerthellales|f_Eggerthellaceae|g_Gordonibacter|s
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_GGB1154|s_GGB11
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidaceae|g_Mediterranea|s_M
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidales_unclassified|g_Bacteroid
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_Family_XIII_Incertae_Sedis|g_Ba
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Clostridiales_unclassified|g_Clostridiales_uncl
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Eubacteriaceae|g_Eubacterium|s_Eubacteriu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Hungateiclostridiaceae|g_GGB3012|s_GGB3
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Faecalicatena|s_Faecalic
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_GGB3632|s_GGB3632_S
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 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnoclostridium|s_Lac
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Lachnospiraceae_unclassif
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Lachnospiraceae|g_Stomatobaculum|s_Ston
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_Paraclostridium|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Peptostreptococcaceae|g_Peptostreptococcu
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Anaeromassilibacillus|s_
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Candidatus_Soleaferrea|
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Flavonifractor|s_Flavon
 k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Ruminococcaceae|g_Gemmiger|s_Gemmige
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 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Acidaminococcales|f_Acidaminococcaceae|g_Acidamino
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Megasphaera|s_Meg
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Finegoldia|s_Finegoldi
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Helcococcus|s_Helcoc
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Peptoniphilus|s_Pepto
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellia_unclassified|f_Tissierellia_unclassified|g_Ezakiell
 k_Bacteria|p_Fusobacteria|c_Fusobacteriia|o_Fusobacteriales|f_Fusobacteriaceae|g_Fusobacterium|

k_Bacteria|p_Proteobacteria|c_Betaproteobacteria|o_Burkholderiales|f_Sutterellaceae|g_GGB6572|
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 k_Bacteria|p_Proteobacteria|c_CFBG2397|o_OFGB2397|f_FGB2397|g_GGB6561|s_GGB6561_SGB9
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 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacterales|f_Enterobacteriaceae|g_I
 k_Bacteria|p_Proteobacteria|c_Gammaproteobacteria|o_Enterobacterales|f_Enterobacteriaceae|g_I
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 k_Bacteria|p_Verrucomicrobia|c_CFBG2165|o_OFGB2165|f_FGB2165|g_GGB6133|s_GGB6133_SGE
 k_Bacteria|p_Verrucomicrobia|c_CFBG6128|o_OFGB6128|f_FGB6128|g_GGB52930|s_GGB52930_S
 k_Archaea|p_Euryarchaeota|c_Methanobacteria|o_Methanobacteriales|f_Methanobacteriaceae|g_M
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Actinotign
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Arcanobac
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Gleimia|s_
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Actinomycetales|f_Actinomycetaceae|g_Schaalia|s_
 k_Bacteria|p_Actinobacteria|c_Actinobacteria|o_Bifidobacteriales|f_Bifidobacteriaceae|g_Bifidobact
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 k_Bacteria|p_Actinobacteria|c_Coriobacteriia|o_Coriobacteriales|f_Atopobiaceae|g_Olsenella|s_Ol
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Muribaculaceae|g_Muribaculum|s_M
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Odoribacteraceae|g_Culturomica|s_C
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Prevotellaceae|g_GGB1239|s_GGB12

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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Rikenellaceae|g_GGB1621|s_GGB1621
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 k_Bacteria|p_Bacteroidetes|c_CFGB637|o_OFGB637|f_FGB637|g_GGB1562|s_GGB1562_SGB2149|s_GGB1562_SGB2149
 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_Melainabacteria_unclassified|s_Candidatus_Melainabacteria_unclassified
 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_Melainabacteria_unclassified|s_Candidatus_Melainabacteria_unclassified
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 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Nanosyncoccalia|o_Candidatus_Nanosingivale|s_Candidatus_Nanosingivale
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 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Saccharibacteria_unclassified|o_Candidatus_Saccharibacteria_unclassified|s_Candidatus_Saccharibacteria_unclassified
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillaceae|g_Lysinibacillus|s_Lysinibacillus_boroni|s_Lysinibacillus_boroni
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillaceae|g_Lysinibacillus|s_Lysinibacillus_sp_2016|s_Lysinibacillus_sp_2016
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillaceae|g_Peribacillus|s_Peribacillus_psychroaerophilus|s_Peribacillus_psychroaerophilus
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillaceae|g_Peribacillus|s_Peribacillus_simplex|s_Peribacillus_simplex
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillaceae|g_Psychrobacillus|s_Psychrobacillus_petrolearius|s_Psychrobacillus_petrolearius
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillales_unclassified|g_Gemella|s_Gemella_asaccharophila|s_Gemella_asaccharophila
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Bacillales_unclassified|g_Gemella|s_Gemella_bergii|s_Gemella_bergii
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Paenibacillaceae|g_Paenibacillus|s_Paenibacillus_eurothermus|s_Paenibacillus_eurothermus
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Paenibacillaceae|g_Paenibacillus|s_Paenibacillus_citri|s_Paenibacillus_citri
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacillales|f_Staphylococcaceae|g_Staphylococcus|s_Staphylococcus_sciuri|s_Staphylococcus_sciuri
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_Bacilli_unclassified|s_Bacilli_unclassified
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s_Bacilli_unclassified|s_Bacilli_unclassified|s_Bacilli_unclassified|s_Bacilli_unclassified|s_Bacilli_unclassified
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4640|s_GGB4640
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4672|s_GGB4672
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_GGB4687|s_GGB4687
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enterococcus_faecalis|s_Enterococcus_faecalis
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enterococcus_faecalis|s_Enterococcus_faecalis
 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Companilactobacillus|s_Companilactobacillus|s_Companilactobacillus

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lacticaseibacillus|s__Lactic

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lactiplantibacillus|s__Lactipl

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lactiplantibacillus|s__Lactipl

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lactobacillus|s__Lactobacil

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lentilactobacillus|s__Lentili

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Lentilactobacillus|s__Lentili

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Ligilactobacillus|s__Ligilacto

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Limosilactobacillus|s__Lacto

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Limosilactobacillus|s__Lacto

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Lactobacillaceae|g__Limosilactobacillus|s__Lacto

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Leuconostocaceae|g__Leuconostoc|s__Leucono

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Leuconostocaceae|g__Weissella|s__Weissella_p

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Leuconostocaceae|g__Weissella|s__Weissella_v

k__Bacteria|p__Firmicutes|c__Bacilli|o__Lactobacillales|f__Streptococcaceae|g__Streptococcus|s__Strepto

k__Bacteria|p__Firmicutes|c__CFGB1192|o__OFGB1192|f__FGB1192|g__GGB2945|s__GGB2945_SGB3918|

k__Bacteria|p__Firmicutes|c__CFGB1281|o__OFGB1281|f__FGB1281|g__GGB3095|s__GGB3095_SGB4103|

k__Bacteria|p__Firmicutes|c__CFGB12952|o__OFGB12952|f__FGB12952|g__GGB36472|s__GGB36472_SGE

k__Bacteria|p__Firmicutes|c__CFGB1394|o__OFGB1394|f__FGB1394|g__GGB3385|s__GGB3385_SGB4471|

k__Bacteria|p__Firmicutes|c__CFGB1677|o__OFGB1677|f__FGB1677|g__GGB4197|s__GGB4197_SGB5684|

k__Bacteria|p__Firmicutes|c__CFGB2832|o__OFGB2832|f__FGB2832|g__GGB9054|s__GGB9054_SGB13959

k__Bacteria|p__Firmicutes|c__CFGB3546|o__OFGB3546|f__FGB3546|g__GGB58071|s__GGB58071_SGB797

k__Bacteria|p__Firmicutes|c__CFGB3601|o__OFGB3601|f__FGB3601|g__GGB42674|s__GGB42674_SGB660

k__Bacteria|p__Firmicutes|c__CFGB42358|o__OFGB42358|f__FGB42358|g__GGB51510|s__GGB51510_SGE

k__Bacteria|p__Firmicutes|c__CFGB9153|o__OFGB9153|f__FGB9153|g__GGB27097|s__GGB27097_SGB393

k__Bacteria|p__Firmicutes|c__CFGB9572|o__OFGB9572|f__FGB9572|g__GGB45461|s__GGB45461_SGB631

k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Candidatu

k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_

k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_

k__Bacteria|p__Firmicutes|c__Clostridia|o__Clostridia_unclassified|f__Clostridia_unclassified|g__Clostridia_

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k_Bacteria|p_Fusobacteria|c_Fusobacteriia|o_Fusobacteriales|f_Fusobacteriaceae|g_Cetobacterium|
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 k_Bacteria|p_Lentisphaerae|c_Lentisphaeria|o_Lentisphaeria_unclassified|f_Lentisphaeria_unclassified|
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Muribaculaceae|g_GGB14009|s_GGB
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 k_Bacteria|p_Bacteroidetes|c_CFBG636|o_OFGB636|f_FGB636|g_GGB1554|s_GGB1554_SGB2141|
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 k_Bacteria|p_Bacteroidetes|c_Flavobacteriia|o_Flavobacteriales|f_Flavobacteriaceae|g_GGB5975|s_
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 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_Eggerthia|s_
 k_Bacteria|p_Firmicutes|c_Erysipelotrichia|o_Erysipelotrichales|f_Erysipelotrichaceae|g_GGB31184|
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 k_Bacteria|p_Firmicutes|c_Firmicutes_unclassified|o_Firmicutes_unclassified|f_Firmicutes_unclassifie
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Acidaminococcales|f_Acidaminococcaceae|g_Acidamino
 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Acidaminococcales|f_Acidaminococcaceae|g_GGB4237|s_
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 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Negativicoccus|s_Ne
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 k_Bacteria|p_Firmicutes|c_Negativicutes|o_Veillonellales|f_Veillonellaceae|g_Veillonellaceae_unclas
 k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Anaerococcus|s_Anaer

k_Bacteria|p_Firmicutes|c_Tissierellia|o_Tissierellales|f_Peptoniphilaceae|g_Anaerococcus|s_Anaer
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k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidales_unclassified|g_Bacteroid
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidales_unclassified|g_GGB1530
 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Bacteroidales_unclassified|g_GGB1543
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 k_Bacteria|p_Bacteroidetes|c_Bacteroidia|o_Bacteroidales|f_Barnesiellaceae|g_Barnesiella|s_Barn
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 k_Bacteria|p_Bacteroidetes|c_CFGB671|o_OFGB671|f_FGB671|g_GGB1669|s_GGB1669_SGB2285|
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 k_Bacteria|p_Candidatus_Melainabacteria|c_Candidatus_Melainabacteria_unclassified|o_Candidatus_C
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 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Saccharibacteria_unclassified|o_Candidatus_S
 k_Bacteria|p_Candidatus_Saccharibacteria|c_Candidatus_Saccharibacteria_unclassified|o_Candidatus_S
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 k_Bacteria|p_Elusimicrobia|c_Elusimicrobia|o_Elusimicrobiales|f_Elusimicrobiales_unclassified|g_Elu
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k_Bacteria|p_Firmicutes|c_Bacilli|o_Bacilli_unclassified|f_Bacilli_unclassified|g_Bacilli_unclassified|s

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Aerococcaceae|g_Aerococcus|s_Aerococcus_

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Aerococcaceae|g_Aerococcus|s_Aerococcus_

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Carnobacteriaceae|g_Carnobacterium|s_Carn

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Carnobacteriaceae|g_Carnobacterium|s_Carn

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Carnobacteriaceae|g_Marinilactibacillus|s_Ma

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Enterococcaceae|g_Enterococcus|s_Enteroco

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Companilactobacillus|s_Co

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Companilactobacillus|s_Co

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lactobacillus|s_Lactobacil

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lentilactobacillus|s_Lentili

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lentilactobacillus|s_Lentili

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lentilactobacillus|s_Lentili

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lentilactobacillus|s_Lentili

k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lentilactobacillus|s_Lentili

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k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Lactobacillaceae|g_Lentilactobacillus|s_Lentil
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Leuconostocaceae|g_Fructobacillus|s_Fructob
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 k_Bacteria|p_Firmicutes|c_Bacilli|o_Lactobacillales|f_Streptococcaceae|g_Lactococcus|s_Lactococci
 k_Bacteria|p_Firmicutes|c_CFGB10238|o_OFGB10238|f_FGB10238|g_GGB31227|s_GGB31227_SGE
 k_Bacteria|p_Firmicutes|c_CFGB11480|o_OFGB11480|f_FGB11480|g_GGB33664|s_GGB33664_SGE
 k_Bacteria|p_Firmicutes|c_CFGB1287|o_OFGB1287|f_FGB1287|g_GGB3103|s_GGB3103_SGB4112|
 k_Bacteria|p_Firmicutes|c_CFGB1289|o_OFGB1289|f_FGB1289|g_GGB3106|s_GGB3106_SGB4115|
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k_Bacteria|p_Firmicutes|c_Clostridia|o_Clostridiales|f_Oscillospiraceae|g_Oscillospiraceae_unclassifi
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 k_Bacteria|p_Kiritimatiellaeota|c_Kiritimatiellae|o_Kiritimatiellae_unclassified|f_Kiritimatiellae_unclassified
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k_Bacteria|p_Lentisphaerae|c_Lentisphaeria|o_Victivallales|f_Victivallales_unclassified|g_Victivallale
 k_Bacteria|p_Planctomycetes|c_Planctomycetia|o_Pirellulales|f_Pirellulaceae|g_GGB6567|s_GGB6
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 k_Bacteria|p_Planctomycetes|c_Planctomycetia|o_Planctomycetales|f_Planctomycetaceae|g_GGB41
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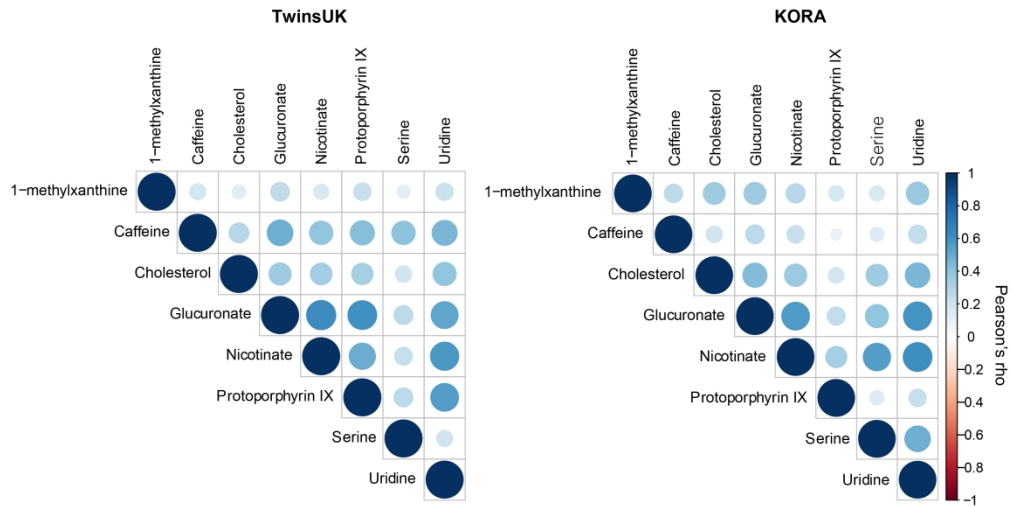
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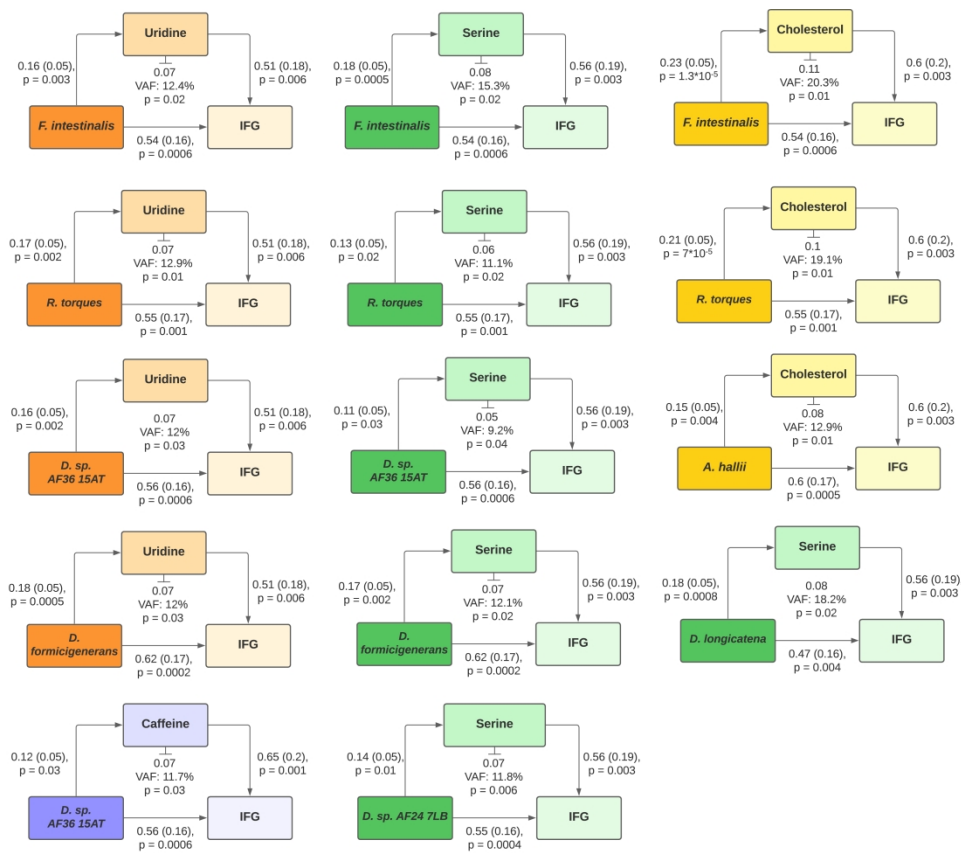
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