

GUT MICROBIOME TEST



Detailed Report: Test Report + Dietary Recommendations

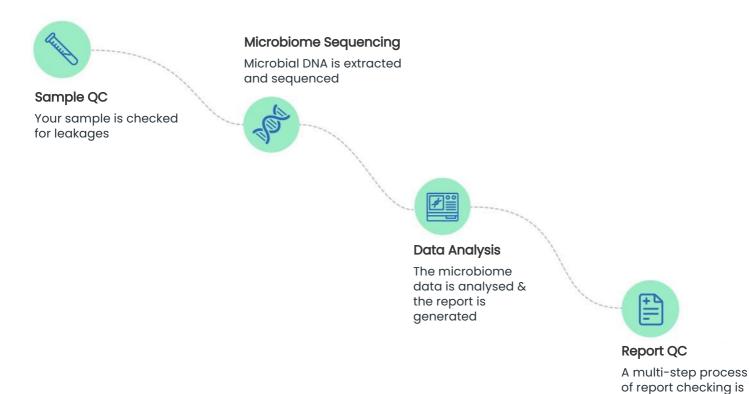


Join us in shifting from SickCare to HealthCare!

Sova is on a mission to enhance lives through Microbiome Health. Led by Clinical Nutritionists, Scientists and Gut Health Experts, we harness the power of microbes to help you prevent and manage conditions linked to Gut, Skin, Oral Health, Metabolic Health & more.



What we do once we get your sample?



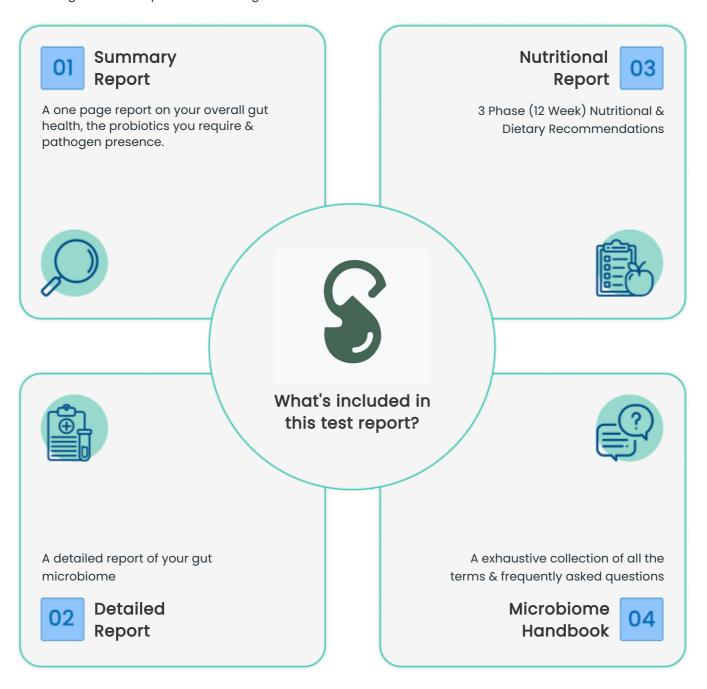
performed



Summary Report

This is your Sova Health Gut Microbiome Summary Report. With this report, our endeavour is to provide key insights, with the hope that it will guide you to better understand your health and make necessary changes to your lifestyle to lead a healthier life. You can always refer our complete Scientific Report for a more detailed evidence-based interpretation of your gut microbiome data.

We have categorized the report into following sections:



Please Note:

1. This is not a diagnostic report and should be interpreted or used exclusively by or under the guidance of a practitioner, including but not limited to, certified physicians, clinicians, dietitians, nutritionists, sports therapists, and such other persons in similar profession having appropriate validation to undertake such practice. (Please See Disclaimers).



Summary Report



One page report on your overall gut health, the probiotics you require & pathogen presence



Rych Index - Your Gut Health Score

Scores in the Green Range represents a Healthy Gut and in the Red Range represents an Unhealthy Gut. Know More about "Rych Index" within the FAQ Section.



Probiotics - The Good Microbes

You may require supplements that contain these probiotics. For more details please read the detailed report.

Lentilactobacillus kefiri

Alkalihalobacillus clausii

Metabacillus indicus



- Bifidobacterium animalis
- Bifidobacterium infantis VIII-240
- Limosilactobacillus reuteri
- Lactobacillus delbrueckii
- Lactobacillus helveticus
- Lacticaseibacillus casei
- Supplementation Needed
- Lactobacillus gasseri
- Lactiplantibacillus pentosus
- Lactobacillus acidophilus
- Saccharomyces boulardii (nom. inval.)

Pathogen - The Bad Microbes

The following "pathogens" abundance was found to be more than the average healthy individuals. Please correlate clinically and follow recommendations. For more details please read the detailed report.



Follow Nutrition

Guidelines

- Clostridioides difficile
- 🎊 Candida albicans
- 🎊 [Candida] glabrata
- Aspergillus terreus
- 🎊 Fusobacterium nucleatum
- Cryptosporidium

Name:

Sample Received Date:

Page 03



Detailed Report



A detailed report of your gut microbiome



Rych Index - Your Gut Health Score

Rych Index is a proprietary algorithm based output that tends to indicate the overall gut health with respect to the microbiota profile. Various parameters such as abundance, diversity and richness have been used to come up with the Rych Index score. Know more about the 'Rych Index' in the FAQ section (Microbiome handbook section).



Pictorial graph representation of various components of your microbiome. Green colour represents healthy / good /favorable, red colour represents unhealthy / bad / unfavorable.

Category Tag

Sova Diversity	Ideal
Kingdom Distribution	Below Average
Foundation Microbiota	Average
Probiotic Characterization	Average
Pathogen Characterization	Non-Ideal
Antibiotic Resistance	Ideal
Antibiotic Recovery Potential	Ideal
SCFA Production	Non-Ideal
Vitamin Production	Average
Neurotransmitters	Ideal
Propensity to Disease Development	Above Average

Name:



Sova Diversity

Category Tag



This is a proprietary diversity score developed by us taking into consideration individual kingdom diversities and internal data analysis of healthy and unhealthy.

Kingdom Distribution

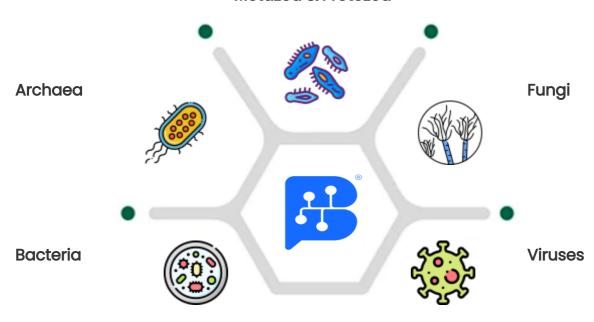
Category Tag

Below Average

Composition of gut microbiome is defined by 4 major groups of microorganisms - Bacteria, Archaea, Virus and Eukaryota (Fungi, Protozoa and Metazoa). Below is a representation highlighting these 4 groups, its corresponding abundance and what it means to you, in context of gut microbiome.

Kingdom Distribution	Range(%)	Your Sample Value	Тад
Bacteria	97.94% - 99.07%	89.26%	Atypical
Fungi	0.36% - 0.86%	0.635%	Typical
Metazoa & Protozoa	0.21% - 0.51%	0.425%	Typical
Archaea	0.11% - 0.28%	9.376%	Atypical
Viruses	0.25% - 1.06%	0.304%	Typical

Metazoa & Protozoa



Name:

Sample Received Date:



Top Abundant Species

Faecalibacterium prausnitzii	8.363 %	Akkermansia muciniphila	2.314 %
Prevotella copri	3.849 %	Bacteroides eggerthii	1.699 %
Dialister succinatiphilus	3.63 %	Coprococcus eutactus	1.448 %
Roseburia faecis	3.038 %	Ligilactobacillus ruminis	1.33 %
Lachnospira pectinoschiza	2.473 %	Oscillibacter sp. MSJ-31	1.221 %
Top abundant species of Archaea in	your sample		
Methanobrevibacter smithii	9.97 %	Methanobrevibacter thaueri	0.023 %
Methanobrevibacter oralis	0.046 %	Methanobrevibacter sp. 87.7	0.018 %
Methanobrevibacter woesei	0.041 %	Methanobrevibacter curvatus	0.014 %
Methanobrevibacter sp. A54	0.036 %	Methanospirillum lacunae	0.014 %
Methanobrevibacter millerae	0.027 %	Methanotorris igneus	0.009 9
Top abundant species of Eukaryota i	n your sample		
Tetrahymena thermophila	0.096 %	lchthyophthirius multifiliis	0.023 %
Trichomonas vaginalis	0.032 %	Acytostelium subglobosum	0.018 %
Plasmodium vinckei	0.027 %	Cavenderia fasciculata	0.018 %
Dictyostelium discoideum	0.023 %	Plasmodium chabaudi	0.018 %
Entamoeba dispar	0.023 %	Plasmodium gallinaceum	0.018 %
Top abundant species of Viruses in y	our sample		
crAssphage cr7_1	0.2 %	Buzura suppressaria nucleopolyhedrovirus	0.005 %
crAssphage cr124_1	0.169 %	Cellulophaga phage phi39:1	0.005 %
Megavirus chiliensis	0.009 %	Yellowstone lake phycodnavirus 2	0.005 %
Tipula oleracea nudivirus	0.009 %	Cbastvirus ST	0.005 9
African swine fever virus	0.005 %	Orpheovirus IHUMI-LCC2	0.005 %
Top abundant species of Fungi in you	ur sample		
Rhizophagus irregularis	0.073 %	Aspergillus steynii	0.014 %
Blastomyces gilchristii	0.018 %	Candida albicans	0.014 %
Lobosporangium transversale	0.018 %	Letharia columbiana	0.014 %
Pyricularia grisea	0.018 %	Puccinia graminis	0.014 %
Wickerhamomyces ciferrii	0.018 %	Sclerotinia sclerotiorum	0.014 %

Please Note: All values are % relative abundances.



Foundation Microbiota

Category Tag

Average

Perturbations of these keystone species can have large effects on the overall microbiome. If any keystone species is in atypical range, please strictly follow the dietary recommendations. Know More about "Foundation Microbiota" within the FAQ Section.

Keystone Species	Relative Abundance Range(%)	Your Sample Value	Conclusion
Akkermansia muciniphila	0.003% - 0.014%	2.314%	Typical
Bifidobacterium longum	1.142% - 3.743%	0.232%	Atypical
Faecalibacterium prausnitzii	0.235% - 3.008%	8.363%	Typical
Roseburia intestinalis	0.285% - 0.690%	0.332%	Typical
Ruminococcus bromii	0.061% - 0.171%	0.123%	Typical
Lactobacillus helveticus	0.003% - 0.010%	0.000%	Atypical
Lactobacillus delbrueckii	0.004% - 0.013%	0.000%	Atypical
Lacticaseibacillus paracasei	0.004% - 0.014%	0.005%	Typical
Ligilactobacillus salivarius	0.005% - 0.011%	0.027%	Typical
Limosilactobacillus fermentum	0.006% - 0.019%	0.005%	Atypical
Limosilactobacillus reuteri	0.007% - 0.021%	0.000%	Atypical
Lactiplantibacillus mudanjiangensis	0.028% - 0.099%	0.005%	Atypical
Limosilactobacillus mucosae	0.044% - 0.200%	0.000%	Atypical
Lacticaseibacillus rhamnosus	0.047% - 0.102%	0.041%	Atypical
Ligilactobacillus ruminis	0.273% - 0.586%	1.33%	Typical



Probiotic Characterization

Category Tag

Average

Sova Health identifies and characterizes many probiotics commonly known to be present and beneficial to gut health. These probiotics are reported with "indicative tags", which can be interpreted as described below.

Supplementation Needed - These probiotics were found either absent or very less in abundance in your sample.

Follow Recommendation - These probiotics were found to be present but less abundant.

Follow your current diet - These probiotics were present in adequate abundance in your sample.



Supplementation Needed

- Bifidobacterium animalis
- Bifidobacterium infantis VIII-240
- Limosilactobacillus reuteri
- Lactobacillus delbrueckii
- Lactobacillus helveticus
- Lacticaseibacillus casei
- Lactobacillus gasseri
- Lactiplantibacillus pentosus
- Lactobacillus acidophilus
- Saccharomyces boulardii
- Lentilactobacillus kefiri
- Alkalihalobacillus clausii
- Metabacillus indicus



Follow Recommendations

- Bifidobacterium longum
- Bifidobacterium adolescentis
- Bifidobacterium breve
- Lacticaseibacillus rhamnosus
- Limosilactobacillus fermentum
- Bacillus subtilis



Follow your Current Diet

- Bifidobacterium bifidum
- Lacticaseibacillus paracasei
- Lactiplantibacillus plantarum
- Levilactobacillus brevis
- Lactobacillus johnsonii
- Saccharomyces cerevisiae
- Akkermansia muciniphila
- Leuconostoc mesenteroides
- Weizmannia coagulans
- Enterococcus durans
- Ligilactobacillus salivarius
- Streptococcus thermophilus



Pathogen Characterization

Category Tag Non-Ideal

Sova Health identifies and characterizes many pathogens commonly known to cause gut infections and other health issues. These pathogens are reported with "indicative tags", which can be interpreted as described below.

This is not a diagnostic and are not correlated clinically with cfu/ug. Know More about "Pathogen Characterization" within the FAQ Section.



Nothing to Worry Please follow recommendations and if any symptoms present then correlate clinically and

Species	Species
Bacterial Pathogens / Primary Pathogens	Opportunistic Bacteria
Campylobacter jejuni	Bacillus cereus 💢
Clostridioides difficile	Enterococcus faecalis 💢
Escherichia coli	Enterococcus faecium 💢
Helicobacter pylori	Listeria monocytogenes
Salmonella enterica	Pseudomonas aeruginosa 😮
Shigella dysenteriae	Staphylococcus aureus
Vibrio cholerae	Staphylococcus epidermidis
Yersinia enterocolitica	Staphylococcus saprophyticus
Potential Autoimmune Triggers	Streptococcus agalactiae
Klebsiella pneumoniae	Streptococcus pneumoniae
Mycobacterium avium	Worms
Proteus mirabilis	Giardia intestinalis
Citrobacter freundii	Necator americanus
Fusobacterium nucleatum	Trichuris trichiura
	Ancylostoma duodenale
	Ascaris lumbricoides

Name:

Sample Received Date:



Species		Species	
Protozoa		Fungi / Yeast	
Blastocystis hominis	8	Candida albicans	①
Chilomastix mesnili	8	[Candida] glabrata	①
Cryptosporidium	①	Candida tropicalis	8
Dientamoeba fragilis	8	Candida parapsilosis	8
Endolimax nana	8	Pichia kudriavzevii	8
Entamoeba coli	8	Aspergillus fumigatus	8
Entamoeba histolytica	8	Aspergillus flavus	8
Pentatrichomonas hominis	8	Aspergillus niger	8
Dysbiotic / Overgrowth Bacteria		Aspergillus terreus	①
Citrobacter freundii	8	Aspergillus nidulans	8

Disclaimer:

- 1. This is not a diagnostic report. This is not a microbiology (culture based) report.
- 2. We quantify these pathogens using sequencing-based method, and hence represent quantity only as "% abundances" of these pathogens. Also, the "indicative tags" does not represent standard scientific notation such as colony forming units per gram of stool (CFU/g).
- 3. Please correlate clinically.



Antibiotic Resistance

Category Tag



Some bacteria are known to possess genes that can lead to resistance to antibiotics. Our algorithm based output provides information on possible antibiotic resistance based on the genomic analysis of the sample. This is not a microbiological assay based output and hence clinical validation is necessary.

Antibiotic Name		Antibiotic Name	
Amikacin	Susceptible	Ceftriaxone	Susceptible
Aminocoumarin	Susceptible	Cephalothin	Susceptible
Amoxicillin	Susceptible	Cephamycin	Susceptible
Amoxicillin+Clavulanic_Acid	Susceptible	Ciprofloxacin	Susceptible
Ampicillin	Susceptible	Clindamycin	Susceptible
Ampicillin+Clavulanic_Acid	Susceptible	Colistin	Susceptible
Avilamycin	Susceptible	Dalfopristin	Susceptible
Azithromycin	Susceptible	Diaminopyrimidine	Susceptible
Aztreonam	Susceptible	Doxycycline	Susceptible
Benzalkonium_Chloride	Susceptible	Elfamycin	Susceptible
Bicyclomycin	Susceptible	Ertapenem	Susceptible
Bleomycin	Susceptible	Erythromycin	Susceptible
Carbapenem	Susceptible	Florfenicol	Susceptible
Carbomycin	Susceptible	Fosfomycin	Susceptible
Cefepime	Susceptible	Fusidic_Acid	Susceptible
Cefixime	Susceptible	Gentamicin	Susceptible
Cefotaxime	Susceptible	Glycylcycline	Susceptible
Cefotaxime+Clavulanic_Acid	Susceptible	Hygromycin	Susceptible
Cefoxitin	Susceptible	Imipenem	Susceptible
Ceftazidime	Susceptible	Isoniazid	Susceptible
Ceftazidime+Avibactam	Susceptible	Kanamycin	Susceptible



Antibiotic Name		Antibiotic Name	
Kasugamycin	Susceptible	Spectinomycin	Susceptible
Lincomycin	Susceptible	Spiramycin	Susceptible
Lincosamide	Susceptible	Streptomycin	Susceptible
Linezolid	Susceptible	Streptothricin	Susceptible
Meropenem	Susceptible	Sulfamethoxazole	Susceptible
Methicillin	Susceptible	Teicoplanin	Susceptible
Minocycline	Susceptible	Telithromycin	Susceptible
Monobactam	Susceptible	Temocillin	Susceptible
Mupirocin	Susceptible	Tetracenomycin	Susceptible
Nalidixic_Acid	Susceptible	Tetracycline	Susceptible
Nitrofuran	Susceptible	Thiostrepton	Susceptible
Nitroimidazole	Susceptible	Tiamulin	Susceptible
Oleandomycin	Susceptible	Ticarcillin	Susceptible
Penicillin	Susceptible	Ticarcillin+Clavulanic_Acid	Susceptible
Phenicol	Susceptible	Tigecycline	Susceptible
Piperacillin	Susceptible	Tobramcyin	Susceptible
Piperacillin+Tazobactam	Susceptible	Tobramycin	Susceptible
Pleuromutilin	Susceptible	Triclosan	Susceptible
Pristinamycin_la	Susceptible	Trimethoprim	Susceptible
Pristinamycin_lia	Susceptible	Tylosin	Susceptible
Quinupristin	Susceptible	Vancomycin	Susceptible
Quinupristin+Dalfopristin	Susceptible	Viomycin	Susceptible
Rhodamine	Susceptible	Virginiamycin_M	Susceptible
Rifampin	Susceptible	Virginiamycin_S	Susceptible
Rifamycin	Susceptible	Zorbamycin	Susceptible



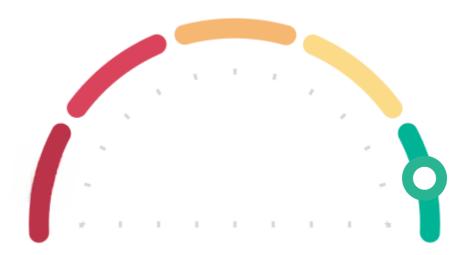
Microbiota Recovery Potential Post Antibiotic Course

Category Tag



Antibiotics are known to disrupt the microbiota ecosystem dramatically. Research suggest that recovery of the microbial ecosystem may be dependent on few species of bacteria among other factors. Our proprietary matrix and algorithm-based output predicts the microbiota recovery potential after a course of antibiotics. Know More about "Microbiota Recovery Potential" within the FAQ Section.

Poor potential to recover to a good microbiota
Good potential to recover to a good microbiota



Please Note:

This is not a diagnostic conclusion and clinical relevance is yet to be ascertained



SCFA Production Potential

Category Tag Non-Ideal

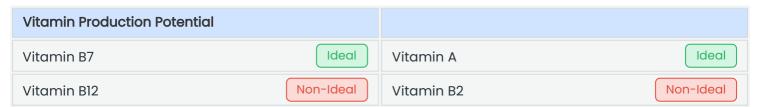
Short Chain Fatty Acids improve the gut health through a number of local effects, ranging from maintenance of intestinal barrier integrity, mucus production, and protection against inflammation. Our proprietary algorithms based output suggests the following status of SCFA production in your gut based on your gut microbiota profile.



Vitamin Production Potential

Category Tag Average

The gut microbiota produce a variety of vitamins. Our proprietary algorithms based output suggests the following status of vitamin production in your gut based on your gut microbiota profile. Please follow your clinician, nutritionist's advice.



Neurotransmitters

Category Tag

Gut microbiome produce neurotransmitters such as serotonin, dopamine and GABA, all of which play a key role in mood and other brain functions. Our proprietary algorithms based output suggests the following status of neurotransmitter production in your gut based on your gut microbiota profile. This has not been clinically validated.



Please Note: * Tryptophan is a precursor of many neurotransmitters.

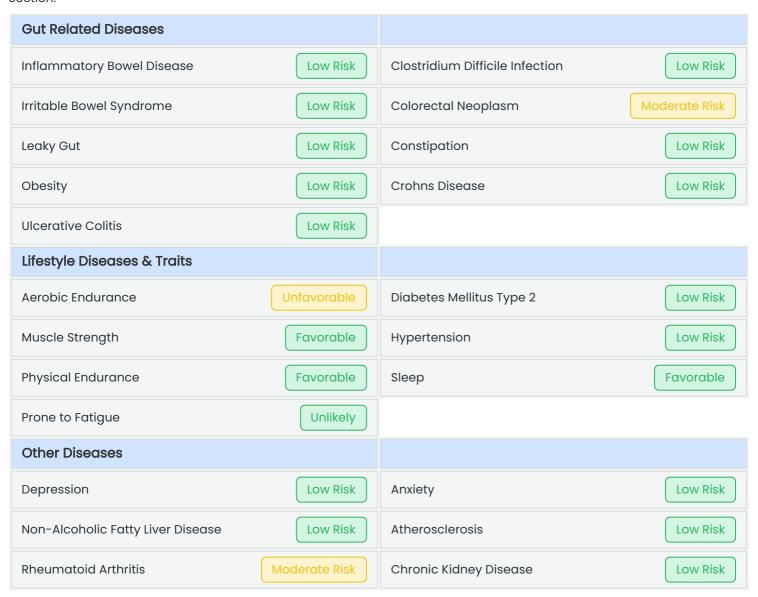
Name: Sample Received Date:



Propensity to Disease Development

Category Tag Above Average

The disease susceptibility index is based on our patent pending algorithm and matrix. Briefly, microorganisms in the gut are linked to various diseases. We have developed technology to assess the vulnerability of an individual to various diseases based on the gut microbiota profile. Know More about "Propensity to Disease Development" within the FAQ Section.



Disclaimer:

This is not a diagnostic report, but an algorithm-based susceptibility score based on the gut microbiota profile. Please correlate clinically. This indicates only susceptibility and not actual disease, hence this does not mean that individuals with diseases under low risk category will not clinically manifest the diseases or individuals with high disease risk will clinically manifest those diseases, as there are many factors apart from the gut microbiota that may result in the disease outcome.

Name:

Sample Received Date:



Nutritional Report



3 Phase (12 Week) Nutritional & Dietary Recommendation



Dietary Recommendations

Our approach to restore the gut balance is based on a three stage strategy:



Phase 1

Restoring your gut microbiome - 2 Weeks

Involves restoration or resetting of your gut microbiome, where we minimize the composition and abundance of pathogenic or opportunistic microorganisms, to create a gut environment ideal for beneficial microorganisms to grow in Phase 2. This phase requires strict changes in your diet for a short period of time and supplementation with anti-inflammatory foods, natural antibiotics, and through restriction of selected inflammatory foods.



Phase 2

Rebuilding your microbiome - 8 Weeks

Involves rebuilding of your healthy gut microbiome, through re-inoculation and replacement with mostly beneficial microorganisms. We achieve this through incorporation of prebiotics and probiotics, via natural dietary sources and commercially available supplements. This lasts for up to 10th week of your diet plan (a total of 8 weeks), which ensure the complete restoration of your gut microbiota.



Phase 3

Maintaining the healthy gut - 2 Weeks

Largely involves a streamlined method for sustaining the healthy gut microbiome built during phase 2. These dietary, prebiotic and probiotic recommendations can be adopted for long term sustenance, spanning up to 2 weeks of your diet plan.

All 3 phases have a total of 6 food categories, each containing a list of foods and a frequency tag. We have used a total of 4 frequency tags that indicates how frequently you can include a specific food in your meal plan.

an be consumed everyday [in 1 meal/day]

once in 3 days [in 1 meal/3 days]

can be consumed every alternate day [in 1 meal/2 days]

Avoid the consumption as much as possible

Please Note:

These recommendations are largely beneficial, with no or minimal negative impact on your health. Even though these dietary charts are evidence based recommendations, we would strongly suggest you to consult a physician/nutritionist, before implementing these in your lifestyle. This is specifically true about the extent of inclusion and exclusion of a specific food and for individuals who are either diabetic, hypertensive and/or having special dietary needs.

Name: Sample Received Date:

Page 16



Greens & Vegetables

Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Ash Gourd				Cucumber			(
Beet Root			(Drumstick			0
Bengal Gram				Fenugreek Leaves			0
Bitter Gourd			(Field Bean			(
Bottle Gourd			(French Beans			0
Brinjal			(Gogu Leaves			0
Broad Beans			0	Green Chillies			(
Broccoli				Green Gram			0
Cabbage			(Green Peas			(
Capsicum			(Horse Gram			©
Carrot							©
Cauliflower				🥻 Knol			
Chickpeas				Ladies Finger			0
Cho Cho			(Moth Bean			0
Cluster Beans				Mung Bean			0
© Cowpea		(0	(



Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Onion			(Snake Gourd			0
Pigeon Pea	0		(Spinach			(
Pointed Gourd	0		©	Sweet Corn			(
Potato			©	Sweet Potato			(
Pumpkin			0	Tinda	0		(
Radish	((Tomatoes	0		(
Ridge Gourd	0		(🍏 Yam	0		(

Cereals, Herbs & Condiments

Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Almond			0	Coriander Leaves			0
Asafoetida			©	Coriander Seeds			©
Cardamom	0		<u></u>	Cumin Seeds			(
Cashew Nut	0		0	Curry Leaves			(
Cloves			0	L Dates			0
Coconut			(Fenugreek Seeds			0
Coconut Oil	<u></u>	<u></u>	©	Finger Millet		O	

Name:

Sample Received Date:



Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Garlic Garlic			(Pistachio Nuts			(
Ghee Ghee	0		0	Poppy Seeds			
Ginger			0	Red Chilli Powder			0
Ground Nut				Rice Bran Oil			0
Honey				Rice Flakes			(
Jaggery			(Rice Puffed			
Kodo Millets			0	Semame Oil			
Little Millets			0	Sesame Seeds			(
Maize Maize			0	§ Shalgam			(
Mint Leaves				Sunflower Oil			(
Mustard Oil			(Sunflower Seeds			(
Mustard Seeds				Turmeric Powder			(
Olive Oil				Walnut			(
Palm Oil	0			Wheat			
Pearl Millet			(Wheat Flour			
Pepper			©	White Rice			©



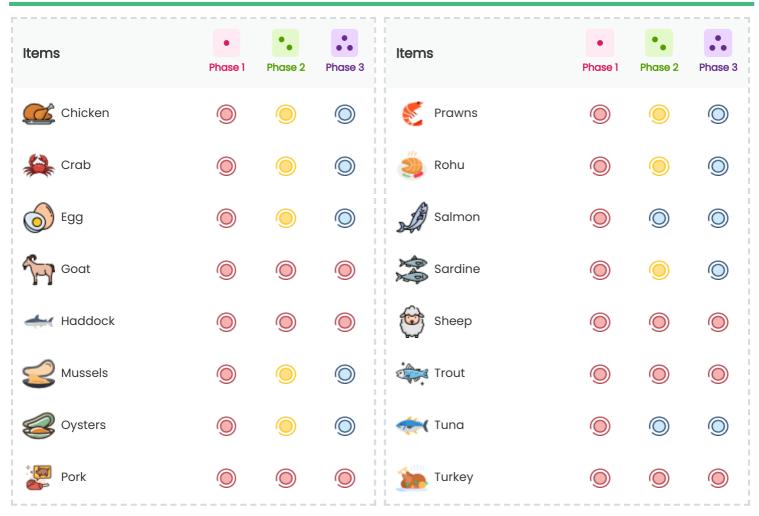
Fruits

Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Apple			©	Mosambi			(
Banana			0	Muskmelon			(
Custard Apple			(Orange			(
k Fig			(Papaya			<u></u>
Goosberry			0	Pear Pear			
Grapes			0	Pineapple			
Guava			(Pomegranate			
Jack Fruit			(Raisins			
Kala Jamun			(Sapota			<u></u>
Kokum			0	Strawberry			
Lychee				Watermelon			
Mango Mango				Wood Apple			(

Egg & Meat

Items	Phase 1	Phase 2	Phase 3	Phase 1	Phase 2	Phase 3
Beef			Catla			(





Milk & Fermented Products

Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Butter Milk			©	Kombucha			(
Cheese			0	Panner Panner			
Soy Products				Sauerkraut			
Kefir			(Shrikhand			
Kimchi			©	Yogurt			(



Processed Foods

Items	• Phase 1	Phase 2	Phase 3	Items	• Phase 1	Phase 2	Phase 3
Artificial Sweeteners			(Ice Cream			(
Bakery Breads			(Milk Chocolate			(
Burger				Noodles			(
Cake			(Pasta			(
Cookies			(Pastry			(
Crackers			(Pizza			(
Dark Chocolate			(Rolls			(
French Toast			(Sandwich			(
Garlic Bread			(Taco			(

Drinks & Beverages



Name:

Sample Received Date:



Supplements

Probiotics

Probiotics are a set of beneficial microorganisms that help you metabolize the food you eat and have significantly positive impact on your overall gut health. Consuming foods or supplements rich in these probiotics will aid in restoring and maintaining a healthy gut in the long run. Below we have listed of probiotics species along with one example of its natural source.

Bifidobacterium infantis VIII-240	Yogurt	Lentilactobacillus kefiri Kefir & Cheese
Limosilactobacillus reuteri	Kefir	Alkalihalobacillus clausii Fruit Juices
Lactobacillus delbrueckii	Greek yogurt	Metabacillus indicus Soyabean Natto
Lactobacillus helveticus	Italian Cheeses	Bifidobacterium animalis Fermented dairy products
Lacticaseibacillus casei	Fermented milk	Limosilactobacillus fermentum Fruits
Lactobacillus gasseri	Kimchi	Bacillus subtilis Tempeh & Miso
Lactiplantibacillus pentosus	Fermented dairy	Bifidobacterium breve Fermented Vegetables
Lactobacillus acidophilus	Fermented foods	Lacticaseibacillus rhamnosus Butter milk
Saccharomyces boulardii (nom. inv	al.) Kefir	Bifidobacterium longum Buffalo milk

Also, these supplements are available for purchase through online retailers. Example of a probiotic supplement include RychBiome.

Prebiotics

PREBIOTICS are a special form of dietary fibers that act as fertilizers for the probiotics in your gut (listed above). Below we have listed a set of prebiotics along with one example of its natural source.

Isomalto-oligosaccharides	Honey	Hemicellulosic oligosaccahride	Garlic
Arabinoxylan oligosaccharides	Cluster beans	Inulin	Onions
Dextran	Artichokes	Lactulose	Oats
Fructo-oligosaccharides	Sugar cane	Mannose and Galactose	Yogurt
Galacto-oligosaccharides	Bamboo shoots	Resistant starch	Rice bran

Also, these supplements are available for purchase through online retailers. Example of a Prebiotic supplement include Prebiotic D - a natural fiber to promote colon and gut health.

Name: Sample Received Date:

Page 23





A exhaustive collection of all the terms & frequently asked questions



Disease Description

Colorectal Neoplasm

Gut bacteria like Escherichia coli, Bacteroides fragilis Enterococcus etc., produces toxins that are reported to be involved in the development of cancers. Specifically, these toxins are called enterotoxigenic (in simpler terms - toxic to genes), which means these toxins can directly damage the DNA resulting in activation of uncontrollable cell proliferation, which eventually leads to cancer.

Non-Alcoholic Fatty Liver Disease

Microbiota promote the absorption of monosaccharides from the gut, thereby triggering lipogenesis in the liver. Dysbiosis is associated with reduced synthesis and secretion of fasting-induced adipocyte factor a powerful metabolism and adiposity regulator belonging to the angiopoietin-like protein family in enterocytes, which results in increased activity of lipoprotein lipase (LPL), responsible for the secretion of triglycerides (TG) from very low-density lipoprotein, eventually resulting in the augmented uptake of fatty acids and accumulation of TG in the adipocytes and leading to NAFLD.

Inflammatory Bowel Disease

The abundant bacteria in the gut needs complex polysaccharides to survive, which if absent in your gut, starts eating the mucus layer shielding the colon lining which leads to many opportunistic infections aided by Roseburia and Actinobacteria, which will further activate several enteric pathogens and triggers inflammatory pathways and causes inflammation in walls of gastrointestinal tract.

Hypertension

The fermentation of dietary fiber by gut microbiota generates short-chain fatty acids (SCFAs) like acetate, propionate, and butyrate. Butyrate is used by colonocytes (cells of the colon) to maintain the intestinal barrier and decrease local inflammation, while small amounts are transported with acetate and propionate to the liver through the portal vein. Most of the propionate is metabolized by the hepatocytes (liver cells), whereas acetate and remaining proportions of propionate and butyrate are released into the systemic circulation, they can reach organs involved in the regulation of blood pressure and help to maintain or reduce the blood pressure.

Crohns Disease

Increased abundance of Enterobacteriaceae activates other enteric pathogens that trigger a set of inflammatory pathways, causing irritation of your gut. For instance, Sulfate reducing bacteria inflame the lining of the gut, while Clostridium and certain fungi trigger the factors that decrease anti-inflammatory bacteria (Lactobacillus, Faecalibacterium), cumulatively triggering or inducing to Crohn's disease.

Ulcerative Colitis

Bifidobacterium and Lactobacillus maintains the gut mucosal integrity through the expression of many tight junction encoding genes (connections that bridge and hold the cells). Reduction of Bifidobacterium results in marked reduction in the tight junction expression, in turn reducing the gut integrity. Parallelly, increased abundance of E. coli activates bacterial TLR2 ligands and other downstream signaling, contributing to colitis pathology.



Clostridium Difficile Infection

A dysbiotic microbiota can result in the loss of colonization resistance due to changes in the structural and/or metabolic environment. The loss of specific community members potentially affects the levels of microbial and host-generated metabolites, resulting in a different functional state that promotes spore germination and vegetative outgrowth. A dysbiotic microbiota may also result in an imbalanced immune response through the loss of immune regulation and a proinflammatory state, both of which may affect disease development. Toxin production by vegetative C. difficile can stimulate the production of inflammatory cytokines, neutrophils, and antitoxin antibodies.

Prone to Fatigue

Tiredness can be a normal response to physical and mental activity. In most normal individuals are quickly relieved from regular fatigue (usually in hours to about a day, depending on the intensity of the activity). However, extreme tiredness resulting from physical exertion defines the state of fatigue. Twitch muscle fibers maintains the contractile responses while performing different motor tasks, and is directly associated with fatigue. Higher abundance of Lactobacillus acidophilus, and supplementation with multi-strain probiotic of Lactobacillus and Bifidobacterium have shown better contractile responses and hence minimizing fatigue.

Atherosclerosis

Trimethylamine-N-oxide (TMAO) is a product of microbial-human co-metabolic pathway, which is derived from dietary (food based) choline and carnitine and converted to trimethylamine (TMA) by anaerobic bacteria residing within the lumen of the gut. TMA is then oxidized by a liver enzyme to TMAO. This TMAO is known to be a pro-atherogenic compound, which is directly implicated in the development of plaques inside the arteries. A dysbiosis in the intestinal microbiota, resulting in increased anaerobic bacteria, is thought to contribute to the chronic inflammatory state, production of TMAO and eventually atherosclerosis.

Chronic Kidney Disease

Delivery of undigested protein to the colon results in the proliferation of proteolytic bacteria. These bacteria ferment proteins and amino acids to generate potential uremic toxins, including p-cresol, indoxyl sulfate and trimethylamine N-oxide. Impaired gut barrier function allows translocation of uremic toxin into systemic circulation. This contributes to chronic kidney disease (CKD) progression.

Diabetes Mellitus Type 2

Diabetes mellitus is associated with chronic (slow developing) low-grade inflammation, and gut microbes have been shown to contribute to this. Lipopolysaccharides (LPS), which are components of the cell walls of Gramnegative bacteria, play a key role in the development of such chronic inflammation, resulting insulin resistance in fat, liver and muscle cells, eventually leading to Diabetes Mellitus Type 2.

Constipation

There are two important luminal (gut) factors, modulated by the gut microbiota, which maintains smooth muscle contraction and balanced bowel movements. The factors include short chain fatty acids (SCFAs) and bile acids. The absence of SCFAs due to low-fiber diet inhibit mucin secretion by intestinal goblet cells, reduce stool volume by stimulating water and electrolyte absorption, and inhibit smooth muscle contraction in the colon, causing imbalanced bowel movements/constipation.



Obesity

Fermentation of polysaccharides by gut microbes results in the production of short chain fatty acids (butyrate, propionate, acetate), carbon dioxide (CO2), and hydrogen (H2). Butyrate is an important energy substrate for the colonic epithelium. Acetate and propionate can be taken up by the liver and used as substrates for lipogenesis and gluconeogenesis. This result in increased availability of calories and adiposity to the host leading to obesity.

Rheumatoid Arthritis

The human gut microbiota and their metabolites can regulate immune cells and cytokines via epigenetic modifications. For example, short-chain fatty acids (SCFAs) produced by gut microbiota promote the differentiation of natural T cell into Treg cells by suppressing histone deacetylases (HDACs). Thus, resulting bacterial metabolites cause aberrant immune responses via epigenetic modifications, leading to Rheumatoid arthritis.

Colorectal Neoplasm

Gut bacteria like Escherichia coli, Bacteroides fragilis Enterococcus etc., produces toxins that are reported to be involved in the development of cancers. Specifically, these toxins are called enterotoxigenic (in simpler terms - toxic to genes), which means these toxins can directly damage the DNA resulting in activation of uncontrollable cell proliferation, which eventually leads to cancer.

Depression

Depression is a syndrome (a group of symptoms) characterized by sad or irritable mood exceeding normal sadness or grief, both in its intensity and duration. On one end, specific gut microbes (like Blautia, Clostridium, Klebsiella etc.) are known to be higher in individuals with depression, which increase inflammation causing biochemicals that cause depression. On the other end, certain beneficial microbes (like Lactobacillus rhamnosus, Bifidobacterium breve etc.) are known to increase serotonin activity, and decrease norepinephrine and dopamine activities, overall reducing symptoms of depression.

Anxiety

It is defined as intense, excessive and persistent worry and fear about everyday situations. Anxiety is mostly induced by stress that triggers immune cells to produce biochemicals (like Interleukin-6) that cause symptoms of anxiety. Several gut microorganisms, like species of Bifidobacterium and other belonging to group of Bacteroides, release tryptophan, a precursor of neurotransmitter serotonin and Bacillus, Enterococcus species produce norepinephrine, and dopamine. All these three biochemicals together reduce the symptoms of anxiety by increasing the action of a brain chemical called gamma-aminobutyric acid (GABA). Hence, gut microbiome has emerged as a key factor to manage anxiety.

Physical Endurance

The ability to perform strenuous, large-muscle exercise or activities for a prolonged period is termed as physical endurance. High endurance sports / training is accompanied with production of oxidative stress, due to over production of reactive oxygen species (ROS) and reactive nitrogen species (RNS). Studies have observed that high abundance of Lactobacillus paracasei, Bifidobacterium sp., Lactobacillus rhamnosus and Faecalibacterium prausnitzii, in the gut aids in management of oxidative stress and hence positively correlated with endurance.



Aerobic Endurance

Aerobic endurance is the ability to sustain an aerobic effort over time, such as distance running or cycling. Aerobic endurance maintains the ability of the cardiovascular system to deliver oxygen to working muscles and the ability of the muscles to utilize that oxygen. The most common quantification of endurance is the maximal rate of oxygen uptake (VO2max). High abundance of Faecalibacterium prausnitzii has been associated with higher aerobic endurance.

Muscle Strength

Muscular strength is a component of fitness that is necessary for optimal well-being and quality of life. In general, physical endurance is directly correlated to muscle strength. Smooth muscle works most efficiently, and needs much less energy for its activity and they display considerable plasticity when healthy and young. However, these cells can switch to largely non-contractile mode in response to inflammatory stimuli, diet or other factors, which result in loss of plasticity and in turn contractibility. Supplementation with multi-strain probiotic of Lactobacillus and Bifidobacterium have shown better contractile responses and hence better muscle strength.

Leaky Gut

The occurrence of harmful bacteria in our gut may cause a leaky gut syndrome, which happens due to the high permeability of the intestinal walls, causing leakage of undigested food particles, bacteria, and many other substances into the nearby tissues. The leaky gut syndrome is directly connected with several health problems, such as chronic fatigue, Stomach aches, Insomnia, Inflammatory Bowel Syndrome, Constipation, Diarrhoea, Headaches, Depression, Cardiac problems, Pancreatic illness, etc. By populating friendly bacteria in your gut for optimal health, in turn through foods for a healthy gut, ensures the best way to restore your gut flora. This also ensures recovery to better gut health, specifically via probiotics which heal leaky gut to a great extent.

Sleep

The researchers have observed that gut microbiome plays a significant role in circadian clock along with other phenotypic characteristics, like, immunity, metabolism, and others. The circadian rhythm is our inner clock, which controls our body's energy disbursement, hunger, and snooze. We usually get about seven hours of sound sleep every night. In the morning, when we wake up, our body warms up to conduct daily chores. To run our body, we need energy, and energy comes from the food we eat during the day. At night, our body needs rest to rewind, so we fast and go to sleep. Gut microbiome resonates with this bodily rhythm. The scientific world now accepts the robust connection between sleep and intestinal wellbeing. A good quality night sleep allows more flourishing and better functioning gut microbiome and vice versa. Gut flora follows the rhythm by secreting specific molecules at certain times of the day. At night, secretion of factors responsible for energy metabolism, DNA repair, and proliferation occurs. During daytime, flora harbouring in the gut releases molecules essential for their colonization. Neurotransmitters like serotonin and GABA secreted by brain control our sleep-wake cycle. Astoundingly, certain intestinal bacteria including, Turicibacter sanguinis and Clostridia sp., release specific signalling molecules that trigger the production of serotonin. By modulating serotonin levels, the gut microbiome can interfere or improve our sleep pattern.



Evidences

- Belkaid Y, Hand TW. Role of the microbiota in immunity and inflammation. Cell. 2014;157(1):12141.
- Bernstein CN, Forbes JD. Gut Microbiome in Inflammatory Bowel Disease and Other Chronic ImmuneMediated Inflammatory Diseases. Inflamm Intest Dis. 2017;2(2):116123.
- Bhattarai Y, Muniz pedrogo DA, Kashyap PC. Irritable bowel syndrome: a gut microbiotarelated disorder?. Am J Physiol Gastrointest Liver Physiol. 2017;312(1):G52G62.
- Bouter KE, Van raalte DH, Groen AK, Nieuwdorp M. Role of the Gut Microbiome in the Pathogenesis of Obesity and ObesityRelated Metabolic Dysfunction. Gastroenterology. 2017;152(7):16711678.
- Engevik MA, Versalovic J. Biochemical Features of Beneficial Microbes: Foundations for Therapeutic Microbiology. Microbiol Spectr. 2017;5(5)
- Evrensel A, Ceylan ME.The GutBrain Axis: The Missing Link in Depression. Clin Psychopharmacol Neurosci. 2015;13(3):23944.
- Guarner F, Khan AG, Garisch J, et al. World Gastroenterology Organisation Global Guidelines: probiotics and prebiotics October 2011. J Clin Gastroenterol. 2012;46(6):46881.
- Han S, Gao J, Zhou Q, Liu S, Wen C, Yang X. Role of intestinal flora in colorectal cancer from the metabolite perspective: a systematic review. Cancer Manag Res. 2018;10:199206.
- Jiang HY, Zhang X, Yu ZH, et al. Altered gut microbiota profile in patients with generalized anxiety disorder. J Psychiatr Res. 2018;104:130136.
- Jie Z, Xia H, Zhong SL, et al. The gut microbiome in atherosclerotic cardiovascular disease. Nat Commun. 2017;8(1):845.
- Karlsson FH, Fåk F, Nookaew I, et al. Symptomatic atherosclerosis is associated with an altered gut metagenome. Nat Commun. 2012;3:1245.
- Kedia S, Rampal R, Paul J, Ahuja V. Gut microbiome diversity in acute infective and chronic inflammatory gastrointestinal diseases in North India. J Gastroenterol. 2016;51(7):66071.
- Krych Ł, Nielsen DS, Hansen AK, Hansen CH. Gut microbial markers are associated with diabetes onset, regulatory imbalance, and IFN_γ level in NOD mice. Gut Microbes. 2015;6(2):1019.
- Li J, Zhao F, Wang Y, et al. Gut microbiota dysbiosis contributes to the development of hypertension. Microbiome. 2017;5(1):14.
- Ma N, Guo P, Zhang J, et al. Nutrients Mediate Intestinal BacteriaMucosal Immune Crosstalk. Front Immunol. 2018;9:5.
- Pérezcobas AE, Artacho A, Ott SJ, Moya A, Gosalbes MJ, Latorre A. Structural and functional changes in the gut microbiota associated to Clostridium difficile infection. Front Microbiol. 2014;5:335.
- Belkaid Y, Hand TW. Role of the microbiota in immunity and inflammation. Cell. 2014;157(1):12141.
- Bernstein CN, Forbes JD. Gut Microbiome in Inflammatory Bowel Disease and Other Chronic ImmuneMediated Inflammatory Diseases. Inflamm Intest Dis. 2017;2(2):116123.
- Bouter KE, Van raalte DH, Groen AK, Nieuwdorp M. Role of the Gut Microbiome in the Pathogenesis of Obesity and ObesityRelated Metabolic Dysfunction. Gastroenterology. 2017;152(7):16711678.



Frequently Asked Questions

1. Is Sova Health diagnostic report?

No, Sova Health is not a diagnostic report however the information provided can be used to take complimentary/supplementary measures along with standard treatment if needed. A lot of information contained in the report are actionable and provides guidance for living healthy!

2. What is Rych Index and how it can help?

Rych Index is a patent pending algorithm based intestinal health score developed by us. It tries to give a snapshot of the intestinal health with respect to the microbiota profile (microorganisms in the gut). It is not a diagnostic marker but can be used as an information to ascertain the gut health.

3. Is Rych Index only criteria for determining the gut health?

Rych index has been designed to take into consideration various gut microbiota characteristics, which in turn are known to influence the host health. However, this is an evolving research area and gut microbiota alone is not responsible of the complete gut health, although it plays a primary role. Genetics, gut architecture, gender, hormones, food, lifestyle etc. also play a role in defining the gut health.

4. Can "disease susceptibility" section be used as diagnostic?

No, disease susceptibility is a score-based prediction that is dependent on the microbiota profile. This is not a diagnostic assessment, but only a risk assessment. This can be used a guide for health. Preventive health check-ups can be performed if required.

5. Can pathogen characterization be used directly as indicator of pathogen load?

Pathogen characterization section uses bioinformatics tools to ascertain relative abundance of the various microbes. It is not based on culture assays and is not an indicator of absolute abundance of the microbes represented. However, this information can be used to correlate clinically and/or validated by other assays as may deem fit by the medical practitioner.

6. What is the "antibiotic recovery potential" section all about?

This is a unique score developed by us to provide an estimate of how well one's gut microbiota may recover post an antibiotic course. As it is known, antibiotics not only kills that pathogen in question but can also destroy other bacteria in the gut leading to short term to long term deleterious effects. Everyone takes different time to recover their gut microbiota post an antibiotic course. Our effort here is to provide a prediction of the potential of this recovery, post an antibiotic course. A lower score/potential means the person might need additional nutritional/supplemental support during or post an antibiotic course to recover faster and better.



7. What is foundation microbiota?

Foundation microbiota, also called as keystone species, are a set of organisms fundamental for the ecosystem to survive. These organisms help hold the system together and hence any perturbation in their abundance may have a deleterious effect on the overall ecosystem.

8. Is the nutritional recommendation personalized and can it cure my disease?

The nutritional recommendation is based on the gut microbiota profile of the individual. As the gut microbiota gets influenced by the food we eat, it is possible to modulate them by changing the food habit. Therefore, the microbiota profile based nutritional recommendation in this report tries to modulate the microbes in the gut to a balanced state (eubiosis) from a disbalanced or dysbiotic state. The nutritional recommendation in this report is disease agnostic, in other words it is not specifically targeted against any disease per se. However, if the balance is restored in the gut by following the nutritional recommendations, then there is a good chance that many of the clinical manifestations of various diseases that cropped up due to dysbiosis in the gut can be rectified.

9. Do I need to follow the nutritional recommendation for 3 months only?

Nutritional recommendations are designed in 3 phases for 3 months for better compliance. However, you may continue with the recommendations beyond 3 months till the time it is convenient for you.

10. What technology is used for making this report?

We use next generation sequencing or NGS. More specifically we use whole genome shotgun metagenomics approach that can profile all microbes including bacteria, viruses, fungi, helminths etc. We have our own curated databases and patent pending algorithms and interpretation engine that led to the generation of this unique report.

For more "Frequently Asked Questions" please visit <u>www.Sova.Health</u>



Disclaimer

- Throughout this Disclaimer (hereinafter referred to as "Disclaimer"), Leucine Rich Bio Private Limited is referred to as "We/Us/Our" and the person to whom the specimen belongs (including such person's guardian or any person acting on his/her behalf) shall be referred to as "You/Your".
- This is not a diagnostic report (hereinafter referred to as this "Report") and therefore should be used for Research Use Only (RUO) or Investigational Use Only (IUO) and should be interpreted or used exclusively by or under the guidance of a practitioner, including but not limited to, certified physicians, clinicians, dietitians, nutritionists, sports therapists nd such other persons in similar profession having appropriate validation to undertake such practice (from here on referred to as "Professional Practitioners"). It is imperative that any preventative or therapeutic measures taken, by placing reliance on this Report, for any of the diagnosis should be solely under the guidance of a "Professional Practitioner". In the event of You executing any preventative or therapeutic measures by virtue of practicing self-medication and/or undergoing diagnosis from persons other than Professional Practitioners, then We cannot be held responsible in any manner for any loss, liability, ounter-effect and so on suffered by You as a result of ignorance of this Disclaimer. Further, We shall not be held responsible for any misinterpretation by Your "Professional Practitioner" of this Report or for any other matter arising out of this Report.
- This Report's role is limited to providing insights of Your gut microbiome, with a general set of dietary recommendations and risk managements. General risk management strategies provided in Our Report are for information purpose only and in this regard, it is essential to understand that every person's resistance, immunity, sensitivity and response to medication is different and therefore not all general risk management strategies may be suitable to everyone. It is also essential to note that, while assessing Your Report and providing these recommendations, We assume that You are in a general state of good health, and do not consider Your past or existing health conditions and or any medication taken by You (either in the past or currently), even if You have provided Us with such information. Therefore, it is essential that, You consult a Professional Practitioners for detailed recommendations or risk managements that may be specific / customized for You. In other words, information contained in this Report is not intended to replace medical or professional advice offered by Professional Practitioners.
- We would like to bring it to Your notice that not all disease-associated microbial groups may have been identified, validated and recorded by the scientific community, and the clinical significance of many microbial groups are also not well understood. Hence, it should be noted that this analysis and this Report does not cover all clinically relevant microbes' that have been identified or reported till date. This Report is limited only to those variants within Your gut microbiome which has strong evidence of causing or contributing to a disease or a drug response or a metabolism related issue till date.
- We would also like to bring to Your attention that the microbiome sequencing data is being constantly updated both with new taxonomic groups and curation of old microbial databases. Hence, it is subject to revision-based updates, based on the latest scientific research. Therefore, it is important to note that it is possible that the interpretation of the results that have been reported herein may vary or be altered, subject to these revisions. Hence, We would recommend that You to undergo periodical reinterpretation of Your microbiome data that You possess, especially when a specific disease is confirmed through diagnosis or new symptoms arise, in the future.



- Microbiome information must always be considered in conjunction with other information about Your health, including, but not limited to, Your age, sex, ethnicity, lifestyle, bio-medical history, family health history and any other information that You may provide to the "Professional Practitioner". This is especially critical with respect to the pharmacogenomics data (therapies and drugs), where a person's response to various medications is determined by the above listed factors.
- We would like to bring to Your attention that very specific and rare microbial groups are not reliably detected by current sequencing methods or downstream analysis pipelines, hence they are not analyzed and interpreted within the current Report.
- Overall, Your reliance upon this Report is solely at Your own discretion. Adequate care should be exercised in using all health and medical related information and recommendations provided in this Report. We cannot be held responsible in any manner for non adherence by You to the terms and conditions contained in this Disclaimer. Further, We shall not be responsible for any findings in this Report and disclaims any responsibility for any errors, including but not limited to human error in reporting, and/or omissions by the sampler or agent either during collection of DNA samples (stool etc.,) or delivery of the DNA sample to Us. With respect to this Report or process undertaken to arrive at the findings reflected or reported in the Report, We make no warranties of any kind including, without limitation, the implied warranties as to its merchantability, fitness for a specific purpose, accuracy and non-infringement.

This report has been researched & developed by:







