VibrantWellness

Final Report Date:	04-06-2017 11:08	**Specimen Collected:**	11-30-2015
Accession ID:	1512010000	**Specimen Received:**	12-01-2015 00:00

Last Name	First Name	Middle Name	Date of Birth	Gender	Physician ID
TESTNAME	PATIENT		1980-10-10	Male	999994

PATIENT

Name: PATIENT TESTNAME
Date of Birth: 1980-10-10
Gender: Male
Age: 36

Medical Record Number:
Telephone #: 1-866-364-0963
Street Address: 1021 HOWARD AVENUE SUITE B
City: SAN CARLOS
State: CA
Zip #: 94070

Email: support@vibrant-america.com

PROVIDER

Practice Name: Demo Client, MD
Provider Name: Demo Client, MD (999994)
Street Address: 1021 HOWARD AVENUE
City: SAN CARLOS
State: CA
Zip #: 94070
Telephone #: 1-800-842-7268
Fax #:

For doctor's reference

Vibrant Wellness is pleased to present to you, **Gut Zoomer** testing, to help you make healthy lifestyle choices in consultation with your physician and dietitian. It is intended to be used as a tool to encourage general healthy lifestyle choices.

Gut Zoomer is a health analytics tool based on the gut microbiome which provides potential risks for leaky gut, intestinal, cardiovascular, autoimmune, metabolic, and nutritional health conditions. It is intended to be used to improve functions associated with a general state of health, and where it is well understood and accepted that healthy lifestyle choices may play an important role in these health outcomes.

Interpretation of Report: The following terminologies are used consistently in the report and are explained below.

Relative Abundance is the percent composition of an organism of a particular kind relative to the total number of organisms in your gut microbiome.

The **Abundance** of individual bacterial phylum/family/genus/species is calculated by comparing the relative abundance to the healthy reference range. Reference ranges have been established using 192 healthy individuals.

The abundance results are displayed as HIGH↑, LOW↓ or OPTIMAL↔ . A HIGH↑ result indicates that you may have a higher relative abundance of the particular bacteria corresponding to the healthy reference range. A LOW↓ result indicates that you may have a lower relative abundance of the particular bacteria corresponding to the healthy reference range. An OPTIMAL↔ result indicates that you have an optimal relative abundance of the particular bacteria corresponding to the healthy reference range.

In some cases, a high abundance is potentially associated with an increased risk for a condition and in some cases a low abundance is potentially associated with an increased risk for a condition. The abundance is always mentioned in the report along with the potential associated risk, however, it is applicable only when indicated in RED.

Ratings are calculated based on the Impact Factor, Citations, and Study Population of the references which correlate the bacterial organism with the associated conditions. It is indicated with a star based system (1 star – 5 stars) with 5 stars indicating the best correlation of the bacteria with the potential associated risk. The Impact Factor of the journal in which the reference is published is the number of citations received by articles published in that journal during the two preceding years, divided by the total number of articles published in that journal during the two preceding years. Study population includes the number of samples tested along with gender, age and ethnicity of the population.

Vibrant Wellness is a personalized health analytics company founded out of our passion to serve patients and providers. The Vibrant Wellness platform provides tools for you to track and analyze your general wellness profile. All testing offered by Vibrant Wellness is performed at a CLIA approved lab testing facility and licensed by California Department of Public Health.

Please Note - It is important that you discuss any modifications to your diet, exercise and nutritional supplementation with your physician before making any changes.

To schedule an appointment with Vibrant Clinical Dietitians please call: Toll-Free 866-364-0963.

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Gut Microbiome and Phylum	Abundance	Previous (08/20/2015)
Actinobacteria	HIGH↑	HIGH↑
Bacteroidetes	OPTIMAL↔	OPTIMAL↔
Firmicutes	OPTIMAL↔	OPTIMAL↔
Proteobacteria	LOW↓	LOW↓

Gut Microbiome and Ratios

Floral Balance	Result	Previous (08/20/2015)	Rating	Potential Associated Risk*
Firmicutes/ Bacteriodetes	OPTIMAL↔	OPTIMAL↔	★★★★	
Gram+/ Gram-	HIGH↑	HIGH↑	★★★	Obesity
Diversity Index	LOW↓	LOW↓	★★★★	Gut Dysbiosis

Potential Risk Mitigation Choices

Considerations

Consider working with a Vibrant clinical dietitian to optimize your individualized diet and lifestyle recommendations.

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Gut Microbiome and Intestinal Permeability

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Bacteroides	OPTIMAL↔	OPTIMAL↔	★★★	Lower SCFA production
Bifidobacterium	LOW↓	LOW↓	★★★	
Propionibacterium	OPTIMAL↔	OPTIMAL↔	★★★	
Eubacterium	OPTIMAL↔	OPTIMAL↔	★★★	
Lactobacillus	OPTIMAL↔	LOW↓	★★★	
Clostridium	LOW↓	LOW↓	★★★	
Roseburia	OPTIMAL↔	OPTIMAL↔	★★★	
Prevotella	OPTIMAL↔	LOW↓	★★★	
Eubacterium rectale	OPTIMAL↔	OPTIMAL↔	★★★	
Butyrivibrio	LOW↓	LOW↓	★★★★	
Blautia	OPTIMAL↔	OPTIMAL↔	★★★	
Enterobacteriaceae (family)	OPTIMAL↔	OPTIMAL↔	★★★★	Tight junction integrity impaired
Akkermansia muciniphila	OPTIMAL↔	OPTIMAL↔	★★★★★	
Lactobacillus rhamnosus	OPTIMAL↔	OPTIMAL↔	★★★★	
Lactobacillus reuteri	LOW↓	LOW↓	★★★★	
Lactobacillus plantarum	LOW↓	LOW↓	★★★	
Streptococcus thermophilus	OPTIMAL↔	OPTIMAL↔	★★★	
Lactobacillus bulgaricus	OPTIMAL↔	OPTIMAL↔	★★★	
Lactobacillus acidophilus	OPTIMAL↔	OPTIMAL↔	★★★	
Bifidobacterium longum	OPTIMAL↔	OPTIMAL↔	★★★	

Potential Risk Mitigation Choices

Prebiotics

Consider taking prebiotic fibers

Probiotics

Consider taking probiotics containing Lactobacillus reuteri, Lactobacillus rhamnosus, Bifidobacterium infantis and Lactobacillus plantarum

Considerations

Consider butyrate supplements, further testing to confirm intestinal permeability and working with a Vibrant clinical dietitian to follow an anti-inflammatory diet.
Consider L-glutamine supplements, colostrum peptides and further testing to confirm intestinal permeability.

Diet

Consider a diet supplemented with fermented foods, dietary polyphenols and food sources of butyrate.

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Gut Microbiome and Intestinal Health

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Dorea	OPTIMAL↔	OPTIMAL↔	★★★★★	IBS
Ruminococcus	OPTIMAL↔	OPTIMAL↔	★★★★★	
Faecalibacterium prausnitizii	OPTIMAL↔	OPTIMAL↔	★★★	
Bifidobacterium	LOW↓	LOW↓	★★★	
Coprobacillus	OPTIMAL↔	OPTIMAL↔	★	
Ruminococcus productus	OPTIMAL↔	OPTIMAL↔	★★★★★	
Bifidobacterium catenulatum	OPTIMAL↔	OPTIMAL↔	★★★★★	
Desulfovibrio piger	OPTIMAL↔	OPTIMAL↔	★★★★★	
Coprococcus eutactus	OPTIMAL↔	OPTIMAL↔	★★★★★	
Escherichia coli	OPTIMAL↔	OPTIMAL↔	★★	
Clostridium leptum	OPTIMAL↔	OPTIMAL↔	★★	IBD
Enterobacterium	OPTIMAL↔	OPTIMAL↔	★★★	
Akkermansia muciniphila	OPTIMAL↔	OPTIMAL↔	★	
Lachnospira	LOW↓	LOW↓	★★★★★	
Phascolarctobacterium	OPTIMAL↔	OPTIMAL↔	★★★★★	
Gardnerella	OPTIMAL↔	OPTIMAL↔	★★	
Bacillus	OPTIMAL↔	OPTIMAL↔	★★★	
Lactobacillus	OPTIMAL↔	LOW↓	★★★★★	IBS-D
Veillonella	OPTIMAL↔	OPTIMAL↔	★★★★★	IBS-C

Potential Risk Mitigation Choices

Probiotics

Consider taking multi-strain probiotics containing Lactobacillus reuteri, Lactobacillus plantarum and Lactobacillus salivarius

Considerations

Possible supplements include curcumin, omega 3's, and Quercetin. Consider working with a Vibrant clinical dietitian to follow an anti-inflammatory diet.
Consider prebiotic fibers based on individual symptoms and evaluate possible food sensitivities.

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Gut Microbiome and Cardiovascular Health

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Collinsella	OPTIMAL↔	OPTIMAL↔	★★★★★	Atherosclerosis
Eubacterium	OPTIMAL↔	OPTIMAL↔	★★★★★	
Lactobacillus reuteri	LOW↓	LOW↓	★★★★★	High LDL-Cholesterol
Lactobacillus acidophilus	OPTIMAL↔	OPTIMAL↔	★★★★★	
Lactobacillus plantarum	LOW↓	LOW↓	★★★★★	Atherosclerosis and Triglyceride levels
Prevotella	OPTIMAL↔	LOW↓	★★★★★	Potentially increased TMAO levels leading to atherosclerosis
Sporobacter	OPTIMAL↔	OPTIMAL↔	★★★★★	
Peptostreptococcaceae (family)	OPTIMAL↔	OPTIMAL↔	★★★★★	
Peptostreptococcaceae incertae sedis	OPTIMAL↔	OPTIMAL↔	★★★★★	
Clostridiaceae	OPTIMAL↔	OPTIMAL↔	★★★★★	
Fusibacter	OPTIMAL↔	OPTIMAL↔	★★★★★	
Lachnospira	LOW↓	LOW↓	★★★★★	
Clostridium	LOW↓	LOW↓	★★★★★	
Clostridiales incertae sedis XII (family)	OPTIMAL↔	OPTIMAL↔	★★★★★	
Anaerococcus hydrogenalis	OPTIMAL↔	OPTIMAL↔	★★★★	
Clostridium asparagiforme	OPTIMAL↔	OPTIMAL↔	★★★★	
Clostridium hathewayi	OPTIMAL↔	OPTIMAL↔	★★★★	
Clostridium sporogenes	OPTIMAL↔	OPTIMAL↔	★★★★	
Escherichia fergusonii	OPTIMAL↔	OPTIMAL↔	★★★★	
Proteus penneri	OPTIMAL↔	OPTIMAL↔	★★★★	
Providencia rettgeri	OPTIMAL↔	OPTIMAL↔	★★★★	
Edwardsiella tarda	LOW↔	LOW↔	★★★★	

Potential Risk Mitigation Choices

Prebiotics

Consider prebiotic supplements inulin and fructooligosaccharide fibers.

Probiotics

Consider taking probiotics containing Lactobacillus reuteri, Lactobacillus acidophilus and Bifidobacterium lactis

Considerations

Consider evaluating clinical cardiovascular tests including lipids and inflammatory markers.

Diet

Consider a diet high in plant-based fibers and oils and evaluate the intake of L-carnitine and choline (red meat, eggs, liver).

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Gut Microbiome and Autoimmune Health

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Helicobacter	OPTIMAL↔	OPTIMAL↔	★★★★★	Celiac Disease
Serratia	OPTIMAL↔	OPTIMAL↔	★★	
Lactobacillus	OPTIMAL↔	LOW↓	★★	
Bifidobacterium	LOW↓	LOW↓	★★★	
Streptococcus	OPTIMAL↔	OPTIMAL↔	★★★	
Papilibacter	OPTIMAL↔	OPTIMAL↔	★★	
Prevotella	OPTIMAL↔	LOW↓	★★★★★	
Tannerella	OPTIMAL↔	OPTIMAL↔	★★★	Rheumatoid Arthritis (RA)
Yersinia	LOW↔	LOW↔	★★	
Aggregatibacter	OPTIMAL↔	OPTIMAL↔	★★★	
Porphyromonas	OPTIMAL↔	OPTIMAL↔	★★★	
Coprococcus	OPTIMAL↔	OPTIMAL↔	★	Psoriasis and Psoriatic Arthritis
Pseudobutyrivibrio	OPTIMAL↔	LOW↓	★	Psoriatic Arthritis
Klebsiella pneumoniae	LOW↔	LOW↔	★★★	Crohn's Disease
Veillonella	OPTIMAL↔	OPTIMAL↔	★★	
Dialister	LOW↓	LOW↓	★★★★★	

Potential Risk Mitigation Choices

Probiotics

Consider probiotics containing Lactobacillus and Bifidobacterium species.

Considerations

Consider further testing for celiac/gluten sensitivity and other autoimmune related antibodies.

Diet

Consider working with a Vibrant clinical dietitian to follow an anti-inflammatory diet.

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Gut Microbiome and Metabolic Health

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Lactobacillus reuteri	LOW↓	LOW↓	★★★★	Obesity
Lactobacillus casei	OPTIMAL↔	OPTIMAL↔	★★★	
Lactobacillus paracasei	OPTIMAL↔	OPTIMAL↔	★★★★★	
Methanobacteriales	OPTIMAL↔	OPTIMAL↔	★	
Bifidobacterium Animalis	OPTIMAL↔	OPTIMAL↔	★★★★	
Methanobrevibacter smithii	LOW↓	LOW↓	★★★★	
Staphylococcus	OPTIMAL↔	OPTIMAL↔	★★★	
Blautia	OPTIMAL↔	OPTIMAL↔	★★	
Oscillospira	OPTIMAL↔	OPTIMAL↔	★★★★★	
Alistipes	OPTIMAL↔	OPTIMAL↔	★★★	
Roseburia	OPTIMAL↔	OPTIMAL↔	★★★★★	Type II Diabetes
Eubacterium	OPTIMAL↔	OPTIMAL↔	★★★★★	
Eggerthella	OPTIMAL↔	OPTIMAL↔	★★★★★	

Potential Risk Mitigation Choices

Probiotics

Consider taking probiotics containing Lactobacillus reuteri, Lactobacillus paracasei, Lactobacillus rhamnosus, and Bifidobacterium animalis.

Considerations

Consider appropriate weight loss techniques in consultation with your physician

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Gut Microbiome and Nutrition I

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Bifidobacterium bifidum	LOW↓	LOW↓	★★★★	K Vitamins and B Vitamins Production affected
Bifidobacterium longum	OPTIMAL↔	OPTIMAL↔	★★★★	
Lactobacillus plantarum	LOW↓	LOW↓	★★★	
Bifidobacterium breve	OPTIMAL↔	OPTIMAL↔	★★★★	
Bifidobacterium adolescentis	OPTIMAL↔	OPTIMAL↔	★★★★	
Bacillus subtilis	OPTIMAL↔	OPTIMAL↔	★★	Vitamin K2 production affected
Lactobacillus reuteri	LOW↓	LOW↓	★★	Vitamin B12 production affected
Propionibacterium freudenreichii subsp. shermanii	OPTIMAL↔	OPTIMAL↔	★★	
Lactobacillus fermentum	OPTIMAL↔	OPTIMAL↔	★★	

Potential Risk Mitigation Choices

Probiotics

Consider multi-strain probiotic supplements containing Lactobacillus plantarum.

Considerations

Consider evaluating serum folate levels, genetic MTHFR testing and working with your provider or a Vibrant clinical dietitian to optimize diet and nutraceutical supplements
Consider working with your provider or a Vibrant clinical dietitian to optimize diet and nutraceutical supplements

Diet

Consider increasing the intake of fermented foods, particularly fermented dairy.

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Gut Microbiome and Nutrition II

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Bifidobacterium animalis subspe lactis	OPTIMAL↔	OPTIMAL↔	★★★	Oxalate metabolism affected
Lactobacillus animalis	OPTIMAL↔	LOW↓	★	
Eggerthella lenta	OPTIMAL↔	OPTIMAL↔	★★	
Enterococcus faecalis	LOW↓	LOW↓	★★	
Providencia rettgeri	OPTIMAL↔	OPTIMAL↔	★★	
Streptococcus thermophilus	OPTIMAL↔	OPTIMAL↔	★★	
Lactobacillus plantarum	LOW↓	LOW↓	★★	
Lactobacillus gasseri	OPTIMAL↔	LOW↓	★★	
Lactobacillus casei	OPTIMAL↔	OPTIMAL↔	★★	
Lactobacillus acidophilus	OPTIMAL↔	OPTIMAL↔	★★	
Lactobacillus rhamnosus	OPTIMAL↔	OPTIMAL↔	★★	
Lactobacillus salivarius	OPTIMAL↔	LOW↓	★★	
Lactobacillus johnsonii	OPTIMAL↔	OPTIMAL↔	★★	
Bifidobacterium infantis	OPTIMAL↔	OPTIMAL↔	★★	
Bifidobacterium animalis	OPTIMAL↔	OPTIMAL↔	★★	
Oxalobacter formigenes	OPTIMAL↔	LOW↓	★★	
Allisonella	OPTIMAL↔	OPTIMAL↔	★★★	Potential gut inflammation - High Histamine production
Methanobrevibacter smithii	LOW↓	LOW↓	★★★★★	Extraction of nutrients affected

Potential Risk Mitigation Choices

Prebiotics

Consider prebiotic fibers

Considerations

Consider working with your provider or a Vibrant clinical dietitian to optimize diet and nutraceutical supplements

Diet

Evaluate dietary oxalate foods

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Gut Parasites

Genus/Species	Result	Previous (08/20/2015)	Rating	Potential Associated Risk*
Cryptosporidium	NEGATIVE↔	NEGATIVE↔	★★★★	
Entamoeba histolytica	NEGATIVE↔	NEGATIVE↔	★★★★	
Giardia lamblia	POSITIVE↑	POSITIVE↑	★★★★	Giardiasis

Potential Risk Mitigation Choices

Considerations

Please consult with your physician and refer to the CDC for recommendations.

Gut Fungi & Yeast

Genus/Species	Abundance	Previous (08/20/2015)	Rating	Potential Associated Risk*
Candida albicans	LOW↔	HIGH↑	★★★★	

Pathogenic Bacteria

Genus/Species	Abundance	Previous (08/20/2015)
Shigella	LOW↔	LOW↔
Helicobacter pylori	HIGH↑	LOW↔
Clostridium difficile	LOW↔	LOW↔
Campylobacter sp	LOW↔	LOW↔
Enterotoxigenic Escherichia coli	LOW↔	LOW↔
Yersinia	LOW↔	LOW↔
Klebsiella pneumoniae	LOW↔	LOW↔
Edwardsiella tarda	LOW↔	LOW↔
Escherichia coli 0157	HIGH↑	
Salmonella sp	HIGH↑	
Listeria sp	HIGH↑	

Considerations

Please refer to the results of the culture based test(s) below for confirmation.

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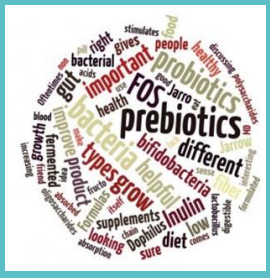
Pathogenic Bacteria (Culture)

Genus/Species	Abundance	Previous
Helicobacter pylori	POSITIVE ↑	
Escherichia coli 0157	POSITIVE ↑	
Salmonella sp	POSITIVE ↑	
Listeria sp	POSITIVE ↑	

VibrantWellness

PROBIOTICS AND PREBIOTICS FOR A HEALTHY GUT



Probiotics support a healthy gut microbiome, as well as maintain the integrity of the gut lining, boost immune function, promote healthy inflammatory responses, improve digestive function, help to heal inflammatory bowel conditions, manage and prevent skin conditions, fight food-borne illnesses, and improve psychological function. Probiotics are friendly bacteria that can be found in a variety of foods.

Prebiotics are carbohydrate-based sources of fiber that are food for beneficial bacteria in your gut. These fibers help them grow and thrive. Prebiotic fibers are helpful in the treatment of irritable bowel syndrome, inflammatory bowel disease and intestinal permeability. They also help to regulate bowel function.

Prebiotic rich foods

VEGGIES

Artichokes
Tomatoes
Onions
Leafy Greens
Asparagus
Garlic
Leeks

FRUITS

Berries
Bananas
Kiwis
Cherries
Apples
Pears
Mangoes

GRAIN AND LEGUMES

Quinoa
Flaxseeds
Oatmeal
Lentils
Chickpeas
White Beans
Black Beans

Probiotic rich foods

FERMENTED FOODS

Sauerkraut
Kimchi
Kombucha
Kefir
Yogurt (Dairy and Non-Dairy)
Lassi (Indian Yogurt Drink)
Natto
Miso
Fermented Pickles
Tempeh

PREBIOTICS	PROBIOTICS
Asparagus: Asparagus is packed with fiber, folate and other B vitamins.	**Live cultured yogurt and Kefir:** Naturally high in lactobacilli and bifido bacteria, yogurt can also be a healthy source of protein and calcium. Both dairy and non-dairy varieties are available.
Bananas: Bananas contain both soluble and insoluble fiber. This provides a food source for a variety of beneficial gut bacteria.	**Kombucha tea:** Kombucha is a fermented black or green tea made from live cultures of beneficial bacteria and yeast. It is high in B vitamins, which can also provide an energy boost.
Garlic: Garlic is a good source of inulin as well as contains natural antibacterial compounds. It is also a good source of sulfur compounds and vitamin B6, which aid in metabolism and nervous system health.	**Tempeh:** Tempeh is a fermented food made from soybeans. Soy is a complete protein, containing all the essential amino acids. Look for organic varieties of soy.
Onions: Onions are a natural source of inulin, which is a type of fiber that feeds beneficial bacteria in your gut.	**Kimchi**: Kimchi is a traditional Korean food rich in Lactobacillus bacteria. It is also high in fiber and vitamins A and C.
Artichokes: Artichokes are a very high fiber, low glycemic index vegetable. They are also good sources of folic acid and vitamin K.	**Sauerkraut:** Made from fermented cabbage and other vegetables, sauerkraut contains lactobacilli as well as soil-based organisms. It is a good source of vitamins C and K, calcium, magnesium and iron.

All Vibrant Wellness patients have the opportunity to work with our team of Clinical Dietitians.
To schedule an appointment please call: Toll-Free 866-364-0963

VibrantWellness

What are Polyphenols?

Polyphenols *(pol-ee-fee-nawls)* are chemical compounds that come from plants. They are used by your gut bacteria to make beneficial substances for you, and they help to keep your gut bacteria balanced by some of their antimicrobial effects.

Eating more polyphenol-rich foods has been shown to create an optimal gut bacterial balance, which, in turn, can reduce your risk for many diseases. If you have a decreased abundance of some beneficial gut bacteria, increasing your intake of polyphenol-rich foods is one thing you can do to improve your gut bacteria balance.

Higher Polyphenol Content

48 Highest Polyphenol Foods to Consume Often		
Cloves (spice)	Peppermint, dried (herb)	Celery seed
Cocoa powder	Mexican oregano, dried (herb)	Dark chocolate (70% or higher) *
Flaxseed meal	Black elderberry (fruit)	Chestnut (nut)
Sage, dried (herb)	Rosemary, dried (herb)	Thyme, dried (herb)
Blueberry (fruit)	Capers (herb/seasoning)	Black Olive (veg.)
Hazelnut (nut)	Pecan nut (nut)	Plum (fruit)
Green olive (veg.)	Sweet basil, dried (herb)	Curry powder (spice)
Sweet cherry (fruit)	Blackberry (fruit)	Roasted soybean (seed)
Milk chocolate *	Strawberry (fruit)	Red raspberry (fruit)
Coffee	Ginger, dried (root)	Whole grain wheat flour *
Prune (fruit)	Almond (nut)	Black grape (fruit)
Red onion (veg.)	Thyme, fresh (herb)	Refined maize flour *
Soy, tempeh	Whole grain rye flour *	Apple (fruit)
Spinach (veg.)	Black tea	Red wine
Green tea	Yellow onion (veg.)	Pure apple juice
Pure pomegranate juice	Extra virgin olive oil	Peach

***** *indicates a food that contains or may contain gluten*

Glossary

Antibiotic – antibiotics, or antibacterial treatments, are a type of antimicrobial product used to target bacteria, and are often used in medical treatment of bacterial infections. They can either kill or inhibit the growth of bacteria.

Archaea are a kingdom of single-celled prokaryotic microorganisms that are often mutualists (two different species that exist in a mutually beneficial relationship) or commensals (a species that benefits from other organisms without affecting them).

Atherosclerosis (also known as arteriosclerotic vascular disease or ASVD) is a specific form of arteriosclerosis in which an artery wall thickens as a result of invasion and accumulation of white blood cells (WBCs) or foam cells and proliferation of intimal-smooth-muscle cell creating a fibrous fatty plaque.

Bacterial classification - All organisms are classified in a hierarchical manner. For bacteria, we begin with the broadest division, the phylum, and work all the way down through sub-phylum, class, order, family, genus, and species, to strain. Most bacterial names that we encounter are described in terms of their genus, species and strain, which provides a very precise description of an individual organism.

Bacteroides are a phylum of bacteria commonly found in the human intestine, where they have a symbiotic host-bacterial relationship with humans. They assist in breaking down food and producing valuable nutrients and energy that the body needs. However, Bacteroides can be pathogenic when introduced to parts of the body other than the gastrointestinal area. They can cause or exacerbate abscesses and other infections.

Diversity index is calculated as the negative sum of each genus and species proportional abundance multiplied by the log of its proportional abundance and then normalizing the index with respect to the reference diversity index (calculated from running 192 healthy control stool samples).

Dysbiosis (also called dysbacteriosis) refers to microbial imbalance resulting from a change in the number or types of bacteria on or inside the body. Dysbiosis is most prominent in the digestive tract or on the skin, but can also occur on any exposed surface or mucous membrane.

Fermentation – a chemical process that converts sugar and carbohydrates into acids, gases, and/or alcohol. It occurs with yeast and bacteria, but humans also use fermentation to produce certain food and beverages.

Firmicutes are a phylum of bacteria, most of which have Gram-positive cell wall structure. Firmicutes make up the largest portion of the human gut microbiome. The division Firmicutes as part of the gut flora has been shown to be involved in energy resorption and obesity. Many Firmicutes produce endospores, which are resistant to desiccation and can survive extreme conditions. They are found in various environments, and the group includes some notable pathogens.

Fungus refers to any member of a large group of eukaryotic organisms that includes microorganisms such as yeasts and molds, as well as mushrooms. These organisms are classified as a kingdom, Fungi, which are separate from plants, animals, and bacteria.

Gastrointestinal tract/Digestive System – an organ system responsible for consuming and digesting foodstuffs, absorbing nutrients, and expelling waste. Bacteria constitute a large domain of prokaryotic microorganisms. They were among the first life forms to appear on Earth, and are present in most of its habitats. Bacteria also live in symbiotic and parasitic relationships with plants and animals. The majority of bacteria in the human body are harmless or beneficial, the largest number being in the gut flora. However, some species of bacteria are pathogenic and cause infectious diseases.

Gram-negative bacteria are a group of bacteria that do not retain the crystal violet stain used in the Gram staining method of bacterial differentiation. They are characterized by their cell envelopes, which are composed of a thin peptidoglycan cell wall sandwiched between an inner cytoplasmic cell membrane and a bacterial outer membrane.

Gram-positive bacteria are bacteria that give a positive result in the Gram stain test. Gram-positive bacteria take up the crystal violet stain used in the test, and then appear to be purple-colored when seen through a microscope. This is because the thick peptidoglycan layer in the bacterial cell wall retains the stain after it is washed away from the rest of the sample, in the decolorization stage of the test.

Gut microbiota refers to the community of microorganisms that live in the gastrointestinal tract. Gut refers to the intestine. Gut microbiota consists of tens of trillions of microorganisms, including at least 1,000 different species of known bacteria with millions of genes. Gut microbiota perform a host of useful functions, such as fermenting unused energy substrates, training the immune system, preventing growth of harmful, pathogenic bacteria, regulating the development of the gut, producing vitamins for the host, such as biotin and vitamin K, and producing hormones to direct the host to store nutrients.

Microbiota (or microbiome) is the community of microorganisms that typically inhabits a bodily organ or part. Microbial cells are more abundant in the human body than are human cells. These microorganisms may be commensal (living in close association that allows one species to benefit without harming the other), symbiotic (having an interdependent relationship), and pathogenic (disease- producing).

Short Chain Fatty Acids (SCFA), also referred to as volatile fatty acids (VFAs), are fatty acids with an aliphatic tail of less than six carbon atoms. Short-chain fatty acids are produced when dietary fiber is fermented in the colon.

Trimethylamine N-oxide (TMAO) is the organic compound in the class of amine oxides with the formula $(CH_3)_3NO$. This colorless solid is usually encountered as the dihydrate. It is a product of the oxidation of trimethylamine. The concentration of TMAO in the blood increases after consuming foods containing carnitine or lecithin if the bacteria that convert those substances to TMAO are present in the gut. High concentrations of carnitine are found in red meat, some energy drinks, and some dietary supplements.

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References

	BACTERIA	REFERENCE/ABSTRACT	RATING
Gut Microbiome and leaky gut	**Enterobacteriaceae**	**Kim K. A., Gu W., Lee I. A., Joh E. H., Kim D. H. (2012). "High fat diet-induced gut microbiota exacerbates inflammation and obesity in mice via the TLR4 signaling pathway".** The Study investigated the effect of endotoxin-induced inflammation at both systemic and intestinal levels in response to a high-fat diet (HFD). The below following observations were seen in the HFD mice reduction in the expression of tight junction-associated proteins claudin-1 and occludin in the colon, induced the growth of Enterobacteriaceae and the production of endotoxin and induced macrophage infiltration and inflammation in the adipose tissue, as well as an increase in the circulating proinflammatory cytokines.	★★★★
	Bacteroides, Bifidobacterium, Propionibacterium, Eubacterium, Lactobacillus, Clostridium, Roseburia, Prevotella	**Macfarlane G. T., Macfarlane S. (2012). "Bacteria, colonic fermentation, and gastrointestinal health."** This review summarizes the role of short-chain fatty acid (SCFA) in energy metabolism in large intestine, starting from the fermentation by the gut microbiota to the uptake by the colon and ending with the effects on gastrointestinal health. Bacteroides are one of the major species involved in the production of the SCFA acid, Acetate which plays an important physiological role in immune system, anti-carcinogenesis, increase colonic blood flow and adipogenesis.	★★★
	Akkermansia muciniphila	**Everard A., Belzer C., Geurts L., Ouwerkerk J. P., Druart C., Bindels L. B., et al. . (2013). "Cross-talk between Akkermansia muciniphila and intestinal epithelium controls diet-induced obesity".** This study aims demonstrate the link between the obesity and type 2 diabetes with the altered gut microbiota. Result indicates a significant contribution from species Akkermansia muciniphila which seen in decreased amount in genetically and diet-induced obese and type 2 diabetic mice .Furthermore the study demonstrated that prebiotic (oligo fructose) treatment restored A. muciniphila abundance and improved gut barrier and metabolic parameters in obese mice.	★★★★★
	Lactobacillus reuteri, Lactobacillus rhamnosus	**Rosenfeldt V., Benfeldt E., Valerius N. H., Paerregaard A., Michaelsen K. F. (2004). "Effect of probiotics on gastrointestinal symptoms and small intestinal permeability in children with atopic dermatitis".** A total of 41 children with moderate and severe atopic dermatitis completed a 6 week randomized, double-blind, placebo-controlled, crossover study. Subjects were given Lactobacillus supplements containing (L. rhamnosus and L. reuteri). Result showed a significant decrease in gastrointestinal symptoms over the period of the study with the probiotic treatment.	★★★★
Gut Microbiome and Intestinal Health	**Dorea, Ruminococcus**	**Rajili-Stojanovi M1, Biagi E, Heilig HG, Kajander K, Kekkonen RA, Tims S, de Vos WM "Global and deep molecular analysis of microbiota signatures in fecal samples from patients with irritable bowel syndrome".** The microbiota composition was assessed by global and deep molecular analysis of fecal samples from 62 patients with IBS patients and 46 healthy individuals (controls). Result indicated that the intestinal microbiota of IBS patients have a 2 fold increase in number of Dorea, Ruminococcus, and Clostridium.	★★★★★
	Lachnospira, Phascolarctobacterium	**Xochitl C Morgan, Timothy L Tickle, Harry Sokol, Dirk Gevers, Kathryn L Devaney, Doyle V Ward, Joshua A Reyes, Samir A Shah, Neal LeLeiko, Scott B Snapper, Athos Bousvaros, Joshua Korzenik, Bruce E Sands, Ramnik J Xavier and Curtis Huttenhower".** Dysfunction of the intestinal microbiome in inflammatory bowel disease and treatment". We analyzed the microbiota of intestinal biopsies and stool samples from 231 IBD and healthy subjects by 16S gene pyrosequencing and followed up a subset using shotgun metagenomics. Result indicated Inflammatory bowel diseases (IBD) Crohn's disease (CD), proportions of the Clostridia are altered: the Roseburia and Faecalibacterium genera of the Lachnospiraceae and Ruminococcaceae families are decreased, whereas Ruminococcus gnavus increased.	★★★★★
	Desulfovibrio piger	**Loubinoux J, Bronowicki JP, Pereira IA, Mougenel JL, Faou AE "Sulfate-reducing bacteria in human feces and their association with inflammatory bowel disease".** Sulfate-reducing bacteria were isolated from 10 healthy individuals (24%), 15 patients presenting with inflammatory bowel diseases (68%), and 33 patients with other symptoms (37%). The prevalence of D. piger was significantly higher in inflammatory bowel disease patients (55%) as compared to healthy individuals (12%) or patients with other symptoms (25%) (P<0.05).	★★★★★
	Coprococcus Euctatus	**Kassinen, A., Krogius-Kurikka, L., Makivuokko, H., Rinttil, T.Paulin, L., Corander, J., Malinen, E., Apajalahti, J. & Palva, A. "The fecal microbiota of irritable bowel syndrome patients differs significantly from that of healthy subjects".** Microbial genomes from fecal samples of 24 patients with IBS and 23 controls were collected and analyzed. Coprococcus eutactus species were significantly decreased in all IBS subtypes (IBS-C, IBS-D) compared with the healthy controls samples.	★★★★★
	Lactobacillus, Veillonella, Ruminococcus productus, Bifidobacterium catenulatum	**Malinen E, Rinttila T, Kajander K et al. "Analysis of the fecal microbiota of irritable bowel syndrome patients and healthy controls with real-time PCR".** Fecal Samples of 27 IBS patients were compared with 22 control subjects to extensively analyze the intestinal microbes in IBS. Extensive individual variation was observed in GI microbiota among both IBS and control group, furthermore Result indicated a lower amount of lactobacillus in the samples of diarrhea predominant IBS patients.	★★★★★
Gut Microbiome and Cardiovascular Health	**Collinsella, Eubacterium**	**Karlsson FH, Fåk F, Nookaew I, Tremaroli V, Fagerberg B, Petranovic D, Bäckhed F, and Nielsen J "Symptomatic atherosclerosis is associated with an altered gut metagenome".** The patient samples were from the Goteborg atheroma study group biobank, which includes sample from patients who had undergone surgery to excise an atherosclerotic plaque. All sample were sequenced in the Illumina HISeq2000 instrument, the finding shows an increased amount of Collinsella in cardio vascular patients having relative abundance score >0.015 compared to the control group having lesser than 0.005.	★★★★★
	Prevotella, Sporobacter, Peptostreptococcaceae, Peptostreptococcaceae incertae sedis, Clostridiaceae, Fusibacter, Lachnospira, Clostridium, Clostridiales Incertae Sedis XII	**R A Koeth et al. "Intestinal microbiota metabolism of L-carnitine, a nutrient in red meat, promotes atherosclerosis".** The study links the contribution of intestinal microbiota towards the L-carnitine, a nutrient in red meat with the increased risk of cardiovascular disease. Based on the result they hypothesized that the dietary l-carnitine in humans, like choline and phosphatidylcholine, might be metabolized to produce TMA and TMAO in a gut microbiota–dependent fashion and be associated with atherosclerosis risk. The major gut microbiota contributed to increase levels of TMAO levels in CVD patients were Prevotella, Sporobacter, Peptostreptococcaceae, and Peptostreptococcaceae incertae sedis, Clostridiaceae, Fusibacter, Lachnospira, Clostridium, and Clostridiales Incertae Sedis XII.	★★★★★
	Anaerococcus hydrogenalis, Clostridium asparagiforme, Clostridium hathewayi	**T. Liu et al. "Intestinal Microbiota Metabolism and Atherosclerosis".** Study details the link between cardiovascular disease and TMAO. It has been observed that several TMA-containing compounds may be catabolized by specific intestinal microbiota, resulting in TMA release which then converted into TMAO in liver. The major intestinal microbiota contributed to increase levels of TMAO levels were Anaerococcus hydrogenalis, Clostridium asparagiforme, Clostridium hathewayi.	★★★★

	BACTERIA	REFERENCE/ABSTRACT	RATING
Gut Bacteria and Autoimmune Health	**Helicobacter**	**Lebwohl B, Blaser MJ, Ludvigsson JF, Green PH, Rundle A, Sonnenberg A, Genta RM "Decreased risk of celiac disease in patients with Helicobacter pylori colonization".** In a study consisting of 136,179 patients, a total of 2,689 (2.0) % had celiac disease and Helicobacter pylori prevalence was significantly lower in patients with CD (4.4%) than in those without CD (8.8%) with the odd ratio of 0.48.	★★★★★
	Aggregatibacter, Porphyromonas	**Luigi Nibali, Brian Henderson, Syed Tariq Sadiq, and Nikos Donos "Genetic Dysbiosis: the role of microbial insults in chronic inflammatory diseases".** A recent survey in an US adult population of 3,742 individuals revealed a prevalence of 47% for periodontitis. Periodontopathogenic bacteria include gram-negative bacteria such as Aggregatibacter actinomycetemcomitans, Porphyromonas gingivalis and Tannerella forsythia. These bacteria are thought be able to enter the bloodstream through infected periodontal, have been found in atheromatous plaques, amniotic fluid of pregnant women and are thought to initiate rheumatoid arthritis in susceptible individuals.	★★★
	Dialister	**Joossens M1, Huys G, Cnockaert M, De Preter V, Verbeke K, Rutgeerts P, Vandamme P, Vermeire S "Dysbiosis of the fecal microbiota in patients with Crohn's disease and their unaffected relatives".** Focusing on families with at least three members affected with CD, fecal samples of 68 patients with Crohn's disease (CD), 84 of their unaffected relatives and 55 matched controls were subjected to community fingerprinting of the predominant microbiota using denaturing gradient gel electrophoresis (DGGE). Results suggests that there is a decrease in Dialister invisus (p=0.04) in positive CD patients compared to the control group.	★★★★★
	Prevotella	**Gangwei Ou , MD, PhD , Maria Hedberg , PhD , Per H ö rstedt , PhD , Vladimir Baranov , MD, PhD , G ö te Forsberg , MD, PhD , Mirva Drobni , PhD , Olof Sandstr ö m , MD, PhD , Sun Nyunt Wai , MD, PhD , Ingegerd Johansson , OD, PhD , Marie-Louise Hammarstr ö m , PhD , Olle Hernell , MD, PhD and Sten Hammarstr ö m , PhD "Proximal Small Intestinal Microbiota and Identification of Rod-Shaped Bacteria Associated With Childhood Celiac Disease".** 45 children with CD and 18 clinical controls were studied. s. The proximal small intestine microbiota in biopsies from CD patients collected during 2004 – 2007 differed only marginally from that of controls, and only one biopsy (4 %) had rod-shaped bacteria by SEM (SEM +). In nine frozen SEM +CD biopsies from the previous study, microbiotas were significantly enriched in Clostridium, Prevotella, and Actinomyces compared with SEM biopsies. Bacteria of all three genera were isolated from children born during the Swedish CD epidemic. New Clostridium and Prevotella species and Actinomyces graevenitzii were tentatively identified.	★★★★★
Gut Microbiome and Metabolic Health	**Lactobacillus Reuteri, Lactobacillus paracasei, Bifidobacterium Animalis, Methanobrevibacter smithii**	**M Million, E Angelakis, M Maraninchi, M Henry, R Giorgi4, R Valer, B Vialettes and D Raoult, "Correlation between body mass index and gut concentrations of Lactobacillus reuteri, Bifidobacterium animalis, Methanobrevibacter smithii and Escherichia coli".** 263 individuals, including 134 obese, 38 overweight, 76 lean and 15 anorexic were subjects to test for the correlation between bacterial concentration and body mass index (BMI). M. smithii was found in 63% of individuals. The fecal concentration of Methanobrevibacter smithii OR= 0.43 were negatively associated with the BMI.	★★★★
	Oscillospira	**Julia K. Goodrich, Jillian L. Waters, Angela C. Poole, Jessica L. Sutter, Omry Koren, Ran Blekhman, Michelle Beaumont, William Van Treuren, Rob Knight, Jordana T. Bell, Timothy D. Spector, Andrew G. Clark, and Ruth E. Ley".** Human genetics shape the gut microbiome". In a study consisted of microbiotas across > 1,000 fecal samples obtained from the Twins UK population, including 416 twin-pairs. Results indicates an increase in Oscillospira in lean subjects compared to high BMI candidates.	★★★★★
	Roseburia, Eubacterium	**Junjie Qin, Yingrui Li, and Zhiming Cai et.al "A metagenome-wide association study of gut microbiota in type 2 diabetes".** A two-stage case-control metagenome-wide association study (MGWAS) was developed based on deep next generation shotgun sequencing of DNA extracted from the stool samples from a total of 345 Chinese T2D patients and non-diabetic controls. Using the taxonomic characterization from these MLGs, it was found that almost all of the MLGs enriched in the control samples were from various butyrate producing bacteria, including Roseburia intestinalis and Roseburia inulinivorans.	★★★★★
	Eggerthella	**Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, Liang S, Zhang W, Guan Y, Shen D, Peng Y, Zhang D, Jie Z, Wu W, Qin Y, Xue W, Li J, Han L, Lu D, Wu P, Dai Y, Sun X, Li Z, Tang A, Zhong S, Li X, Chen W, Xu R, Wang M, Feng Q, Gong M, Yu J, Zhang Y, Zhang M, Hansen T, Sanchez G, Raes J, Falony G, Okuda S, Almeida M, LeChatelier E, Renault P, Pons N, Batto JM, Zhang Z, Chen H, Yang R, Zheng W, Li S, Yang H, Wang J, Ehrlich SD, Nielsen R, Pedersen O, Kristiansen K, Wang J "A metagenome-wide association study of gut microbiota in type 2 diabetes."** The gut microbial content in patients (345 Chinese individuals) with type 2 diabetes were analyzed through deep shotgun sequencing method. MGWAS analysis showed that patients with type 2 diabetes were characterized by a moderate degree of gut microbial Dysbiosis amongst which Eggerthella species had an OR of 1.57.	★★★★★
Gut Microbiome and Nutrition	**Bifidobacterium bifidum, Bifidobacterium longum, Bifidobacterium breve, Bifidobacterium adolescentis**	**LeBlanc et al. "Bacteria as vitamin suppliers to their host: a gut microbiota perspective".** In humans it has been shown that members of the gut microbiota are able to synthesize vitamin K as well as most of the water-soluble B vitamins, such as biotin, cobalamin, folates, nicotinic acid, panthotenic acid, pyridoxine, riboflavin and thiamine. The study shows that some species of Bifidobacterium such as Bifidobacterium bifidum, B.Longum, B.Breve, B.adolescentis are claimed to be the key components to exhibit the vitamin production.	★★★★
	Bifidobacterium animalis subspecies lactis	**Turroni et al. "Oxalate-Degrading Activity in Bifidobacterium animalis subsp. lactis: Impact of Acidic Conditions on the Transcriptional Levels of the Oxalyl Coenzyme A (CoA) Decarboxylase and Formyl-CoA Transferase Genes".** Intestinal oxalate degrading bacteria plays an important role in maintaining oxalate homeostasis and reducing the risk of kidney stones. In this study, the oxalate degradation activities of 14 species of Bifidobacterium strains were examined, among which results indicates B. animalis carries the oxc gene, which encodes oxalyl-coenzyme A (CoA) decarboxylase, a key enzyme in oxalate catabolism which then making it a strong candidate for the prophylaxis and management of oxalate-related kidney disease.	★★★
	Methanobrevibacter smithii	**Mark Pimentel MD, Robert P Gunsalus, Satish SC Rao MD and Husen Zhang "Methanogens in Human Health and Disease".** The review examines the impact of methanogens in human health and disease. Methanobrevibacter smithii accounts for 94% of the methanogen population. Methanogens oxidize hydrogen to produce methane and ensure more complete fermentation of carbohydrate substrates, leading to higher production and adsorption of short-chain fatty acids, which may lead to obesity. Recent evidence has linked methane production to the pathogenesis of constipation and irritable bowel syndrome (IBS), as well as obesity.	★★★★★

The complete list of references and the summary of performance studies can be found online at www.vibrant-wellness.com or BY CONTACTING CLIENT SERVICES AT +1(866)364-0963.

Test Risk and Limitations

Gut Zoomer testing is performed at Vibrant Genomics, a CLIA certified laboratory, and utilizes ISO-13485 developed technology. However, laboratory error can occur, which might lead to incorrect results. Some of them may include sample or DNA mislabeling or contamination, operational error or failure to obtain data for certain genes. Vibrant's laboratory may need a second sample to complete the testing.

Vibrant Genomics has effective procedures in place to protect against technical and operational problems. However, such problems may still occur and examples include failure to obtain the Gut Zoomer abundance result for a specific species due to circumstances beyond Vibrant's control. Vibrant may re-test a sample in order to obtain these results but upon re-testing the results may still not be obtained. As with all medical laboratory testing, there is a small chance that the laboratory could report incorrect Gut Zoomer abundance results. A tested individual may wish to pursue further testing to verify any results.

Tested individuals should not change their diet, physical activity, or any medical treatments they are currently using based on the results without consulting their personal health care provider. These risk factors for Gut Zoomer are based on selected peer-reviewed scientific research findings as listed under references.

Tested individuals may find their experience is not consistent with Vibrant's selected peer-reviewed scientific research findings of relative improvement for study groups. The science in this area is still developing and many personal health factors affect diet and health. Since subjects in the scientific studies referenced in this report may have had personal health and other factors different from those of tested individuals, results from these studies may not be representative of the results experienced by tested individuals. Further, some recommendations may or may not be attainable, depending on the tested individuals' physical ability or other personal health factors.

A limitation of this testing is that most scientific studies have been performed in Caucasian populations only. The interpretations and recommendations are done in the context of Caucasian studies, but the results may or may not be relevant to tested individuals of different or mixed ethnicities. Please note that pediatric ranges have not been established for these tests. Interference studies have not been established for individuals on immunosuppressive drugs.

Based on test results and other medical knowledge of the tested individual, health care providers might consider additional independent testing, or consult another health care provider or genetic counselor.