Analysis Report

Sample code:	DMB001
Analysis:	Gut Microbiome Screening
Sample type:	Feces
Gender:	M
Age:	50
Arrival date:	1-1-2022
Analysis complete:	3-1-2022

In this report you will find the results of your gut microbiome analysis. For a quick impression of the results, read the summary below. This is followed by the composition of the gut microbiome and comparison with healthy reference values (page 2). The microbial activity (page 3) indicates the distribution of active and inactive cells per bacterial group. The interpretation of your gut microbiome (page 4) provides an overview of the bacterial groups that deviated from the reference values. In addition, a complete overview is given of potential problems associated with this personal gut microbiome analysis. Additional explanation about the various tables and graphs in this report can be found on the last page.
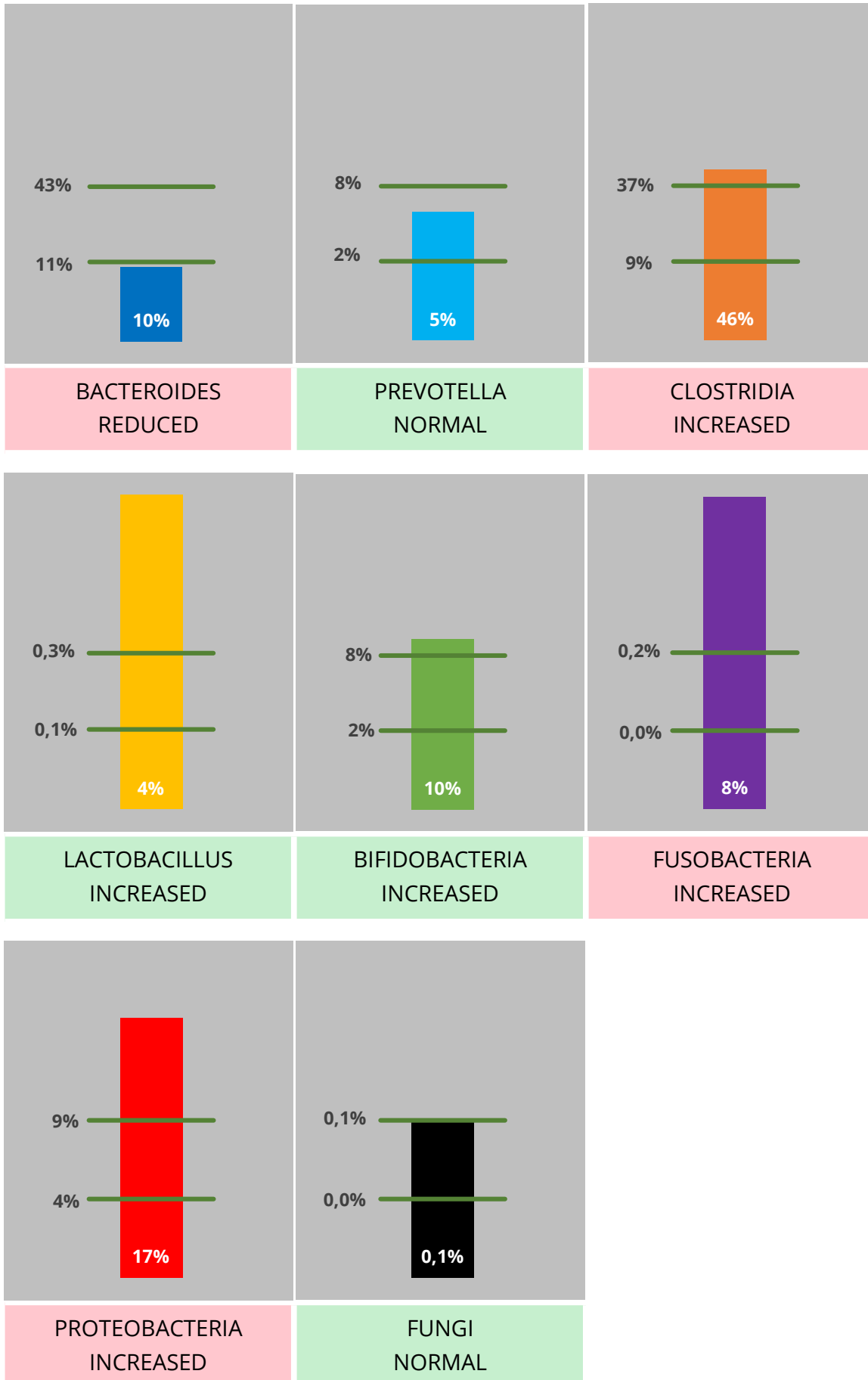
Summary

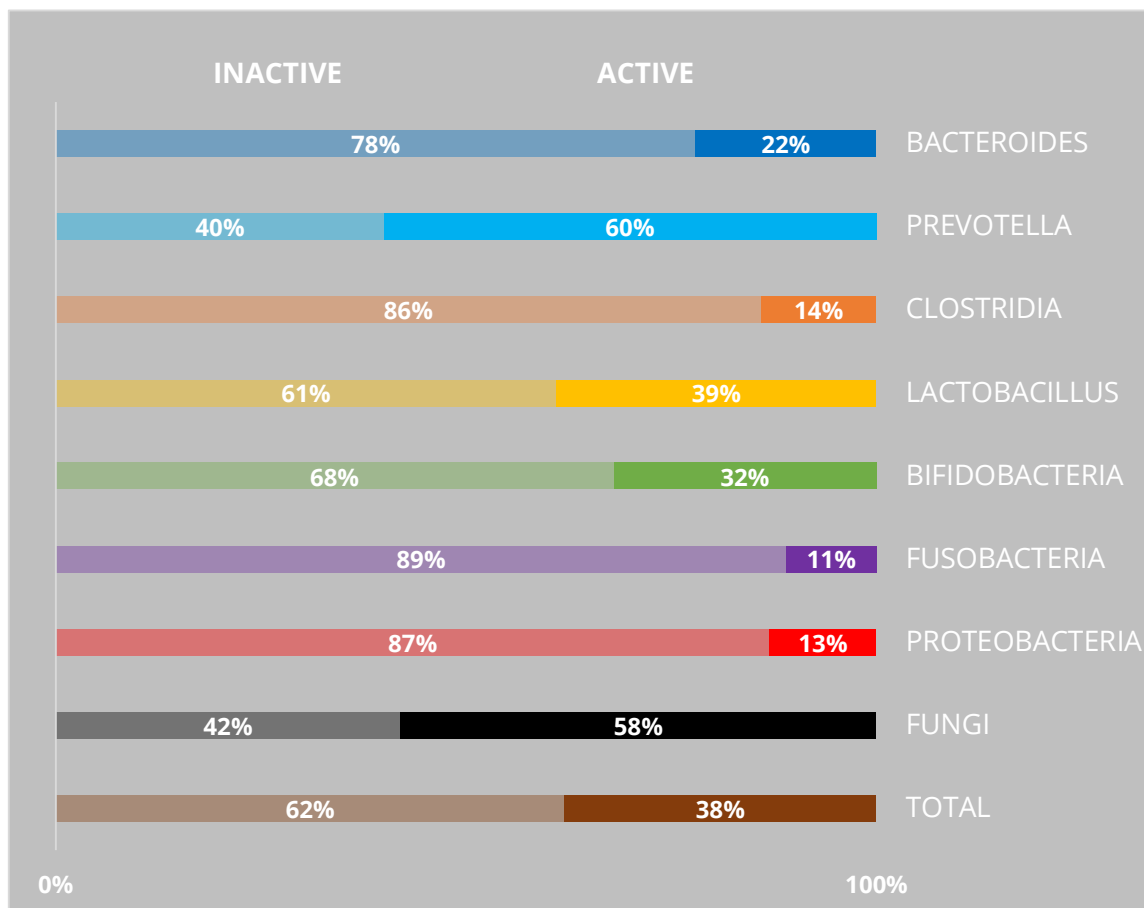| Best scores		Points of attention	
✓✓	**LACTOBACILLUS** INCREASED Lactic acid bacteria are considered probiotic. This means that they can be health-promoting.	‼️‼️	**BACTEROIDES** REDUCED A decreased number of *Bacteroides* is associated with disturbances of the fat metabolism.
✓✓	**BIFIDOBACTERIA** INCREASED Due to the probiotic effects of bifidobacteria, this can be seen as a positive result. Bifidobacteria contribute, among other things, to good colonization resistance.	‼️	**CLOSTRIDIA** INCREASED There is a (slightly) increased risk of concentration problems, sadness and chronic fatigue.
		‼️	**PROTEOBACTERIA** INCREASED The risk of infectious diarrhea, Crohn's disease and irritable bowel syndrome is increased.

Gut Microbiome Composition

Pie chart legend:
- BACTEROIDES — 10%
- PREVOTELLA — 5%
- CLOSTRIDIA — 46%
- LACTOBACILLUS — 4%
- BIFIDOBACTERIA — 10%
- FUSOBACTERIA — 8%
- PROTEOBACTERIA — 17%
- FUNGI — 0,1%
- OTHER

Your gut microbiome compared to reference values

43% ——— 11% ——— **10%**	8% ——— 2% ——— **5%**	37% ——— 9% ——— **46%**
BACTEROIDES REDUCED	**PREVOTELLA NORMAL**	**CLOSTRIDIA INCREASED**
0,3% ——— 0,1% ——— **4%**	8% ——— 2% ——— **10%**	0,2% ——— 0,0% ——— **8%**
LACTOBACILLUS INCREASED	**BIFIDOBACTERIA INCREASED**	**FUSOBACTERIA INCREASED**
9% ——— 4% ——— **17%**	0,1% ——— 0,0% ——— **0,1%**	
PROTEOBACTERIA INCREASED	**FUNGI NORMAL**	
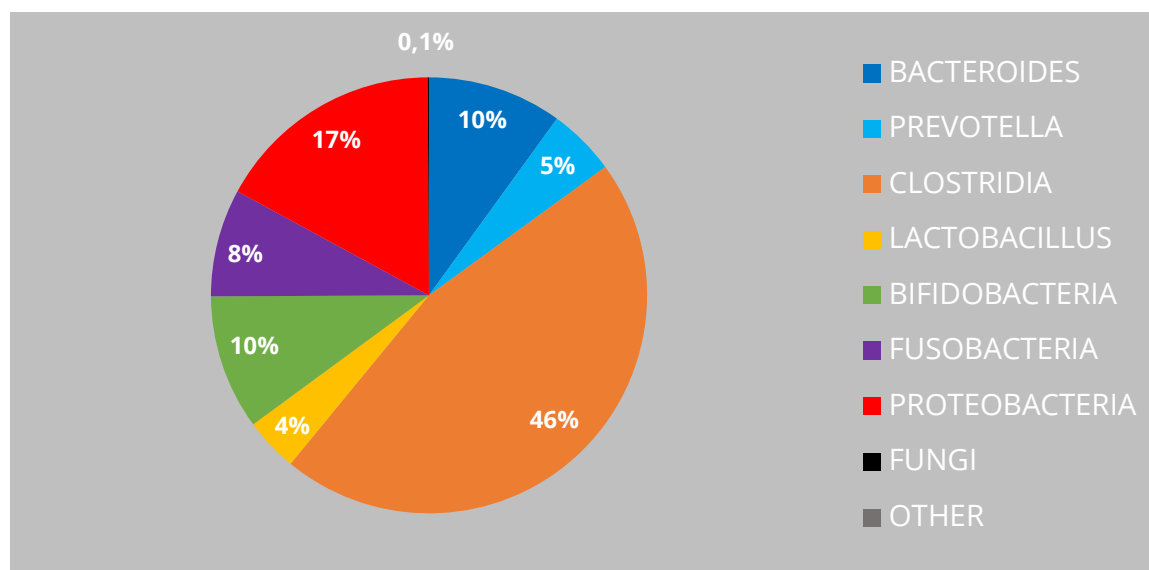
Microbial activity

The graph below shows for each bacterial group the distribution between active (high microbial activity) and inactive (low microbial activity) cells. The microbial activity is based on multiple parameters, including intensity of the fluorescent signal. 'Total' includes the activity of all cells in the gut microbiome (incl. the group 'other').

	INACTIVE	ACTIVE	
BACTEROIDES	78%	22%	
PREVOTELLA	40%	60%	
CLOSTRIDIA	86%	14%	
LACTOBACILLUS	61%	39%	
BIFIDOBACTERIA	68%	32%	
FUSOBACTERIA	89%	11%	
PROTEOBACTERIA	87%	13%	
FUNGI	42%	58%	
TOTAL	62%	38%	

0%   100%

Additional results

	Your sample	Reference value	Indication
Color	(dark) Brown	(dark) Brown	Good
Consistency	**Mushy**	Smooth	**Deviated**
pH value	**<6.5**	6.5 - 7.5	**Acidic**
Colonisation resistance	3,3x10^11 bacteriën/g	≥1x10^11 bacteriën/g	Good
Diversity	1,00	≥0.9[*]	Good
Dysbiosis	**1,70**	0.15 - 0.85[*]	**Elevated**

* Theoretical reference values, based on the reference values of individual bacterial groups.

Interpreting your gut microbiome

Consistency

The stool is mild diarrhea. This can be a natural reaction of the body to (new) nutrients. As long as there is no fever, the situation will pass. In case of (persistent) complaints, a disturbed gut microbiome could be the cause.

pH

Acidification of the stool (faecal acidosis). If there is also a fever, there may be an intestinal infection. If no fever is present, there may be lactose intolerance. In addition, a lowered pH could be the result of a (too) low protein intake. It is useful to investigate whether there is a balanced diet.

Dysbiosis

The gut microbiome is out of balance (dysbiotic). This can be a cause as well as a consequence of various diseases. Incomplete nutrition, use of medicines and little exercise can also disrupt the microbial balance. It is important to restore the relationships between the bacterial groups. An adapted diet can contribute to this.

Bacteroides

A reduced number of *Bacteroides* can lead to a reduced colonization resistance and is also associated with disturbances of the fat metabolism. The result is an increased risk of non-alcoholic fatty liver disease and vasoconstriction. In combination with an increased amount of Clostridia, the risk of obesity is increased. In combination with a reduced amount of Clostridia and an increased amount of Fusobacteria, there is a slightly increased chance of changes in the intestinal mucosa. A diet with less to no fat, sufficient fiber and protein and also sufficient exercise can help to increase the amount of *Bacteroides*.

Clostridia

Possible cause: sudden change in diet. An increased amount of Clostridia could lead to putrefactive dyspepsia, which is often accompanied by an increased pH of the stool and/or an accelerated intestinal passage. There is also a greater chance of the production of harmful substances (toxins) in the intestine by Clostridia. The result is a reduced concentration, gloominess/depression and chronic fatigue. Elevated Clostridia is commonly found in autism spectrum disorders. Clostridia mainly live on proteins and fats, so the amount of Clostridia could be reduced by reducing the protein intake.

Lactobacillus

Lactobacilli improve the functioning of the gut-associated immune system. In addition, the risk of a leaky gut (intestinal permeability) and infectious diarrhea is smaller. Due to the probiotic effects, there is little reason for dietary adjustments with an increased number of Lactobacilli.

Bifidobacteria

Bifidobacteria are probiotic bacteria. In the current numbers there are a number of health-promoting effects: reduction of allergic hypersensitivity, reduced risk of infectious diarrhea and improved digestion and colonization resistance.

Fusobacteria

Fusobacteria are found in both the gut and the mouth and mainly live on proteins and carbohydrates. An increased number of Fusobacteria increases the risk of gum disease, impaired food digestion (constipation), chronic inflammatory bowel disease and increases the risk of changes in the intestinal mucosa.

Proteobacteria

An increased number of Proteobacteria is associated with various diseases. The risk of infectious diarrhea, irritable bowel syndrome and Crohn's disease may be increased. An increased number of Proteobacteria could be caused by a (too) high protein intake. The amount of Proteobacteria could be reduced by increasing fiber intake and decreasing protein intake.

How to read the report?

Summary

Brief overview of positive and negative parameters in this personal gut microbiome. Ranked by degree of impact. The importance of the result is emphasized by means of check marks (good) and exclamation marks (requires attention).

Gut Microbiome Composition

Shows the full gut microbiome composition. The 'other' group includes micro-organisms that are present in the microbiome but have not been identified in this analysis. In a helathy gut microbiome, more than 95% of the bacteria should be identified with this screening (Western European diet).

Your gut microbiome compared to reference values

Overview of all measured bacterial groups in comparison with reference values from scientific publications. An indication of the result is given based on the reference values (normal/reduced/elevated, etc.). Reference values are subject to change due to new scientific insights.

Microbial activity

Per analyzed bacterial group, the ratio between active (high microbial activity) and inactive (low microbial activity) cells is shown. The microbial activity is determined based on multiple parameters, including intensity of the fluorescent signal. 'Total' includes the activity of all measured cells in the gut microbiome (all measured bacterial groups + the 'other' group).

Additional results

Overview of measured and calculated values. In comparison to healthy reference values an indication is given (good/reduced/elevated, etc.).

Interpreting your gut microbiome

An accompanying explanation for each deviating factor is provided. Possible causes and consequences of disruptions in the long term are mentioned. The gut microbiome composition and additional results are assessed in combination with the microbial activities.

All responsibility for actions based on this analysis report rests with the applicant. To all NL-Lab services the general terms and conditions are applicable as stated on the registration form and as published on our website: www.NL-Lab.nl.