

-- ANALYSIS REPORT --

## Summary

Overview of your gut microbiota

ID: RG-TEST-002 | Date: 12/05/2026 | Shotgun Metagenomic Sequencing - 20M reads - PE150

This report presents your results, comparing them with those obtained from the Nahibu cohort.

227

Richness

OPTIMAL

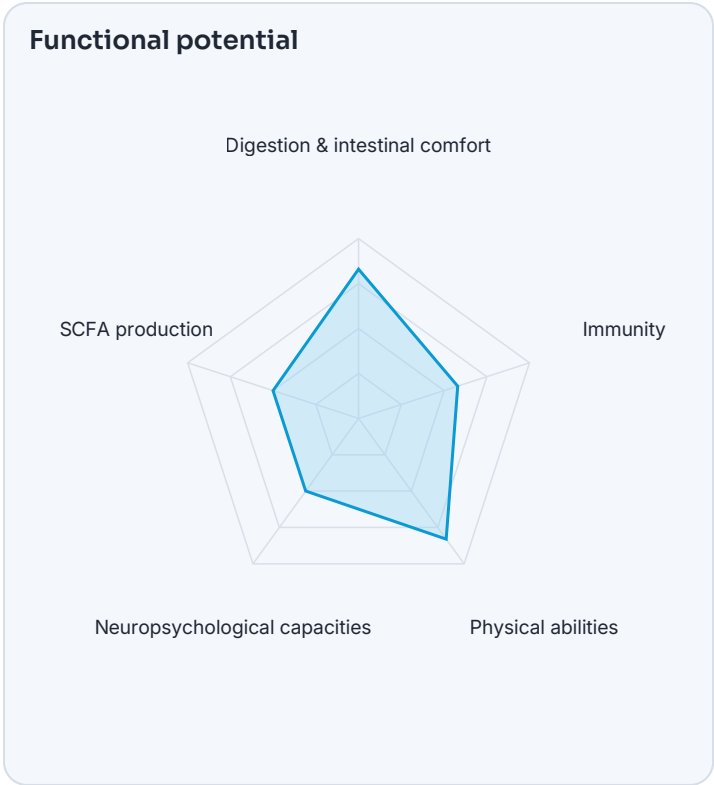
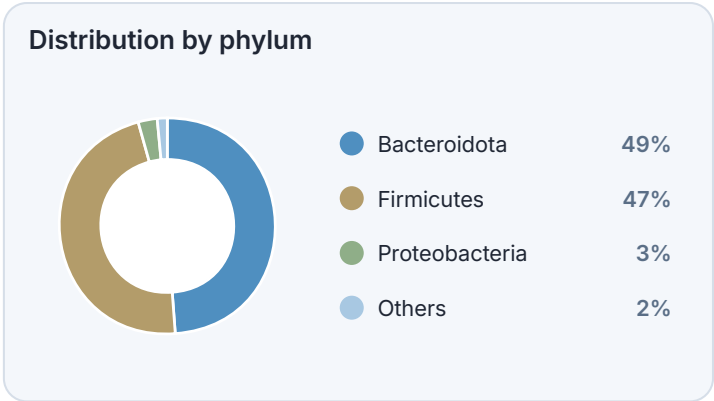
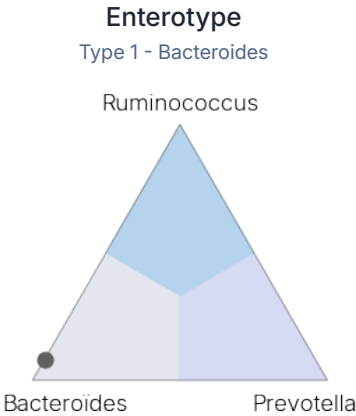
Number of different species detected

4.09

Diversity

OPTIMAL

Shannon Index - Evaluates species distribution



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-- MICROBIAL ACTIVITY --

## Functional potential

Overview of functions carried by the microbiome

*Shotgun sequencing explores the entirety of the sample's genetic material, making it possible to identify the functions that the microorganisms present are capable of performing. These results, based on the genes that were actually sequenced, reflect the functional potential of the microbiome.*

### SCFA production

SHORT CHAIN FATTY ACIDS

| COMPOUND   | STATUS       | COMPARISON COHORT                                       |
|------------|--------------|---------------------------------------------------------|
| Butyrate   | ● Improvable | <div><div></div><div></div><div></div><div></div></div> |
| Acetate    | ● Optimal    | <div><div></div><div></div><div></div><div></div></div> |
| Lactate    | ● Optimal    | <div><div></div><div></div><div></div><div></div></div> |
| Propionate | ● Improvable | <div><div></div><div></div><div></div><div></div></div> |

### Digestion and intestinal comfort

BLOATING AND GAS

| COMPOUND         | STATUS    | COMPARISON COHORT                                       |
|------------------|-----------|---------------------------------------------------------|
| Hydrogen sulfide | ● Correct | <div><div></div><div></div><div></div><div></div></div> |

ACIDS AND REFLUX

| COMPOUND | STATUS    | COMPARISON COHORT                                       |
|----------|-----------|---------------------------------------------------------|
| Lactate  | ● Optimal | <div><div></div><div></div><div></div><div></div></div> |

SATIETY

| COMPOUND                     | STATUS    | COMPARISON COHORT                                       |
|------------------------------|-----------|---------------------------------------------------------|
| Acetate, lactate, propionate | ● Optimal | <div><div></div><div></div><div></div><div></div></div> |

FATTY ACID METABOLISM REGULATION

| COMPOUND   | STATUS    | COMPARISON COHORT                                       |
|------------|-----------|---------------------------------------------------------|
| Spermidine | ● Correct | <div><div></div><div></div><div></div><div></div></div> |

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VITAMIN PRODUCTION

| COMPOUND          | STATUS                        | COMPARISON COHORT                                       |
|-------------------|-------------------------------|---------------------------------------------------------|
| Adenosylcobalamin | <div><div></div>Optimal</div> | <div><div></div><div></div><div></div><div></div></div> |
| Menaquinone       | <div><div></div>Optimal</div> | <div><div></div><div></div><div></div><div></div></div> |

Immunity

DEVELOPMENT AND MAINTENANCE OF GUT TISSUES

| COMPOUND               | STATUS                           | COMPARISON COHORT                                       |
|------------------------|----------------------------------|---------------------------------------------------------|
| Butyrate               | <div><div></div>Improvable</div> | <div><div></div><div></div><div></div><div></div></div> |
| Hydrogen sulfide       | <div><div></div>Correct</div>    | <div><div></div><div></div><div></div><div></div></div> |
| Putrescine, spermidine | <div><div></div>Correct</div>    | <div><div></div><div></div><div></div><div></div></div> |

INFLAMMATION

| COMPOUND  | STATUS                           | COMPARISON COHORT                                       |
|-----------|----------------------------------|---------------------------------------------------------|
| Butyrate  | <div><div></div>Improvable</div> | <div><div></div><div></div><div></div><div></div></div> |
| Acetate   | <div><div></div>Optimal</div>    | <div><div></div><div></div><div></div><div></div></div> |
| Lactate   | <div><div></div>Optimal</div>    | <div><div></div><div></div><div></div><div></div></div> |
| Histidine | <div><div></div>Correct</div>    | <div><div></div><div></div><div></div><div></div></div> |

Physical abilities

| COMPOUND     | STATUS                        | COMPARISON COHORT                                       |
|--------------|-------------------------------|---------------------------------------------------------|
| Acetate      | <div><div></div>Optimal</div> | <div><div></div><div></div><div></div><div></div></div> |
| Histidine    | <div><div></div>Correct</div> | <div><div></div><div></div><div></div><div></div></div> |
| Pantothenate | <div><div></div>Optimal</div> | <div><div></div><div></div><div></div><div></div></div> |

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# Neuropsychological capacities

## GENERAL BRAIN FUNCTION

| COMPOUND  | STATUS  | COMPARISON COHORT                                                  |
|-----------|---------|--------------------------------------------------------------------|
| Histidine | Correct | <div><div></div><div></div><div></div><div></div><div></div></div> |

## COGNITIVE ABILITIES AND MEMORY

| COMPOUND         | STATUS     | COMPARISON COHORT                                                  |
|------------------|------------|--------------------------------------------------------------------|
| Tetrahydrofolate | Improvable | <div><div></div><div></div><div></div><div></div><div></div></div> |
| Butyrate         | Improvable | <div><div></div><div></div><div></div><div></div><div></div></div> |

## SLEEP

| COMPOUND   | STATUS     | COMPARISON COHORT                                                  |
|------------|------------|--------------------------------------------------------------------|
| Butyrate   | Improvable | <div><div></div><div></div><div></div><div></div><div></div></div> |
| GABA       | Correct    | <div><div></div><div></div><div></div><div></div><div></div></div> |
| Tryptophan | Optimal    | <div><div></div><div></div><div></div><div></div><div></div></div> |

## DEPRESSION AND MOOD DISORDERS

| COMPOUND | STATUS  | COMPARISON COHORT                                                  |
|----------|---------|--------------------------------------------------------------------|
| GABA     | Correct | <div><div></div><div></div><div></div><div></div><div></div></div> |
| Tyrosine | Correct | <div><div></div><div></div><div></div><div></div><div></div></div> |

## STRESS, ANXIETY

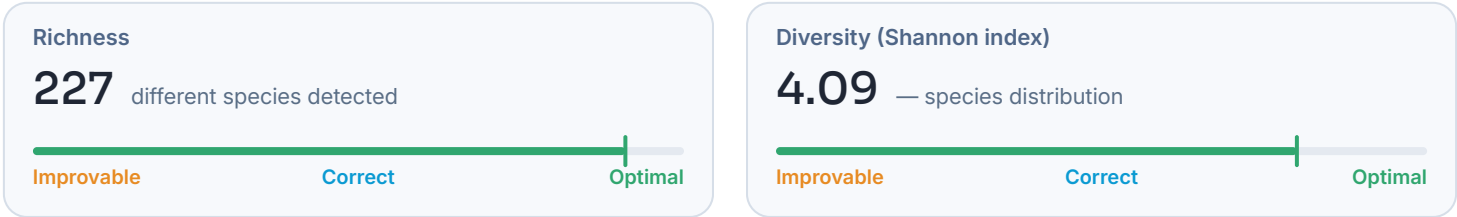
| COMPOUND     | STATUS  | COMPARISON COHORT                                                  |
|--------------|---------|--------------------------------------------------------------------|
| Pantothenate | Optimal | <div><div></div><div></div><div></div><div></div><div></div></div> |
| GABA         | Correct | <div><div></div><div></div><div></div><div></div><div></div></div> |
| Tryptophan   | Optimal | <div><div></div><div></div><div></div><div></div><div></div></div> |
| Tyrosine     | Correct | <div><div></div><div></div><div></div><div></div><div></div></div> |

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-- BACTERIAL ANALYSIS --

## Taxonomic composition

Detected genera and species of interest



Shotgun sequencing identifies the microorganisms present in the sample down to the species level. The relative abundance of each detected taxon corresponds to the proportion (%) it represents within the gut microbiome. A concise description of each bacterium of interest and the complete abundance table are available in the appendix.

### Genera of interest

| TAXON           | %     | STATUS  | COMPARISON COHORT |
|-----------------|-------|---------|-------------------|
| Coprococcus     | 1.79% | Optimal | <div></div>       |
| Bifidobacterium | 0.28% | Correct | <div></div>       |
| Dialister       | 0.27% | Correct | <div></div>       |

### Species with positive impact

| TAXON                              | %     | STATUS     | COMPARISON COHORT |
|------------------------------------|-------|------------|-------------------|
| Faecalibacterium prausnitzii       | 3.54% | Correct    | <div></div>       |
| Eubacterium hallii (Not detected)  | -     | Improvable | <div></div>       |
| Bifidobacterium longum             | 0.01% | Correct    | <div></div>       |
| Roseburia intestinalis             | 0.03% | Correct    | <div></div>       |
| Akkermansia muciniphila            | 0.01% | Correct    | <div></div>       |
| Veillonella atypica (Not detected) | -     | Correct    | <div></div>       |

### Species with negative impact

| TAXON                                   | %     | STATUS  | COMPARISON COHORT |
|-----------------------------------------|-------|---------|-------------------|
| Bilophila wadsworthia                   | 0.13% | Correct | <div></div>       |
| Clostridioides difficile (Not detected) | -     | Optimal | <div></div>       |
| Ruminococcus gnavus (Not detected)      | -     | Optimal | <div></div>       |

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-- NAHIBU PROTOCOL --

## Methodology

Analysis process and pipeline

Shotgun metagenomics involves sequencing all the DNA present in a sample, without prior targeting of a specific genomic region. The resulting fragments are analyzed to identify the microorganisms present and reconstruct the metabolic pathways they carry. In a single experiment, this approach captures both the composition and the functional potential of the gut microbiome.

### Nahibu analysis process and pipeline

- 1

**Collection and storage**

The sample is collected at home using a standardized kit. A stabilizing medium preserves the integrity of microbial DNA throughout the logistics chain at room temperature.
- 2

**DNA extraction**

DNA is extracted from each sample using a standardized protocol in our laboratory, ensuring effective lysis of microbial cell walls and reproducible extraction quality.
- 3

**Shotgun sequencing**

Shotgun sequencing is performed at a targeted depth of 20 million reads (PE150), a standard recommended for the exploration of the gut microbiota.
- 4

**Quality control, decontamination, and normalization**

The analysis relies on subsampling to 3 million reads, quality control, and removal of host sequences to ensure comparability between samples.
- 5

**Taxonomic and functional profiling**

Taxonomic identification down to the species level and exploration of functional potential (major metabolic functions) are performed for each sample.

### Scope and limitations of the analysis

#### Scope of the analysis

By sequencing all the DNA in the sample, this approach captures the full range of microorganisms present, with resolution down to the species level. It also provides access to the functional potential of the microbiome: metabolic pathways are inferred directly from the detected genes, without prior targeting. No amplification bias alters the proportionality of the measurements.

#### Limitations of the analysis

Shotgun sequencing provides a snapshot of the microbiome at a given point in time, as its composition naturally varies depending on diet, intestinal transit, or medical treatments. In addition, the detected genes reflect metabolic potential rather than measured activity. Finally, a fraction of the sequences does not match any known microorganism, as part of the human microbial diversity remains unexplored.

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-- APPENDICES --

## Bacteria of interest

- *Akkermansia muciniphila*

*A. muciniphila* helps strengthen the intestinal barrier, supports weight management, has anti-inflammatory properties, and is associated with overall good health.

- *Bifidobacterium*

*Bifidobacterium* are among the most abundant beneficial bacteria in the gut microbiome. Some contribute to strengthening the immune system and the intestinal barrier, reducing diarrhea, improving digestive discomfort, and protecting against pathogenic bacteria.

- *Bifidobacterium longum*

*B. longum* is a commercially available probiotic. It has anti-inflammatory effects and appears to improve symptoms in people suffering from constipation, celiac disease or ulcerative colitis.

- *Bilophila wadsworthia*

*B. wadsworthia* has pro-inflammatory properties and appears to worsen metabolic disorders in people with a high-fat diet. Its abundance may be increased in high saturated fat diets, or as part of a low FODMAP diet.

- *Clostridioides difficile*

*C. difficile* is a pathogenic bacterium responsible for the majority of nosocomial infections worldwide. Its effects range from mild diarrhea to severe intestinal pathologies.

- *Coprococcus*

The *Coprococcus* genus is associated with a good quality of life. As a butyrate producer, it exhibits anti-inflammatory properties and a potential role in colorectal cancer prevention. Reduced abundance has been observed in individuals with depressive symptoms, although no causal link has been established.

- *Dialister*

*Dialister* is a bacterial genus naturally present in the human microbiome, where it plays an important role in microbial balance. It participates in the metabolism of compounds such as SCFAs, contributes to immune system modulation, and may also be involved in the regulation of mental health.

- *Eubacterium hallii*

*E. hallii* is a butyrate- and propionate-producing species, two compounds with health benefits.

- *Faecalibacterium prausnitzii*

*F. prausnitzii* is one of the most abundant species in the intestinal microbiota. A butyrate producer, an anti-inflammatory compound, it contributes to good intestinal health by nourishing colon cells and reinforcing the intestinal barrier.

- *Roseburia intestinalis*

*R. intestinalis* is one of the dominant species in the gut microbiota. As a butyrate producer, it contributes to the proper functioning of the intestinal barrier and has anti-inflammatory properties.

- *Ruminococcus gnavus*

*R. gnavus* is a commensal (common) species of the intestine. It has a high inflammatory potential.



- *Veillonella atypica*

*V. atypica* seems to promote the growth of many other microorganisms, including beneficial bacteria for the host. It also helps to eliminate potentially harmful compounds produced by bacteria living in the digestive system. Mainly found in the microbiota of athletes, it appears to enhance physical performance by transforming the lactic acid produced during exercise.

## Compounds of interest

- Acetate

This volatile fatty acid, produced by bacteria and transported to organs through the bloodstream, is a preferred source of energy for muscles. Also involved in immune cell expression, its concentration increases during infection to support the adaptive immune response.

- Acetate, Lactate, Propionate

These volatile fatty acids are involved in satiety regulation by inhibiting hormone secretion from colon mucosal cells and promoting the release of peptides and hormones that act on the central nervous system. High concentrations lead to reduced appetite.

- Adenosylcobalamin

Adenosylcobalamin is one of the active forms of vitamin B12. It comes mainly from the diet, but can be produced by certain bacteria, reducing the risk of deficiency. It is involved in the synthesis of essential amino acids for both the microbiota and the host. Additionally, it plays a role in regulating fatty acid metabolism and cell development.

- Butyrate

Short-chain fatty acid produced by intestinal microbiota during fiber fermentation. As the main nutrient for intestinal mucosa cells, it stimulates mucus production, helping to maintain digestive tract tissue. Butyrate also has anti-inflammatory properties and promotes sleep onset and deep sleep phases.

- GABA

GABA (gamma-aminobutyric acid) inhibits neurons to prevent constant excitation. It must be balanced with glutamate to reduce the risk of epilepsy.

- Histidine

An essential compound in hemoglobin synthesis, it plays a crucial role in arterial health. It also contributes to neurological well-being by protecting nerve cells. Sufficient histidine levels help reduce mental fatigue, support memory, and promote quality sleep. However, an excess of histidine can lead to stress and anxiety.

- Lactate

The acidity from lactate inhibits the growth of potentially pathogenic bacteria, but maintaining balance is essential to prevent excessive acidification of the intestine. Its presence is directly linked to increased local acidity through a higher concentration of lactate-producing bacteria and a decrease in lactate-utilizing bacteria.

- Menaquinone

Menaquinone is the form of vitamin K produced by bacteria. It contributes to cardiovascular and bone metabolism, cell growth, and immunity. Menaquinone also promotes the development of beneficial bacteria and limits the growth of pathogens.

- Pantothenate

Pantothenate, or vitamin B5, is involved in the regulatory mechanisms of adrenalin, insulin and porphyrin (hemoglobin precursor). It has anti-stress properties and helps reduce fatigue.



- **Propionate**

Propionate plays a role in the regulation of satiety and inhibits the formation of fats and cholesterol. It is being studied for its potential role in the prevention of obesity and diabetes, and may also exhibit anti-infective properties.

- **Putrescine, spermidine**

Putrescine and spermidine are polyamines found in the intestine, part of which is produced by the intestinal microbiota. They help regulate cell growth and support intestinal maturation. Some of these polyamines are used by bacteria to form biofilms, which play a protective role in the intestinal lining. However, excessive concentrations may be linked to an increased risk of cancer and chronic inflammation.

- **Spermidine**

Spermidine is a polyamine produced by the gut microbiota. It helps reduce adiposity and fat accumulation in the liver. Spermidine thus plays a role in preventing diet-induced obesity.

- **Hydrogen sulfide**

At low concentrations, hydrogen sulfide reduces inflammation in the digestive tract. It stabilizes mucus and bacterial populations, reinforcing the intestinal microbiota's barrier effect. However, excessive bacterial production of hydrogen sulfide can lead to intestinal irritation and inflammation. When absorbed by the body, this gas may be linked to hypertension issues.

- **Tetrahydrofolate**

Tetrahydrofolate is the active form of vitamin B9 and can be synthesized by intestinal bacteria. It is involved in the development of the nervous system and the maintenance of cognitive functions.

- **Tryptophan**

Tryptophan is an essential amino acid precursor of serotonin and melatonin. It promotes sleep and helps to reduce stress.

- **Tyrosine**

Tyrosine is a precursor amino acid of dopamine, adrenalin and noradrenalin. It helps maintain balance within the nervous system, playing an important role in regulating motivation, mood and stress.



-- APPENDICES --

# Taxonomic abundance table

| PHYLUM         | CLASS               | ORDER             | FAMILY                       | GENDER                        | SPECIES                              | ABUNDANCE |
|----------------|---------------------|-------------------|------------------------------|-------------------------------|--------------------------------------|-----------|
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_uniformis                | 10.075%   |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Phocaeicola                   | Phocaeicola_vulgatus                 | 7.846%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Prevotellaceae               | Segatella                     | Segatella_copri                      | 6.901%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Prevotellaceae               | Segatella                     | Segatella_hominis                    | 5.265%    |
| Firmicutes     | CFGB38642           | OFGB38642         | FGB38642                     | GGB9758                       | GGB9758_SGB15368                     | 4.687%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Roseburia                     | Roseburia_faecis                     | 3.998%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | Faecalibacterium              | Faecalibacterium_prausnitzii         | 3.538%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Lachnospira                   | Lachnospira_pectinoschiza            | 3.072%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | Oscillospiraceae_unclassified | Eubacterium_siraeum                  | 2.718%    |
| Bacteroidota   | CFGB35002           | OFGB35002         | FGB35002                     | GGB11117                      | GGB11117_SGB17823                    | 2.538%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Lachnospiraceae_unclassified  | Eubacterium_rectale                  | 2.510%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Rikenellaceae                | Alistipes                     | Alistipes_putredinis                 | 1.926%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Coprococcus                   | Coprococcus_eutactus                 | 1.737%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | Faecalibacterium              | Faecalibacterium_SGB15346            | 1.572%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Tannerellaceae               | Parabacteroides               | Parabacteroides_merdae               | 1.562%    |
| Bacteroidota   | CFGB4405            | OFGB4405          | FGB4405                      | GGB1266                       | GGB1266_SGB1699                      | 1.307%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Rikenellaceae                | Alistipes                     | Alistipes_nderdonkii                 | 1.244%    |
| Proteobacteria | CFGB10055           | OFGB10055         | FGB10055                     | GGB6606                       | GGB6606_SGB9340                      | 1.041%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_ovatus                   | 1.013%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Barnesiellaceae              | Barnesiella                   | Barnesiella_intestinihominis         | 0.973%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_caccae                   | 0.951%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_fragilis                 | 0.847%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Lachnospira                   | Lachnospira_eligens                  | 0.803%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Phocaeicola                   | Phocaeicola_dorei                    | 0.796%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Brotolimicola                 | Brotolimicola_acetigignens           | 0.752%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | Oscillibacter                 | Oscillibacter_sp_ER4                 | 0.728%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_thetaiotaomicron         | 0.725%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Clostridiaceae               | Clostridium                   | Clostridium_SGB4909                  | 0.667%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Clostridiaceae               | Clostridium                   | Clostridium_sp_AF36_4                | 0.613%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | Ruminococcus                  | Ruminococcus_bromii                  | 0.577%    |
| Proteobacteria | Betaproteobacteria  | Burkholderiales   | Sutterellaceae               | Parasutterella                | Parasutterella_excrementihominis     | 0.557%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Odoribacteraceae             | Odoribacter                   | Odoribacter_splanchnicus             | 0.554%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Clostridiaceae               | Clostridium                   | Clostridium_fessum                   | 0.541%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | GGB9635                       | GGB9635_SGB15106                     | 0.538%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Eubacteriales_unclassified   | Gemmiger                      | Gemmiger_formicilis                  | 0.523%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Eubacteriales_incertae_sedis | Candidatus_Cibionibacter      | Candidatus_Cibionibacter_quicibialis | 0.514%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | GGB9699                       | GGB9699_SGB15216                     | 0.511%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Tannerellaceae               | Parabacteroides               | Parabacteroides_distasonis           | 0.510%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Lachnospiraceae              | Lachnospira                   | Lachnospira_sp_NSJ_43                | 0.500%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_cellulosilyticus         | 0.481%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Clostridiaceae               | Clostridium                   | Clostridium_sp_AF20_17LB             | 0.470%    |
| Firmicutes     | Clostridia          | Eubacteriales     | Oscillospiraceae             | Ruminococcus                  | Ruminococcus_bicirculans             | 0.461%    |
| Proteobacteria | Gammaproteobacteria | Enterobacterales  | Enterobacteriaceae           | Escherichia                   | Escherichia_coli                     | 0.459%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales     | Bacteroidaceae               | Bacteroides                   | Bacteroides_xylanisolvens            | 0.427%    |
| Firmicutes     | CFGB74971           | OFGB74971         | FGB74971                     | GGB9334                       | GGB9334_SGB14298                     | 0.421%    |
| Firmicutes     | Negativicutes       | Acidaminococcales | Acidaminococcaceae           | Phascolarctobacterium         | Phascolarctobacterium_faecium        | 0.406%    |

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| PHYLUM                     | CLASS              | ORDER             | FAMILY                     | GENDER                       | SPECIES                               | ABUNDANCE |
|----------------------------|--------------------|-------------------|----------------------------|------------------------------|---------------------------------------|-----------|
| Bacteroidota               | Bacteroidia        | Bacteroidales     | Rikenellaceae              | Alistipes                    | Alistipes_communis                    | 0.403%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | Faecalibacterium             | Faecalibacterium_sp_HTF               | 0.397%    |
| Firmicutes                 | CFGB9119           | OFGB9119          | FGB9119                    | GGB4651                      | GGB4651_SGB6438                       | 0.393%    |
| Bacteroidota               | Bacteroidia        | Bacteroidales     | Bacteroidaceae             | Bacteroides                  | Bacteroides_gallinaceum               | 0.376%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB9595                      | GGB9595_SGB15019                      | 0.354%    |
| Proteobacteria             | CFGB2403           | OFGB2403          | FGB2403                    | GGB6601                      | GGB6601_SGB9333                       | 0.351%    |
| Tenericutes                | CFGB1789           | OFGB1789          | FGB1789                    | GGB4754                      | GGB4754_SGB6584                       | 0.340%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Clostridiaceae             | Clostridium                  | Clostridium_sp_AM22_11AC              | 0.321%    |
| Bacteroidota               | Bacteroidia        | Bacteroidales     | Rikenellaceae              | Alistipes                    | Alistipes_finegoldii                  | 0.311%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Roseburia                    | Roseburia_hominis                     | 0.308%    |
| Bacteroidota               | Bacteroidia        | Bacteroidales     | Rikenellaceae              | Alistipes                    | Alistipes_senegalensis                | 0.301%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB33469                     | GGB33469_SGB15236                     | 0.300%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Roseburia                    | Roseburia_inulinivorans               | 0.299%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | Ruminococcus                 | Ruminococcus_SGB4421                  | 0.293%    |
| Firmicutes                 | CFGB1380           | OFGB1380          | FGB1380                    | GGB3364                      | GGB3364_SGB4449                       | 0.292%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Fusicatenibacter             | Fusicatenibacter_saccharivorans       | 0.280%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB9614                      | GGB9614_SGB15049                      | 0.269%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Eubacteriales_unclassified | Eubacteriales_unclassified   | Bacteroides_pectinophilus             | 0.253%    |
| Firmicutes                 | CFGB79294          | OFGB79294         | FGB79294                   | GGB9677                      | GGB9677_SGB15179                      | 0.253%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB9715                      | GGB9715_SGB15265                      | 0.252%    |
| Firmicutes                 | CFGB47591          | OFGB47591         | FGB47591                   | GGB9746                      | GGB9746_SGB15352                      | 0.241%    |
| Firmicutes                 | CFGB3062           | OFGB3062          | FGB3062                    | GGB9747                      | GGB9747_SGB15356                      | 0.235%    |
| Firmicutes                 | Negativicutes      | Veillonellales    | Veillonellaceae            | Dialister                    | Dialister_hominis                     | 0.234%    |
| Actinobacteria             | Actinomycetia      | Bifidobacteriales | Bifidobacteriaceae         | Bifidobacterium              | Bifidobacterium_adolescentis          | 0.230%    |
| Candidatus_Melainabacteria | CFGB2107           | OFGB2107          | FGB2107                    | GGB6012                      | GGB6012_SGB8640                       | 0.230%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | Oscillibacter                | Oscillibacter_sp_MSJ_31               | 0.227%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB9708                      | GGB9708_SGB15233                      | 0.219%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB51661                     | GGB51661_SGB72064                     | 0.216%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | Lawsonibacter                | Lawsonibacter_asaccharolyticus        | 0.215%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Faecalicatena                | Faecalicatena_fissicatena             | 0.214%    |
| Firmicutes                 | Negativicutes      | Acidaminococcales | Acidaminococcaceae         | Phascolarctobacterium        | Phascolarctobacterium_succinatutens   | 0.211%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Butyrivibrio                 | Butyrivibrio_crossotus                | 0.200%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Eubacteriales_unclassified | GGB9760                      | GGB9760_SGB15374                      | 0.196%    |
| Proteobacteria             | Betaproteobacteria | Burkholderiales   | Sutterellaceae             | Duodenibacillus              | Duodenibacillus_massiliensis          | 0.195%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Roseburia                    | Roseburia_sp_AF02_12                  | 0.194%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Lachnospiraceae_unclassified | Lachnospiraceae_bacterium_CLA_AA_H244 | 0.191%    |
| Firmicutes                 | CFGB9120           | OFGB9120          | FGB9120                    | GGB4642                      | GGB4642_SGB6422                       | 0.190%    |
| Bacteroidota               | Bacteroidia        | Bacteroidales     | Bacteroidaceae             | Bacteroides                  | Bacteroides_salysiae                  | 0.189%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Simiaoa                      | Simiaoa_sunii                         | 0.185%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | GGB9708                      | GGB9708_SGB15234                      | 0.185%    |
| Lentisphaerae              | Lentisphaeria      | Victivallales     | Victivallaceae             | GGB6512                      | GGB6512_SGB9197                       | 0.182%    |
| Firmicutes                 | CFGB9583           | OFGB9583          | FGB9583                    | GGB3490                      | GGB3490_SGB4664                       | 0.181%    |
| Bacteroidota               | Bacteroidia        | Bacteroidales     | Muribaculaceae             | GGB1497                      | GGB1497_SGB2076                       | 0.177%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Lachnospiraceae            | Lacrimispora                 | Lacrimispora_amygdalina               | 0.175%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | Faecalibacterium             | Faecalibacterium_sp_CLA_AA_H233       | 0.173%    |
| Firmicutes                 | CFGB8140           | OFGB8140          | FGB8140                    | GGB3755                      | GGB3755_SGB5106                       | 0.172%    |
| Firmicutes                 | CFGB1765           | OFGB1765          | FGB1765                    | GGB4585                      | GGB4585_SGB6340                       | 0.170%    |
| Firmicutes                 | CFGB79303          | OFGB79303         | FGB79303                   | GGB3725                      | GGB3725_SGB5055                       | 0.169%    |
| Elusimicrobia              | Elusimicrobia      | Elusimicrobiales  | Elusimicrobiaceae          | GGB12693                     | GGB12693_SGB19690                     | 0.167%    |
| Firmicutes                 | Clostridia         | Eubacteriales     | Oscillospiraceae           | Vescimonas                   | Vescimonas_coprocola                  | 0.166%    |

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| PHYLUM         | CLASS               | ORDER              | FAMILY              | GENDER                       | SPECIES                                 | ABUNDANCE |
|----------------|---------------------|--------------------|---------------------|------------------------------|-----------------------------------------|-----------|
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Blautia                      | Blautia_SGB101324                       | 0.161%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | GGB9634                      | GGB9634_SGB15093                        | 0.159%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | Oscillibacter                | Oscillibacter_valericigenes             | 0.151%    |
| Firmicutes     | CFGB1765            | OFGB1765           | FG1765              | GGB4571                      | GGB4571_SGB6317                         | 0.151%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | Dysosmobacter                | Dysosmobacter_welbionis                 | 0.150%    |
| Firmicutes     | CFGB73062           | OFGB73062          | FG73062             | GGB9059                      | GGB9059_SGB13976                        | 0.149%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridium                  | Clostridium_SGB4750                     | 0.139%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | Agathobaculum                | Agathobaculum_butyriciproducens         | 0.137%    |
| Firmicutes     | Negativicutes       | Acidaminococcales  | Acidaminococcaceae  | Acidaminococcus              | Acidaminococcus_intestini               | 0.135%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Bacteroidaceae      | Phocaeicola                  | Phocaeicola_massiliensis                | 0.134%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | GGB9707                      | GGB9707_SGB15229                        | 0.132%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Bacteroidaceae      | Bacteroides                  | Bacteroides_stercoris                   | 0.130%    |
| Firmicutes     | CFGB2832            | OFGB2832           | FG2832              | GGB9054                      | GGB9054_SGB13959                        | 0.128%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Muribaculaceae      | GGB1550                      | GGB1550_SGB2135                         | 0.128%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Lachnospiraceae_unclassified | Lachnospiraceae_bacterium_AM48_27BH     | 0.124%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridiaceae_unclassified  | Clostridiaceae_bacterium                | 0.120%    |
| Proteobacteria | Deltaproteobacteria | Desulfovibrionales | Desulfovibrionaceae | Bilophila                    | Bilophila_wadsworthia                   | 0.120%    |
| Firmicutes     | CFGB1474            | OFGB1474           | FG1474              | GGB3731                      | GGB3731_SGB5063                         | 0.117%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | GGB3640                      | GGB3640_SGB4937                         | 0.116%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Eubacteriaceae      | GGB3277                      | GGB3277_SGB4327                         | 0.109%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Mediterraneibacter           | Ruminococcus_lactaris                   | 0.104%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Prevotellaceae      | GGB1221                      | GGB1221_SGB1590                         | 0.100%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridium                  | Clostridium_sp_AM49_4BH                 | 0.098%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridium                  | Clostridium_SGB48024                    | 0.096%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridiaceae_unclassified  | Clostridiaceae_bacterium_Marselle_Q4145 | 0.092%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridiaceae_unclassified  | Clostridiaceae_bacterium_AF18_31LB      | 0.089%    |
| Firmicutes     | CFGB2984            | OFGB2984           | FG2984              | GGB9347                      | GGB9347_SGB14313                        | 0.088%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Rikenellaceae       | Alistipes                    | Alistipes_shahii                        | 0.086%    |
| Fibrobacteres  | CFGB48799           | OFGB48799          | FG48799             | GGB49836                     | GGB49836_SGB69821                       | 0.082%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Wujia                        | Wujia_chippingensis                     | 0.081%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridiaceae_unclassified  | Clostridiaceae_bacterium_Marselle_Q4143 | 0.079%    |
| Firmicutes     | CFGB2834            | OFGB2834           | FG2834              | GGB9064                      | GGB9064_SGB13983                        | 0.077%    |
| Firmicutes     | CFGB3038            | OFGB3038           | FG3038              | GGB9534                      | GGB9534_SGB14937                        | 0.076%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Odoribacteraceae    | Butyricimonas                | Butyricimonas_faecihominis              | 0.075%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Bacteroidaceae      | Bacteroides                  | Bacteroides_intestinalis                | 0.073%    |
| Firmicutes     | CFGB1765            | OFGB1765           | FG1765              | GGB4543                      | GGB4543_SGB6264                         | 0.073%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Odoribacteraceae    | Butyricimonas                | Butyricimonas_paravirosa                | 0.071%    |
| Firmicutes     | CFGB2830            | OFGB2830           | FG2830              | GGB9047                      | GGB9047_SGB13950                        | 0.070%    |
| Firmicutes     | CFGB9272            | OFGB9272           | FG9272              | GGB9296                      | GGB9296_SGB14253                        | 0.070%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Lachnospira                  | Lachnospira_SGB5083                     | 0.067%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Anaerotignum                 | Anaerotignum_faecicola                  | 0.065%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Blautia                      | Blautia_wexlerae                        | 0.064%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridium                  | Clostridium_sp_AF27_2AA                 | 0.063%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | GGB13489                     | GGB13489_SGB15224                       | 0.060%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Lachnospiraceae     | Lachnospiraceae_unclassified | Lachnospiraceae_unclassified_SGB69346   | 0.060%    |
| Tenericutes    | CFGB1791            | OFGB1791           | FG1791              | GGB4757                      | GGB4757_SGB6588                         | 0.059%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | Clostridium                  | Clostridium_sp_AM33_3                   | 0.058%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Rikenellaceae       | Alistipes                    | Alistipes_dispar                        | 0.057%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Oscillospiraceae    | GGB9593                      | GGB9593_SGB15015                        | 0.056%    |
| Firmicutes     | Clostridia          | Eubacteriales      | Clostridiaceae      | GGB3480                      | GGB3480_SGB20550                        | 0.056%    |
| Bacteroidota   | Bacteroidia         | Bacteroidales      | Bacteroidaceae      | Bacteroides                  | Bacteroides_clarus                      | 0.052%    |

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| PHYLUM                     | CLASS                                   | ORDER                          | FAMILY                                      | GENDER                                      | SPECIES                                  | ABUNDANCE |
|----------------------------|-----------------------------------------|--------------------------------|---------------------------------------------|---------------------------------------------|------------------------------------------|-----------|
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | GGB3653                                     | GGB3653_SGB4964                          | 0.052%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Coprococcus                                 | Coprococcus_comes                        | 0.052%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | Ruthenibacterium                            | Ruthenibacterium_lactatiformans          | 0.048%    |
| Firmicutes                 | CFGB4605                                | OFGB4605                       | FGB4605                                     | GGB13404                                    | GGB13404_SGB14252                        | 0.048%    |
| Bacteroidota               | Bacteroidia                             | Bacteroidales                  | Rikenellaceae                               | Alistipes                                   | Alistipes_ihumii                         | 0.048%    |
| Bacteroidota               | Bacteroidia                             | Bacteroidales                  | Rikenellaceae                               | Alistipes                                   | Alistipes_sp_AF17_16                     | 0.047%    |
| Firmicutes                 | CFGB10318                               | OFGB10318                      | FGB10318                                    | GGB37878                                    | GGB37878_SGB47372                        | 0.046%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Jutongia                                    | Jutongia_hominis                         | 0.046%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Anaerostipes                                | Anaerostipes_hadrus                      | 0.045%    |
| Proteobacteria             | Betaproteobacteria                      | Burkholderiales                | Sutterellaceae                              | Sutterella                                  | Sutterella_SGB9281                       | 0.042%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Eubacteriales_unclassified                  | Eubacteriales_unclassified                  | Clostridiales_bacterium_KLE1615          | 0.041%    |
| Actinobacteria             | Actinomycetia                           | Bifidobacteriales              | Bifidobacteriaceae                          | Bifidobacterium                             | Bifidobacterium_pseudocatenulatum        | 0.041%    |
| Firmicutes                 | CFGB1776                                | OFGB1776                       | FGB1776                                     | GGB4671                                     | GGB4671_SGB6460                          | 0.040%    |
| Bacteroidota               | Bacteroidia                             | Bacteroidales                  | Rikenellaceae                               | GGB1689                                     | GGB1689_SGB2321                          | 0.038%    |
| Actinobacteria             | Coriobacteriia                          | Coriobacteriales               | Coriobacteriaceae                           | Collinsella                                 | Collinsella_aerofaciens                  | 0.038%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Roseburia                                   | Roseburia_sp_831b                        | 0.037%    |
| Firmicutes                 | CFGB1359                                | OFGB1359                       | FGB1359                                     | GGB3321                                     | GGB3321_SGB4395                          | 0.036%    |
| Candidatus_Melainabacteria | Candidatus_Melainabacteria_unclassified | Candidatus_Gastranaerophilales | Candidatus_Gastranaerophilales_unclassified | Candidatus_Gastranaerophilales_unclassified | Candidatus_Gastranaerophilales_bacterium | 0.036%    |
| Firmicutes                 | CFGB3054                                | OFGB3054                       | FGB3054                                     | GGB9686                                     | GGB9686_SGB15190                         | 0.035%    |
| Firmicutes                 | Bacilli                                 | Lactobacillales                | Streptococcaceae                            | Streptococcus                               | Streptococcus_salivarius                 | 0.035%    |
| Firmicutes                 | Erysipelotrichia                        | Erysipelotrichales             | Turicibacteraceae                           | Turicibacter                                | Turicibacter_sanguinis                   | 0.035%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | GGB9730                                     | GGB9730_SGB15291                         | 0.034%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | GGB9715                                     | GGB9715_SGB15260                         | 0.034%    |
| Bacteroidota               | Bacteroidia                             | Bacteroidales                  | Bacteroidaceae                              | Bacteroides                                 | Bacteroides_finegoldii                   | 0.033%    |
| Firmicutes                 | CFGB3023                                | OFGB3023                       | FGB3023                                     | GGB9501                                     | GGB9501_SGB14898                         | 0.033%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Lachnospiraceae_unclassified                | Lachnospiraceae_bacterium                | 0.033%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Eubacteriaceae                              | Eubacterium                                 | Eubacterium_ventriosum                   | 0.031%    |
| Firmicutes                 | CFGB2829                                | OFGB2829                       | FGB2829                                     | GGB9045                                     | GGB9045_SGB13947                         | 0.030%    |
| Firmicutes                 | CFGB1325                                | OFGB1325                       | FGB1325                                     | GGB3175                                     | GGB3175_SGB4191                          | 0.030%    |
| Firmicutes                 | CFGB9119                                | OFGB9119                       | FGB9119                                     | GGB4726                                     | GGB4726_SGB6546                          | 0.030%    |
| Firmicutes                 | CFGB3069                                | OFGB3069                       | FGB3069                                     | GGB9767                                     | GGB9767_SGB15385                         | 0.029%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Roseburia                                   | Roseburia_intestinalis                   | 0.029%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | GGB9616                                     | GGB9616_SGB15052                         | 0.028%    |
| Firmicutes                 | CFGB1765                                | OFGB1765                       | FGB1765                                     | GGB4552                                     | GGB4552_SGB6276                          | 0.028%    |
| Candidatus_Melainabacteria | CFGB2107                                | OFGB2107                       | FGB2107                                     | GGB6006                                     | GGB6006_SGB8630                          | 0.028%    |
| Bacteroidota               | Bacteroidia                             | Bacteroidales                  | Barnesiellaceae                             | Coprobacter                                 | Coprobacter_secundus                     | 0.027%    |
| Firmicutes                 | Negativicutes                           | Veillonellales                 | Veillonellaceae                             | Dialister                                   | Dialister_invisus                        | 0.026%    |
| Candidatus_Melainabacteria | CFGB10197                               | OFGB10197                      | FGB10197                                    | GGB5975                                     | GGB5975_SGB8592                          | 0.025%    |
| Proteobacteria             | Betaproteobacteria                      | Burkholderiales                | Sutterellaceae                              | Sutterella                                  | Sutterella_wadsworthensis                | 0.023%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | Lawsonibacter                               | Lawsonibacter_SGB15145                   | 0.023%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | Hydrogenoanaerobacterium                    | Hydrogenoanaerobacterium_saccharovorans  | 0.022%    |
| Verrucomicrobia            | Opitutae                                | Puniceococcales                | Puniceococcaceae                            | GGB6123                                     | GGB6123_SGB8767                          | 0.022%    |
| Proteobacteria             | Deltaproteobacteria                     | Desulfovibrionales             | Desulfovibrionaceae                         | GGB9819                                     | GGB9819_SGB15460                         | 0.020%    |
| Proteobacteria             | CFGB2404                                | OFGB2404                       | FGB2404                                     | GGB6613                                     | GGB6613_SGB9347                          | 0.019%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Mediterraneibacter                          | Ruminococcus_torques                     | 0.019%    |
| Proteobacteria             | Betaproteobacteria                      | Burkholderiales                | Sutterellaceae                              | Parasutterella                              | Parasutterella_SGB9260                   | 0.019%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Lachnospiraceae                             | Mediterraneibacter                          | Mediterraneibacter_faecis                | 0.019%    |
| Firmicutes                 | CFGB2997                                | OFGB2997                       | FGB2997                                     | GGB9445                                     | GGB9445_SGB14835                         | 0.018%    |
| Firmicutes                 | CFGB72                                  | OFGB72                         | FGB72                                       | GGB105                                      | GGB105_SGB124                            | 0.017%    |
| Firmicutes                 | Clostridia                              | Eubacteriales                  | Oscillospiraceae                            | GGB9636                                     | GGB9636_SGB15108                         | 0.017%    |

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| PHYLUM                     | CLASS                 | ORDER                 | FAMILY                     | GENDER                        | SPECIES                                | ABUNDANCE |
|----------------------------|-----------------------|-----------------------|----------------------------|-------------------------------|----------------------------------------|-----------|
| Firmicutes                 | Clostridia            | Eubacteriales         | Eubacteriales_unclassified | GGB9760                       | GGB9760_SGB15373                       | 0.016%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Oscillospiraceae           | Ruminococcus                  | Ruminococcus_callidus                  | 0.016%    |
| Firmicutes                 | CFGB73223             | OFGB73223             | FG73223                    | GGB9249                       | GGB9249_SGB14193                       | 0.016%    |
| Firmicutes                 | CFGB2833              | OFGB2833              | FG2833                     | GGB74665                      | GGB74665_SGB13972                      | 0.016%    |
| Firmicutes                 | CFGB1765              | OFGB1765              | FG1765                     | GGB4604                       | GGB4604_SGB6371                        | 0.014%    |
| Firmicutes                 | CFGB72899             | OFGB72899             | FG72899                    | GGB4611                       | GGB4611_SGB6385                        | 0.014%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Clostridiaceae             | Clostridium                   | Clostridium_SGB6177                    | 0.013%    |
| Bacteroidota               | Bacteroidia           | Bacteroidales         | Bacteroidaceae             | Bacteroides                   | Bacteroides_eggerthii                  | 0.011%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Lachnospiraceae            | Fusicatenibacter              | Fusicatenibacter_sp_CLA_AA_H277        | 0.010%    |
| Firmicutes                 | CFGB1765              | OFGB1765              | FG1765                     | GGB4599                       | GGB4599_SGB6362                        | 0.010%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Oscillospiraceae           | Oscillospiraceae_unclassified | Oscillospiraceae_bacterium             | 0.010%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Eubacteriales_unclassified | Intestinimonas                | Intestinimonas_massiliensis            | 0.009%    |
| Firmicutes                 | CFGB14936             | OFGB14936             | FG14936                    | GGB3256                       | GGB3256_SGB4303                        | 0.009%    |
| Actinobacteria             | Actinomycetia         | Bifidobacteriales     | Bifidobacteriaceae         | Bifidobacterium               | Bifidobacterium_longum                 | 0.009%    |
| Bacteroidota               | Bacteroidia           | Bacteroidales         | Prevotellaceae             | Paraprevotella                | Paraprevotella_clara                   | 0.008%    |
| Firmicutes                 | Erysipelotrichia      | Erysipelotrichales    | Erysipelotrichaceae        | Faecalibacillus               | Faecalibacillus_intestinalis           | 0.008%    |
| Firmicutes                 | CFGB78560             | OFGB78560             | FG78560                    | GGB9287                       | GGB9287_SGB14242                       | 0.007%    |
| Bacteroidota               | CFGB72567             | OFGB72567             | FG72567                    | GGB1109                       | GGB1109_SGB1423                        | 0.006%    |
| Candidatus_Melainabacteria | CFGB2106              | OFGB2106              | FG2106                     | GGB5980                       | GGB5980_SGB8599                        | 0.006%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Eubacteriales_unclassified | Colidextribacter              | Colidextribacter_sp_210702_DFI_3_9     | 0.006%    |
| Proteobacteria             | CFGB2404              | OFGB2404              | FG2404                     | GGB6608                       | GGB6608_SGB9342                        | 0.006%    |
| Bacteria_unclassified      | Bacteria_unclassified | Bacteria_unclassified | Bacteria_unclassified      | Bacteria_unclassified         | bacterium_210917_DFI_7_65              | 0.005%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Eubacteriales_unclassified | Eubacteriales_unclassified    | Clostridiales_bacterium                | 0.005%    |
| Firmicutes                 | CFGB6280              | OFGB6280              | FG6280                     | GGB6600                       | GGB6600_SGB9331                        | 0.003%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Lachnospiraceae            | Blautia                       | Blautia_faecis                         | 0.003%    |
| Verrucomicrobia            | Verrucomicrobiae      | Verrucomicrobiales    | Akkermansiaceae            | Akkermansia                   | Akkermansia_muciniphila                | 0.002%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Lachnospiraceae            | Dorea                         | Dorea_longicatena                      | 0.002%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Oscillospiraceae           | Oscillospiraceae_unclassified | Oscillospiraceae_bacterium_CLA_AA_H250 | 0.002%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Oscillospiraceae           | Oscillospiraceae_unclassified | Oscillospiraceae_unclassified_SGB4197  | 0.002%    |
| Firmicutes                 | Clostridia            | Eubacteriales         | Lachnospiraceae            | Anaerotignum                  | Anaerotignum_sp_MSJ_24                 | 0.002%    |

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