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GA-map® Dysbiosis Test Lx v2

TEST RESULTS

SAMPLE ID:	Collection Date:	Date Received:	Report Date:

DYSBIOSIS INDEX (DI) *

The patient's gut microbiota is **mildly dysbiotic**

FUNCTIONAL IMBALANCE - BACTERIA PROFILES *

	FUNCTIONAL PROFILES	TEST RESULTS	COMMENTS
A	Butyrate producing bacteria	✗	Reduced levels of major butyrate producers
B	Gut mucosa protective bacteria	✗	Reduced levels of important gut mucosa protective bacteria
C	Gut health marker	✓	Normal level of *Faecalibacterium prausnitzii*, a key bacterium that promotes intestinal health
D	Gut barrier protective bacteria and potentially harmful bacteria	✗	Imbalance between selected gut barrier protective and potentially harmful bacteria
E	Pro-inflammatory bacteria	✓	Low levels of pro-inflammatory bacteria
F	Diversity	✓	Expected diversity

* For a more detailed explanation of the results, please refer to pages 3-4, 'GA-map® Dysbiosis Test Lx - REPORT FORM SUPPLEMENT'.

SAMPLE ID:	Collection Date:	Date Received:	Report Date:

BACTERIA ABUNDANCE TABLE *

		Reduced			Normal **	Elevated		
Actinobacteria		-3	-2	-1		1	2	3
100	Actinobacteria				●			
101	Actinomycetales				●			
103	*Bifidobacterium spp.*				●			
Bacteriodetes								
201	*Alistipes*				●			
202	*Alistipes onderdonkii*					●		
203	*Bacteroides fragilis*				●			
204	*Bacteroides pectinophilus*				●			
205	*Bacteroides spp.*				●			
206	*Bacteroides spp. & Prevotella spp.*					●		
207	*Bacteroides stercoris*				●			
208	*Bacteroides zoogleoformans*							●
209	*Parabacteroides johnsonii*							●
210	*Parabacteroides spp.*							●
Firmicutes								
300	Firmicutes				●			
302	Bacilli				●			
304	*Catenibacterium mitsuokai*				●			
305	Clostridia				●			
306	*Clostridium methylpentosum*			●				
307	*Clostridium sp.*				●			
308	*Coprobacillus cateniformis*				●			
310	*Dialister invisus*				●			
311	*Dialister invisus & Mega-sphaera micronuciformis*				●			
312	*Dorea spp.*				●			
313	*Holdemanella biformis*				●			
314	*Anaerobutyricum hallii*			●				

		Reduced			Normal **	Elevated		
Firmicutes cont.		-3	-2	-1		1	2	3
315	*[Eubacterium] rectale*				●			
316	*Eubacterium siraeum*				●			
317	*Faecalibacterium prausnitzii*			●				
318	*Lachnospiraceae*				●			
319	*Lactobacillus ruminis & Pediococcus acidilactici*				●			
320	*Lactobacillus spp.*				●			
321	*Lactobacillus spp. 2*				●			
322	*Phascolarctobacterium sp.*				●			
323	*Ruminococcus albus & R. bromii*				●			
324	*Ruminococcus gnavus*					●		
325	*Streptococcus agalactiae & [Eubacterium] rectale*					●		
326	*Streptococcus salivarius ssp. thermophilus & S. sanguinis*				●			
327	*Streptococcus salivarius ssp. thermophilus*			●				
328	*Streptococcus spp.*				●			
329	*Streptococcus spp. 2*				●			
330	*Veillonella spp.*				●			
331	Firmicutes (various)				●			
Proteobacteria								
500	Proteobacteria				●			
501	*Acinetobacter junii*				●			
502	*Enterobacteriaceae*				●			
504	*Shigella spp. & Escherichia spp.*				●			
Tenericutes								
601	*Mycoplasma hominis*				●			
Verrucomicrobia								
701	*Akkermansia muciniphila*			●				

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* For a more detailed explanation of the results, please refer to pages 3-4, 'GA-map® Dysbiosis Test Lx - REPORT FORM SUPPLEMENT'.
** Reference population: an unselected group of non-gastrointestinal-symptomatic individuals (age 18-70).

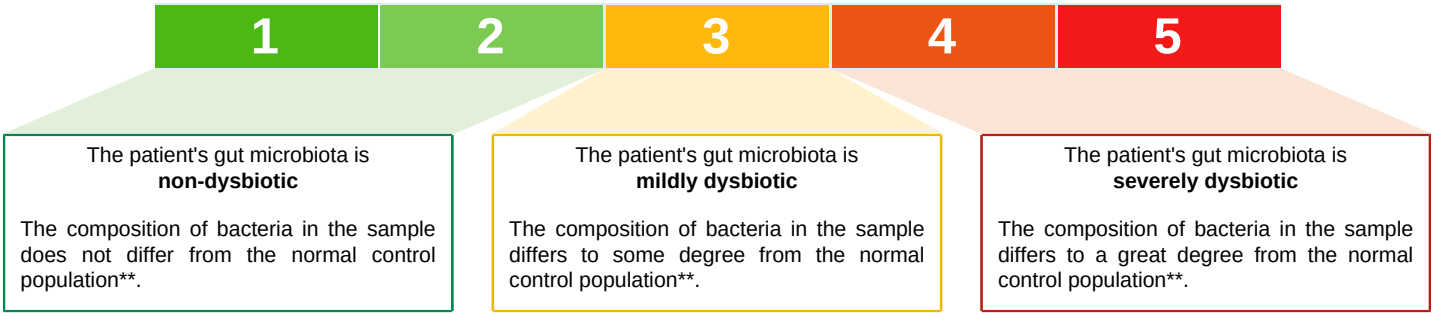
GA-map® Dysbiosis Test Lx – REPORT FORM SUPPLEMENT

The GA-map® Dysbiosis Test Lx is used as a fecal gut microbiota DNA analysis tool to identify and characterize dysbiosis in adults.

Dysbiosis is defined as a permanent or transient imbalance in the gut microbiota composition. This imbalance could be due to an increase in potential harmful bacteria and/or a decrease in commensal bacteria. Under normal conditions the alliance of immune system and gut microbiota prevents the infiltration and proliferation of pathogenic bacteria by inducing and maintaining protective responses. The multiplication of potentially harmful bacteria in the gut may increase the permeability of the intestine, damage intestinal epithelial cells, and affect cell energy metabolism among others. Consequently, imbalances in the gut microbiota population can lead to dysfunction of the intestinal immune system and can trigger a variety of gastrointestinal disorders. Since many of the bacteria in the gut community have important functional relationships with each other, changes in a small number of them and/or in their functions could have broad effects on the individual's health state, directly impacting his/her daily life.

DYSBIOSIS INDEX (DI)

The degree of dysbiosis is reported on a scale from 1 (non-dysbiotic) to 5 (severely dysbiotic).



Clinical studies report that among a healthy population 16% of individuals have a mild dysbiosis (DI 3)[1]. In patients with irritable bowel syndrome (IBS) and inflammatory bowel disease (IBD), about 20-30% have a microbiota profile within the normal range (DI 1-2), while about 70-80% have a microbiota profile that falls outside of the normal range (DI > 2)[1]. IBD patients tend to have a more severe dysbiosis than IBS patients (DI 4-5)[1].

FUNCTIONAL IMBALANCE - BACTERIA PROFILES

Each profile represents a set of unique bacteria signatures linked to their functional properties. The profiles reported as "balance" or "imbalance" may not always correspond with DI, since the profiles are limited to selected bacteria markers associated with gut functions known from literature today.

The profiles are reported as **(Balance)** or **(Imbalance)**, followed by a comment.

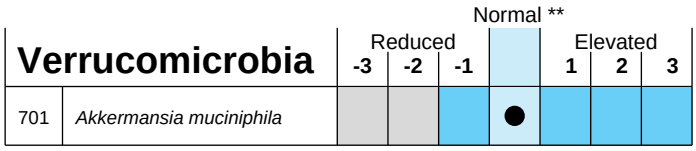
A	Butyrate producing bacteria	
	Description	Insufficient levels of butyrate are associated with an impaired gastrointestinal health. Butyrate is a short-chain fatty acid produced by microbial fermentation in the large intestine of humans. It is important for regulating multiple functions of gut cells, may be important for regulating inflammatory and immunological responses and plays a role in the maintenance of intestinal barrier function. Beneficial bacteria belonging to the phylum Firmicutes are major butyrate producers.
	Bacteria marker	314 - *Anaerobutyricum hallii* 315 - *[Eubacterium] rectale* 317 - *Faecalibacterium prausnitzii*
B	Gut mucosa protective bacteria	
	Description	Mucus and mucosa-associated bacteria form a specific protective environment in the gut. A disruption of the mucosa layer may promote specific bacterial colonization and immunological responses and enhance the development of gastrointestinal diseases. Imbalance of gut mucosa protective bacteria has been associated with various gastrointestinal disorders.
	Bacteria marker	317 - *Faecalibacterium prausnitzii* 701 - *Akkermansia muciniphila*
C	Gut health marker	
	Description	*Faecalibacterium prausnitzii* is one of the most prevalent bacteria within the human gastrointestinal tract. It is recognized as a major butyrate producer and can promote anti-inflammatory processes and testinal barrier function. Lower levels of *Faecalibacterium prausnitzii* in the intestines have been associated with gastrointestinal and metabolomic disorders.
	Bacteria marker	317 - *Faecalibacterium prausnitzii*

** Reference population: an unselected group of non-gastrointestinal-symptomatic individuals (age 18-70).

D	Gut barrier protective bacteria and potentially harmful bacteria	
	Description	The intestinal epithelial barrier is not a static physical barrier but one that can interact with the gut microbiome and cells of the immune system. An imbalance between the gut barrier protective bacteria and potentially harmful bacteria may lead to gut barrier disruption and is associated with an increased susceptibility to certain diseases.
	Bacteria marker	317 - *Faecalibacterium prausnitzii* 324 - *Ruminococcus gnavus* 500 - Proteobacteria 504 - Shigella spp. & Escherichia spp.
E	Pro-inflammatory bacteria	
	Description	Elevated Proteobacteria species are associated with inflammation in various - mainly gastrointestinal - disorders. In a healthy gut microbiota, their increase may promote intestinal inflammation due to molecules present on their surface which are potent triggers of inflammatory responses. Inflammation in itself may also promote the growth of Proteobacteria species. Pro- inflammatory bacteria levels may thus give indications of the susceptibility of the patient to intestinal inflammation and to the possible development of gastrointestinal disorders.
	Bacteria marker	500 - Proteobacteria 504 - Shigella spp. & Escherichia spp.
F	Diversity	
	Description	Diversity displays the distribution of bacteria as "low" or "expected" depending on the number of different species and their abundance in the sample, calculated based on Shannon diversity index.
	Bacteria marker	The diversity is computed using normalized fluorescent signal strengths from a selection of 28 uncorrelated bacteria markers.

THE ABUNDANCE TABLE OF PRESELECTED BACTERIA MARKERS

The results are presented in an easy-to-read abundance table of 48 preselected bacteria markers. Some bacteria markers are specific for one bacterial species (e.g. *Akkermansia muciniphila*), while others cover groups of bacteria (e.g. phylum, Proteobacteria). The selected bacteria have proven to be of high importance and clinically relevant for gut health and disorders in the literature and in laboratory testing.



- The black dot indicates the result of the analysis.
- Each bacteria marker is assigned a unique identification number (e.g. GA ID: 701 - *Akkermansia muciniphila*)
- Bacteria signal levels are reported on a scale from -3 (strongly reduced levels of the bacteria) to +3 (strongly elevated levels of the bacteria).
- The light blue center field indicates the reference relative abundance of bacteria based on a healthy control population **.
- The possible detection range for each bacterium is given as the dark blue shaded boxes.
- The grey shaded boxes indicate levels outside the detection range for each bacterium.
- sp.- one species, the actual specific name unknown
- spp.- two or more species of the same genus

Reference:

1. Casén C, Vebø HC, Sekelja M, Hegge FT, Karlsson MK, Ciemniejewska E, Dzankovic S, Frøyland C, Nestestog R, Engstrand L, Munkholm P, Nielsen OH, Rogler G, Simrén M, Öhman L, Vatn MH, Rudi K. Deviations in human gut microbiota: a novel diagnostic test for determining dysbiosis in patients with IBS or IBD. Aliment Pharmacol Ther. 2015 Jul;42(1):71-83. doi: 10.1111/apt.13236. Epub 2015 May 14. PMID: 25973666; PMCID: PMC5029765.

** Reference population: an unselected group of non-gastrointestinal-symptomatic individuals (age 18-70).