

# What Can Clinicians and Patients Expect from Healthpath Gut Health Testing?

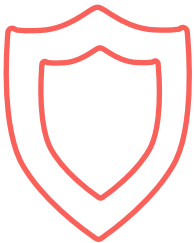
The Healthpath Gut Test shows you what's going on in your gut. By looking at imbalances in bacteria, yeasts, parasites and other intestinal health biomarkers, you find out what's contributing to your symptoms. You also receive targeted diet, supplement and lifestyle recommendations to help you take back control.

**The biomarkers provide clinical information on three key areas:**



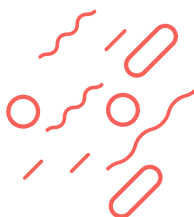
## 1 | Digestion/Absorption

- pH
- Pancreatic elastase
- Zonulin



## 2 | Immune activity/Inflammation

- Calprotectin
- Haemoglobin
- Secretory IgA
- H. Pylori
- Archaea/methanogens
- E. Coli, Lactobacillus species, Enterococcus species
- Akkermansia muciniphila, Faecalibacterium prausnitzii



## 3 | Gut Microbiome/Mycobiome

- Microbiome diversity
- Enterotype
- Dysbiosis index
- Actinobacteria
- Bacteroidetes
- Firmicutes
- Proteobacteria
- Fusobacteria
- Verrucomicrobia
- Hydrogen-sulphide production
- Oxalate-degrading bacteria
- Yeasts/moulds
- Parasites
- Helminths



### Clinical Advantages of The Healthpath Gut Health Test qPCR Technology

This new method of analysis allows for a single sample. This makes the process easier for everyone, and it's particularly helpful for children and those struggling with diarrhoea or constipation.

	Gut Health Test	Advanced Gut Health Test Pro
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### Stool properties

Colour	✓	✓
Consistency	✓	✓
pH	✓	✓

#### Diversity:

Your diversity is key, which is why our microbiome analysis covers hundreds of parameters. High bacterial diversity is known to protect against intestinal infections. But low bacterial diversity is common, especially in disease states or after a course of antibiotics. When diversity is low, opportunistic bacteria like pathogens, fungi and viruses can proliferate.

Rather than focusing on individual species, it's more important to investigate how the different bacteria interact. Together, they're responsible for a host of intestinal functions.

### Biodiversity

Diversity	✓	✓
Dysbiosis index	✓	✓

There are four large phyla (groups) of bacteria: Bacteroidetes, Firmicutes, Actinobacteria and Proteobacteria. We also report on two smaller, clinically relevant phyla: Verrucomicrobia and Fusobacteria.

### Bacterial distribution

Actinobacteria	✓	✓
Bacteroidetes	✓	✓
Firmicutes	✓	✓
Fusobacteria	✓	✓
Proteobacteria	✓	✓
Verrucomicrobia	✓	✓
Other	✓	✓
Firmicutes/ Bacteroidetes Ratio	✓	✓

#### Enterotype:

Recent research suggests there are three different types of gut microbiomes, known as 'enterotypes'. Not only do the different enterotypes influence the absorption of minerals, but they also have different metabolic properties.

Enterotype 1 has high levels of Bacteroides species, which use fat and protein effectively. Enterotype 2 has a strong Prevotella population, which is better at metabolising carbohydrates. Enterotype 3 is the rarest enterotype. It has high levels of Ruminococcus flora, though we don't yet know which macronutrients it prefers.

Enterotypes aren't affected by a person's age or gender and they remain stable for years. They can be influenced, however, by a long-term change of diet and by taking prebiotics.

### Enterotype

1, 2 or 3	✓	✓
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### Actinobacteria

Bifidobacteria	✓	✓
Equol-producing bacteria	✓	✓
Adlercreutzia species		✓
Eggerthella lenta		✓
Slackia species		✓

### Bacteroidetes

Bacteroides	✓	✓
Prevotella	✓	✓
Prevotella copri	✓	✓

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#### Firmicutes:

Butyrate is a short-chain fatty acid that's produced by bacteria in the colon. It's quickly absorbed by the intestinal mucosa, which means the only reliable way to measure it is to look at the number of butyrate-producing bacteria.

Firmicutes bacteria are key butyrate producers. One of these, *Faecalibacterium prausnitzii*, typically makes up 5–15% of human intestinal bacteria. This important butyrate-producing species has anti-inflammatory properties—so much so that an absence of *Faecalibacterium prausnitzii* typically correlates with higher levels of inflammation.

#### Firmicutes

Butyrate-producing bacteria	✓	✓
Faecalibacterium prausnitzii	✓	✓
Eubacterium rectale	✓	✓
Eubacterium hallii	✓	✓
Roseburia species	✓	✓
Ruminococcus species	✓	✓
Coprococcus	✓	✓
Butyrivibrio species		✓
Cl. butyricum		✓
Total bacterial count	✓	✓
Clostridia	✓	✓
Clostridia total bacterial count	✓	✓
Clostridia cluster 1	✓	✓
Clostridia histolytium		✓
Clostridium perfringens		✓
Clostridium sporenges		✓
Other		✓
Christensenellaceae		✓
Dialister invisus		✓

#### Fusobacteria

Fusobacterium species	✓	✓
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#### Verrucomicrobia

Akkermansia muciniphila	✓	✓
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#### Proteobacteria

Potentially pathogenic bacteria	✓	✓
Haemophilus	✓	✓
Acinetobacter	✓	✓
Escherichia coli biovars	✓	✓
Proteus species	✓	✓
Proteus mirabilis		✓
Klebsiella species	✓	✓
Klebsiella pneumoniae		✓
Enterobacter species	✓	✓
Serratia species	✓	✓
Hafnia species	✓	✓
Morganella species	✓	✓
Campylobacter species		✓
Providencia species		✓
Citrobacter species		✓
Histamine-producing bacteria	✓	✓
H2S production	✓	✓
<b>Hydrogen-sulphide production:</b> Bacterial metabolism isn't always a good thing. Some bacteria reduce sulphate to create hydrogen sulphide—a toxic metabolic by-product that can damage the gut lining. The species <i>Bilophila wadsworthii</i> , <i>Desulfomonas pigra</i> and <i>Desulfovibrio piger</i> are thought to be potent hydrogen-sulphide developers.		
Sulphate-reducing bacteria	✓	✓
Desulfovibrio piger		✓
Desulfomonas pigra		✓
Bilophila wadsworthii		✓
Oxalate-degrading bacteria		✓
Oxalobacter formigenes		✓

#### Archaea:

Archaea have been overlooked in microbiome studies until recently. New research suggests that 1) archaea are part of the microbiome in plants, animals and humans, 2) they form biofilms and 3) they interact with the human immune system. Some archaea are also methanogens, which may play a role in chronic constipation.

#### Archaea

Methanobrevibacter	✓	✓
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### Immunogenically effective bacteria

Escherichia coli	✓	✓
Enterococcus species	✓	✓
Lactobacillus species	✓	✓

### Mucin production/mucosal barrier:

A healthy colon has a protective mucous layer. If this layer is damaged—or only small amounts of mucous are produced—pathogens, pollutants and allergens can come into direct contact with the mucosa. This leads to inflammation.

The bacterium Akkermansia muciniphila is important because it encourages goblet cells to produce this protective mucous. Parts of this mucous also provide a special type of carbohydrate called oligosaccharides, which feed the bacteria that make gut-healing butyrate. With the right bacteria, it becomes a virtuous circle!

### Mucin production/mucosal barrier

Akkermansia muciniphila	✓	✓
Faecalibacterium prausnitzii	✓	✓

### Yeasts/moulds

Candida albicans	✓	✓
Candida species	✓	✓
Geotrichum candidum	✓	✓
Moulds	✓	✓

### Functional markers

Calprotectin	✓	✓
Haemoglobin in faeces immunologically	✓	✓
Secretory IgA	✓	✓
Pancreatic elastase	✓	✓
Zonulin		✓

	Gut Health Test	Advanced Gut Health Test Pro
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### Parasites:

The Multiplex Real-time PCR (Multiplex quantitative real-time PCR) is a faster and more effective method for detecting parasites. This new test:


- provides reliable analysis, even with minimal levels
- gives no false positives with non-pathogens
- also gives reliable results in symptom-free patients and also after treatment

### Parasites

Pathobionts	✓	✓
Blastocystis hominis	✓	✓
Dientamoeba fragilis	✓	✓
Helicobacter AG	✓	✓
Pathogenic intestinal protozoa	✓	✓
Giardia lamblia	✓	✓
Entamoeba histolytica	✓	✓
Cryptosporidium species	✓	✓
Cyclospora cayetanensis	✓	✓
Helminths <b>COMING SOON</b>		✓
Taenia species		✓
Taenia solium		✓
Taenia saginata		✓
Ascaris species		✓
Enterobius vermicularis		✓
Ancylostoma species		✓
Ancylostoma duodenale		✓
Hymenolepis species		✓
Hymenolepis nana		✓
Hymenolepis diminuta		✓
Trichuris trichiura		✓
Necator americanus		✓
Strongyloides species		✓
Strongyloides stercoralis		✓
Microsporidia		✓
Enterocytozoon species		✓
Encephalitozoon species		✓

# GUT HEALTH MOT

## PROCESS OVERVIEW



We evaluated  
**your symptoms**



We looked at  
**bacteria, yeasts  
and/or parasites**



We analysed  
**your biomarkers**



## WHAT YOU GET FROM US



Your bespoke supplement package



The Healthpath plate



The Healthpath fundamentals of health programme



Sleep



Activity



Stress



Diet

# GUT HEALTH MOT

## TEST REPORT

*Thank you for taking the Gut Health MOT Test. We're delighted to provide your personalised report.*

The report is divided into four sections:

- I. **Your microbiome**  
This provides insight into the consistency of your poop, the diversity of your bacteria, your 'enterotype' and your dysbiosis index. These are all important and interconnected components that shed light on the health of your digestive system.
- II. **Bacteria, yeasts and/or parasites**  
This section gives details of organisms that have been detected in your digestive system.
- III. **Biomarkers**  
These assess both your ability to break down and absorb your food, and any immune system activity. This helps us understand whether food sensitivities or gut infections are contributing to your symptoms.
- IV. **Recommendations**  
Finally, this section provides your lifestyle and supplement recommendations.










### I. YOUR MICROBIOME



#### Consistency

YOU

						
TYPE 1 Separate hard lumps, like nuts (hard to pass)	TYPE 2 Sausage shaped but lumpy	TYPE 3 Like a sausage but with cracks on its surface	TYPE 4 Like a sausage or snake, smooth and soft	TYPE 5 Soft blobs with clear-cut edges (passed easily)	TYPE 6 Fluffy pieces with ragged edges, a mushy stool.	TYPE 7 Watery, no solid pieces. Entirely liquid.

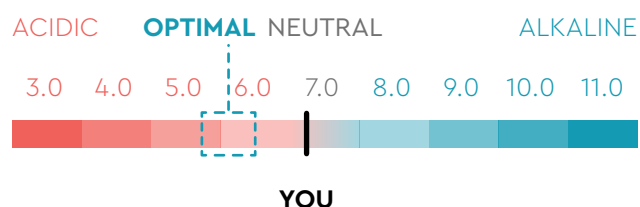
OPTIMAL

**Decreased water activity**, associated with harder stools and prolonged transit time, is thought to limit bacterial growth by reducing nutrient mobility and enzyme activity.

**Species richness** (the number and types of bacteria in the gut) is known to decline with higher BSS scores, reaching its minimum in those with loose stools (type 7).

## pH

**6.9**



### pH is all about balance.

Both very acidic and very alkaline scores represent unhealthy digestive systems.

A **LOW** pH can indicate that carbohydrates aren't being absorbed properly.

A **HIGH** pH suggests inadequate acid production and digestion.

## Biodiversity



Congrats!  
You are quite inhabited.

Species richness is thought to be a major marker for gut health. Ideally, we all want high bacterial richness and diversity, as these often reflect ecosystem stability and resilience.

There's also an association between a reduction in the number of species in a person's poop sample and an increased risk of disease.

What can decrease biodiversity?  
Some factors are travel time, antibiotic therapies, infections, increasing age, unbalanced diets, smoking.

## Enterotype

Recent research suggests that the human microbiome can be assigned to three main groups, known as 'enterotypes'.

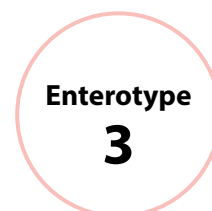
Your result



Enriched with *Bacteroides* and the co-occurring *Parabacteroides*

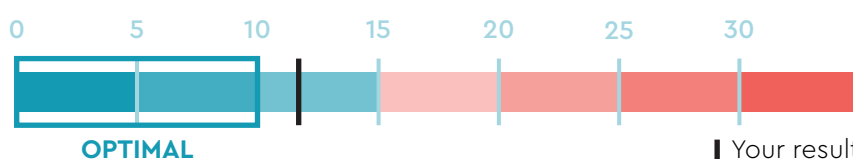


Enriched with *Prevotella* and the co-occurring *Desulfovibrio*



Enriched with *Ruminococcus* and the co-occurring *Akkermansia*

## Dysbiosis index



The dysbiosis index is a measure of deviation with the microbiome. In other words, if you have too much of one type of bacteria, or not enough of another, it can affect your index.

## II. BACTERIA, FUNGI AND PARASITES

### Lactobacilli

LOW

**What is it?** A type of bacteria

**What does it do?** Even though Lactobacilli is only a subgroup within the community of gut bacteria, it's an important one. A low level of Lactobacilli has been linked to an increased risk for certain diseases and chronic conditions.

**What does this level mean?** Two key conditions linked to a low level of intestinal Lactobacilli are IBS and ulcerative colitis. However, it's also possible for people with low Lactobacilli to have no symptoms.

### Bacteroidetes

HIGH

**What is it?** Bacteroidetes are a family of bacteria. Along with Firmicutes, they are one of two dominant families of bacteria in the gut. In fact, Bacteroidetes bacteria generally make up half of the gut microbiome.

**What does it do?** We do need Bacteroidetes, but more isn't necessarily better. This family of bacteria helps to break down food, thereby enabling us to harvest more energy from it.

**What does this level mean?** Some studies suggest that high levels of Bacteroidetes can contribute to metabolic diseases in certain people. Bacteroidetes also have a molecule on their surface called LPS, which is very inflammatory. When LPS crosses the gut wall (e.g. in cases of leaky gut), it can contribute to body-wide inflammation and chronic disease.

### Bifidobacterium spp

LOW

**What is it?** A type of bacteria that's a normal component of a healthy microbiome.

**What does it do?** Bifidobacteria play an important role in breaking down fiber that humans can't digest on their own. They also help to train the immune system. Supplementing with bifidobacteria has been shown to reduce inflammation, improve allergic rhinitis and intermittent asthma, and enhance immune cell function. It can also help to improve cardiovascular risk markers and the production of B vitamins.

**What does this level mean?** A low abundance of bifidobacteria is more common in obese people.

### III. BIOMARKERS

#### Secretory IgA

HIGH

**What is it?** Secretory IgA is an antibody (an immune cell) that is released into the gastrointestinal tract to fight infection.

**What does it do?** It forms part of the lining that protects the gut from infection and toxins, and it also helps to fight inflammation.

**What does this level mean?** Chronic infection, long-term stress, nutrient deficiencies.

#### Elastase-1

LOW

**What is it?** An enzyme.

**What does it do?** Pancreatic elastase is an enzyme that digests protein. It's produced in the pancreas, which means it can be used to measure how well the gut and pancreas are functioning together. It's important our pancreas is working well, as its enzymes allow us to digest our food properly.

**What causes low levels?** Age; smoking; small intestine infection; small intestine bacterial overgrowth (SIBO); inflammation in the small intestine; type-1, type-2 or gestational diabetes; celiac disease; inflammatory bowel disease; chronic stress; excess alcohol intake.

## IV. RECOMMENDATIONS

### *Based on your results, we recommend the following:*

- ✓ Eat 28g of fermented food or drink 200ml fermented drink daily. Fermented foods include sauerkraut and kimchi, while good fermented drink choices are kefir and kombucha.
- ✓ Eat at least two probiotic foods daily. Choose from garlic, onions, asparagus, bananas, Jerusalem artichokes, leeks, barley, oats and apples.
- ✓ Fill up on fibre. We should all aim to eat 30g of fibre daily. Good sources of fibre are fruits and vegetables, whole grains, nuts, pulses and legumes. A good starting point is to fill half your plate with vegetables at both lunch and dinner, and snack on fruit and nuts if you're hungry.
- ✓ Be mindful of your saturated fat intake. We do need some saturated fat, but your gut bacteria don't like too much (especially if you're not eating enough fibre). A good starting point is to cut back on processed foods.
- ✓ Keep a gratitude diary. Treat yourself to a notebook and write down 3 things that you feel grateful for every day. You can also download The Five Minute Journal app.

### *Take the following supplements:*

PRODUCT NAME	DOSE	HOW TO TAKE	DURATION
Saccharomyces Boulardii by Seeking Health	2 capsules	Take whenever is most convenient.	6-8 weeks
Culturelle	2 capsules	Take 1 with breakfast and 1 with dinner.	6-8 weeks
Pro Digestion Intensive by Seeking Health	6 capsules	Take 2 with each meal.	6-8 weeks
AD Pro by Apex Energetics	1 capsule	Take whenever is most convenient.	6-8 weeks
GI Synergy by Apex Energetics	1 packet per day	Take whenever is most convenient.	6-8 weeks



These supplements can be bought individually.  
Many of the nutrients can also be found in the **Healthpath Gut Repair supplement bundle**.




*Disclaimer: if you're pregnant, breastfeeding, taking medications or suffering from a disease or medical condition, please consult your doctor before following these recommendations.*


# ANNEX

## Original Test Report

### Before Healthpath interpretation

Test	Result	Unit	Standard Range	Previous Result
<b>Stool Diagnostics</b>				
<b>Moleculargenetic Microbiomeanalysis MIDI</b>				
<b>Stool Properties</b>				



Colour	dark brown			braun <small>FE NAJ VISU</small>
Consistency	mushy			breiig <small>FE NAJ VISU</small>
pH	6,5		5,8 - 6,5 	6,0 <small>FE NAJ TESTS</small>


<b>Biodiversity</b>				
Diversity	5,29		> 5,0 	<small>FE NAJ MGSEQ</small>

The bacterial diversity in the intestinal tract may vary considerably from person to person. Antibiotic therapies, infections, increasing age, unbalanced diets or smoking are causes of declining diversity.

Grad

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<b>Bacteria Phyla (Distribution)</b>				
Bacteroidetes	55,4	%	30 - 60 	<small>FE NAJ MGSEQ</small>
Firmicutes	39,3	%	30 - 60 	<small>FE NAJ MGSEQ</small>

<b>Ratio</b>				
Firmicutes/Bacteroidetes	0,71	Quotient	< 1,5 	<small>FE NAJ RECHN</small>

<b>Enterotype</b>				
Bacteroides				<small>FE NAJ MGSEQ</small>

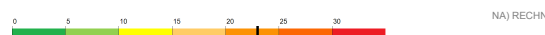
Human intestinal microbiomes can be differentiated into three Enterotypes. Enterotypes are defined by dominant bacterial clusters with distinct metabolic properties.

Enterotyp

1











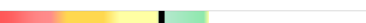









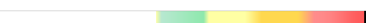





<b>Dysbiosis index</b>				
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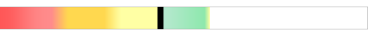









The dysbiosis index represents a measure of deviations within the microbiome. Depending on their relevance, all detected phyla, genera and species are considered.





























Index

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Test	Result	Unit	Standard Range		Previous Result
<b>Bacteria Phyla - most important genera and species</b>					
<b>Actinobacteria</b>					
Bifidobacteria	9,8 x 10 <sup>8</sup>	CFU/g faeces	> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Bifidobacterium longum	79	%			FE NA) MGSEQ
Equol producing bacteria	4,1 x 10 <sup>9</sup>	CFU/g faeces	> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
<b>Bacteroidetes</b>					
Bacteroides	5,0 x 10 <sup>11</sup>	CFU/g faeces	> 1,5 x 10 <sup>11</sup>		FE NA) MGSEQ
Prevotella	< 1,0 x 10 <sup>6</sup>	CFU/g faeces	> 1,0 x 10 <sup>10</sup>		FE NA) MGSEQ
<b>Firmicutes</b>					
<b>Butyrate producing bacteria</b>					
Faecalibacterium prausnitzii	5,4 x 10 <sup>10</sup>	CFU/g faeces	> 5,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Eubacterium rectale	6,5 x 10 <sup>9</sup>	CFU/g faeces	> 1,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Eubacterium hallii	2,4 x 10 <sup>9</sup>	CFU/g faeces	> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Roseburia spp.	3,4 x 10 <sup>10</sup>	CFU/g faeces	> 2,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Ruminococcus spp.	6,2 x 10 <sup>10</sup>	CFU/g faeces	> 3,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Coprococcus	4,6 x 10 <sup>9</sup>	CFU/g faeces	> 2,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Total bacterial count	1,9 x 10 <sup>11</sup>	CFU/g faeces	> 1,3 x 10 <sup>11</sup>		FE NA) MGSEQ
<b>Clostridia</b>					
Clostridia total bacterial count	1,2 x 10 <sup>10</sup>	CFU/g faeces	< 4,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Clostridia cluster I	1,5 x 10 <sup>9</sup>	CFU/g faeces	< 2,0 x 10 <sup>9</sup>		FE NA) MGSEQ
<b>Fusobacteria</b>					
Fusobacterium spp.	< 1,0 x 10 <sup>6</sup>	CFU/g faeces	< 1,0 x 10 <sup>7</sup>		FE NA) MGSEQ
<b>Verrucomicrobia</b>					
Akkermansia muciniphila	3,6 x 10 <sup>7</sup>	CFU/g faeces	> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
<b>Proteobacteria</b>					
<b>Pathogenic or potentially pathogenic bacteria</b>					
Haemophilus	8,9 x 10 <sup>8</sup>	CFU/g faeces	< 1,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Acinetobacter	< 1,0 x 10 <sup>6</sup>	CFU/g faeces	< 1,0 x 10 <sup>6</sup>		FE NA) MGSEQ
Escherichia coli BioVare	< 1,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Proteus species	< 1,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Klebsiella species	< 1,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Enterobacter species	4,0 x 10 <sup>8</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		4,0 x 10 <sup>8</sup> FE A) KULTAZ
Serratia species	< 1,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Hafnia species	< 1,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Morganella spp.	< 1,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>4</sup>		FE NA) MIB
<b>Histamin Developing Bacteria</b>					
Histaminbildende Bakterien	1,6 x 10 <sup>8</sup>	CFU/g faeces	< 5,0 x 10 <sup>8</sup>		FE NA) MGSEQ
<b>H2S production</b>					
Sulphate reducing bacteria	5,2 x 10 <sup>8</sup>	CFU/g faeces	< 2,0 x 10 <sup>9</sup>		FE NA) MGSEQ

Test	Result	Unit	Standard Range		Previous Result
<b>Immunogenicity / Mucus production</b>					
<b>Immunogenically effective bacteria</b>					
Escherichia coli	4,0 x 10 <sup>8</sup>	CFU/g faeces	10 <sup>6</sup> - 10 <sup>7</sup>		2,0 x 10 <sup>8</sup> FE A) KULTAZ
Enterococcus species	1,0 x 10 <sup>8</sup>	CFU/g faeces	10 <sup>6</sup> - 10 <sup>7</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Lactobacillus species	1,0 x 10 <sup>5</sup>	CFU/g faeces	10 <sup>5</sup> - 10 <sup>7</sup>		4,0 x 10 <sup>4</sup> FE A) KULTAZ
<b>Mucin production / Mucosa barrier</b>					
Akkermansia muciniphila	3,6 x 10 <sup>7</sup>	CFU/g faeces	> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Faecalibacterium prausnitzii	5,4 x 10 <sup>10</sup>	CFU/g faeces	> 5,0 x 10 <sup>10</sup>		FE NA) MGSEQ
<b>Yeasts / Molds</b>					
Candida albicans	< 1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		< 1,0 x 10 <sup>3</sup> FE A) KULTAZ
Candida species	2,0 x 10 <sup>4</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		4,0 x 10 <sup>3</sup> FE A) KULTAZ
Geotrichum candidum	< 1,0 x 10 <sup>3</sup>	CFU/g faeces	< 1,0 x 10 <sup>3</sup>		< 1,0 x 10 <sup>3</sup> FE A) KULTAZ
Moulds	negative		negative		negativ FE A) KULTAZ
<b>Parasites</b>					
Giardia lamblia	negative		negative		negativ FE NA) MOLEK
Entamoeba histolytica	negative		negative		negativ FE NA) MOLEK
Cryptosporidium spp.	negative		negative		negativ FE NA) MOLEK
Blastocystis hominis	positive		negative		positiv FE NA) MOLEK
Dientamoeba fragilis	negative		negative		negativ FE NA) MOLEK
Cyclospora cayetanensis	negative		negative		negativ FE NA) MOLEK

Test	Result	Unit	Standard Range		Previous Result
<b>Bacteria Phyla - most important genera and species</b>					
<b>Actinobacteria</b>					
Bifidobacteria	<b>9,8 x 10<sup>8</sup></b> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Bifidobacterium longum	79	%			FE NA) MGSEQ
Equol producing bacteria	<b>4,1 x 10<sup>9</sup></b> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
<b>Bacteroidetes</b>					
Bacteroides	5,0 x 10 <sup>11</sup> CFU/g faeces		> 1,5 x 10 <sup>11</sup>		FE NA) MGSEQ
Prevotella	<b>&lt; 1,0 x 10<sup>6</sup></b> CFU/g faeces		> 1,0 x 10 <sup>10</sup>		FE NA) MGSEQ
<b>Firmicutes</b>					
<b>Butyrate producing bacteria</b>					
Faecalibacterium prausnitzii	5,4 x 10 <sup>10</sup> CFU/g faeces		> 5,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Eubacterium rectale	<b>6,5 x 10<sup>9</sup></b> CFU/g faeces		> 1,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Eubacterium hallii	<b>2,4 x 10<sup>9</sup></b> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Roseburia spp.	3,4 x 10 <sup>10</sup> CFU/g faeces		> 2,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Ruminococcus spp.	6,2 x 10 <sup>10</sup> CFU/g faeces		> 3,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Coprococcus	<b>4,6 x 10<sup>9</sup></b> CFU/g faeces		> 2,0 x 10 <sup>10</sup>		FE NA) MGSEQ
Total bacterial count	1,9 x 10 <sup>11</sup> CFU/g faeces		> 1,3 x 10 <sup>11</sup>		FE NA) MGSEQ
<b>Clostridia</b>					
Clostridia total bacterial count	<b>1,2 x 10<sup>10</sup></b> CFU/g faeces		< 4,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Clostridia cluster I	1,5 x 10 <sup>9</sup> CFU/g faeces		< 2,0 x 10 <sup>9</sup>		FE NA) MGSEQ
<b>Fusobacteria</b>					
Fusobacterium spp.	< 1,0 x 10 <sup>6</sup> CFU/g faeces		< 1,0 x 10 <sup>7</sup>		FE NA) MGSEQ
<b>Verrucomicrobia</b>					
Akkermansia muciniphila	<b>3,6 x 10<sup>7</sup></b> CFU/g faeces		> 5,0 x 10 <sup>9</sup>		FE NA) MGSEQ
<b>Proteobacteria</b>					
<b>Pathogenic or potentially pathogenic bacteria</b>					
Haemophilus	8,9 x 10 <sup>8</sup> CFU/g faeces		< 1,0 x 10 <sup>9</sup>		FE NA) MGSEQ
Acinetobacter	< 1,0 x 10 <sup>6</sup> CFU/g faeces		< 1,0 x 10 <sup>6</sup>		FE NA) MGSEQ
Escherichia coli BioVare	< 1,0 x 10 <sup>4</sup> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Proteus species	< 1,0 x 10 <sup>4</sup> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Klebsiella species	< 1,0 x 10 <sup>4</sup> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Enterobacter species	<b>4,0 x 10<sup>8</sup></b> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		<b>4,0 x 10<sup>8</sup></b> FE A) KULTAZ
Serratia species	< 1,0 x 10 <sup>4</sup> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Hafnia species	< 1,0 x 10 <sup>4</sup> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		< 1,0 x 10 <sup>4</sup> FE A) KULTAZ
Morganella spp.	< 1,0 x 10 <sup>4</sup> CFU/g faeces		< 1,0 x 10 <sup>4</sup>		FE NA) MIB
<b>Histamin Developing Bacteria</b>					
Histaminbildende Bakterien	1,6 x 10 <sup>8</sup> CFU/g faeces		< 5,0 x 10 <sup>8</sup>		FE NA) MGSEQ
<b>H2S production</b>					
Sulphate reducing bacteria	5,2 x 10 <sup>8</sup> CFU/g faeces		< 2,0 x 10 <sup>9</sup>		FE NA) MGSEQ