US BioTek LABORATORIES

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1620 Linden Av N
Shoreline WA, 98133
-.- US BIOTEK

TEST PATIENT
01-Jan-1962 Female

123 TEST STREET
BURWOOD VIC 3125

LAB ID : 3949011
UR NO. :
Collection Date : 17-Jan-2024
Received Date: 17-Jan-2024

3949011

Gut-IQ

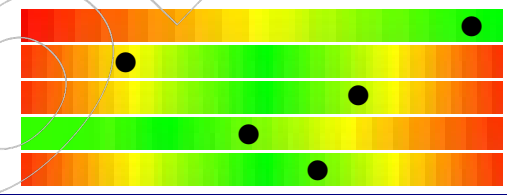
General Macroscopic Description

	Result	Markers
Stool Colour	**Brown**	**Colour** - Brown is the colour of normal stool. Other colours may indicate abnormal gut health.
Stool Form	**Unformed**	**Form** -Sample form is categorised using the Bristol stool chart. A comment on stool appearance can be found in the comments section.
Mucous	**DETECTED**	**Mucous** - Mucous production may indicate the presence of an infection and/or inflammation.
Occult Blood	**POSITIVE**	**Blood (Macro)**- The presence of blood in the stool may be the result of several causes besides colorectal bleeding, including hemorrhoids or gastrointestinal infection.

Short Chain Fatty Acids

Methodology: GC/MS

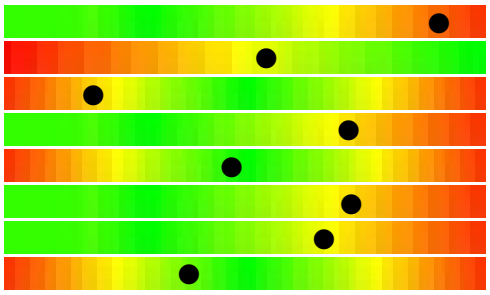
	Result	Range	Units
Short Chain Fatty Acids, Beneficial	30.0	> 13.6	umol/g
Butyrate	11.0	10.8 - 33.5	%
Acetate	69.0	44.5 - 72.4	%
Propionate	15.0	0.0 - 32.0	%
Valerate	5.0	0.5 - 7.0	%



GIT Functional Markers

Methodology: FEIA, EIA, CLIA, pH electrode

	Result	Range	Units
Calprotectin.	*65.0* *H	0.0 - 50.0	ug/g
Pancreatic Elastase	*180.0* *L	> 200.0	ug/g
Secretory (sIgA)	*400.0* *L	510.0 - 2040.0	ng/mL
Zonulin	96.0	0.0 - 107.0	ng/mL
Beta glucuronidase	3486.0	368.0 - 6266.0	U/g
Steatocrit	9.0	0.0 - 10.0	%
a-Transglutaminase IgA	87.0	0.0 - 100.0	units/L
pH	6.6	6.3 - 7.7	



Parasites & Worms

Blastocystis hominis.
Dientamoeba fragilis.
Hymenolepis spp, Tapeworm

Bacteria & Viruses

Campylobacter species.
Yersinia species.
Helicobacter pylori
H.pylori Virulence Factor, dupA

Fungi and Yeasts

Candida albicans.

SAMPLE REPORT

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Parasites and Worms:	Result	Range	Units
Parasitic Organisms.			
Cryptosporidium species	<dl	< 1.0	x10^5 org/g
Entamoeba histolytica.	<dl	< 1.0	x10^5 org/g
Giardia intestinalis	<dl	< 1.0	x10^5 org/g
Blastocystis hominis.	*11.0* *H	< 1.0	x10^5 org/g
Dientamoeba fragilis.	*17.0* *H	< 1.0	x10^5 org/g

Blastocystis Subtypes	Result	Range	Units
Subtype 1	Not Detected		
Subtype 3	DETECTED		
Subtype 9	Not Detected		

Comment: Not Detected results indicate the absence of detectable DNA in the sample for the subtypes and worms reported.

Worms.

Ascaris lumbricoides, Roundworm	Not Detected	Necator americanus, Hookworm	Not Detected
Trichuris trichiura, Whipworm	Not Detected	Enterobius vermicularis,Pinworm	Not Detected
Enterocytozoon spp	Not Detected	Hymenolepis spp, Tapeworm	DETECTED
Strongyloides spp, Roundworm	Not Detected	Taenia species, Tapeworm	Not Detected

Bacterial Pathogens.	Result	Range	Units
Aeromonas hydrophila.	<dl	< 1.00	x10^3 CFU/g
Campylobacter species.	*3.10* *H	< 1.00	x10^5 CFU/g
C. difficile, Toxin B	<dl	< 1.00	x10^4 CFU/g
Enteroaggregative E. coli	<dl	< 1.00	x10^3 CFU/g
Enteropathogenic E. coli	<dl	< 1.00	x10^3 CFU/g
E. coli O157	<dl	< 1.00	x10^2 CFU/g
Hypervirulent Clostridium difficile	<dl	< 1.00	x10^3 CFU/g
Enterotoxigenic E. coli LT/ST	<dl	< 1.00	x10^5 CFU/g
Salmonella species.	<dl	< 1.00	x10^5 CFU/g
Shiga toxigenic E.coli	<dl	< 1.00	x10^3 CFU/g
Shigella spp	<dl	< 1.00	x10^3 CFU/g
Vibrio species.	<dl	< 1.00	x10^4 CFU/g
Yersinia species.	*2.50* *H	< 1.00	x10^5 CFU/g
Helicobacter pylori	8.70*H	< 1.0	x10^3 CFU/g

Comment: H.Pylori virulence factors and gene resistant markers will be listed below if detected .

H. pylori Resistance Genes	Result		
Gene: A2142C	Not Detected		
Gene: A2142G	Not Detected		
Gene: A2143G	Not Detected		
H.pylori Virulence Factor, babA	Not Detected	H.pylori Virulence Factor, cagA	Not Detected
H.pylori Virulence Factor, dupA	DETECTED	H.pylori Virulence Factor, iceA	Not Detected
H.pylori Virulence Factor, oipA	Not Detected	H.pylori Virulence Factor, vacA	Not Detected
H.pylori Virulence Factor, virB	Not Detected	H.pylori Virulence Factor, virD	Not Detected

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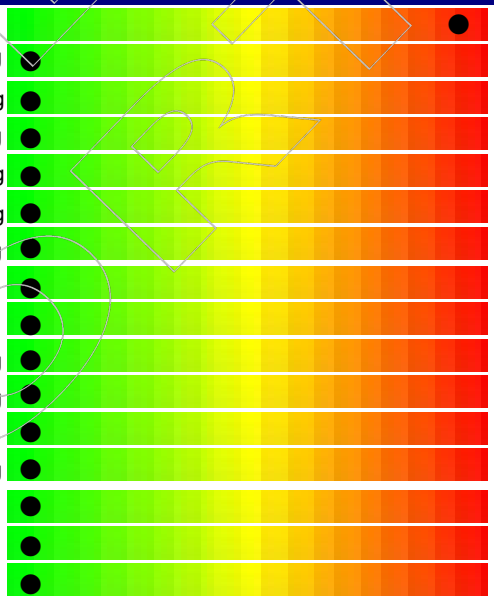
Viral Pathogens	Result	Range	Units
Viral Pathogens			
Adenovirus 40/41	Not Detected		
Norovirus GI/II	Not Detected		
Rotavirus A	Not Detected		
Sapovirus (I,II,IV,V)	Not Detected		
Astrovirus (hAstro)	Not Detected		

Comment: Not Detected results indicate the absence of detectable DNA in the sample for the viral pathogens reported.

Mycology	Result	Range	Units
Candida albicans.	*6.30* *H	< 5.00	x10^4 CFU/g
Candida dubliniensis	<dl	< 5.00	x10^3 CFU/g
Candida famata	<dl	< 5.00	x10^3 CFU/g
Candida glabrata	<dl	< 5.00	x10^3 CFU/g
Candida guilliermondii	<dl	< 3.00	x10^3 CFU/g
Candida intermedia	<dl	< 1.00	x10^3 CFU/g
Candida keyfr	<dl	< 5.00	x10^3 CFU/g
Candida krusei.	<dl	< 5.00	x10^3 CFU/g
Candida parapsilosis.	<dl	< 5.00	x10^3 CFU/g
Candida lambica	<dl	< 5.00	x10^3 CFU/g
Candida lipolytica	<dl	< 3.00	x10^3 CFU/g
Candida lustaniae	<dl	< 1.00	x10^3 CFU/g
Candida tropicalis.	<dl	< 5.00	x10^3 CFU/g
Geotrichum species.	<dl	< 5.00	x10^3 CFU/g
Rhodotorula species.	<dl	< 5.00	x10^3 CFU/g
Saccharomyces cerevisiae:	<dl	< 5.00	x10^3 CFU/g



SAMPLE REPORT

<dl = result below detectable limit. *H = Result greater than the reference range. *L = Result less than the reference range

Summary

Diversity

Gut microbial diversity ↓

Species

Faecalibacterium prausnitzii: ↓
Bacteroides fragilis: ↑
Enterococcus faecalis: ↑
Enterococcus faecium: ↑
Methanobrevibacter smithii: ↑

Functions

Basic Function: ↑
Protein & Other Energy Metabolism: ↑
Iron & Other Ion Metabolism: ↑
Aging Factor: ↑
SCFA Production: ↓
Ammonia(urease): ↓
BCAAs Production: ↓

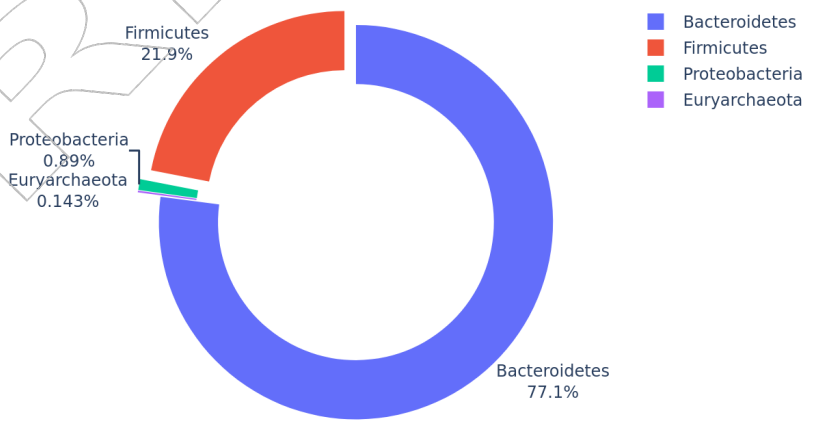
Risks

Type 2 Diabetes: Elevated
Colon Cancer: Elevated
Crohn's Disease: Elevated
Fatty Liver: Typical

The Dominant Microbial Phyla

The fecal microbiota is basically composed of seven major phyla: *Firmicutes*, *Bacteroidetes*, *Proteobacteria*, *Actinobacteria*, *Verrucomicrobia*, *Fusobacteria*, and *Tenericutes*. In healthy individuals, *Firmicutes* and *Bacteroidetes* usually make up 90-95% of the entire microbiome. This showcases the composition of your main gut microbiota at the phylum level, along with key gut microbial biomarker parameters.

Phylum	Population Average(%)	Your Value(%)
Actinobacteria	0.545	Not Detected
Bacteroidetes	68	77.1
Euryarchaeota	0.00814	0.143
Firmicutes	24	21.9
Proteobacteria	5.56	0.89
Verrucomicrobia	0.551	Not Detected



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Gut Microbiota Parameters:

Ratio	Your Value
Firmicutes/Bacteroidetes	0.28
Fusobacterium nucleatum/Faecalibacterium prausnitzii	NA, Faecalibacterium prausnitzii Not detected
Gram-positive/Gram-negative	0.28
Prevotella/Bacteroides	0
Proteobacteria/Actinobacteria	NA, Actinobacteria Not detected

Description of the gut microbiota parameters:

***Firmicutes/Bacteroidetes* Ratio (F/B Ratio):** The F/B ratio is investigated for its association with obesity, metabolic syndrome, and other health conditions, indicating the balance between two major bacterial phyla in the gut microbiome (90–95% of the entire consortium). A higher F/B ratio may indicate an increased capacity for energy extraction from the diet, potentially leading to greater fat storage and impacting weight gain. The F/B ratio typically varies from 0.1 to 10, with a more common range between 0.2 and 4. Ratios of 0.8 to 1.2 are often considered as a possible reference .

***Fusobacterium nucleatum/Faecalibacterium prausnitzii* Ratio (Fn/Fp Ratio):** The Fn/Fp ratio differentiates between healthy individuals and those with conditions such as colorectal cancer, adenomas, and inflammatory bowel diseases. An increase in the Fn/Fp ratio is associated with disease severity, serving as a potential marker for gut health and disease progression. Reference ranges indicate that a ratio less than 1 is observed in healthy and non-intestinal disease individuals, while higher values are noted in disease states.

Gram-positive/Gram-negative Ratio (G+/G− Ratio): The G+/G− ratio serves as a marker for the potential inflammatory state of the gut microbiota, reflecting the balance between G+ and G- bacteria. It's associated with the presence of bacterial lipopolysaccharide (LPS), a potent immune system stimulant. The standard reference range under typical conditions suggests that G- species are on average double the G+ species, with reference values between 0.4 and 0.5. A very low or very high ratio may indicate an altered gut microbiota with potential health implications.

***Prevotella/Bacteroides* Ratio (P/B Ratio):** The P/B ratio serves as a biomarker for identifying individuals likely to benefit from a low-calorie, high vegetable fiber diet, especially for overweight or obese subjects. A higher P/B ratio correlates with better weight loss outcomes when the diet is rich in vegetable fiber. The significance of the P/B ratio lies not just in caloric intake but in the diet's composition, emphasizing the role of fiber and its fermentation by gut microbiota into short-chain fatty acids (SCFAs), which influence energy utilization and possibly satiety, contributing to weight management.

***Proteobacteria/Actinobacteria* Ratio (P/A Ratio):** In general, the P/A ratio could serve as a potential indicator of gut microbiota balance or dysbiosis. Actinobacteria, particularly members like *Bifidobacterium*, are known for their health-promoting properties, including the production of short-chain fatty acids (SCFAs) and modulation of the immune system. In contrast, an overrepresentation of *Proteobacteria* is often associated with a state of dysbiosis and has been linked to various inflammatory and metabolic diseases. A higher P/A ratio might indicate a shift towards a less favorable gut microbiota composition, potentially signifying an increased risk of inflammation or disease.

SAMPLE REPORT

Gut-Centric Personalised Suggestions:

According to the test, in your gut: Multiple probiotics are within typical ranges. However, there are still 1 probiotics that are found in low levels. There are 4 opportunistic pathogens found in elevated levels. *Bacteroides fragilis*: Elevated *Enterococcus faecalis*: Elevated *Enterococcus faecium*: Elevated *Methanobrevibacter smithii*: Elevated *Faecalibacterium prausnitzii*: Low

It is recommended to adopt a low-protein, high-fiber diet, focusing mainly on grains, especially those rich in resistant starch like oats, corn, and sweet potatoes. Decrease the consumption of pork, beef, and lamb; increase the intake of sulfur amino acid-rich foods, including sesame, dairy products, sunflower seeds, yogurt, egg yolks, and oats. Consume fish in moderation, and control daily calorie intake. Ensure an ample daily intake of fresh vegetables (especially dark green leafy ones), fruits, and fiber; consume soy products and nuts in moderation. Maintain a varied diet for balanced nutrition.

1. Persist in regular physical activity, with a minimum of 5 days per week of moderate-intensity exercises like brisk walking, jogging, cycling, yoga, table tennis, basketball, totaling over 150 minutes weekly; aim for an average of 6,000 steps of active physical activity daily. Exercise appropriately to boost immunity and keep energy balanced. 2. Develop good sleep habits, try to sleep early and avoid staying up late, ensure sufficient sleep; relieve stress, maintain a joyful mood.

You have 1 antibiotic resistance genes (vancomycin) with levels higher than the typical range. High resistance gene levels might reduce the effectiveness of these antibiotics. Misuse also contributes to low gut diversity. Carefully select medications to avoid further damage to gut diversity.

SAMPLE REPORT

Gut Microbial Diversity

The human intestinal tract constitutes a complex and ever-changing ecological habitat, harboring an extensive array of microorganisms. The adage "preserve species diversity, uphold ecological equilibrium" holds true for the microecology within the intestines as well. Research has revealed strong associations between gut microbial diversity and conditions such as obesity, insulin resistance, and inflammation.

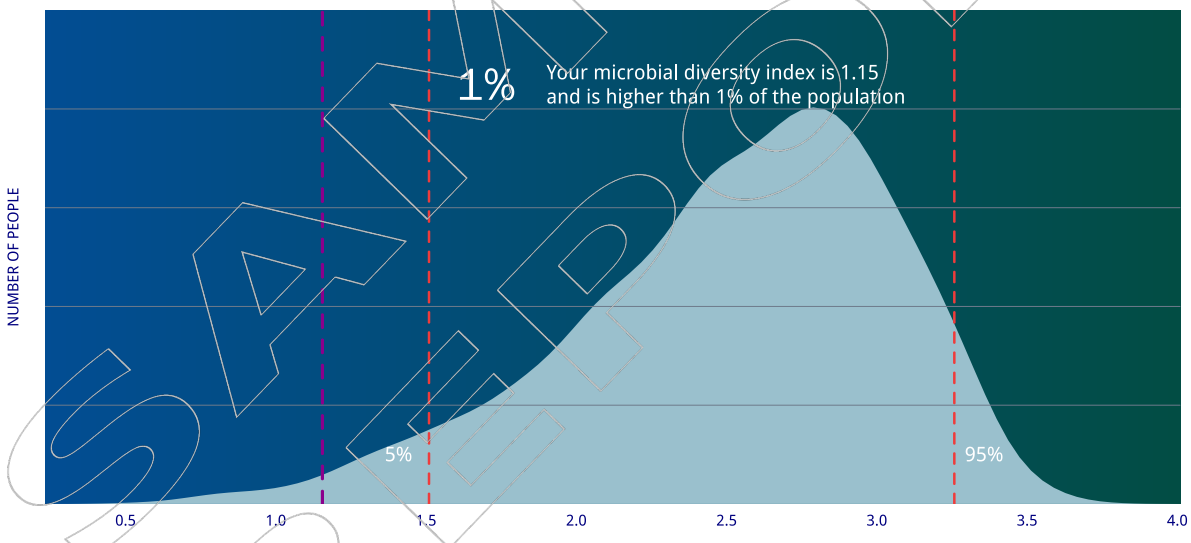
The Shannon Diversity Index is used here, which is a quantitative measure used in ecology and environmental science to describe the biodiversity of a habitat. It takes into account both the number of species present (species richness) and the evenness or proportion of each species (species abundance).

Shannon diversity index **H** is defined as:

$$H = -\sum_{i=1}^{s} (p_i \ln p_i)$$

Where s is the total number of species in the community, and p_i is the relative abundance of the species i.

Your gut microbial diversity index is: 1.15, which is higher than 1% of the reference population.



Gut Microbiota Diversity Index Distribution

Note: The purple dashed line represents your position, while the red dashed line signifies the reference range. The x-axis represents the index of gut microbial diversity, while the y-axis corresponds to the count of individuals.

As depicted in the preceding figure, in comparison to our reference group, your gut microbial diversity index falls below our reference range, being higher than 1% of individuals. Typically, a higher gut microbial diversity index is indicative of a healthier gut environment.

SAMPLE REPORT

Probiotics, Pathogens and Other

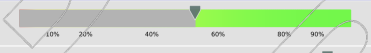
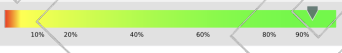
This section focusing on Probiotics, Pathogens, and Other, underscores the critical balance between beneficial microbes and harmful organisms in the gut.

Probiotics and beneficial bacteria, such as *Bifidobacteria* and *Lactobacilli*, play essential roles in nutrient absorption, immune function regulation, and maintaining gut barrier integrity. They contribute to the host's health by synthesizing vitamins and producing short-chain fatty acids, which have various positive effects on gut health.

Conversely, pathogens and opportunistic pathogens can disrupt this balance, leading to inflammation and disease. These organisms might be part of the gut's normal flora but can become harmful under certain conditions, such as a weakened immune system or after the disruption of the microbial balance.

Understanding the dynamics between these beneficial and harmful microbes is crucial for developing personalized nutrition and treatment plans aimed at optimizing gut health and preventing or treating diseases associated with microbial imbalances.

Understanding Your Results

Name	Your Value	Your Position in the Reference Population
Akkermansia muciniphila	0	
Bacteroides thetaiotaomicron	3.9086	

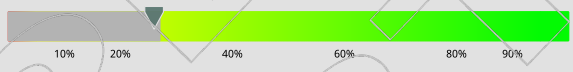
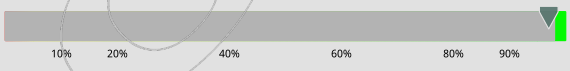
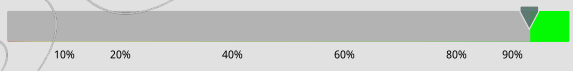
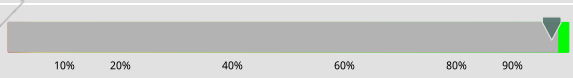
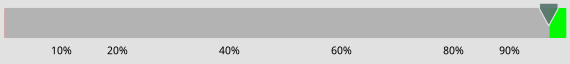
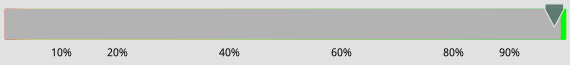
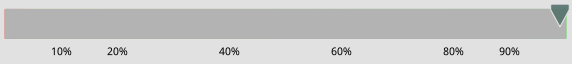
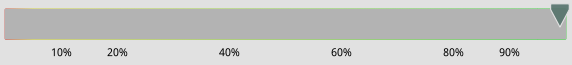
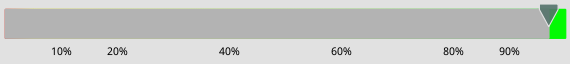
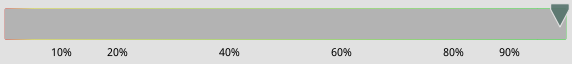
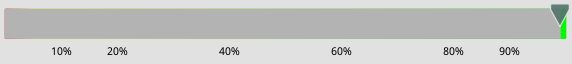
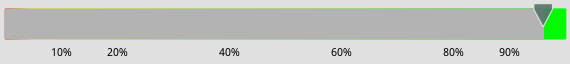
The first graph for "*Akkermansia muciniphila*" indicates a value of 0, meaning this bacterium is not detected in the sample. The gray bar suggests this bacterium is undetectable in about 52% of the population.

The second graph for "*Bacteroides thetaiotaomicron*" shows a value of 3.9086, which places the individual's bacteria level higher than the majority, as indicated by the arrow, past the 90th percentile.

Note: When your values deviate from the normal range, we denote the direction of deviation using arrows. The arrow depicted on the bar graph to the right signifies your position relative to our reference population. The gray segment represents the proportion of the population where the bacterium is undetectable due to its low levels.

SAMPLE REPORT

Probiotics and beneficial bacteria

Name	Your Value(%)	Your Position in the Reference Population
Akkermansia muciniphila	0	
Bacteroides thetaiotaomicron	0.5444	
Bacteroides uniformis	0.0274	
Bifidobacterium adolescentis	0	
Bifidobacterium animalis	0	
Bifidobacterium bifidum	0	
Bifidobacterium breve	0	
Bifidobacterium longum	0	
Bifidobacterium pseudolongum	0	
Clostridium butyricum	0	
Faecalibacterium prausnitzii	0↓	
Lactobacillus acidophilus	0	
Lactobacillus casei paracasei	0	
Lactobacillus crispatus	0	
Lactobacillus delbrueckii	0	
Lactobacillus fermentum	0	
Lactobacillus gasseri	0	
Lactobacillus helveticus	0	
Lactobacillus johnsonii	0	
Lactobacillus plantarum	0	
Lactobacillus reuteri	0	
Lactobacillus rhamnosus	0	
Lactobacillus salivarius	0	

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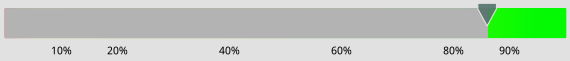
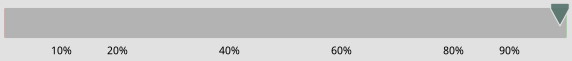
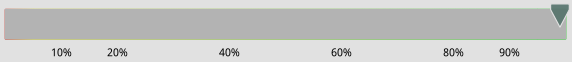
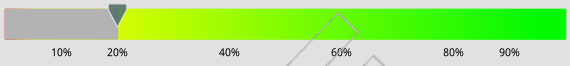
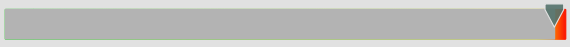
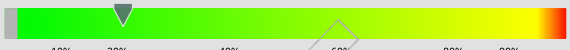
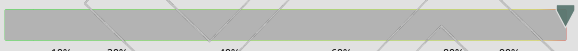
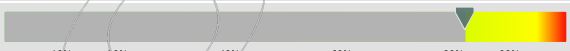
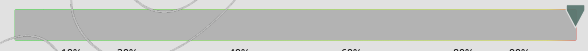
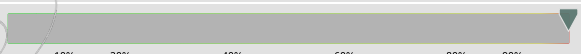
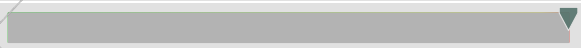
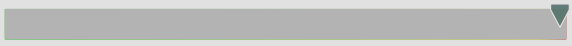
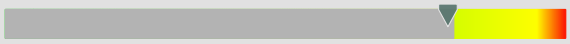
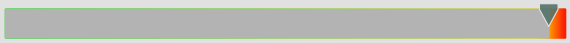
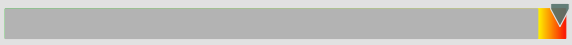
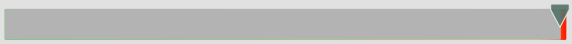
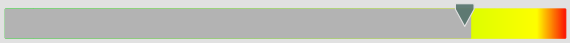
Lactococcus lactis	0	
Oxalobacter formigenes	0	
Pediococcus acidilactici	0	
Pediococcus pentosaceus	0	
Roseburia hominis	0	
Roseburia intestinalis	0	
Roseburia inulinivorans	0	
Streptococcus thermophilus	0	

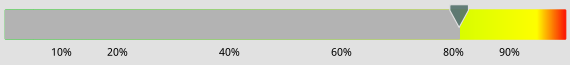
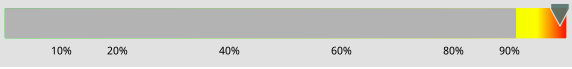
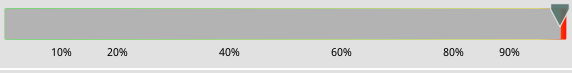
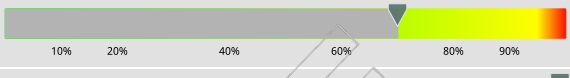
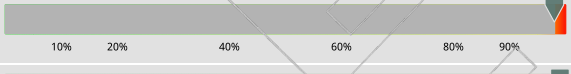
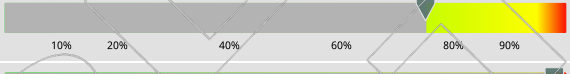
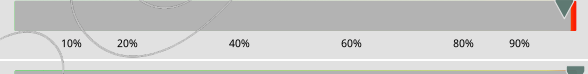
Out of 31 probiotics, 1 (3.2%) are lower than the typical ranges , 0 (0.0%) are higher than the typical ranges .

SAMPLE REPORT

Pathogens and opportunistic pathogens

Name	Your Value(%)	Your Position in the Reference Population
Abiotrophia defectiva	0	
Acinetobacter baumannii	0	
Acinetobacter haemolyticus	0	
Acinetobacter junii	0	
Bacteroides caccae	0.0268	
Bacteroides fragilis	44.6382↑	
Bacteroides vulgatus	0.2697	
Bilophila wadsworthia	0.0169	
Borrelia burgdorferi	0	
Citrobacter freundii	0	
Citrobacter koseri	0	
Citrobacter youngae	0	
Clostridium botulinum	0	
Clostridium perfringens	0	
Clostridium tetani	0	
Corynebacterium diphtheriae	0	
Corynebacterium urealyticum	0	
Cronobacter sakazakii	0	
Cronobacter turicensis	0	
Desulfovibrio piger	0	
Enterobacter cloacae	0.0289	
Enterococcus casseliflavus	0	
Enterococcus faecalis	0.2730↑	
Enterococcus faecium	1.6520↑	
Enterococcus gallinarum	0	
Escherichia coli	0↓	
Fusobacterium nucleatum	0	
Fusobacterium ulcerans	0	

SAMPLE REPORT

Klebsiella oxytoca	0	
Klebsiella pneumoniae	0.3133	
Methanobrevibacter smithii	0.1435↑	
Morganella morganii	0	
Mycoplasma hominis	0	
Prevotella amnii	0	
Prevotella bivia	0	
Prevotella melaninogenica	0	
Proteus mirabilis	0	
Providencia rettgeri	0	
Pseudoflavonifractor capillosus	0	
Pseudomonas aeruginosa	0	
Staphylococcus aureus	0	
Streptococcus agalactiae	0	
Streptococcus anginosus	0	
Streptococcus dysgalactiae	0	
Streptococcus mutans	0	
Streptococcus pyogenes	0	
Streptococcus salivarius	0↓	
Streptococcus suis	0	
Veillonella parvula	0	

SAMPLE REPORT

Out of 48 opportunistic pathogens, 2 (4.2%) are lower than the typical ranges , 4 (8.3%) are higher than the typical ranges .

Summary and Suggestions

Multiple probiotics are within typical ranges. However, there are still 1 probiotics that are found in low levels. 4 opportunistic pathogens are found in high levels. It is recommended to adjust your diet and incorporate probiotic-rich foods like yogurt to rebalance the gut microbiota and inhibit the growth of these bacteria.

Faecalibacterium prausnitzii: An important commensal bacterium in the human gut. It constitutes over 5% of the gut bacteria in healthy adults, making it one of the most common gut bacteria. A major butyrate-producing bacterium in the intestine, butyrate plays a crucial role in intestinal physiology and host health. Lower than normal levels of *Faecalibacterium prausnitzii* are associated with Crohns disease and obesity.

Bacteroides fragilis: Bacteroides fragilis is an obligately anaerobic, Gram-negative, rod-shaped bacterium. It is part of the normal flora of the human colon and is generally commensal, but can cause infection if displaced into

the bloodstream or surrounding tissue following surgery, disease, or trauma. B. fragilis has enormous capsule with NO cell membrane endotoxin, which limit their pathogenicity . Although B. fragilis makes up from 1-2% of the normal flora in our body, they are responsible for 80% of anaerobic infections. As an anaerobic pathogen, B. fragilis also competes with other organisms inside the colon/intestinal lumen for nutrients and food. This can be of great benefit to our body because when organisms compete, it decreases the availability of nutrients for other dangerous pathogens to grow, harming our body. It is highly important to study B. fragilis because it is well known to have caused many intestinal infections and it's highly associated with abscess formation. Abscess formation results in the formation of a fibrous membrane surrounding the infected site caused by B. fragilis. If left untreated, it will cause major harm to humans and animals. Studies have identified an enterotoxin that is associated with B. fragilis and it's the main caused of diarrhea in children and many types of inflammatory diseases in adults. But most importantly, studying B. fragilis will enable scientists to develop antibiotics to cure the infections cause by the organism.

Enterococcus faecalis: Enterococcus faecalis is a Gram-positive, commensal bacterium inhabiting the gastrointestinal tracts of humans and other mammals. Like other species in the genus Enterococcus, E. faecalis can cause life-threatening infections in humans, especially in the nosocomial (hospital) environment, where the naturally high levels of antibiotic resistance found in E. faecalis contribute to its pathogenicity. E. faecalis has been frequently found in root canal-treated teeth in prevalence values ranging from 30% to 90% of the cases. Root canal-treated teeth are about nine times more likely to harbor E. faecalis than cases of primary infections.

Enterococcus faecium: Enterococcus faecium was known as Streptococcus faecium until its name changed in 1984 due to a re-categorization. Enterococcus faecium is a Gram-positive, alpha-hemolytic or nonhemolytic bacterium in the genus Enterococcus. E. faecium is a human pathogen that causes nosocomial bacteremia, surgical wound infection, endocarditis, and urinary tract infections. Nosocomial infections are those acquired in medical setting during treatment of a prior complaint. E. faecium is the normal habitat includes the gastrointestinal tract of a multitude of animals but it can also be found in the oral cavity and vaginal tract. The microbe can survive for long periods of time in soil, sewage, and inside hospitals on a variety of surfaces. It can grow in temperatures ranging from 10 to 45 degrees Celsius, in basic or acidic environments, and in environments which are isotonic or hypertonic. E. faecium can be highly drug resistant and acquires its drug resistance by plasmids and conjugative transposons as well as chromosomal genes that encode resistance. Some strains have become resistant to vancomycin, penicillin, gentamicin, tetracycline, erythromycin and teicoplanin. Spread of the disease occurs between patients in hospitals due to transfer of the pathogen by hands or medical instruments. Also antibiotic use can decrease the number of other intestinal bacteria that are susceptible to the antibiotic and decrease competition for the drug resistant E. faecium.

Methanobrevibacter smithii: Methanobrevibacter smithii is an archaeon found in the human gut. It produces methane, helps with digestion by consuming hydrogen, and influences gut health. Its activity affects the gut microbiome's balance and can be linked to conditions like constipation and irritable bowel syndrome.

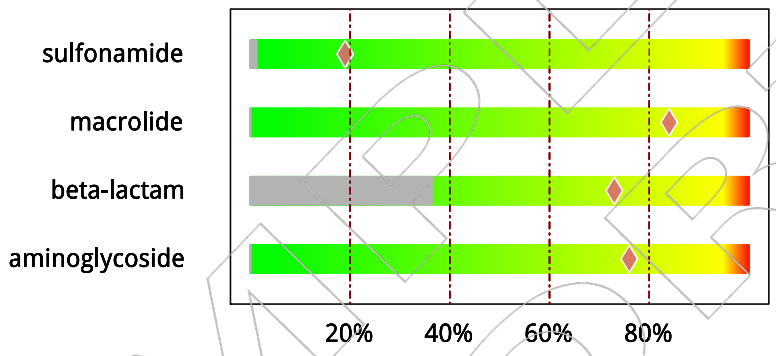
SAMPLE REPORT

Antibiotic Resistance Genes

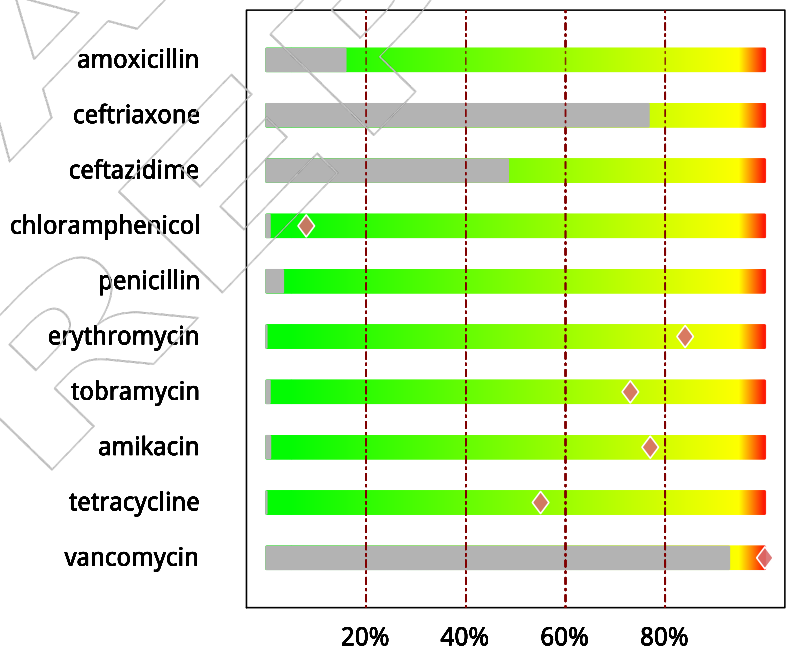
We compared 22 types of antibiotic resistance genes in your gut bacteria to a database. Four major categories (Aminoglycosides, β-lactams, Macrolides, Sulfonamides) and the resistance genes content for ten common antibiotics (Vancomycin, Amikacin, Tobramycin, Tetracycline, Amoxicillin, Penicillin, Erythromycin, Chloramphenicol, Ceftriaxone, Cefotaxime) were assessed against a reference population.

If you have higher resistance genes for other antibiotics, we'll provide details. High levels of specific antibiotic resistance genes may affect treatment effectiveness. Consult a healthcare professional before using antibiotics in such cases.

The diamonds in the figure below indicate the positions of the four major types of antibiotic resistance genes in your body in the reference population:



The diamonds in the figure below indicate the positions of the 10 common antibiotics and high-content antibiotic resistance genes in your body in the reference population:



SAMPLE REPORT

Antibiotic	Your Value	Proportion of the Reference Population with Zero Antibiotic Resistance Genes
Amikacin	3.81e-06	0.73%
Amoxicillin	0.0	15.84%
Ceftazidime	0.0	48.44%
Ceftriaxone	0.0	76.66%
Chloramphenicol	1.67e-07	0.63%
Erythromycin	1.06e-04	0.00%
Penicillin	0.0↓	3.31%
Tetracycline	5.81e-05	0.00%
Tobramycin	3.81e-06	0.63%
Vancomycin	2.75e-06↑	92.79%

Summary and Suggestions

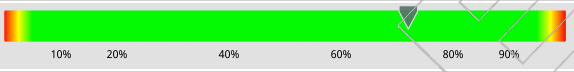
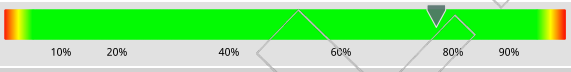
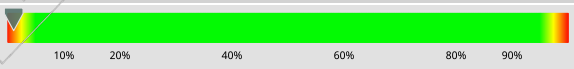
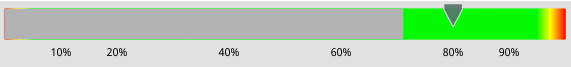
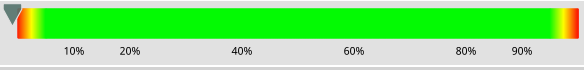
1 antibiotic resistance genes (vancomycin) are found in high abundance. A high level of antibiotic resistance genes may lead to suboptimal outcomes when using these antibiotics.

SAMPLE REPORT

Important Biochemical Functions

We have evaluated the levels of various biochemical functions in your gut microbiota and compared them with the values of our healthy reference population.

Note: In the bar chart below, the arrow indicates your value's position within the reference population.

Your Value	Your Position in the Reference Population
Basic Function	Involves replication and repair of genetic material in intestinal microbiota, fundamental for maintaining a stable gut microbiome; this function is often diminished in overweight populations.
6.31e-03 ↑	
Carbohydrate Metabolism	Encompasses polysaccharide synthesis and decomposition processes mediated by intestinal microbiota; elevated levels are associated with increased risk of various complex diseases.
6.14e-04	
Lipid Metabolism	Involves biosynthesis of fatty acids mediated by intestinal microbiota; elevated levels are associated with increased risk of various complex diseases.
6.50e-04	
Protein & Other Energy Metabolism	Covers metabolism of proteins and synthesis/decomposition of other energy substances by intestinal microbiota; elevated levels are associated with increased risk of various complex diseases.
2.99e-03 ↑	
Iron & Other Ion Metabolism	Involves metabolism of iron and other ions mediated by intestinal microbiota; elevated levels may relate to high long-term red meat consumption, increasing risks of obesity and colorectal cancer.
5.43e-04 ↑	
LPS	Refers to lipopolysaccharide and bacterial secretion; lipopolysaccharides, also known as endotoxins released by certain pathogenic bacteria, along with other substances secreted by gut microbiota, can trigger strong immune responses, leading to chronic inflammation in the intestines. Elevated levels increase risks of obesity, type 2 diabetes, and colorectal cancer.
6.51e-04	
Sulfate Production	Refers to sulfate metabolism; normal sulfate metabolism by intestinal microbiota ensures adequate synthesis of hydrogen sulfide, which is crucial for maintaining stable blood pressure and protecting blood vessels. However, excessive activity leading to elevated levels can result in obesity and inhibit insulin release, thereby increasing the risk of type 2 diabetes.
1.61e-04	
Aging Factor	Refers to oxidative stress resistance; increased oxidative stress is closely linked to aging. Elevated oxidative stress resistance in gut microbiota indicates a high oxidative stress environment in the body. Elevated levels increase the risk of various diseases, such as aging, immune deficiency, cardiovascular diseases.
3.78e-04 ↑	
SCFA Production	Refers to short-chain fatty acid synthesis; these acids, produced by beneficial bacteria acting on indigestible dietary fibers or resistant starch, play a crucial role in maintaining intestinal epithelial cell morphology and function, thus protecting the gut environment. Often reduced in overweight individuals, affecting normal intestinal barrier functions and increasing the risk of obesity and type 2 diabetes.
1.36e-04 ↓	
Histamine	Gut microbiota-derived histamine is produced by certain bacteria, through histidine decarboxylation. This histamine helps regulate the immune system, gut movement, and gut barrier health. However, too much histamine can cause food intolerances, allergies, and gut issues like IBS.
0.00e+00	
Ammonia(urease)	Gut microbiota-derived urease breaks down urea into ammonia. Ammonia can affect gut health by altering pH levels, which can lead to inflammation and damage to the gut lining.
0.00e+00 ↓	
BCAAs Production	Gut bacteria produce branched-chain amino acids (BCAAs) like leucine, isoleucine, and valine. These BCAAs are important for muscle health, metabolism, and the immune system. However, high levels of BCAAs are linked to metabolic diseases like obesity and type 2 diabetes. The gut microbial ability to produce BCAAs can be influenced by diet and overall gut health.
1.39e-04 ↓	

SAMPLE REPORT

Summary and Suggestions

Aging Factor: High oxidative stress resistance in gut microbiota indicates a high oxidative stress environment, potentially triggering various diseases like aging, immune deficiency, and cardiovascular diseases. Protein & Other

Energy Metabolism: Elevated levels indicate active absorption, release, and transport of energy, potentially increasing the risk of various complex diseases. Scfa Production: Reduced function may impact intestinal permeability, leading to obesity and type 2 diabetes risks.

SAMPLE REPORT

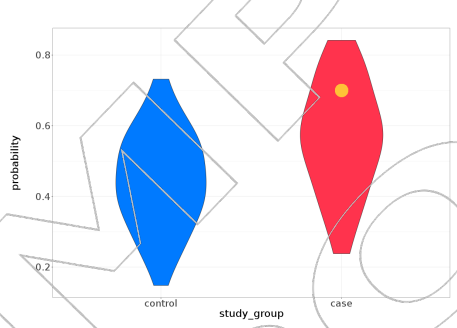
Type 2 Diabetes Risk

Previously, the impact of gut microbiota on type 2 diabetes was often overlooked. Recent research, including that of Professor Patrice D. Cani, highlighted the role of endotoxins from gut microbiota in causing insulin resistance. Professor Zhao Liping's experiments showed that mice developed insulin resistance after exposure to *Enterobacter cloacae B29*. BGI's research found a decrease in butyrate-producing bacteria and an increase in opportunistic pathogens in diabetics. These studies emphasize the close link between gut microbiota and type 2 diabetes.

Drawing from these research findings, we have conducted an assessment of your risk for type 2 diabetes by considering the information pertaining to the microbiota in your gut that is associated with this condition. The results are as follows:

Disease	Risk	Explanation
Type 2 Diabetes		Risk Value: 0.7000, Your risk of developing Type 2 Diabetes is higher then the average.

When compared to our population of individuals with the disease and the healthy control group, your Type 2 Diabetes risk index is positioned as follows:



Species Markers Related to Type 2 Diabetes:

Species Name	Population Average(%)	Your Value(%)
Bacteroides vulgatus	4.3570	0.26969
Clostridium bolteae	0.1453	0.27287

Summary and Suggestions

Based on our test results, your risk of developing Type 2 Diabetes appears to be higher then the average. Suggestions: 1. Change unhealthy lifestyle factors like poor sleep habits, lack of physical activity, sedentary lifestyle, negative emotions; 2. Low-salt, low-fat, low-sugar diet, increase intake of fruits, vegetables, and high-fiber foods, control total calories; 3. Increase physical activity, sports exercises; prefer rhythmic, relaxing activities like walking, jogging, cycling, swimming, dancing, Tai Chi; daily or at least five times a week exercise; 4. Avoid obesity, maintain ideal weight, ideal BMI between 18.5 and 22.9【BMI = weight (kg) / height squared (m^2)】; 5. Maintain good mindset, avoid stress, fatigue, mental stimulation, trauma, and use of blood sugar-raising hormones; 6. Quit smoking, limit alcohol; 7. Regular health check-ups, covering blood sugar, lipids, blood pressure.

SAMPLE REPORT

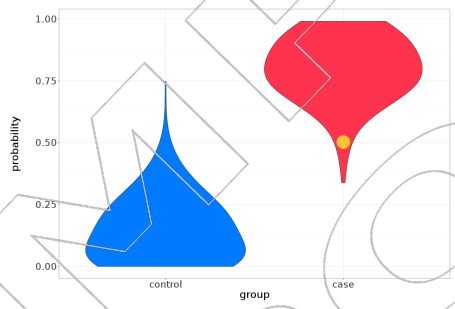
Colon Cancer Risk

Colon cancer, often presenting with subtle early symptoms, is a frequent gastrointestinal malignancy. Chronic intestinal inflammation, influenced by "pathogenic bacteria" in the gut, plays a crucial role in its development, as numerous studies have linked these bacteria to inflammation-induced colon cancer.

We've assessed your colon cancer risk based on gut microbiota associated with this condition. The results are as follows:

Disease	Risk	Explanation
Colon Cancer		Risk value: 0.5024, Your risk of developing Colon Cancer is higher then the average.

When compared to our population of individuals with the disease and the healthy control group, the position of your Colon Cancer risk index is as follows:



Species Markers Related to Colon Cancer:

Species Name	Population Average(%)	Your Value(%)
Actinomyces graevenitzii	0.0034	0
Anaerotruncus colihominis	0.0135	0
Bacteroides fragilis	2.1832	44.63816
Clostridium hathewayi	0.0583	0
Clostridium leptum	0.0678	0
Clostridium symbiosum	0.0325	0
Escherichia coli	2.0023	0
Fusobacterium nucleatum	0.0039	0
Gemella morbillorum	0.0010	0
Lachnospiraceae bacterium 3_1_57FAA_CT1	0.0476	0
Parvimonas micra	0.0002	0
Peptostreptococcus stomatis	0.0014	0
Porphyromonas asaccharolytica	0.0196	0
Prevotella copri	14.5384	0
Streptococcus parasanguinis	0.0297	0

Summary and Suggestions

According to our test results, it appears that your risk of developing colon cancer is relatively higher then the average. Advise regular lifestyle, good sleep habits, avoiding overwork, stress, maintaining a pleasant mood; healthy diet, promote intake of high-fiber fruits, green leafy vegetables, whole grains, reduce fat, animal protein, and "pickled foods"; maintain regular bowel movements.

SAMPLE REPORT

Fatty Liver Risk

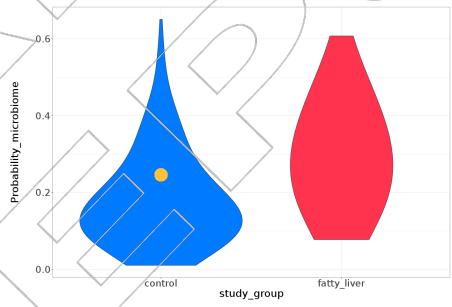
Fatty liver disease, or hepatic steatosis, occurs due to excessive fat accumulation in liver cells, resulting from both alcohol-related and non-alcohol-related factors. This common condition, affecting a significant population segment, is usually reversible. Fatty liver is more common in overweight, obese, or excessive alcohol consumers but can also occur in people with normal weight, known as nonalcoholic fatty liver disease (NAFLD).

A healthy liver contains a small amount of fat (about 3% to 5% of its total weight). Fatty liver diagnosis is confirmed when fat exceeds 5% of liver weight or over 50% of liver cells show fatty degeneration. Diagnosis involves medical history, liver function tests, imaging, and sometimes a biopsy. While mild cases may not be immediately concerning, prolonged fat accumulation can lead to serious issues like hepatitis, cirrhosis, and potentially fatal liver failure.

Recent research indicates a link between fatty liver disease and gut microorganism composition. Abnormal quantities of specific bacteria in individuals with fatty liver suggest a complex interplay between diet, lifestyle, gut microbiome, and liver health. The exact connection between gut microbiota and fatty liver disease remains an active research topic. We have conducted an assessment of your risk for Fatty Liver by considering the information pertaining to the microbiota in your gut that is associated with this condition. The results are as follows:

Disease	Risk	Explanation
Fatty Liver		Risk value: 0.2461, Your risk of developing Fatty Liver is lower than the average.

When compared to our population of individuals with the disease and the healthy control group, the position of your Fatty Liver risk index is as follows:



Species Markers Related to Fatty Liver:

Species Name	Population Average(%)	Your Value(%)
Alistipes indistinctus	0.1127	0.70407
Alistipes shahii	0.6756	0.00316
Bacteroides dorei	1.9980	0.03664

Summary and Suggestions

According to our test results, it appears that your risk of developing fatty liver is relatively lower then the average. Advise balanced and varied diet, limit high-fat, high-sugar foods, and alcohol consumption, maintain exercise habits, including aerobic and strength training, control weight and waist circumference.

SAMPLE REPORT

Inflammatory Bowel Disease Risk

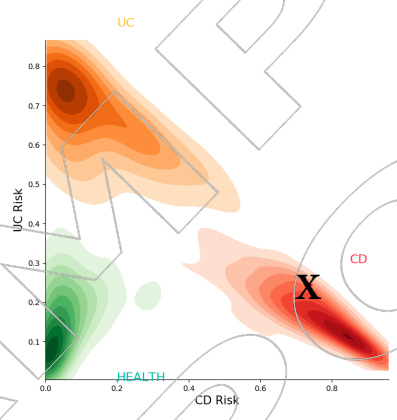
Inflammatory bowel disease (IBD) encompasses two conditions: ulcerative colitis (UC) and Crohn's disease (CD).

UC's development often involves environmental factors impacting genetically susceptible individuals, alongside intestinal microbiota, which incite immune responses and inflammation. This could result from persistent antigen stimulation or immune regulation issues, leading to an excessive immune-inflammatory reaction. UC and CD vary in their root causes, specific triggers, and how they damage tissue.

Ulcerative colitis, a chronic inflammation of the colon's mucous membrane, typically begins in the left half of the colon and may spread to the entire colon. Diet, especially the consumption of red meat and artificial butter, is associated with the development and recurrence of UC.

Disease	Risk
Inflammatory Bowel Disease	Your UC risk value: 0.24, Your CD risk value: 0.73, Relatively high risk of developing IBD, more likely to develop CD.

When compared to our population of individuals with the disease and the healthy control group, the position of your Inflammatory Bowel Disease risk index is as follows:



Species Markers Related to Inflammatory Bowel Disease:

Species Name	Enriched in	Population Average(%)	Your Value(%)
Bifidobacterium breve	UC	0.0023	0
Blautia producta	IBD	0.0007	0
Clostridium clostridioforme	CD	0.0142	0.35424↑
Clostridium symbiosum	UC	0.0325	0
Dorea formicigenerans	Control	0.0731	0↓
Escherichia coli	CD	2.0023	0
Fusobacterium nucleatum	IBD	0.0039	0
Roseburia hominis	Control	0.1834	0↓
Ruminococcus gnavus	CD	0.2605	0
Ruminococcus obeum	Control	0.1042	0↓

Your test results show a certain disease risk in 4 out of 9 (44.44%) inflammatory bowel disease-related species markers.

Summary and Suggestions

Based on our model, it appears that you are at Relatively high risk of developing IBD, more likely to develop CD.

SAMPLE REPORT

References

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