GUT

PETITION NUMBER: TEST001

Requested analysis:	Type of sample:	Age:	Gender:	Report date:
GUT AMPLICON	**Faeces**	**35**	**Not reported**	**22/01/2025**

GUT is a test based on the analysis of a gut microbiome with the aim of identifying the bacterial species present (microbiota). When present, GUT also highlights imbalances in the microbiome (dysbiosis) and provides dietary and lifestyle recommendations to correct it. This test is based on the next generation sequencing of hypervariable regions (V3-V4) of the bacterial gene that encodes the 16S rRNA subunity.
The composition of an individual's microbiota is unique and some microbiome profiles have been associated to better health conditions. A healthy microbiota is characterized by a high diversity of bacteria and stability over time. The analysis of the bacterial microbiome can help maintain good health as well as prevent or treat intestinal (for example recurrent diarrhea or colitis) or systemic (obesity, metabolic syndrome, etc.) diseases.

HOW DOES IT WORK?

The gut microbiome test has no diagnostic value but represents a snapshot of the bacterial component of the intestinal microbiota at the time of sampling. Based on the main phyla, genera and species the report identifies the tester's enterosignature. Each enterosignature is related to a prevailing diet and represents an indication of the reference composition for the microbiota being analyzed.
These results are then compared with the microbiomes of hundreds of healthy individuals (control database). In this way, it is possible to assess whether particular bacterial genera are in excess compared to the average of the control database in order to identify and characterize situations of dysbiosis.
Together with the results, dietary recommendations are provided, including probiotics and dietary supplements to improve the diet regime. These indications must be evaluated by a qualified professional based on the subject's overall medical history.

GENERAL INFORMATION

Boxes highlighted with color green represent an optimal value of the microbiome. Boxes in red show a value that differs significantly from the optimal value while those in yellow show a neutral or intermediate value, neither optimal nor harmful. The blue boxes have simply informative purpose.

INDEXES

✓

MICROBIAL EQUILIBRIUM INDEX

Slight disbiosis

The Microbial Equilibrium Index evaluates the health and composition of the gut microbiota. It measures multiple parameters, including diversity, the balance between Gram+ and Gram- bacteria, the ratios of aerobic/anaerobic species, Bacillota/Bacteroidota and Prevotella/Bacteroides, the presence of Pseudomonadota, a group often associated with dysbiosis, and a measure of similarity between an individual's microbiome and a healthy reference population.

!

SIMILARITY

Low

Patient: **59.5%**

The similarity value suggests how close a microbiome is from another microbiome from a healthy reference population. It ranges from 0 to 100% similarity: 0% would indicate a sample without similarity at all (no taxa in common), while 100% would indicate highly similar taxonomic composition to a sample from the healthy reference population. The similarity value derives from the Bray-Curtis divergence metric.

DIVERSITY

Unavailable or insufficient sequencing depth

A healthy microbiota is rich in different species; therefore, a high diversity represents a sign of its good health. This value shows the Shannon diversity index of bacteria present in the intestine at the time of sampling.

✓

GRAM+ / GRAM-

On average

Patient: **-0.33 (Log10 Ratio)**
Population: -1.21 ~ 1.95

The Gram+ and Gram- are two groups of bacteria which basically differ from each other for their cell wall composition and structure. The differences between gram+ and gram- are primarily related to their cell wall composition

✓

AEROBIC / ANAEROBIC

On average

Patient: **-2.47 (Log10 Ratio)**
Population: -3.89 ~ -0.15

Aerobic bacteria, different from anaerobic, require oxygen to grow. Two groups of anaerobic bacteria exist: 'obligate anaerobes bacteria' which cannot survive in the presence of oxygen, and the facultative anaerobes which are capable of surviving both in presence and absence of oxygen.

ENTEROSIGNATURE

Bacteroides

Enterosignatures can be defined as a characteristic microbial profile that reflects compositional and functional aspects of the gut microbiome. Five enterosignatures have been suggested: Prevotella, Bacteroides, Bifidobacterium, Bacillota, and Escherichia. Prevotella, Bacteroides and Bacillota are the typical enterosignatures in adults.

✓

BACILLOTA / BACTEROIDOTA

On average

Patient: **-0.15 (Log10 Ratio)**
Population: -0.77 ~ 2.22

Previously known as Firmicutes/Bacteroidetes (F/B) ratio. Bacillota and Bacteroidota are two dominant phyla in the fecal microbiota, which represent up to 90% of the total bacterial species. The Bacillota and Bacteroidetes ratio (B/B ratio) is believed to be highly correlated with certain diseases, such as obesity and diabetes.

✓

BACILLOTA + BACTEROIDOTA

On average

Patient: **15.1 (CLR)**
Population: 13.8 ~ 17.0

Assessing the combined abundance of Bacillota and Bacteroidota, formerly known as Firmicutes and Bacteroidetes, is crucial for the clinical interpretation of the intestinal microbiome. These two bacterial phyla are the most abundant in the gut microbiome and play fundamental roles in intestinal health, influencing digestion, metabolism, and immune response.

✓

PREVOTELLA / BACTEROIDES

On average

Patient: **0 (Log10 Ratio)**
Population: -3.70 ~ 2.00

An elevated Prevotella-to-Bacteroides (P/B) ratio is often linked to diets high in fiber and plant-based foods. Higher Prevotella abundance, thus higher P/B ratio, has been associated with improved glycaemic control. Furthermore, individuals with a high P/B ratio are more likely to experience weight loss when consuming a low-calorie fiber-rich diet. Prevotella is more efficient producing propionate, which bypasses the enterocyte line, enters the hepatic gluconeogenesis circuit, and contributes to a satiating effect.

✓

PSEUDOMONADOTA

On average

Patient: **11.3 (CLR)**
Population: 9.47 ~ 13.6

Pseudomonadota (formerly Proteobacteria) is a phylum of bacteria usually present in the gut microbiome in low levels of abundance. However, some Pseudomonadota can also be opportunistic pathogens and are associated with gut inflammation. In this context, high levels of Pseudomonadota might indicate an alteration of the gut microbiome.

NUTRITION

METABOLIC AND NUTRITIONAL FUNCTIONS

✓

GLUTEN DEGRADING BACTERIA

On average

Patient: **14.9 (CLR), 4.96%**
Population: 13.2 ~ 17.6

Gluten is a protein found in wheat, rye, spelt, barleys, among other grains. This protein has characteristics that make it hard to be digested by human enzymes. Several studies show that there are several bacteria that can help to digest gluten.

!

LACTOSE DEGRADING BACTERIA

Low

Patient: **15.8 (CLR), 12.6%**
Population: 16.2 ~ 17.8

Lactose is a common sugar present in milk products that is usually digested in the small intestine. It has been found that intolerance to this sugar has a genetic background. However, some gut bacteria are able to degrade lactose due to their endogenous lactase activity, mainly Lactobacillus and Bifidobacterium species.

✓

GLUTATHIONE REDUCERS

On average

Patient: **15.3 (CLR), 7.60%**
Population: 12.1 ~ 17.5

Glutathione is an antioxidant molecule that is synthesized by our body using amino acids like glycine. The gut microbiome itself does not produce glutathione. It has been observed that glycine can be consumed by the microbiota, thus resulting in a deficiency of glutathione. Decreased glutathione levels may contribute to the development of certain gut-related diseases and neurodegeneration.

OXALATE HOMEOSTASIS

Very low

Patient: **-0.56 (CLR), 0%**
Population: 9.20 ~ 16.5

Most kidney stones are made of calcium oxalate, thus hyperoxaluria (excess of oxalate) is a major risk factor in this kidney disease. While some oxalate is absorbed in the small intestine and excreted in the urine, a significant portion can be metabolized by the gut microbiome, specially by members of the genus Oxalobacter.

EQUOL PRODUCERS

On average

Patient: **8.17 (CLR), 0.0061%**
Population: 7.87 ~ 13.5

Equol-producing bacteria generate this soy isoflavone metabolite, equol, as humans do not synthesize it themselves. Equol has demonstrated a reduction in estrogen-dependent and age-related disorders such as menopausal symptoms, osteoporosis, cardiovascular diseases, and cancer. However, an increased presence of equol-consuming bacteria could counteract its effects by reducing its bioavailability.

SHORT CHAIN FATTY ACIDS

ENERGY PRODUCERS

On average

Patient: **16.1 (CLR), 15.9%**
Population: 14.9 ~ 17.6

A portion of indigestible fiber reaches the colon without undergoing degradation by intestinal enzymes, where microorganisms break it down into crucial metabolic conversions for the host. These conversions, involving the degradation of proteins and structurally diverse complex polysaccharides from both animal and plant origins, provide the organism with essential energy and nutrients. The fermentation of these compounds by the intestinal microbiota generates metabolites such as short-chain fatty acids, pivotal for colon health.

BUTYRATE PRODUCERS

On average

Patient: **15.3 (CLR), 7.09%**
Population: 13.9 ~ 15.8

Butyrate is a Short-Chain Fatty Acid (SCFA) and is one of the main products generated from gut microbial fermentation of dietary fiber. The most important function of butyrate is to be an energy source for the colonocytes and maintain human gut health.

✓

ACETATE PRODUCERS

On average

Patient: **15.8 (CLR), 12.6%**
Population: 14.8 ~ 17.5

Acetate is the most abundant Short-Chain Fatty Acid (SCFA) produced from gut microbiota fermentation reactions of carbohydrates, especially dietary fiber. It is related to the whole-body energy homeostasis, since it can be used both as an energy source and stimulates cholesterol metabolism and lipogenesis.

✓

PROPIONATE PRODUCERS

On average

Patient: **15.1 (CLR), 6.07%**
Population: 13.5 ~ 17.6

The presence of propionate in the gut, a Short-Chain Fatty Acid (SCFA), which is the main source of energy for intestinal epithelial cells, has some health effects, such as decreased cholesterol levels and antilipogenic effects. In addition, it has antiproliferative effects and apoptosis induction related to cancer.

HEALTH STATUS

PRODUCTION OF SPECIFIC COMPOUNDS

✓

METHANOGENS

On average

Patient: **-0.56 (CLR), 0%**
Population: -1.01 ~ -0.37

Methane producers (methanogens) are a group of microorganisms that can produce methane gas in the gut by fermenting carbohydrates. The most well-known methane producers in the gut microbiome are members of the Archaea domain, specifically the Methanobrevibacter and Methanosphaera genera. Methane production in the gut has been associated with functional bowel disease such as constipation and bloating.

✓

HISTAMINE PRODUCERS

On average

Patient: **-0.56 (CLR), 0%**
Population: -0.88 ~ -0.36

Histamine is a chemical created by our immune cells that can also be produced by certain bacteria. Histamines boost blood flow in the area of your body it targets, in this case the intestines. This causes inflammation and, in fact, it has been shown that histamine might promote abdominal pain specially in patients suffering from Inflammatory Bowel Disease (IBD).

INTERACTION WITH TOXIC SUBSTANCES

✓

ALCOHOL TOXICITY

Low

Alcohol (ethanol) is metabolized to acetaldehyde, a toxin involved in alcoholic diseases. In the presence of ethanol, some bacteria produce the reactive and toxic compound acetaldehyde (from the alcohol dehydrogenase enzymatic activity of these bacteria). This product can bind to different enzymes and molecules with negative effects. As a consequence, there is an increase in the chances of developing diverse diseases.

TRYPTOPHAN METABOLISM

✓

INDOLE PRODUCERS

On average

Patient: **16.2 (CLR), 19.0%**
Population: 13.9 ~ 17.4

Indole producers are a group of bacteria in the gut microbiome that can produce indole by means of tryptophan metabolism. Some studies have shown that indole produced by gut bacteria can have beneficial effects on the host, such as promoting gut barrier function, reducing inflammation, and modulating immune responses.

NEUROTRANSMITTERS

✓

GABA PRODUCERS

On average

Patient: **15.6 (CLR), 10.5%**
Population: 14.9 ~ 17.5

GABA producers are bacteria synthesizing gamma-aminobutyric acid (GABA), a neurotransmitter that regulates brain activity. Although GABA is primarily produced in the brain, it can also be generated in the intestinal microbiome from glutamate. Elevated levels of GABA producers have shown to reduce inflammation, improve intestinal motility, and decrease anxiety and depression-like behaviours. Conversely, GABA-consuming bacteria counteract this effect by reducing the bioavailability of GABA in the gut lumen.

IMMUNE REGULATION

✓

IMMUNE HOMEOSTASIS

On average

Patient: **-0.36 (Log10 Ratio)**
Population: -1.66 ~ 0.76

The composition of the gut microbiome can influence the immunitary response, thus influencing the immune homeostasis. Some bacteria produce Short Chain Fatty Acids (SCFA), which have anti-inflammatory properties. Other gram-negative bacteria are highly immunogenic due to their lipopolysaccharides (LPS). This index assesses the ratio of pro-inflammatory to anti-inflammatory bacteria: the higher the ratio, the higher probability of inflammation.

✓

PERMEABILITY AND MUCOLYTIC ACTIVITY

On average

Patient: **16.3 (CLR), 20.8%**
Population: 15.7 ~ 17.7

The protective mucus layer lining the intestinal epithelium is composed of mucin, a complex glycoprotein. This mucosal barrier acts as a defence against pathogens. Mucolytic bacteria, by degrading mucin, can compromise the mucosal layer, especially in low-fiber diets. Excessive degradation may increase permeability and susceptibility to pathogens, while insufficient degradation affects the availability of nutrients for beneficial bacteria.

✓

LPS PRODUCERS

On average

Patient: **13.8 (CLR), 1.78%**
Population: 10.4 ~ 15.5

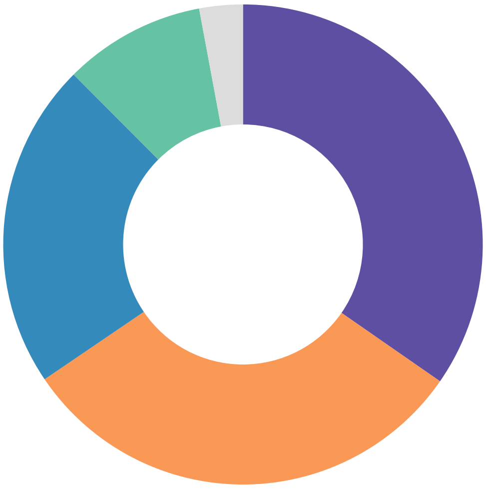
Lipopolysaccharides (LPS) are lipid-polysaccharide chemical complexes commonly found in the outer membrane of gram-negative bacteria. It is known that these molecules promote intestinal inflammation and increase gut permeability.

COMPOSITION OF THE MICROBIOME

The pie chart illustrates the taxonomic classification of the sample at the level of phyla and genus. The data present in the graph and in the legend are ordered in descending order: from the bacteria present in greater quantity to those present in smaller quantities.

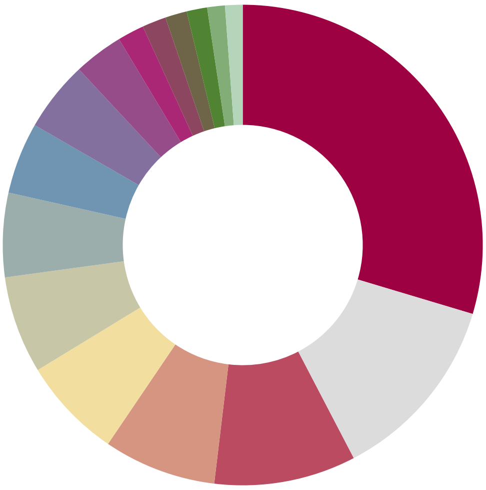
BACTERIA

PHYLA



	PHYLUM	DETECTED VALUE (%)	DETECTED VALUE (CLR)	REFERENCE VALUES (CLR)	RESULT	
🟪	Actinomycetota	34.7	14.34	7.74 ~ 13.94	High	⌃
🟧	Bacteroidota	30.9	14.22	9.39 ~ 16.25	On average	=
🟦	Bacillota	22.0	13.88	12.29 ~ 16.07	On average	=
🟩	unkn. Bacteria(d)	9.55	13.05	8.41 ~ 13.11	On average	=
⬜	Other merged taxa	2.93				

GENUS



	GENUS	DETECTED VALUE (%)	DETECTED VALUE (CLR)	REFERENCE VALUES (CLR)	RESULT	
🟥	unkn. Actinomycetes(c)	29.6	16.65	Absent in DB	Very high	︽
🟥	unkn. Bacteria(d)	9.55	15.52	10.50 ~ 15.10	High	︿
🟧	Bacteroides	7.59	15.29	12.26 ~ 17.39	On average	=
🟨	unkn. Bacteroidia(c)	6.81	15.18	8.49 ~ 14.71	High	︿
🟨	Alistipes	6.55	15.14	10.12 ~ 15.25	On average	=
⬜	unkn. Eubacteriales(o)	5.65	14.99	13.91 ~ 15.70	On average	=
🟦	Clostridium	4.81	14.83	12.67 ~ 14.71	High	︿
🟪	unkn. Bacteroidota(p)	4.73	14.81	8.86 ~ 14.63	High	︿
🟪	unkn. Actinomycetota(p)	3.33	14.46	8.02 ~ 14.49	On average	=
🟪	Parabacteroides	1.78	13.84	7.48 ~ 15.40	On average	=
🟫	unkn. Propionibacteriales(o)	1.62	13.74	Absent in DB	Very high	︽
🟫	unkn. Clostridia(c)	1.46	13.64	9.60 ~ 14.83	On average	=
🟩	Ligilactobacillus	1.38	13.58	Absent in DB	Very high	︽
🟩	unkn. Clostridiaceae(f)	1.19	13.43	10.67 ~ 12.99	High	︿
🟩	unkn. Oscillospiraceae(f)	1.18	13.43	11.37 ~ 15.21	On average	=
⬜	Other merged taxa	12.7				

ARCHAEA

GENUS

None detected above 0.0001%

NUTRITION

LEGENDA

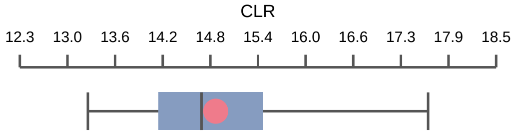
- ︽ Very high
- ︿ High
- = On average
- ﹀ Low
- ︾ Very low
- ○ Not significant

- 🟩 Good
- 🟨 Indifferent
- 🟥 Bad
- ◼ Not Significant

METABOLIC AND NUTRITIONAL FUNCTIONS

GLUTEN DEGRADING BACTERIA

Clostridium 14.83 CLR *Pseudomonas* 11.26 CLR
Streptococcus 8.57 CLR



Patient: **14.9 CLR (4.96%)**
Population: 13.2 ~ 17.6

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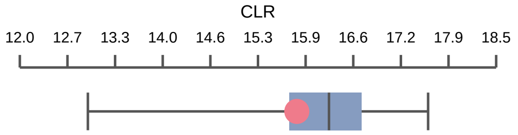
The amino acid sequence of gluten confers resistance to hydrolysis by human digestive enzymes. This results in a partial digestion of the protein, yielding relatively large peptides that can behave as antigens and promote the activation of inflammatory processes. People suffering from celiac disease develop intolerance to gluten proteins, which results in an inflammatory immune response and the production of antibodies against gluten and tissue transglutaminase. There are some bacteria in our gut microbiome (gluten-digesters) that can help us with gluten digestion. It has been seen that some gluten-digesters are altered in celiac people. Celiac disease may cause symptoms such as abdominal pain, diarrhea, nausea, lactose intolerance and weight loss.

REFERENCES: DOI:10.1038/NRGASTRO.2015.90, DOI:10.3390/NU11102375, DOI:10.1111/1574-6941.12295, DOI:10.1016/B978-0-12-401716-0.00013-1, DOI:10.1017/S0007114515002767, DOI:10.4161/19490976.2014.969635, DOI:10.1001/JAMA.2017.9730

AMINO ACID-METABOLIZING MICROBES

Bacteroides 15.29 CLR *Clostridium* 14.83 CLR
Odoribacter 9.67 CLR *Streptococcus* 8.57 CLR
Propionibacterium 8.17 CLR



Patient: **15.8 CLR (12.4%)**
Population: 12.9 ~ 17.6

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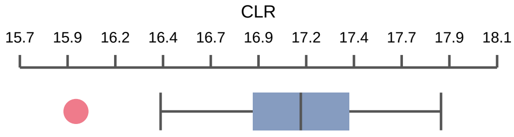
Some bacteria can use amino acids from food for protein synthesis and energy metabolism along the large intestine and colon. Protein intake will have a direct impact on the metabolic pathways of gut bacteria, shifting towards protein fermentation. When amino acids are fermented by the gut microbiota, primary and secondary metabolites (e.g. ammonia and sulfides) are produced and are thought to have a toxic effect on the colonic lumen. High amounts of these byproducts could contribute to gastrointestinal discomfort and other health issues, such as inflammation, ulcerative colitis and colorectal cancer.

REFERENCES: DOI:10.1007/S00726-017-2493-3, DOI:10.2741/3820, DOI:10.1093/JN/130.7.1857S, DOI:10.3390/NU7042930, DOI:10.1038/S41551-019-0397-0, DOI:10.1080/19490976.2016.1270809

CARBOHYDRATE-METABOLIZING MICROBES

Bacteroides 15.29 CLR
Clostridium 14.83 CLR
Eubacterium 13.36 CLR
Oscillospira 13.15 CLR
Roseburia 11.19 CLR
Odoribacter 9.67 CLR
Ruminococcus 9.26 CLR
Dorea 8.86 CLR
Blautia 8.17 CLR



Patient: **16.0 CLR (14.6%)**
Population: 16.4 ~ 17.9

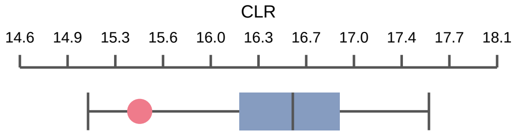
⌄

The degradation and fermentation of carbohydrates has an impact on gut health. Complex carbohydrates (dietary fiber) are metabolized into Short Chain Fatty Acids (SCFAs) by colonic microbiota. SCFAs decrease the luminal pH, thus modulating metabolic absorption and microbiota composition. The Prevotella enterotype is associated with high-fiber diets. In addition, an increase of butyrate-producing bacteria in the gut microbiome has been observed in high-carbohydrate diets. Also, gut microbiota can influence host gene expression in tissues such as the liver and adipose tissues modifying lipogenesis, and glycogenosis.

REFERENCES: DOI:10.1097/MCO.0B013E3283619E63, DOI:10.1097/MCO.0B013E32833A8B60, DOI:10.1080/19490976.2016.1270809

LIPID-METABOLIZING MICROBES

Bacteroides 15.29 CLR
Oscillospira 13.15 CLR
Pseudomonas 11.26 CLR
Odoribacter 9.67 CLR
Ruminococcus 9.26 CLR
Dorea 8.86 CLR
Akkermansia 8.86 CLR
Blautia 8.17 CLR



Patient: **15.5 CLR (8.70%)**
Population: 15.1 ~ 17.6

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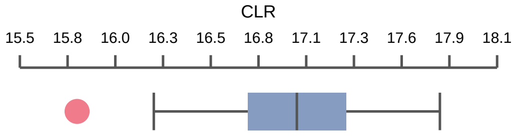
Diet can modulate the gut microbiota and, as an essential part of the diet, lipids also modulate host physiology and the gut microbiota. High-fat diets are correlated with the Bacteroides enterotype and with a slowed intestinal transit. In addition, high-fat diets seem to facilitate the translocation of bacterial lipopolysaccharides (LPS) upon being dissolved into lipid micelles, thus contributing to higher inflammatory statuses. On the other hand, a diet high in fats causes circulating triglycerides and cholesterol to increase by the gut microbiota. Nevertheless, not all fats have the same effect; meat-derived fats promote higher metabolic dysfunction than fish-derived fats.

REFERENCES: DOI:10.1007/S11154-019-09512-0, DOI:10.1080/19490976.2016.1270809, DOI:10.1097/MOL.0000000000000278

LACTOSE DEGRADING BACTERIA

Bacteroides 15.29 CLR
Clostridium 14.83 CLR
Roseburia 11.19 CLR
Ruminococcus 9.26 CLR
Streptococcus 8.57 CLR
Blautia 8.17 CLR



Patient: **15.8 CLR (12.6%)**
Population: 16.2 ~ 17.8

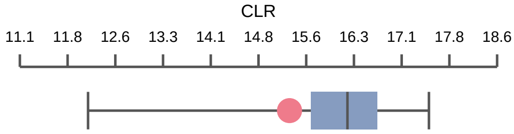
⌄

Lactose intolerance appears due to lactase deficiency or down-regulation of its activity, and lactose malabsorption. However, a regular lactose intake may lead to a higher bacterial metabolism of undigested lactose, thus leading to a colonic adaptation and increased tolerance. Microorganisms involved in lactose digestion encode a ß-galactosidase enzyme. In this context, lactose-digesters hydrolyze lactose to glucose and galactose; then, glucose and galactose are fermented to produce the byproduct lactic acid. Without lactose-digesters, lactose would be fermented by other bacteria producing gas and intestinal discomfort.

REFERENCES: DOI:10.1093/AJCN/NQZ104, DOI:10.3390/NU11040886, DOI:10.1155/2010/649312, DOI:10.3390/NU10121994, DOI:10.3390/NU10101517

GLUTATHIONE REDUCERS

Bacteroides 15.29 CLR | *Streptococcus* 8.57 CLR



Patient: **15.3 CLR (7.60%)**
Population: 12.1 ~ 17.5

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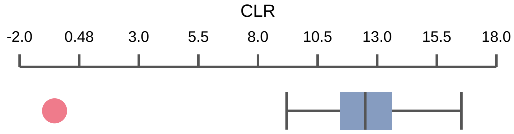
Glutathione is an antioxidant molecule that is synthesized by our body using amino acids like glycine. The gut microbiome itself does not produce glutathione. It has been observed that glycine can be consumed by the microbiota, thus resulting in a deficiency of glutathione. Decreased glutathione levels may contribute to the development of certain gut-related diseases and neurodegeneration.

REFERENCES: 10.1016/J.JARE.2021.09.005, 10.15252/MSB.20156487, 10.1016/J.REDOX.2018.01.009

OXALATE HOMEOSTASIS



Patient: **-0.56 CLR (0%)**
Population: 9.20 ~ 16.5

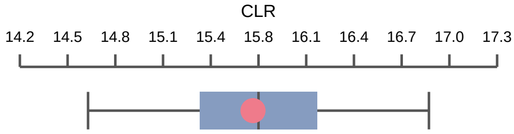
⏬

Most kidney stones are made of calcium oxalate, thus hyperoxaluria (excess of oxalate) is a major risk factor in this kidney disease. While some oxalate is absorbed in the small intestine and excreted in the urine, a significant portion can be metabolized by the gut microbiome, specially by members of the genus Oxalobacter.

REFERENCES: 10.21037/ATM.2016.12.70, 10.1007/S00240-016-0952-Z

WEIGHT-INFLUENCING MICROBES

Alistipes 15.14 CLR | *Clostridium* 14.83 CLR
Roseburia 11.19 CLR | *Ruminococcus* 9.26 CLR
Barnesiella 8.86 CLR



Patient: **15.7 CLR (11.5%)**
Population: 14.6 ~ 16.9

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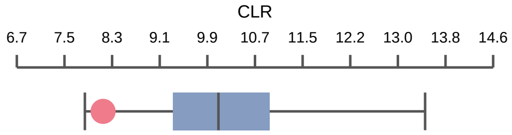
Intestinal bacteria might influence in a certain manner whether you are obese or thin. In this sense, certain bacteria are correlated to maintaining a healthy weight. Usually, an overall enrichment equal or higher than the population is beneficial for our health. Some bacteria have been described as negatively correlated with obesity. One example is Akkermansia muciniphila, which is involved in glucose and lipid metabolism as well as in the maintenance of the intestinal barrier mechanism. Changes in abundance of these microbes will not reflect directly your body shape since other factors such as exercise play a role.

REFERENCES: CASTANER, O., GODAY, A., PARK, Y. M., LEE, S. H., MAGKOS, F., SHIOW, S., & SCHRÖDER, H. (2018). THE GUT MICROBIOME PROFILE IN OBESITY: A SYSTEMATIC REVIEW. INTERNATIONAL JOURNAL OF ENDOCRINOLOGY, 2018, 4095789. DOI:10.1155/2018/4095789, CLARKE, S. F., MURPHY, E. F., NILAWEERA, K., ROSS, P. R., SHANAHAN, F., O'TOOLE, P. W., & COTTER, P. D. (2012). THE GUT MICROBIOTA AND ITS RELATIONSHIP TO DIET AND OBESITY: NEW INSIGHTS. GUT MICROBES, 3(3), 186–202. DOI:10.4161/GMIC.20168, ANDOH, A., NISHIDA, A., TAKAHASHI, K., INATOMI, O., IMAEDA, H., BAMBA, S., ... KOBAYASHI, T. (2016). COMPARISON OF THE GUT MICROBIAL COMMUNITY BETWEEN OBESE AND LEAN PEOPLES USING 16S GENE SEQUENCING IN A JAPANESE POPULATION. JOURNAL OF CLINICAL BIOCHEMISTRY AND NUTRITION, 59(1), 65–70. DOI:10.3164/JCBN.15-152, NAITO, Y., UCHIYAMA, K., & TAKAGI, T. (2018). A NEXT-GENERATION BENEFICIAL MICROBE: AKKERMANSIA MUCINIPHILA. JOURNAL OF CLINICAL BIOCHEMISTRY AND NUTRITION, 63(1), 33–35. DOI:10.3164/JCBN.18-57

EQUOL HOMEOSTASIS

EQUOL PRODUCERS

Adlercreutzia 8.17 CLR



Patient: **8.17 CLR (0.0061%)**
Population: 7.87 ~ 13.5

=

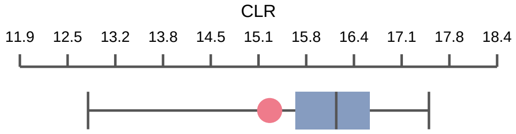
Equol-producing bacteria are a type of bacteria that can produce equol, which is a metabolite of the soy isoflavone daidzein. Humans do not synthesize equol as it is produced by some members of the gut microbiome. Equol-producing strains like Lactococcus, Adlercreutzia, and Slackia are crucial for health benefits associated with soy intake. It has been seen that equol reduces the incidence of estrogen-dependent and aging-associated disorders (e.g., menopause symptoms in women, osteoporosis, cardiovascular diseases and cancer). On the other hand, higher abundance of Equol-consuming bacteria might counteract the beneficial effects of Equol by reducing its bioavailability.

REFERENCES: 10.3390/NU11092231, 10.1186/S12864-022-08426-7

VITAMINS

VITAMIN K-PRODUCING MICROBES

Bacteroides 15.29 CLR



Patient: **15.3 CLR (7.59%)**
Population: 12.8 ~ 17.5

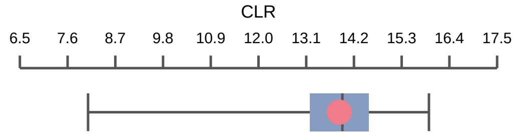
=

Vitamin K is a fat-soluble molecule divided into two forms: phylloquinone (K1) and menaquinone (K2). While phylloquinone is abundant in several vegetables, menaquinone has a microbial origin and is present in fermented food. Both forms of vitamin K are involved in coagulation regulation and bone formation and maintenance, though menaquinone is preferentially used in the bone. The concentration of vitamin K in newborns is very low due to immature gut microbiome and lack of consumption of foods rich in vitamin K; in this context, doctors administer an extra amount of vitamin K by injection. The principal causes of vitamin K deficiency are alteration of intestinal absorption (e.g. alcoholism) or gastrointestinal injury. Symptoms include ecchymosis, petechiae, bruising due to slower coagulation, abdominal pain, alopecia, risk of massive bleeding, abundant menstruation, calcification of cartilage, a severe malformation in bone development and calcium deposition in blood vessels.

REFERENCES: DOI:10.1081/E-EDS-120022055, DOI:10.1038/JP.2016.30, DOI:10.1111/JTH.13217

VITAMIN B9-PRODUCING MICROBES

Parabacteroides 13.84 CLR



Patient: **13.8 CLR (1.78%)**
Population: 8.06 ~ 15.9

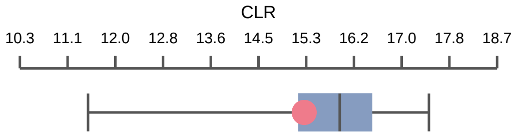
=

Vitamin B9 is a water-soluble molecule that cannot be synthesized by us so it must be supplied by taking foods like animal viscera (e.g. liver), legumes, green leafy vegetables, certain fruits, and nuts. Nevertheless, this vitamin can be produced in our gut by different species within the Bifidobacterium genus, among others. There is evidence that folate concentration decreases after sun exposition since solar ultraviolet (UV) radiation degradates it. In adults, folate deficiency manifests with anemia. In addition, in pregnant women, deficiency of folate might lead to neural tube defects (NTD) during the first month of pregnancy and its associated symptoms include physical problems like paralysis, blindness, and neurological problems such as intellectual disability and lack of consciousness.

REFERENCES: DOI:10.1111/J.1753-4887.2012.00485.X, DOI:10.1007/S12161-016-0647-7, DOI:10.1016/J.JPHOTOBIOL.2018.10.012

VITAMIN H-PRODUCING MICROBES

Bacteroides 15.29 CLR



Patient: **15.3 CLR (7.59%)**
Population: 11.5 ~ 17.5

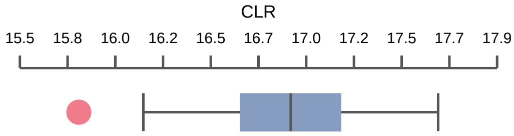
=

Vitamin H is a water and alcohol soluble molecule present in some foods like egg, milk, banana, sardines, or mushrooms, among other foods. It can also be synthesized in the gut microbiome from Lactobacillus species, among others. Its coenzyme role in certain carboxylases makes vitamin H a key factor for specific metabolism steps but also for gene regulation through epigenetics. Biotin deficiency could be caused by alcoholism or high egg white consumption, which contain high levels of avidin, a protein that tightly binds to biotin. Its deficiency can lead to symptoms such as loss of pigment in hair and hair loss, red rashes, depression, among others.

REFERENCES: DOI:10.2174/1389557516666160725095729, DOI:10.1159/000462981, DOI:10.1080/14728214.2018.1463370

VITAMIN B12-PRODUCING MICROBES

Bacteroides 15.29 CLR
Clostridium 14.83 CLR
Pseudomonas 11.26 CLR
Ruminococcus 9.26 CLR
Streptococcus 8.57 CLR
Propionibacterium 8.17 CLR



Patient: **15.8 CLR (12.6%)**
Population: 16.1 ~ 17.6

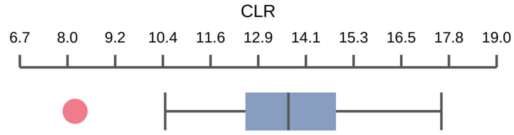
⌄

Vitamin B12 is mainly present in animal food like meat, fish, or milk. Nevertheless, it is only synthesized by certain bacteria and archaea. This vitamin is a water-soluble molecule with essential roles in brain and nervous system function, blood formation, protein metabolism, synthesis, and regulation of DNA. Vitamin B12 deficiency can cause symptoms such as anemia, weight loss, or neurological alterations such as Alzheimer's disease, depression, or decreased mental abilities. The man-made form of vitamin B12 used in some dietary supplements is called cyanocobalamin.

REFERENCES: DOI:10.1186/S12934-017-0631-Y, DOI:10.1007/S00253-001-0902-7

VITAMIN B2-PRODUCING MICROBES

Propionibacterium 8.17 CLR



Patient: **8.17 CLR (0.0061%)**
Population: 10.5 ~ 17.6

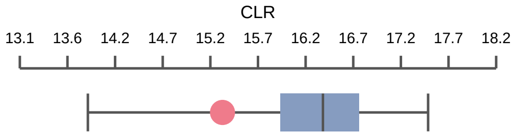
⌄

Vitamin B2 has to be daily consumed because of the small amount that the human body stores and the ease of excretion. It is present in foods such as eggs, meat, and milk. It is a water-soluble molecule absorbed in the small intestine and helps to convert carbohydrates, amino acids, and lipids into energy (ATP). The antioxidant function of vitamin B2 plays an important role in protecting eyes (especially the cornea), and preventing oxidative stress. Some diseases such as hypothyroidism could cause riboflavin deficiency. In addition, alcoholics or anorexics are more prone to have this deficiency too. Principal symptoms are tongue and lip inflammations, skin disorders, and anemia. Vitamin B2 deficiency is potentially dangerous for pregnant women because it concludes with eclampsia, an illness that causes maternal and fetal death.

REFERENCES: DOI:10.1146/ANNUREV.MICRO.58.030603.123615, DOI:10.1017/S0007114514000178, DOI:10.1017/CBO9781107415324.004

VITAMIN B5-PRODUCING MICROBES

Bacteroides 15.29 CLR | *Ruminococcus* 9.26 CLR



Patient: **15.3 CLR (7.61%)**
Population: 13.9 ~ 17.5

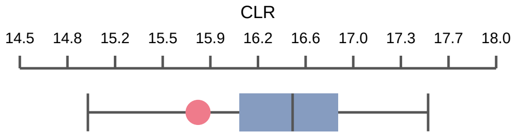
=

Vitamin B5 is part of coenzyme A (CoA), a cofactor involved in multitude of enzymatic reactions and mainly related to carbohydrate, protein, and lipid metabolism. It is present in several foods like liver, kidney, egg, fish, or milk. It helps to fight against fatigue and takes part in the synthesis of stress-related hormones. Vitamin B5 deficiency causes symptoms like headache, numbness, stomachache, or irritability, and one of its triggers is excessive alcohol consumption thus difficulting vitamin absorption. Because of its important role in fat synthesis, some studies suggest a positive influence of vitamin B5 on cholesterol and triglycerides.

REFERENCES: DOI:10.1016/J.BBRC.2020.05.015, DOI:10.2147/VHRM.S57116

VITAMIN B1-PRODUCING MICROBES

Bacteroides 15.29 CLR | *Clostridium* 14.83 CLR
Ruminococcus 9.26 CLR



Patient: **15.8 CLR (12.4%)**
Population: 15.0 ~ 17.5

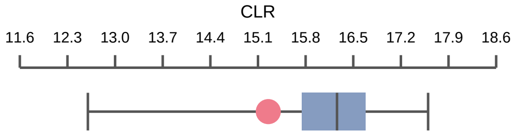
=

Vitamin B1 is a water-soluble vitamin that plays an important role in pyruvate metabolism, nervous signal conductivity, and energy supply. It is primarily derived from dietary sources and absorbed throughout the intestines. There are some bacteria that can synthesize thiamine in the gut from precursors thiamine pyrophosphate (TPP) and thiazole, which has been identified in coffee, roasted peanuts, cooked beef or chicken, and baked potato. Vitamin B1 deficiency comes from low vitamin diets and alcoholism. All symptoms such as neurological effects and weight loss are caused because of the influence that thiamine has on glucose metabolism. Deficiency of vitamin B1 also causes the beriberi disorder, which is divided into two subcategories: “wet”, which has an effect on the cardiovascular system, and “dry”, which is also called Wernicke-Korsakoff syndrome and has an effect on the nervous system.

REFERENCES: DOI:10.3181/00379727-144-37642, DOI:10.1128/MSYSTEMS.00116-17, DOI:10.1016/C2009-0-02724-X

VITAMIN B6-PRODUCING MICROBES

Bacteroides 15.29 CLR | *Streptococcus* 8.57 CLR



Patient: **15.3 CLR (7.60%)**
Population: 12.6 ~ 17.6

=

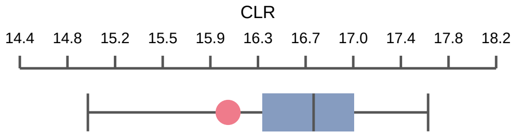
Vitamin B6 is a water-soluble molecule that cannot be synthesized by us. Therefore, it needs to be taken from food sources like fish, especially salmon and tuna, legumes, or meat. Certain groups of bacteria can also synthesize it in our gut. An excess of vitamin B6 could cause stomachache and sensorial changes. In contrast, a deficiency of vitamin B6 causes vascular damage, mouth damage like ulcers, and lip inflammation. In addition, there might be neurological symptoms such as irritability, depression, and confusion. Kidney or liver disorders or alcoholism are causes of vitamin B6 deficiency.

REFERENCES: ISBN:1420029665, DOI:10.1016/J.BIOTECHADV.2016.11.004, DOI:10.1002/JIMD.12060

SHORT CHAIN FATTY ACIDS

ENERGY PRODUCERS

Bacteroides 15.29 CLR
Alistipes 15.14 CLR
Parabacteroides 13.84 CLR
Ruminococcus 9.26 CLR
Blautia 8.17 CLR



Patient: **16.1 CLR (15.9%)**
Population: 14.9 ~ 17.6

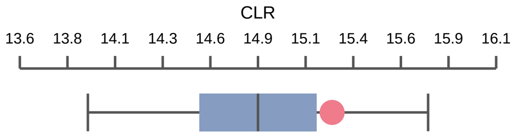
=

A portion of indigestible fiber reaches the colon without undergoing degradation by intestinal enzymes, where microorganisms break it down into crucial metabolic conversions for the host. These conversions, involving the degradation of proteins and structurally diverse complex polysaccharides from both animal and plant origins, provide the organism with essential energy and nutrients. The fermentation of these compounds by the intestinal microbiota generates metabolites such as short-chain fatty acids, pivotal for colon health

REFERENCES: 10.1038/S42255-018-0017-4, 10.1194/JLR.R036012

BUTYRATE PRODUCERS

Clostridium 14.83 CLR
Eubacterium 13.36 CLR
Oscillospira 13.15 CLR
Pseudomonas 11.26 CLR
Lachnoclostridium 10.61 CLR
Butyrivibrio 10.52 CLR
Porphyromonas 9.08 CLR



Patient: **15.3 CLR (7.09%)**
Population: 13.9 ~ 15.8

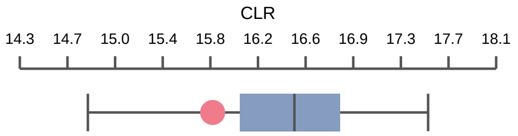
=

Butyrate-producers are strict anaerobes and carry out fermentative metabolism from non-digestible carbohydrates. It is involved in gene expression, inflammation, cell differentiation, and apoptosis. Butyrate is essential for colonocytes since it is their main energy source. Butyrate metabolism by colonocytes consume large amounts of oxygen, leading towards a state of hypoxia that maintains oxygen balance in the gut and prevents gut microbiota dysbiosis driven by the expansion of facultative anaerobic bacteria. Butyrate has also antiproliferative activity on colon cancer cells inducing apoptosis. In addition, butyrate regulates glucose levels by activating intestinal gluconeogenesis. There is growing evidence that a low abundance of butyrate-producers is correlated with prediabetic and obese individuals.

REFERENCES: DOI:10.1111/J.1574-6968.2009.01514.X, DOI:10.1038/ISMEJ.2011.109, DOI:10.1136/BMJ.K2179, DOI:10.3390/NU10101499, DOI:10.1007/S11892-013-0409-5, DOI:10.1111/J.1365-2036.2007.03562.X, DOI:10.1093/ADVANCES/NMX009

ACETATE PRODUCERS

Bacteroides 15.29 CLR
Clostridium 14.83 CLR
Pseudomonas 11.26 CLR
Anaerotignum 9.26 CLR
Porphyromonas 9.08 CLR
Streptococcus 8.57 CLR



Patient: **15.8 CLR (12.6%)**
Population: 14.8 ~ 17.5

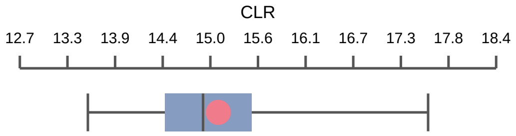
=

Together with butyrate and propionate, acetate is a Short-Chain Fatty Acid (SCFA). It is partly consumed by some luminal bacteria, which in turn convert part of it to butyrate. However, most acetate escapes luminal bacteria and reaches to peripheral tissues that will use acetate for their metabolism. Acetate can be used by peripheral tissues for cholesterol metabolism and lipogenesis. In addition, it regulates leptin secretion, thus regulating energy balance by inhibiting hunger. On the other hand, excessive acetate levels in high-fat diets have been correlated with glucose-stimulated insulin secretion, leading to obesity and insulin resistance.

REFERENCES: DOI:10.1097/MCO.0B013E32833A8B60, DOI:10.1038/NRENDO.2015.128, DOI:10.1080/19490976.2015, DOI:10.1079/PNS2002207, DOI:10.1042/BJ1420401, DOI:10.1038/NATURE18309

PROPIONATE PRODUCERS

Clostridium 14.83 CLR *Eubacterium* 13.36 CLR
Pseudomonas 11.26 CLR *Anaerotignum* 9.26 CLR
Propionibacterium 8.17 CLR



Patient: **15.1 CLR (6.07%)**
Population: 13.5 ~ 17.6

=

Propionate-producers have as substrate non-digestible carbohydrates processed mostly through the succinate, propanediol, and acrylate pathways depending on the sugar structure and peptides and amino acids through their fermentation. This molecule may travel to other body parts such as the liver. The inhibition role that propionate plays in hepatic lipid synthesis is the reduction of acetate incorporation to triglycerides and cholesterol, decreasing their concentrations from blood. Moreover, propionate induces intestinal gluconeogenesis and influences food intake behaviour thus increasing satiety. On the other hand, excessive propionate levels have been associated with gradual weight gain and insulin resistance in the long term. There is also evidence that suggests propionate plays a role in reducing inflammation and proliferation of colon cancer cells.

REFERENCES: DOI:10.1111/J.1467-3010.2008.00706.X, DOI:10.1111/J.1753-4887.2011.00388.X, DOI:10.1136/GUT.35.1_SUPPL.S35, DOI:10.1038/ISMEJ.2014.14, DOI:10.1038/BJC.2012.409

HEALTH STATUS

LEGENDA

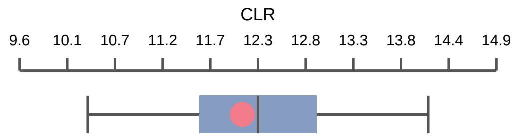
⏫ Very high
⌃ High
= On average
⌄ Low
⏬ Very low
○ Not significant

🟩 Good
🟨 Indifferent
🟥 Bad
⬜ Not Significant

PRODUCTION OF SPECIFIC COMPOUNDS

HYDROGEN SULFIDE (H_2S) PRODUCERS

Desulfotomaculum 11.50 CLR *Pseudomonas* 11.26 CLR



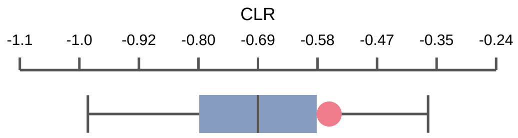
Patient: **12.1 CLR (0.31%)**
Population: 10.4 ~ 14.1

=

Different functions have been attributed to hydrogen sulfide (H2S). It is currently being used for clinical treatment for inflammation, thrombosis, and cancer since it is an antithrombotic and inflammation modulator. Focusing on the gut microbiome, H2S can reduce mucosal inflammation and promote tissue damage repair. A number of studies have shown that H2S is a positive mediator in the circulatory system: it provides a cardioprotective effect, decreases blood pressure and decreases the heart rate, and causes vasodilation. However, excessive levels can be toxic and related to increased inflammation. Following a sulfate-rich diet (e.g. cabbage, onion and mushrooms) can boost the abundance of hydrogen sulfide-producers.

REFERENCES: DOI:10.3390/MOLECULES21111558, DOI:10.1089/ARS.2011.4351, DOI:10.1152/AJPCELL.00329.2016, DOI:10.1097/MCO.0000000000000526, DOI:10.3390/MICROORGANISMS3040866, DOI:10.1016/J.JARE.2020.03.003

METHANOGENS



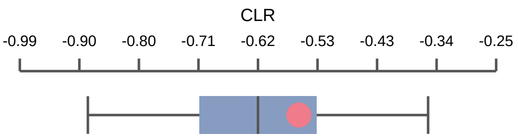
Patient: **-0.56 CLR (0%)**
Population: -1.01 ~ -0.37

=

Methane producers (methanogens) are a group of microorganisms that can produce methane gas in the gut by fermenting carbohydrates. The most well-known methane producers in the gut microbiome are members of the Archaea domain, specifically the Methanobrevibacter and Methanosphaera genera. Methane production in the gut has been associated with functional bowel disease such as constipation and bloating.

REFERENCES: 10.1016/J.JFF.2022.105367

HISTAMINE PRODUCERS



Patient: **-0.56 CLR (0%)**
Population: -0.88 ~ -0.36

=

Histamine is a chemical created by our immune cells that can also be produced by certain bacteria. Histamines boost blood flow in the area of your body it targets, in this case the intestines. This causes inflammation and, in fact, it has been shown that histamine might promote abdominal pain specially in patients suffering from Inflammatory Bowel Disease (IBD).

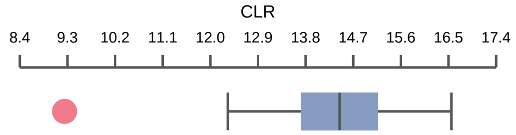
REFERENCES: 10.1126/SCITRANSLMED.ABJ1895, 10.3389/FNUT.2022.1018463, 10.1186/S12864-021-08004-3

INTERACTION WITH TOXIC SUBSTANCES

ALCOHOL TOXICITY

ACETALDEHYDE-PRODUCERS

Ruminococcus 9.26 CLR

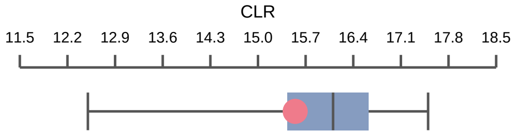


Patient: **9.26 CLR (0.018%)**
Population: 12.4 ~ 16.6

✓

ACETALDEHYDE-DEGRADERS

Bacteroides 15.29 CLR
Parabacteroides 13.84 CLR
Streptococcus 8.57 CLR



Patient: **15.5 CLR (9.38%)**
Population: 12.5 ~ 17.5

=

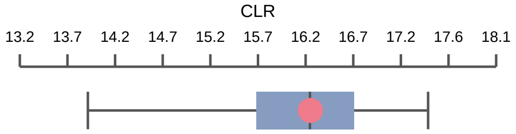
The union between acetaldehyde and macromolecules or proteins produce acetaldehyde adducts that can promote different biochemical and immunological reaction chains. These reaction chains have been highly related to liver injuries due to an abnormal cellular function such as DNA repair. One of the consequences of excessive acetaldehyde concentration is inflammation and metaplasia of tracheal epithelium and this can lead to laryngeal carcinoma. Besides the liver, another important organ for ethanol degradation to acetaldehyde production is the bowel through the gut microbiome and an excessive acetaldehyde concentration can be related to an increased risk of gastrointestinal morbidity, diarrhea and colon cancer.

REFERENCES: DOI:10.1016/J.ORALONCOLOGY.2006.02.005, DOI:10.1038/NRMICRO3344, DOI:10.1080/13556219772840, DOI:10.1002/(SICI)1097-0215(20000415)86:2<169::AID-IJC4>3.0.CO;2-3

TRYPTOPHAN METABOLISM

INDOLE PRODUCERS

Bacteroides 15.29 CLR
Alistipes 15.14 CLR
Clostridium 14.83 CLR
Propionibacterium 8.17 CLR



Patient: **16.2 CLR (19.0%)**
Population: 13.9 ~ 17.4

=

Indole producers are a group of bacteria in the gut microbiome that can produce indole by means of tryptophan metabolism. Some studies have shown that indole produced by gut bacteria can have beneficial effects on the host, such as promoting gut barrier function, reducing inflammation, and modulating immune responses.

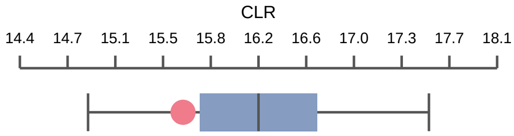
REFERENCES: 10.1016/J.CHOM.2018.05.003

NEUROTRANSMITTERS

GABA HOMEOSTASIS

GABA PRODUCERS

Bacteroides 15.29 CLR
Parabacteroides 13.84 CLR
Eubacterium 13.36 CLR

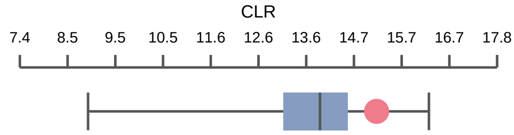


Patient: **15.6 CLR (10.5%)**
Population: 14.9 ~ 17.5

=

GABA CONSUMERS

Alistipes 15.14 CLR
Pseudomonas 11.26 CLR



Patient: **15.2 CLR (6.69%)**
Population: 8.91 ~ 16.3

=

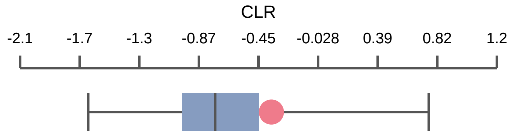
GABA-producers are bacteria that can synthesize gamma-aminobutyric acid (GABA), important for regulating brain activity. GABA can also be produced in the gut microbiome from glutamate through decarboxylation. Increased levels of GABA-producers might reduce inflammation, improve gut motility, and reduce anxiety and depression-like behaviours. In contrast, GABA-consuming bacteria counteract the effect of GABA-producers by reducing GABA bioavailability in the gut lumen.

REFERENCES: 10.1038/S41598-020-70986-Z, 10.3389/FMICB.2021.656895, 10.1038/S41564-018-0307-3

IMMUNE REGULATION

IMMUNE HOMEOSTASIS

Bacteroides 15.29 CLR
Alistipes 15.14 CLR
Clostridium 14.83 CLR
Parabacteroides 13.84 CLR
Eubacterium 13.36 CLR
Oscillibacter 13.04 CLR
Pseudomonas 11.26 CLR
Roseburia 11.19 CLR
Lachnoclostridium 10.61 CLR
Butyrivibrio 10.52 CLR



Patient: **-0.36 Log10 Ratio**
Population: -1.66 ~ 0.76

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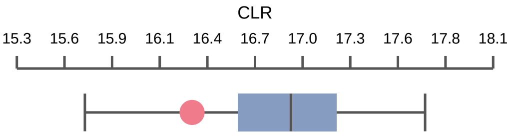
The composition of the gut microbiome can influence the response of the immune system, thus influencing the immune homeostasis. Some bacteria produce Short Chain Fatty Acids (SCFA), which are compounds that have been shown to have anti-inflammatory properties. Instead, other gram-negative bacteria are highly immunogenic due to their lipopolysaccharides (LPS). This index assesses the ratio of pro-inflammatory to anti-inflammatory bacteria: the higher the ratio, the higher probability of inflammation.

REFERENCES: 10.3390/IJERPH17207618, 10.3389/FNUT.2021.818902, 10.1038/S41422-020-0332-7, 10.1136/GUTJNL-2020-322670

PERMEABILITY AND MUCOLYTIC ACTIVITY

Bacteroides 15.29 CLR | *Alistipes* 15.14 CLR
Clostridium 14.83 CLR | *Parabacteroides* 13.84 CLR
Ruminococcus 9.26 CLR | *Akkermansia* 8.86 CLR
Streptococcus 8.57 CLR | *Blautia* 8.17 CLR



Patient: **16.3 CLR (20.8%)**
Population: 15.7 ~ 17.7

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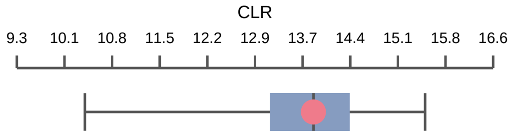
The protective mucus layer lining the intestinal epithelium is composed of mucin, a complex glycoprotein. This mucosal barrier acts as a defence against pathogens. Mucolytic bacteria, by degrading mucin, can compromise the mucosal layer, especially in low-fiber diets. Excessive degradation may increase permeability and susceptibility to pathogens, while insufficient degradation affects the availability of nutrients for beneficial bacteria.

REFERENCES: DOI:10.1016/J.GENDIS.2014.08.001, DOI:10.1016/J.CELL.2016.10.043

LPS PRODUCERS

Parabacteroides 13.84 CLR



Patient: **13.8 CLR (1.78%)**
Population: 10.4 ~ 15.5

=

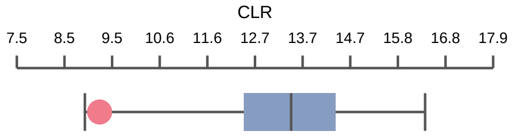
Lipopolysaccharides (LPS) are identified by immune cells as molecules associated with pathogens. This results in an activation of proinflammatory cytokines. Bacteroidetes and Proteobacteria are the main contributors to LPSs.

REFERENCES: DOI:10.3390/MOLECULES21111558, DOI:10.1016/J.AJPATH.2017.08.005, DOI:10.1097/MCO.0000000000000526

BENEFICIAL MICROBES

PROBIOTICS

Akkermansia 8.86 CLR | *Propionibacterium* 8.17 CLR



Patient: **9.27 CLR (0.018%)**
Population: 8.95 ~ 16.4

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Probiotics can modulate the human microbiota by reducing luminal pH, competing for nutrients, secreting different kinds of beneficial compounds, preventing bacterial adhesion, or invasion of epithelial cells. Probiotics are thought to act in three different ways: acting directly on the gastrointestinal tract by interaction with the intestinal microbiota and enzymes, interacting with the mucus layer (mucosa), or acting outside the gastrointestinal tract such as on the systemic immune system and organs like the liver and the brain. Moreover, probiotics can have direct beneficial effects by providing us enzymes like beta-galactosidase, which deficiency causes lactose intolerance.

REFERENCES: DOI:10.1016/J.MEDMAL.2013.10.002, DOI:10.1002/MNFR.201600240, DOI:10.1007/S12263-011-0229-7, DOI:10.1016/J.FOODRES.2019.108788, PMID:23426535

POTENTIALLY PATHOGENIC MICROORGANISMS

Potentially pathogenic microorganisms may be present in small amounts in the intestinal microbiota of healthy people. Under certain conditions they can exponentially grow, proliferate and cause intestinal disorders. When their abundance is higher than expected (abundance above the population average), it is advisable to consult a physician and possibly perform further diagnostic investigations. When *not detected* is indicated, it does not exclude the possibility that the searched microorganisms may be found with a physiological quantification.

MICROORGANISM	NOT DETECTED / NOT SIGNIFICANT	DETECTED IN PHYSIOLOGICAL RANGE	DETECTED BEYOND PHYSIOLOGICAL LEVELS
Clostridioides	✓		
Enterococcus	✓		
Klebsiella	✓		
Morganella	✓		
Salmonella	✓		
Shigella	✓		

ACTIONS

ANALYSIS SUMMARY

A low abundance of vitamin B2-producing bacteria has been found. Vitamin B2, also known as riboflavin, plays an important role in energy generation as it is the precursor to coenzymes FMN and FAD, essential for the metabolism of carbohydrates, amino acids, and lipids. Its deficiency can cause symptoms such as skin disorders, edema, hair loss, or cataracts.

A low abundance of vitamin B12-producing bacteria has been observed. This vitamin is a water-soluble molecule that plays an essential role in the nervous system function, blood cell formation, and protein and DNA metabolism. Lack of vitamin B12 can lead to symptoms such as anemia, weight loss, or neurological alterations.

A low quantity of lactose-digesting bacteria has been found. Lactose intolerance occurs when the intestine doesn't produce enough lactase, and increasing the abundance of lactose-digesting bacteria could aid in lactose digestion.

A low abundance of oxalate-degrading bacteria has been found. Most kidney stones are composed of calcium oxalate, so hyperoxaluria (excess oxalate) is one of the main risk factors for this kidney disease. Although some oxalate is absorbed in the small intestine and excreted in the urine, a significant portion can be metabolized by the intestinal microbiome, especially by members of the *Oxalobacter* genus.

A low similarity in the microbial composition of the sample compared to healthy profiles has been observed. The uniqueness of a healthy intestinal microbiome means that samples with low similarity can still be considered a healthy profile, although very low similarity suggests a composition far from eubiosis, indicating possible dysbiosis.

RECOMMENDATIONS

From a dietary point of view, it is recommended to increase the consumption of: Kefir, Yogurt, Unpasteurized Cheese, Fermented soy products, Meat, Fish, Milk, Eggs.


Kefir


Yogurt


Unpasteurized Cheese


Fermented soy products

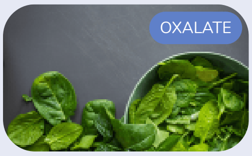

Meat


Fish


Milk


Eggs

From a dietary point of view, it is recommended to decrease the consumption of: Spinach, Chard, Beetroot, Almonds, Peanuts, Chocolate, Black tea, Coffee, Potato, Kale, Nuts, Asparagus.



Spinach

Chard

Beetroot

Almonds

Peanuts

Chocolate

Black tea

Coffee

Potato

Kale

Nuts

Asparagus

The following supplements are also recommended: Lactobacillus Genus, Vitamin B12 supplements, Galactooligosaccharides (GOS).

Lactobacillus Genus

Vitamin B12 supplements

Galactooligosaccharides (GOS)

Legend:

OXALATE	If you have kidney stones and your microbiota with the ability to metabolize oxalate is below the control population, you may consider excluding oxalate-rich foods from your diet.

References:

10.3389/fcimb.2018.00314
10.3389/fmicb.2017.00846
10.1186/s12934-017-0631-y
10.1007/s00253-001-0902-7
10.1073/pnas.160672211
10.3390/nu10101517
10.1111/1574-6941.12186
10.21037/atm.2016.12.70
10.1007/s00240-016-0952-z

TEST LIMITS

GUT has no diagnostic purpose; the test allows to identify the composition of the intestinal microbiota population and to correlate it with the main physiological functions of the host. The identified profile does not absolutely exclude the possibility that some microorganism have not been detected. Furthermore, the method does not allow to evaluate the vitality of the identified microbes. The result obtained represents a photograph of the situation at the time of sampling and may vary due to changes in dietary habits or the use of supplements or drugs. Suggestions and recommendations for probiotics or food supplements do not in any way represent food or therapeutic plans. Any change in lifestyle and diet or any pharmacological intervention must be decided as a result of a specialized medical examination and must be based on the correct anamnestic evaluation of the individual and on potential further investigations.

Signature (Name and surname)

ANNEX I - TAXONOMIC TABLE

Detection level minimun: 0.0001 % prokaryote abundance
WHEN THE GENUS IS UNKNOWN, IT INDICATES THE TAXONOMIC GROUP DETECTED
unkn: genus unidentified - f: family - o: order - c: class - p: phylum

- ︽ Very high
- ︿ High
- = On average
- ﹀ Low
- ︾ Very low
- ○ Not significant

DOMAIN	PHYLUM	GENUS	PATIENT (%)	PATIENT (CLR)	POPULATION	
Bacteria	**Actinomycetota**	**unkn. Actinomycetes(c)**	**29.63**	**16.65**	**Absent in DB**	︽
Bacteria	**unkn. Bacteria(d)**	**unkn. Bacteria(d)**	**9.55**	**15.52**	**10.50 ~ 15.10**	︿
Bacteria	Bacteroidota	Bacteroides	7.59	15.29	12.26 ~ 17.39	=
Bacteria	**Bacteroidota**	**unkn. Bacteroidia(c)**	**6.81**	**15.18**	**8.49 ~ 14.71**	︿
Bacteria	Bacteroidota	Alistipes	6.55	15.14	10.12 ~ 15.25	=
Bacteria	Bacillota	unkn. Eubacteriales(o)	5.65	14.99	13.91 ~ 15.70	=
Bacteria	**Bacillota**	**Clostridium**	**4.81**	**14.83**	**12.67 ~ 14.71**	︿
Bacteria	**Bacteroidota**	**unkn. Bacteroidota(p)**	**4.73**	**14.81**	**8.86 ~ 14.63**	︿
Bacteria	Actinomycetota	unkn. Actinomycetota(p)	3.33	14.46	8.02 ~ 14.49	=
Bacteria	Bacteroidota	Parabacteroides	1.78	13.84	7.48 ~ 15.40	=
Bacteria	**Actinomycetota**	**unkn. Propionibacteriales(o)**	**1.62**	**13.74**	**Absent in DB**	︽
Bacteria	Bacillota	unkn. Clostridia(c)	1.46	13.64	9.60 ~ 14.83	=
Bacteria	**Bacillota**	**Ligilactobacillus**	**1.38**	**13.58**	**Absent in DB**	︽
Bacteria	**Bacillota**	**unkn. Clostridiaceae(f)**	**1.19**	**13.43**	**10.67 ~ 12.99**	︿
Bacteria	Bacillota	unkn. Oscillospiraceae(f)	1.18	13.43	11.37 ~ 15.21	=
Bacteria	Bacillota	Eubacterium	1.10	13.36	11.26 ~ 14.70	=
Bacteria	Bacteroidota	unkn. Bacteroidales(o)	1.07	13.33	9.37 ~ 14.86	=
Bacteria	Bacillota	Oscillospira	0.90	13.15	7.40 ~ 14.20	=
Bacteria	**Bacteroidota**	**unkn. Rikenellaceae(f)**	**0.88**	**13.14**	**6.52 ~ 12.95**	︿
Bacteria	Bacillota	Oscillibacter	0.80	13.04	7.94 ~ 13.38	=
Bacteria	**Tenericutes**	**unkn. Anaeroplasmataceae(f)**	**0.76**	**12.98**	**Absent in DB**	︽
Bacteria	**Proteobacteria**	**unkn. Desulfovibrionaceae(f)**	**0.75**	**12.97**	**6.51 ~ 10.89**	︿
Bacteria	**Bacteroidota**	**unkn. Odoribacteraceae(f)**	**0.75**	**12.97**	**5.89 ~ 11.22**	︿
Bacteria	**Proteobacteria**	**unkn. Desulfovibrionales(o)**	**0.47**	**12.51**	**6.57 ~ 10.24**	︿
Bacteria	Bacillota	unkn. Lachnospiraceae(f)	0.43	12.41	11.78 ~ 14.65	=
Bacteria	Bacillota	Lacrimispora	0.31	12.08	7.84 ~ 13.40	=

DOMAIN	PHYLUM	GENUS	PATIENT (%)	PATIENT (CLR)	POPULATION	
Bacteria	**Bacteroidota**	**Culturomica**	**0.28**	**11.98**	**Absent in DB**	⏫
Bacteria	**Candidatus Melainabacteria**	**unkn. Candidatus Melainabacteria(p)**	**0.25**	**11.87**	**Absent in DB**	⏫
Bacteria	Bacillota	unkn. Bacillota(p)	0.24	11.84	11.39 ~ 14.88	=
Bacteria	**Deferribacteres**	**Mucispirillum**	**0.24**	**11.84**	**Absent in DB**	⏫
Bacteria	Bacillota	Eisenbergiella	0.23	11.79	7.10 ~ 13.68	=
Bacteria	**Bacillota**	**Angelakisella**	**0.22**	**11.76**	**Absent in DB**	⏫
Bacteria	Bacillota	unkn. Eubacteriaceae(f)	0.18	11.57	8.41 ~ 14.47	=
Bacteria	Proteobacteria	unkn. Alphaproteobacteria(c)	0.18	11.57	7.12 ~ 13.73	=
Bacteria	**Bacillota**	**Desulfotomaculum**	**0.17**	**11.50**	**6.71 ~ 9.90**	˄
Bacteria	Bacillota	Butyricicoccus	0.15	11.34	8.97 ~ 13.53	=
Bacteria	Bacillota	Flintibacter	0.14	11.30	7.64 ~ 11.39	=
Bacteria	Proteobacteria	Pseudomonas	0.14	11.26	6.10 ~ 12.99	=
Bacteria	**Bacillota**	**Pseudoflavonifractor**	**0.13**	**11.21**	**7.65 ~ 10.73**	˄
Bacteria	Bacillota	Roseburia	0.13	11.19	8.98 ~ 16.14	=
Bacteria	Bacillota	Enterocloster	0.12	11.14	7.55 ~ 14.22	=
Bacteria	Bacillota	Mediterraneibacter	0.10	10.97	8.48 ~ 14.54	=
Bacteria	**Bacillota**	**Phocea**	**0.092**	**10.87**	**7.02 ~ 10.44**	˄
Bacteria	**Bacteroidota**	**unkn. Tannerellaceae(f)**	**0.089**	**10.84**	**Absent in DB**	⏫
Bacteria	Bacillota	Hespellia	0.086	10.80	6.55 ~ 11.88	=
Bacteria	Bacillota	Anaerotruncus	0.074	10.65	7.12 ~ 11.26	=
Bacteria	Bacteroidota	unkn. Bacteroidaceae(f)	0.074	10.65	8.76 ~ 11.45	=
Bacteria	Bacillota	Lachnoclostridium	0.071	10.61	8.60 ~ 13.87	=
Bacteria	**Bacillota**	**Acetatifactor**	**0.068**	**10.56**	**Absent in DB**	⏫
Bacteria	Bacillota	Butyrivibrio	0.064	10.52	8.15 ~ 15.27	=
Bacteria	Bacteroidota	unkn. Porphyromonadaceae(f)	0.064	10.52	7.62 ~ 11.50	=
Bacteria	**Bacillota**	**Schaedlerella**	**0.061**	**10.47**	**Absent in DB**	⏫
Bacteria	**Bacteroidota**	**unkn. Barnesiellaceae(f)**	**0.061**	**10.47**	**Absent in DB**	⏫
Bacteria	**Bacillota**	**Lachnoanaerobaculum**	**0.058**	**10.42**	**Absent in DB**	⏫
Bacteria	**Actinomycetota**	**unkn. Propionibacteriaceae(f)**	**0.055**	**10.36**	**Absent in DB**	⏫
Bacteria	**Bacillota**	**Lachnotalea**	**0.043**	**10.11**	**Absent in DB**	⏫
Bacteria	Bacillota	Intestinimonas	0.040	10.04	8.40 ~ 12.69	=
Bacteria	Bacteroidota	unkn. Sphingobacteriia(c)	0.037	9.96	6.04 ~ 10.95	=
Bacteria	Bacteroidota	Odoribacter	0.028	9.67	8.50 ~ 12.84	=
Bacteria	Tenericutes	Anaeroplasma	0.028	9.67	6.72 ~ 11.19	=
Bacteria	Bacillota	unkn. Christensenellaceae(f)	0.025	9.55	Absent in DB	○
Bacteria	Bacillota	Murimonas	0.025	9.55	Absent in DB	○
Bacteria	Bacillota	Flavonifractor	0.025	9.55	7.60 ~ 13.64	=

DOMAIN	PHYLUM	GENUS	PATIENT (%)	PATIENT (CLR)	POPULATION	
Bacteria	Tenericutes	unkn. Anaeroplasmatales(o)	0.025	9.55	Absent in DB	○
Bacteria	Bacillota	Marvinbryantia	0.021	9.42	7.36 ~ 11.44	=
Bacteria	Bacillota	unkn. Erysipelotrichales(o)	0.021	9.42	6.34 ~ 10.31	=
Bacteria	Bacillota	Anaerotignum	0.018	9.26	7.00 ~ 14.08	=
Bacteria	Bacillota	Robinsoniella	0.018	9.26	6.79 ~ 11.92	=
Bacteria	**Bacillota**	**Ruminococcus**	**0.018**	**9.26**	**9.50 ~ 15.52**	∨
Bacteria	Proteobacteria	unkn. Proteobacteria(p)	0.018	9.26	8.42 ~ 14.50	=
Bacteria	Bacillota	Hungatella	0.015	9.08	7.94 ~ 13.92	=
Bacteria	Bacillota	unkn. Erysipelotrichia(c)	0.015	9.08	6.19 ~ 11.44	=
Bacteria	Bacteroidota	Porphyromonas	0.015	9.08	7.44 ~ 14.35	=
Bacteria	Proteobacteria	Mailhella	0.015	9.08	Absent in DB	○
Bacteria	Bacillota	unkn. Bacillaceae(f)	0.012	8.86	6.80 ~ 11.36	=
Bacteria	Bacillota	Ihubacter	0.012	8.86	7.36 ~ 10.64	=
Bacteria	Bacillota	Anaerobium	0.012	8.86	6.27 ~ 10.84	=
Bacteria	**Bacillota**	**Dorea**	**0.012**	**8.86**	**10.92 ~ 14.12**	∨
Bacteria	Bacteroidota	Barnesiella	0.012	8.86	7.81 ~ 14.98	=
Bacteria	Bacteroidota	Rikenella	0.012	8.86	Absent in DB	○
Bacteria	Candidatus Saccharibacteria	unkn. Candidatus Saccharimonadales(o)	0.012	8.86	Absent in DB	○
Bacteria	Proteobacteria	unkn. Enterobacterales(o)	0.012	8.86	7.58 ~ 13.87	=
Bacteria	Verrucomicrobia	Akkermansia	0.012	8.86	7.28 ~ 16.40	=
Bacteria	Bacillota	unkn. Lactobacillaceae(f)	0.0092	8.57	7.25 ~ 12.54	=
Bacteria	Bacillota	Streptococcus	0.0092	8.57	8.12 ~ 14.05	=
Bacteria	Bacteroidota	unkn. Sphingobacteriales(o)	0.0092	8.57	Absent in DB	○
Bacteria	Proteobacteria	unkn. Deltaproteobacteria(c)	0.0092	8.57	6.86 ~ 10.89	=
Bacteria	Tenericutes	Malacoplasma	0.0092	8.57	7.22 ~ 11.19	=
Bacteria	Actinomycetota	Propionibacterium	0.0061	8.17	7.39 ~ 15.07	=
Bacteria	Actinomycetota	Adlercreutzia	0.0061	8.17	Absent in DB	○
Bacteria	Actinomycetota	unkn. Eggerthellaceae(f)	0.0061	8.17	7.62 ~ 11.89	=
Bacteria	Bacillota	Falcatimonas	0.0061	8.17	6.84 ~ 9.98	=
Bacteria	Bacillota	unkn. Desulfotomaculaceae(f)	0.0061	8.17	Absent in DB	○
Bacteria	Bacillota	Anaerocolumna	0.0061	8.17	6.54 ~ 9.99	=
Bacteria	**Bacillota**	**Blautia**	**0.0061**	**8.17**	**10.73 ~ 15.49**	∨
Bacteria	Bacillota	Syntrophococcus	0.0061	8.17	6.79 ~ 10.58	=
Bacteria	Bacillota	Agathobaculum	0.0061	8.17	7.27 ~ 12.68	=
Bacteria	Bacillota	Candidatus Stoquefichus	0.0061	8.17	Absent in DB	○
Bacteria	Bacteroidota	unkn. Prevotellaceae(f)	0.0061	8.17	7.16 ~ 14.29	=