

Casual Friday Series

# GI Assessments, Interventions, and Applications

A Biogenetix Clinical Presentation

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# Disclaimer

- *Information in this presentation is not intended, in itself, to diagnose, treat, reverse, cure, or prevent any disease. While this presentation is based on medical literature, findings, and text, The following statements have not been evaluated by the FDA.*
- *The information provided in this presentation is for your consideration only as a practicing health care provider. Ultimately you are responsible for exercising professional judgment in the care of your own patients.*

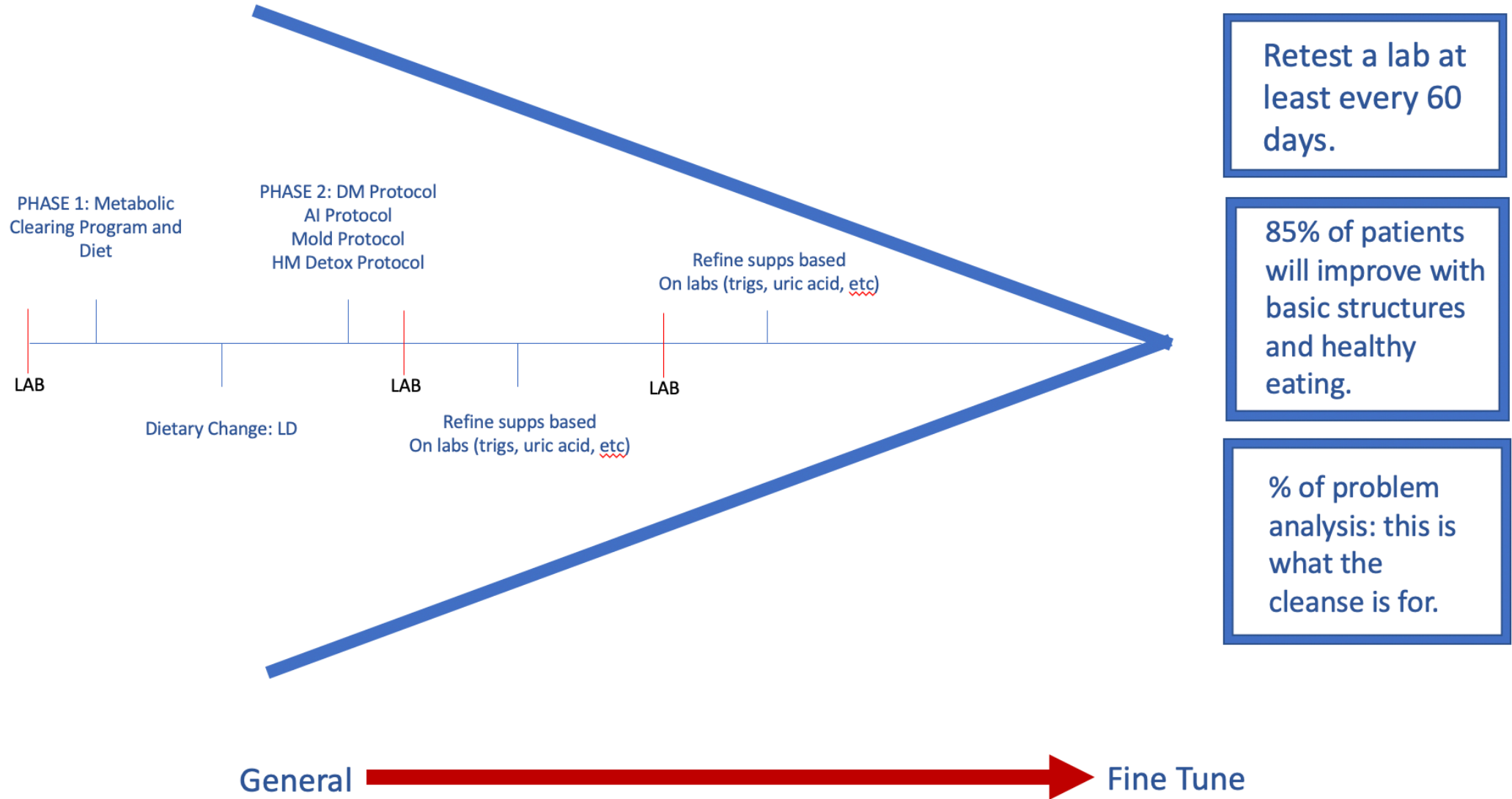




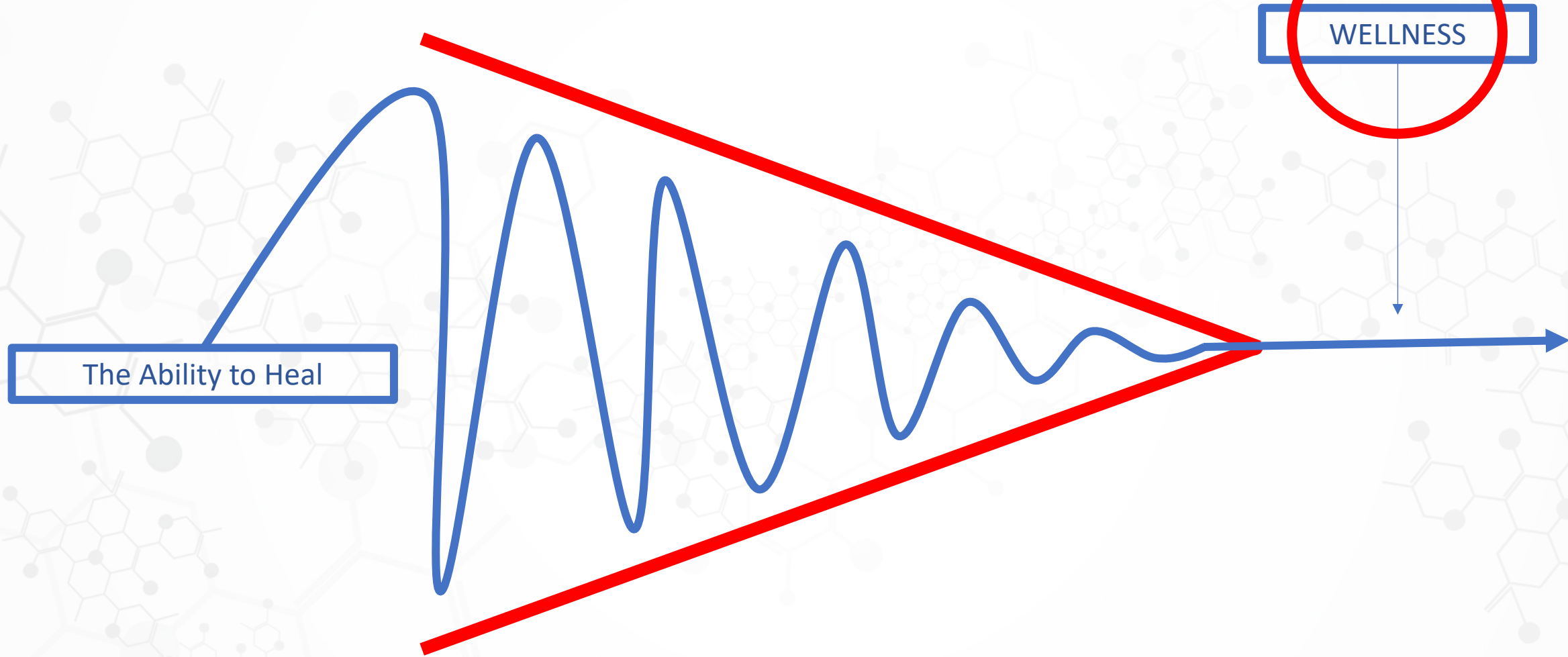
(Lifestyle + Genetics) x Time = Chronic Health IMPROVEMENT



# Supplement and Diet Protocols



# Building Protocols



The Ability to Heal

WELLNESS



[Int J Mol Sci.](#) 2015 Apr; 16(4): 7493–7519.

Published online 2015 Apr 2. doi: [10.3390/ijms16047493](https://doi.org/10.3390/ijms16047493)

PMCID: PMC4425030

PMID: [25849657](https://pubmed.ncbi.nlm.nih.gov/25849657/)

## Impacts of Gut Bacteria on Human Health and Diseases

[Yu-Jie Zhang](#),<sup>1</sup> [Sha Li](#),<sup>2</sup> [Ren-You Gan](#),<sup>3</sup> [Tong Zhou](#),<sup>1</sup> [Dong-Ping Xu](#),<sup>1</sup> and [Hua-Bin Li](#)<sup>1,\*</sup>

Manickam Sugumaran, Academic Editor

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Gut bacteria are an important component of the microbiota ecosystem in the human gut, which is colonized by  $10^{14}$  microbes, ten times more than the human cells. Gut bacteria play an important role in human health, such as supplying essential nutrients, synthesizing vitamin K, aiding in the digestion of cellulose, and promoting angiogenesis and enteric nerve function. However, they can also be potentially harmful due to the change of their composition when the gut ecosystem undergoes abnormal changes in the light of the use of antibiotics, illness, stress, aging, bad dietary habits, and lifestyle. Dysbiosis of the gut bacteria communities can cause many chronic diseases, such as inflammatory bowel disease, obesity, cancer, and autism. This review summarizes and discusses the roles and potential mechanisms of gut bacteria in human health and diseases.

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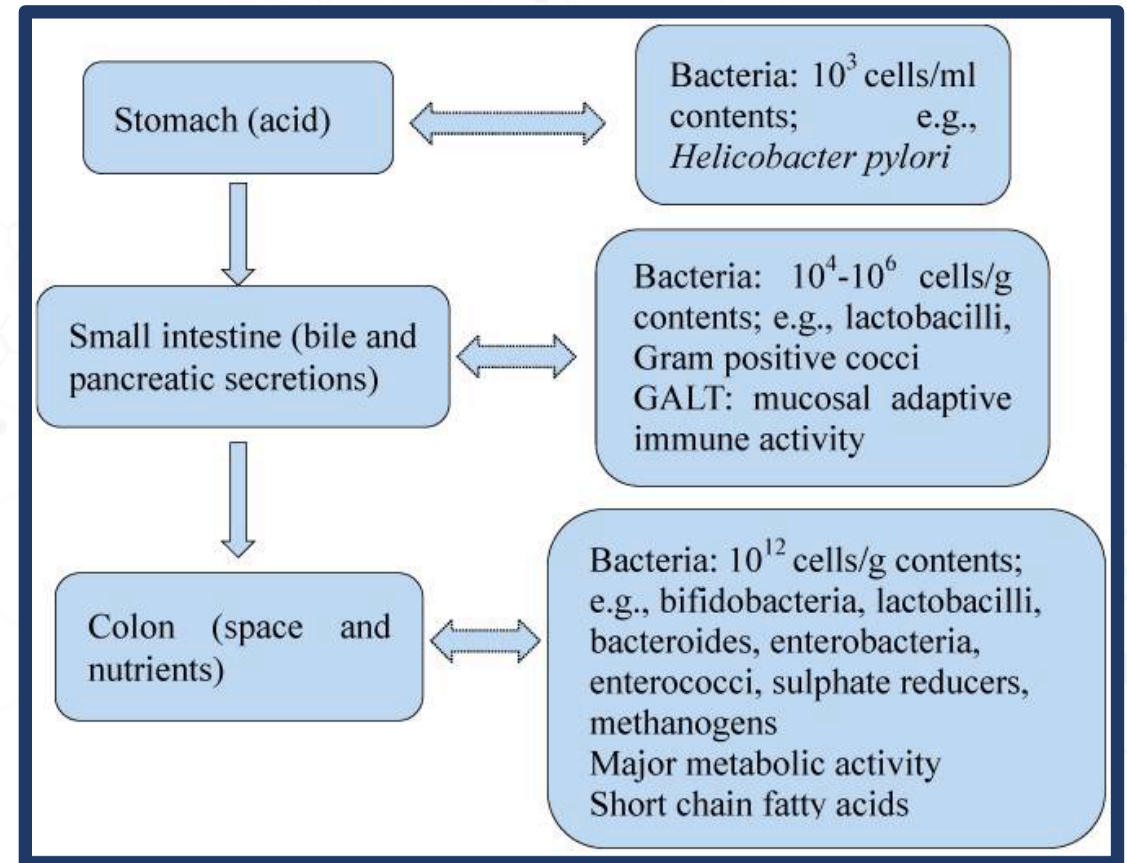
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stabilizes to a more adult-like profile around the age of one year, usually after the introduction of solid foods [4]. In addition, the composition of the gut bacteria community in the stomach and colon is distinctive, which is mainly due to different physicochemical conditions, such as intestinal motility, pH value, redox condition, nutrients, host secretions (e.g., gastric acid, bile, digestive enzymes, and mucus), and the presence of an intact ileocaecal valve [5]. Additionally, they can be influenced by many factors, such as the use of antibiotics, illness, stress, aging, bad dietary habits and lifestyle [5,6].



# Bacterial Impacts

- Supply Essential Nutrients
- Synthesize Vit K
- Digest Cellulose
- Promote Angiogenesis
- Promote enteric nerve function
- Reductive Reactions (PRE-tox?)
- Prevent antigen and pathogen invasion
- Immune homeostasis

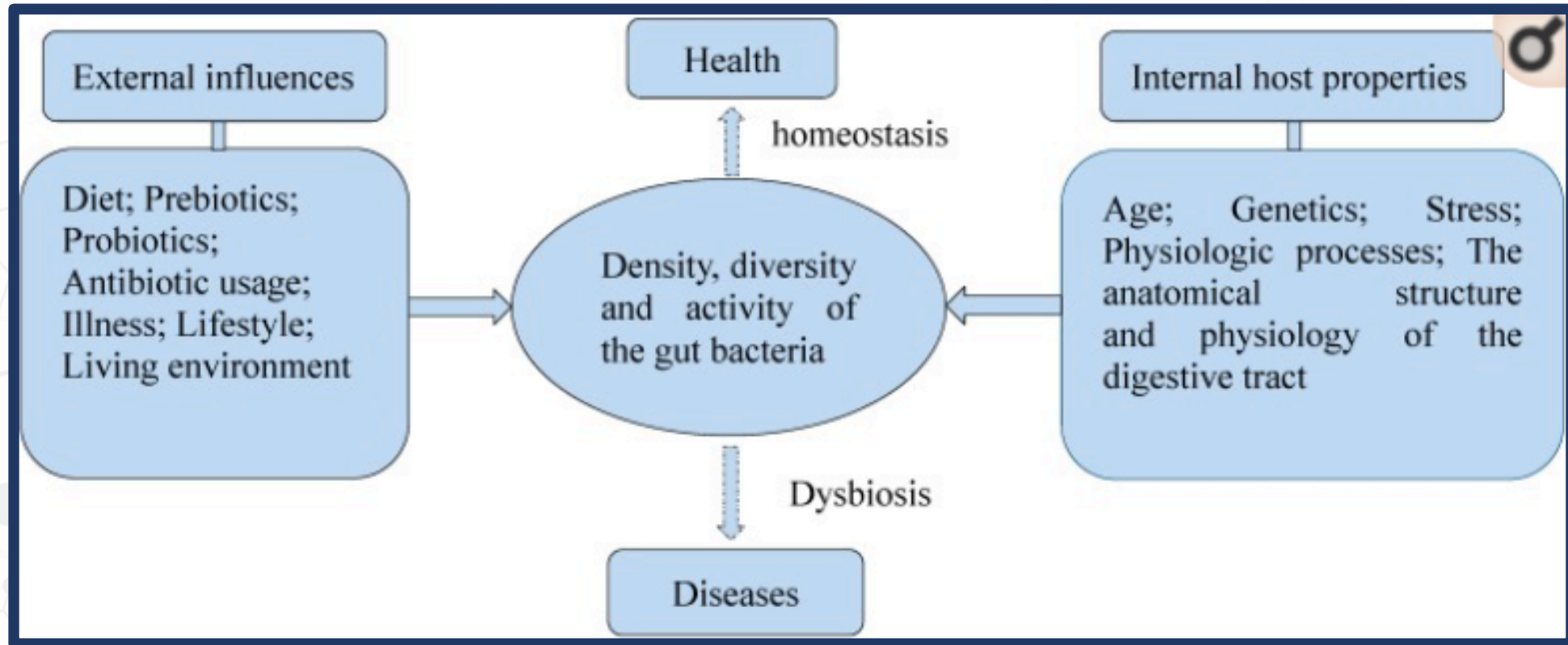


<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4425030/>





# Avoid or Adapt?



<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4425030/>



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### 3.2. Gut Bacteria and Obesity

Normal gut bacteria play an important role in diet-induced obesity, because germ-free mice have been reported to be thinner and did not become adipose when subjected to high-fat diet [66]. The high-fat diet altered the composition of bacteria to display higher levels of luminal *Firmicutes* and *Proteobacteria* and lower levels of *Bacteroidetes* [67], indicating that obesity may be associated with decreased diversity and changes in composition of the gut bacteria. Gut bacteria is an important determinant of susceptibility to obesity and related metabolic diseases. The ratio of *Firmicutes* to *Bacteroides* has been found to be correlated to body weight, with the ratio being higher in obese people [68]. Gut bacteria could also affect obesity by promoting chronic inflammatory status [69]. In addition, *Clostridium difficile* infections may be another possibility of causing obesity [70]. Gut bacteria may affect obesity through regulation of the microbiota-brain-gut axis by its metabolites. Overweight individuals have more faecal SCFAs than lean



# Condition Specific

- Obesity
- Diabetes, both type 1 and type 2
- Liver disease
- Pancreatic dysfunction (enzymatic)
- Heart Disease
- Cancer
- HIV
- Autism

Some examples of dysbiosis found in human diseases.

Disease	Model	Dysbiosis	Sample	References
Ulcerative colitis	Mice	↓ <i>Lactobacilli</i> ↑ <i>Clostridiales</i>	Colonic	[56]
	Mice	↑ <i>E. coli</i>	Colonic	[57]
	Humans	↓ <i>R. hominis</i> ↓ <i>F. prausnitzii</i>	Fecal	[58]
Crohn's disease	Humans	↓ <i>Bacteroides</i> ↓ <i>Bifidobacteria</i>	Fecal	[61]
Obesity	Mice	↓ <i>Bacteroides</i> ↑ <i>Firmicutes</i> ↑ <i>Proteobacteria</i>	Fecal	[67]

Rheumatic arthritis	Humans	↓ <i>Bifidobacteria</i> ↓ <i>Bacteroides fragilis</i>	Fecal	[127]
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## Functional Imbalance Scores

Key **<2** : Low Need for Support   **2-3** : Optional Need for Support   **4-6** : Moderate Need for Support   **7-10** : High Need for Support

	Need for Digestive Support	Need for Inflammation Modulation	Need for Microbiome Support	Need for Prebiotic Support	Need for Antimicrobial Support
	<b>MALDIGESTION</b>	<b>INFLAMMATION</b>	<b>DYSBIOSIS</b>	<b>METABOLIC IMBALANCE</b>	<b>INFECTION</b>
	<b>1</b>	<b>0</b>	<b>7</b>	<b>9</b>	<b>0</b>
<b>Biomarkers</b>	Fecal Fats ▲ Pancreatic Elastase ● Products of Protein Breakdown ●	Calprotectin ● Eosinophil Protein X ● Secretory IgA ● Occult Blood ●	Total Abundance ▼ PP Bacteria/Yeast ▲ Reference Variance ▲ IAD/Methane Score ●	Total SCFA's ▼ SCFA (%) ▼ n-Butyrate Conc. ● Beta-glucuronidase ●	Total Abundance ▼ PP Bacteria/Yeast ▲ Parasitic Infection ● Pathogenic Bacteria ●
<b>Therapeutic Support Options</b>	<ul style="list-style-type: none"> <li>Digestive Enzymes</li> <li>Betaine HCl</li> <li>Bile Salts</li> <li>Apple Cider Vinegar</li> <li>Mindful Eating Habits</li> <li>Digestive Bitters</li> </ul>	<ul style="list-style-type: none"> <li>Elimination Diet/ Food Sensitivity Testing</li> <li>Mucosa Support: Slippery Elm, Althea, Aloe, DGL, etc.</li> <li>Zinc Carnosine</li> <li>L-Glutamine</li> <li>Quercetin</li> <li>Turmeric</li> <li>Omega-3's</li> <li>GI Referral (If Calpro is Elevated)</li> </ul>	<ul style="list-style-type: none"> <li>Pre-/Probiotics</li> <li>Increase Dietary Fiber Intake</li> <li>Consider SIBO Testing</li> <li>Increase Resistant Starches</li> <li>Increase Fermented Foods</li> <li>Meal Timing</li> </ul>	<ul style="list-style-type: none"> <li>Pre-/Probiotics</li> <li>Increase Dietary Fiber Intake</li> <li>Increase Resistant Starches</li> <li>Increase Fermented Foods</li> <li>Calcium D-Glucarate (for high beta-glucuronidase)</li> </ul>	<ul style="list-style-type: none"> <li>Antibiotics (if warranted)</li> <li>Antimicrobial Herbal Therapy</li> <li>Antiparasitic Herbal Therapy (if warranted)</li> <li><i>Saccharomyces boulardii</i></li> </ul>

59 YO Male DM2, HBP, Obesity



## Commensal Microbiome Analysis

### Commensal Abundance

#### Patient Total Commensal Abundance



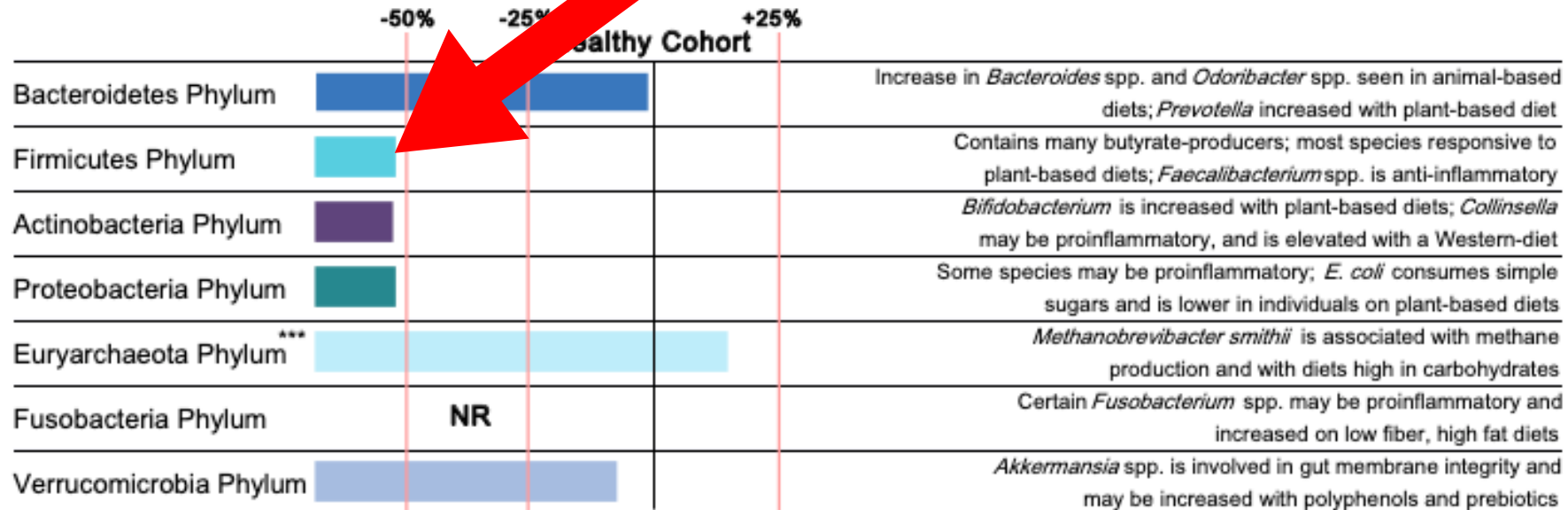
**Total Commensal Balance:** The total commensal abundance is a sum-total of the reported commensal bacteria compared to a healthy cohort. Low levels of commensal bacteria are often observed after antimicrobial therapy, or in diets lacking fiber and/or prebiotic-rich foods and may indicate the need for microbiome support. Conversely, higher total commensal abundance may indicate potential bacteria overgrowth or probiotic supplementation.

59 YO Male DM2, HBP, Obesity



# Lactobacillus Family

## Relative Commensal Abundance



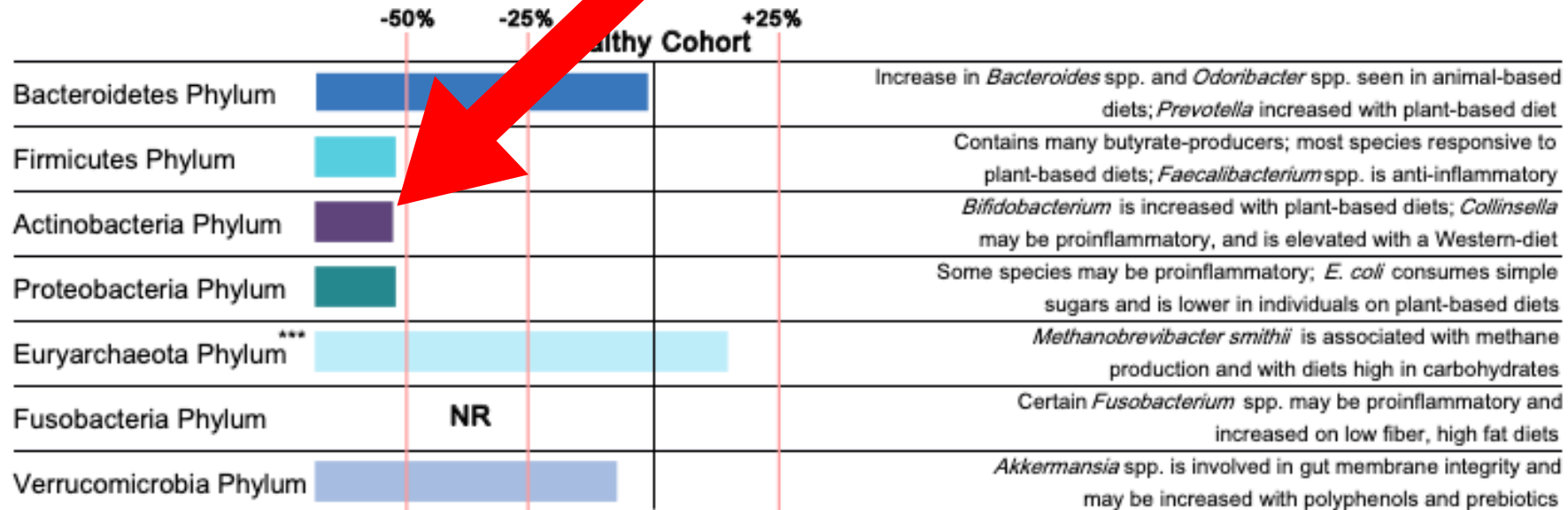
**Relative Abundance:** The relative abundance compares the quantity of each of 7 major bacterial phyla to a healthy cohort. This can indicate broader variances in the patient's gut microbiome profile. Certain interventions may promote or limit individual phyla when clinically appropriate. Please refer to Genova's Stool Testing Support Guide for more information on modulation of commensal bacteria through diet & nutrient interventions. \*\*\*Approximately 75% of the healthy cohort had below detectable levels of *Methanobrevibacter smithii*.

59 YO Male DM2, HBP, Obesity



# Bifidobacterium Family

## Relative Commensal Abundance



**Relative Abundance:** The relative abundance compares the quantity of each of 7 major bacterial phyla to a healthy cohort. This can indicate broader variances in the patient's gut microbiome profile. Certain interventions may promote or limit individual phyla when clinically appropriate. Please refer to Genova's Stool Testing Support Guide for more information on modulation of commensal bacteria through diet & nutrient interventions. \*\*\*Approximately 75% of the healthy cohort had below detectable levels of *Methanobrevibacter smithii*.



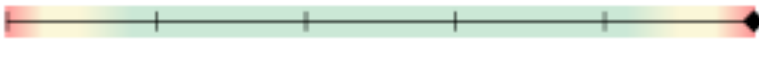




59 YO Male DM2, HBP, Obesity



Methodology: GC-FID, Automated Chemistry, EIA

Result | 1st | 2nd | 3rd | 4th | 5th | Reference Range

### Digestion and Absorption

	Result	QUINTILE DISTRIBUTION	Reference Range
Pancreatic Elastase 1 †	>500		>200 mcg/g
Products of Protein Breakdown (Total*) (Valerate, Isobutyrate, Isovalerate)	6.8		1.8-9.9 micromol/g
Fecal Fat (Total*)	39.2 <b>H</b>		3.2-38.6 mg/g
Triglycerides	1.0		0.3-2.8 mg/g
Long-Chain Fatty Acids	28.0		1.2-29.1 mg/g
Cholesterol	8.7 <b>H</b>		0.4-4.8 mg/g
Phospholipids	1.5		0.2-6.9 mg/g

59 YO Male DM2, HBP, Obesity





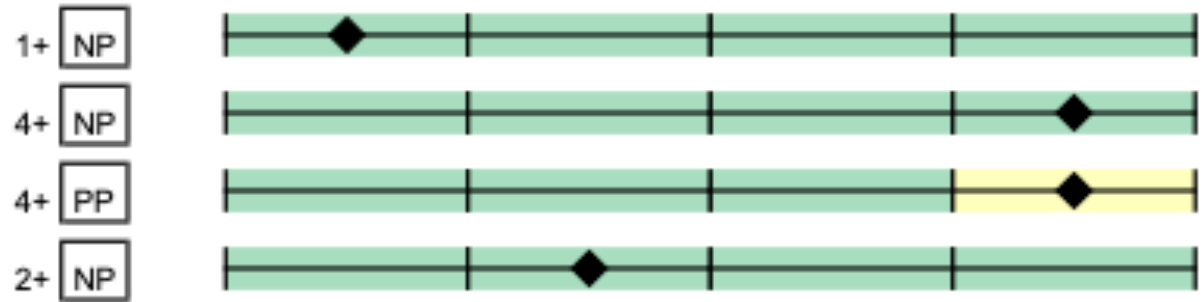
### Additional Bacteria

*alpha haemolytic Streptococcus*

*Haemolytic Escherichia coli*

*Klebsiella pneumoniae*

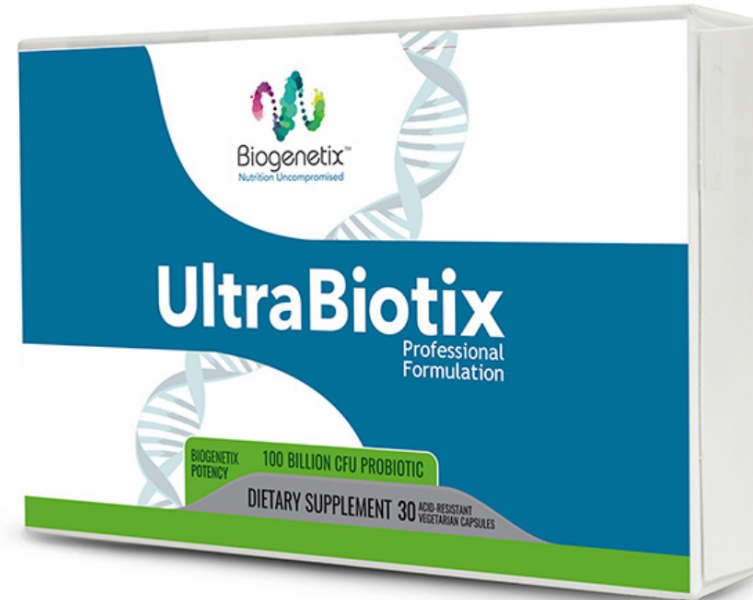
*Enterococcus faecium*



59 YO Male DM2, HBP, Obesity



# Phase 2 Intervention



## Functional Imbalance Scores

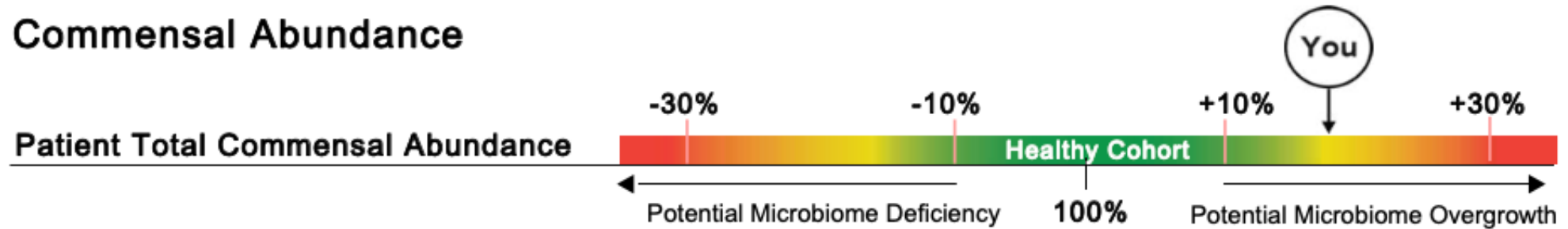
Key < 2 : Low Need for Support 2-3 : Optional Need for Support 4-6 : Moderate Need for Support 7-10 : High Need for Support

	Need for Digestive Support	Need for Inflammation Modulation	Need for Microbiome Support	Need for Prebiotic Support	Need for Antimicrobial Support
	<b>MALDIGESTION</b> <span style="border: 1px solid gray; border-radius: 50%; padding: 10px; font-size: 24px;">2</span>	<b>INFLAMMATION</b> <span style="border: 1px solid red; border-radius: 50%; padding: 10px; font-size: 24px;">7</span>	<b>DYSBIOSIS</b> <span style="border: 1px solid red; border-radius: 50%; padding: 10px; font-size: 24px;">10</span>	<b>METABOLIC IMBALANCE</b> <span style="border: 1px solid green; border-radius: 50%; padding: 10px; font-size: 24px;">0</span>	<b>INFECTION</b> <span style="border: 1px solid gray; border-radius: 50%; padding: 10px; font-size: 24px;">2</span>
<b>Biomarkers</b>	Products of Protein Breakdown <span style="color: green;">▲</span> Pancreatic Elastase <span style="color: green;">●</span> Fecal Fats <span style="color: green;">●</span>	Eosinophil Protein X <span style="color: red;">▲</span> Calprotectin <span style="color: green;">●</span> Secretory IgA <span style="color: green;">●</span> Occult Blood <span style="color: green;">●</span>	Reference Variance <span style="color: red;">▲</span> IAD/Methane Score <span style="color: yellow;">▲</span> PP Bacteria/Yeast <span style="color: yellow;">▲</span> Total Abundance <span style="color: yellow;">▲</span>	Beta-glucuronidase <span style="color: red;">▼</span> Total SCFA's <span style="color: green;">●</span> n-Butyrate Conc. <span style="color: green;">●</span> SCFA (%) <span style="color: green;">●</span>	PP Bacteria/Yeast <span style="color: yellow;">▲</span> Total Abundance <span style="color: yellow;">▲</span> Parasitic Infection <span style="color: green;">●</span> Pathogenic Bacteria <span style="color: green;">●</span>
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68 YO female DM2, Chronic diarrhea, HBP, AI



## Commensal Abundance

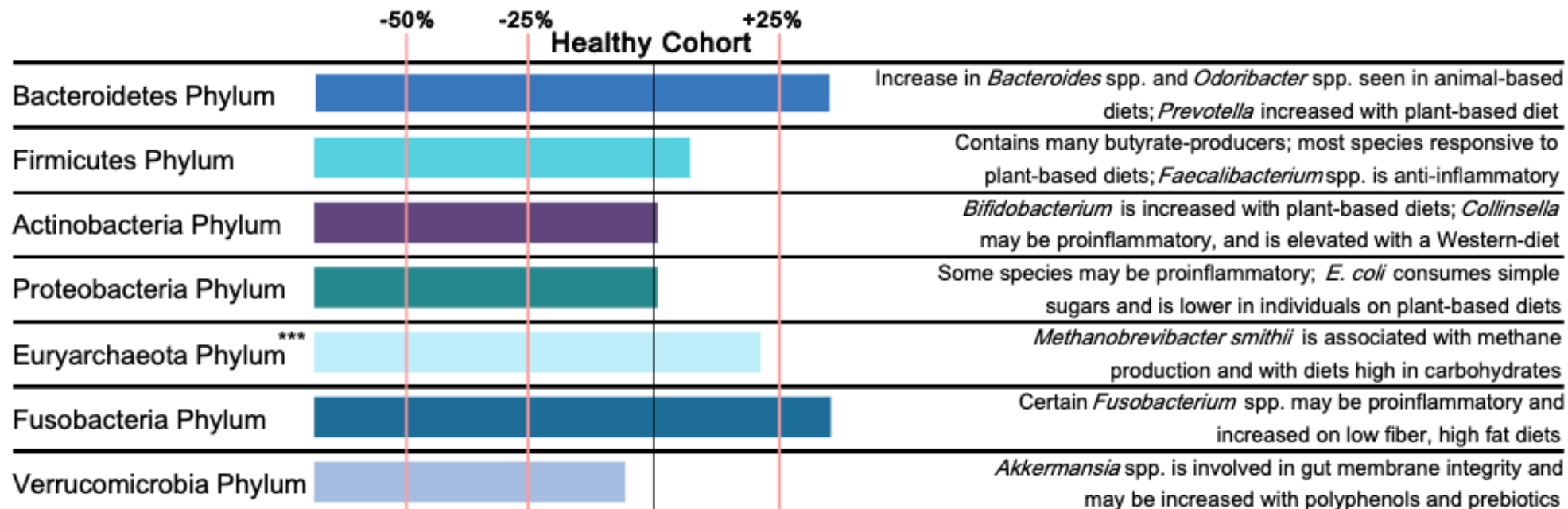


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68 YO female DM2, Chronic diarrhea, HBP, AI



## Relative Commensal Abundance



68 YO female DM2, Chronic diarrhea, HBP, AI



### Additional Bacteria

*Haemolytic Escherichia coli*



*Proteus vulgaris*



*Enterococcus avium*



*Enterobacter species*



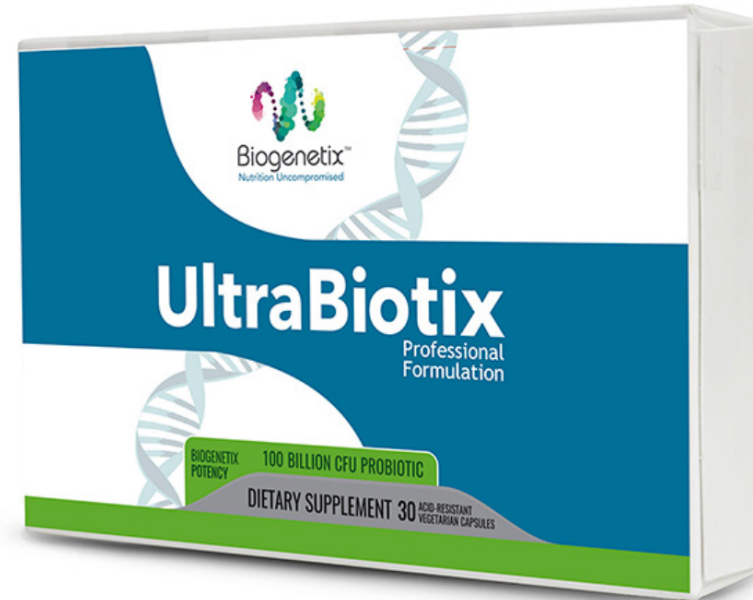
*Pseudomonas aeruginosa*



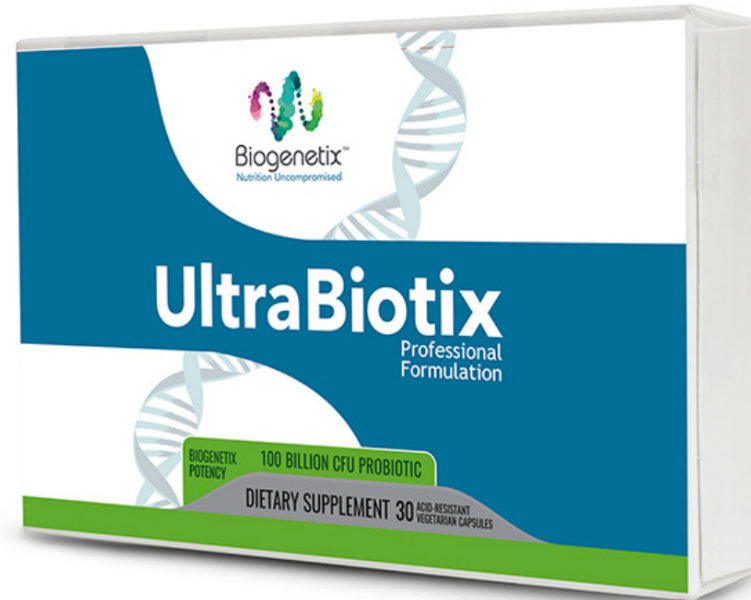
68 YO female DM2, Chronic diarrhea, HBP, AI



# Phase 2 Intervention

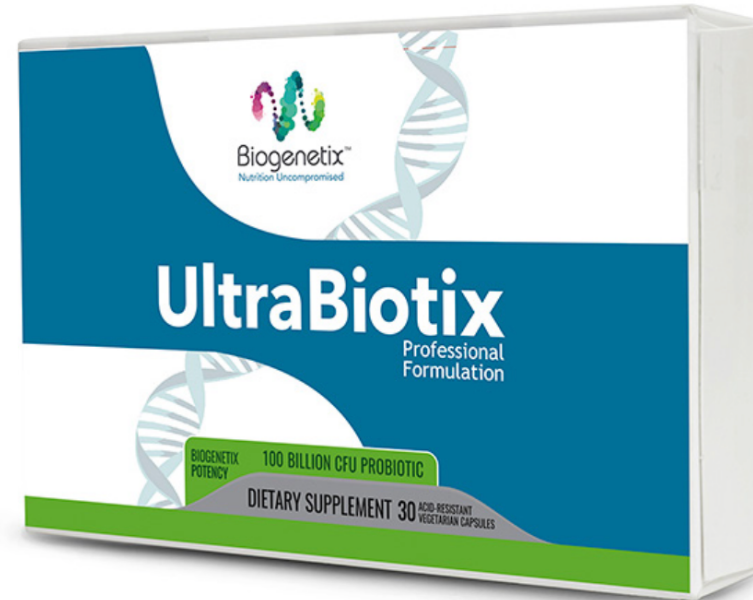


# Phase 2 Intervention





# Phase 2 Intervention



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