

Patient		Sample		Order	
Name	Sam Sample	Type	Swab	Report Date	February 12, 2019
DOB	N/A	Source	Fecal	Provider	John Doe, MD
Age	N/A	Collected	December 07, 2018	Provider NPI	8889823333
Gender	Male	Received	December 12, 2018	Order Date	April 01, 2018
Patient ID	12039810938190123				

Results and interpretation of this test

Your SmartGut test results indicate that your **microbial diversity score** is **normal**. This indicates that your gut microbiome is similar to that of individuals within the healthy reference range.




Your sample tested **negative** for all 5 pathogens reported on the SmartGut test: *Campylobacter*, *Clostridium difficile*, *Escherichia/Shigella*, *Salmonella enterica*, and *Vibrio cholerae*.

Microbial Diversity ● Normal

The microbial diversity score measures how many different kinds of microorganisms are present in your sample and how they are distributed. Higher microbial diversity is generally considered to be an indicator of a healthy gut.

How Your Results Compare: Gut Conditions Highlights

Each of the percentiles below shows how your test results compare with those of our healthy users (people who don't have the condition). A result above the 50th percentile means that you have more out-of-range organisms than most healthy users.

<p>Irritable Bowel Syndrome (IBS)</p>  <p>60th</p>	<p>Inflammatory Bowel Disease (IBD): Crohn's Disease</p>  <p>50th</p>	<p>Inflammatory Bowel Disease (IBD): Ulcerative Colitis</p>  <p>40th</p>
---	--	---

SmartGut results do not imply a diagnosis or lack of diagnosis. Please consult your healthcare provider to interpret the results provided in this report.

Pathogenic Species

<p><i>Clostridium difficile</i></p> <p>● Negative</p>	<p><i>Salmonella enterica</i></p> <p>● Negative</p>	<p><i>Vibrio cholerae</i></p> <p>● Negative</p>
---	---	---






















Pathogenic Genera

<p><i>Campylobacter</i></p> <p>● Negative</p>	<p><i>Escherichia/Shigella</i></p> <p>● Negative</p>
---	--

Probiotic Organisms

The World Health Organization defines probiotics as "live microorganisms which, when administered in adequate amounts, confer a health benefit on the host." The probiotic bacteria presented in this section are typically found in foods or probiotic supplements. The indicated abundance is based upon the average abundance in gut samples from self-reported healthy individuals from our internal database.

The levels of these bacteria do not necessarily correlate with health or disease. They are not naturally present in the gut and are derived from eating probiotic foods or supplements containing these bacteria. Many healthy people do not have detectable probiotic bacteria in their stool. This section is offered for informational purposes and is not intended to replace professional medical advice, diagnosis, or treatment. Always consult with your healthcare provider before making any changes to your diet, medications, or treatments.

Microorganism	Result	Foods that are high in this probiotic
<i>Bacillus coagulans</i>	 Normal	Probiotic supplements
<i>Bifidobacterium*</i>	 Normal	Cheese, Kefir, Raw cow milk, Yogurt, and Probiotic supplements
<i>Bifidobacterium animalis</i>	 Normal	Cheese and Probiotic supplements
<i>Bifidobacterium bifidum</i>	 Normal	Kefir, Yogurt, and Probiotic supplements
<i>Clostridium butyricum</i>	 Normal	Bee products
<i>Enterococcus italicus</i>	 Normal	Cheese and Raw cow milk
<i>Lactobacillus*</i>	 Low	Cheese, Kefir, Raw Cow Milk, Yogurt, Kimchi, Pickles, Sauerkraut, Bee Products, and Probiotic supplements
<i>Lactobacillus brevis</i>	 Normal	Kefir, Kimchi, Sauerkraut, Bee Products, and Probiotic supplements
<i>Lactobacillus coryniformis</i>	 Normal	Probiotic supplements
<i>Lactobacillus delbrueckii</i>	 Normal	Raw cow milk
<i>Lactobacillus fermentum</i>	 Normal	Kefir, Raw cow milk, and Probiotic supplements
<i>Lactobacillus helveticus</i>	 Normal	Raw cow milk, Kefir, and Probiotic supplements
<i>Lactobacillus kefiranoformis</i>	 Normal	Kefir
<i>Lactobacillus kunkeei</i>	 Normal	Bee Products
<i>Lactobacillus rhamnosus</i>	 Normal	Raw cow milk and Probiotic supplements
<i>Lactobacillus salivarius</i>	 Normal	Cheese and Probiotic supplements
<i>Lactococcus lactis</i>	 Normal	Cheese, Raw cow milk, Kimchi, Bee Products, and Probiotic supplements
<i>Leuconostoc kimchii</i>	 Normal	Kimchi
<i>Pediococcus pentosaceus</i>	 Normal	Raw cow milk, Kimchi, Pickles, and Sauerkraut
<i>Propionibacterium freudenreichii</i>	 Normal	Raw cow milk, Kimchi, Pickles, and Sauerkraut
<i>Weissella koreensis</i>	 Normal	Kimchi

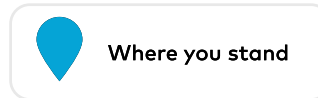
*This result shows the amount of a probiotic group of bacteria at the genus level. The genus level result combines the amounts of all species within this group, including, but not limited to, the ones listed above. It is very normal to have **low** levels of the *Lactobacillus* and *Bifidobacterium* probiotic genera while having **normal - medium** levels of the species reported on the SmartGut test.

Health Conditions and the Gut Microbiome

On the following pages you will find information about how your gut microbiome correlates with 18 different health conditions. Microorganisms presented here have been associated with each health condition based on scientific literature. Some organisms have a more significant impact on conditions than others. Where possible, the results for each condition are summarized in the Significance Index, which weighs how your intestinal microbiome differs from that of healthy individuals.

How Your Results Compare

This value looks at how many out-of-range organisms you have for a condition, compared with our healthy users (people who don't have the condition). Having out-of-range organisms is not unusual. This simply means that one or more of the microorganisms associated with the condition were outside of the healthy range in your sample. Some healthy users also have out-of-range organisms.




Having a result below the 50th percentile means that you have **fewer out-of-range organisms** than most of our healthy users. In contrast, having a result above the 50th percentile means that you have **more out-of-range organisms** than most of our healthy users.


Having a result at the 50th percentile means you're in the middle (median), with a **similar number** of healthy users having **more out-of-range organisms** and **fewer out-of-range organisms** than you.

The percentiles in this report are calculated using the most current knowledge as of the reporting date. This information does not predict the likelihood of developing a specific disease, nor does it imply protection against a specific disease. Detection of a microorganism by this test does not imply a diagnosis. Similarly, a lack of detection does not exclude the presence of a disease-causing microorganism or a diagnosis of disease. Please consult your healthcare provider to interpret the results provided in this report.


Gut Conditions


Your microbiome may include microorganisms associated with conditions such as irritable bowel syndrome (IBS), Crohn's disease, ulcerative colitis, and infectious diarrhea. Use the section below to find out more about the relationship between these gut conditions and your microbiome. Please consult with your healthcare provider for follow-up regarding these results.

Infectious Diarrhea		How Your Results Compare: 60th 	
Association	Organism	Result	Out of Range
Associated	<i>Bacteroides fragilis</i> [1,2]	● Normal	
	<i>Campylobacter</i> [3,4]	● Negative	
	<i>Clostridium</i> [5,6]	● Normal	
	<i>Clostridium difficile</i> [4,7]	● Negative	
	<i>Escherichia/Shigella</i> [4,8]	● Negative	
	<i>Salmonella enterica</i> [4,8]	● Negative	
	<i>Vibrio cholerae</i> [4,9]	● Negative	
Inversely Associated	<i>Lactobacillus</i> [10]	● Low	⚠ Condition more likely
	Microbial Diversity [11,12]	● Normal	


Irritable Bowel Syndrome (IBS)		How Your Results Compare: 60th 	
Association	Organism	Result	Out of Range
Associated	<i>Campylobacter</i> [13]	● Negative	
	<i>Escherichia/Shigella</i> [13]	● Negative	
	<i>Methanobrevibacter smithii</i> [14]	● Low	
	<i>Salmonella enterica</i> [15]	● Negative	
	<i>Veillonella</i> [16]	● Normal	
Inversely associated	<i>Alistipes</i> [17]	● Normal	
	<i>Bifidobacterium</i> [18]	● Normal	
	<i>Collinsella aerofaciens</i> [19-21]	● Normal	
	<i>Paraprevotella</i> [17]	● Low	⚠ Condition more likely
	<i>Lactobacillus</i> [16]	● Low	⚠ Condition more likely

Gut Conditions (continued)

Inflammatory Bowel Disease (IBD)		How Your Results Compare: 0 	
Association	Organism	Result	Out of Range
Associated	<i>Campylobacter</i> [22]	● Negative	
	<i>Desulfovibrio piger</i> [23]	● Normal	
	<i>Fusobacterium</i> [24]	● Normal	
Inversely associated	<i>Roseburia</i> [25]	● Normal	

Crohn's Disease		How Your Results Compare: 50th 	
Association	Organism	Result	Out of Range
Associated	<i>Clostridium</i> [25,26]	● Normal	
	<i>Clostridium difficile</i> [27]	● Negative	
	<i>Escherichia/Shigella</i> [25]	● Negative	
	<i>Methanobrevibacter smithii</i> [28]	● Low	
	<i>Parabacteroides</i> [26]	● Normal	
Inversely associated	<i>Akkermansia muciniphila</i> [29]	● Low	⚠ Condition more likely
	<i>Bacteroides</i> [28,30]	● Normal	
	<i>Bacteroides fragilis</i> [30]	● Normal	
	<i>Bifidobacterium</i> [26,28,30]	● Normal	
	<i>Dialister invisus</i> [31]	● Low	⚠ Condition more likely
	<i>Lactobacillus</i> [28]	● Low	⚠ Condition more likely
	<i>Odoribacter</i> [25]	● Normal	
	<i>Phascolarctobacterium</i> [25]	● Normal	
	<i>Prevotella</i> [30]	● Normal	
	<i>Roseburia</i> [25]	● Normal	
	<i>Ruminococcus</i> [28]	● Normal	
	Microbial Diversity [32]	● Normal	

Gut Conditions (continued)

Ulcerative Colitis		How Your Results Compare: 40th 	
Association	Organism	Result	Out of Range
Associated	<i>Campylobacter</i> [22,26,33]	● Negative	
	<i>Clostridium</i> [25]	● Normal	
	<i>Clostridium difficile</i> [27,34]	● Negative	
	<i>Methanobrevibacter smithii</i> [28]	● Low	
	<i>Ruminococcus albus</i> [35]	● Normal	
	<i>Salmonella enterica</i> [15]	● Negative	
Inversely associated	<i>Akkermansia muciniphila</i> [29]	● Low	⚠ Condition more likely
	<i>Bacteroides</i> [28,30]	● Normal	
	<i>Bacteroides fragilis</i> [30]	● Normal	
	<i>Bifidobacterium</i> [28,30]	● Normal	
	<i>Lactobacillus</i> [28]	● Low	⚠ Condition more likely
	<i>Odoribacter</i> [25]	● Normal	
	<i>Phascolarctobacterium</i> [25]	● Normal	
	<i>Prevotella</i> [30]	● Normal	
	<i>Roseburia</i> [25]	● Normal	
	<i>Ruminococcus</i> [28]	● Normal	
	Microbial Diversity [36]	● Normal	

Asymptomatic Diverticulosis			
Association	Organism	Result	Out of Range
Associated	<i>Akkermansia muciniphila</i> [44]	● Low	

Gut Symptoms


Your microbiome may include microorganisms associated with gut symptoms such as constipation, abdominal pain, bloating, and flatulence. Use the section below to find out more about the relationship between these gut symptoms and your microbiome. Please consult with your healthcare provider for follow-up regarding these results.

Abdominal Pain		How Your Results Compare: 20th	
Association	Organism	Result	Out of Range
Associated	<i>Ruminococcus flavefaciens</i> [37]	● Low	
Inversely associated	<i>Methanobrevibacter smithii</i> [38]	● Low	⚠ Condition more likely
	<i>Ruminococcus</i> [37]	● Normal	

Bloating		How Your Results Compare: 0	
Association	Organism	Result	Out of Range
Associated	<i>Anaerotruncus colihominis</i> [37]	● Low	
	<i>Butyrivibrio crossotus</i> [37]	● Low	
	<i>Ruminococcus flavefaciens</i> [37]	● Low	


Constipation		How Your Results Compare: 0	
Association	Organism	Result	Out of Range
Associated	<i>Butyricimonas</i> [39,40]	● Normal	
	<i>Coprococcus</i> [39,40]	● Normal	
	<i>Faecalibacterium</i> [40]	● Normal	
	<i>Gelria</i> [39]	● Normal	
	<i>Holdemania</i> [39]	● Normal	
	<i>Methanobrevibacter smithii</i> [41]	● Low	
	<i>Paraprevotella</i> [39]	● Low	
	<i>Phascolarctobacterium</i> [39]	● Normal	
	<i>Veillonella</i> [19]	● Normal	
Inversely associated	<i>Bifidobacterium</i> [42]	● Normal	
	<i>Roseburia</i> [39,40]	● Normal	


Gut Symptoms (continued)

Flatulence		How Your Results Compare: 70th	
Association	Organism	Result	Out of Range
Associated	<i>Bacteroides fragilis</i> [43]	● Normal	
	<i>Blautia</i> [43]	● Normal	
	<i>Clostridium</i> [43]	● Normal	
	<i>Coprococcus</i> [43]	● Normal	
	<i>Phascolarctobacterium</i> [43]	● Normal	
Inversely associated	<i>Oscillospira</i> [43]	● Low	 Condition more likely

Metabolic Conditions

The composition of the gut microbiome has been linked to metabolic conditions, including diabetes, obesity, and non-alcoholic fatty liver disease. Use the section below to find out more about the relationship between metabolic health and your microbiome. Please consult with your healthcare provider for follow-up regarding these results.

Obesity		How Your Results Compare: 70th 	
Association	Organism	Result	Out of Range
Associated	<i>Bacteroides</i> [45]	● Normal	
	<i>Fusobacterium</i> [46]	● Normal	
	<i>Lactobacillus</i> [47]	● Low	
Inversely associated	<i>Akkermansia muciniphila</i> [48,49]	● Low	⚠ Condition more likely
	<i>Alistipes</i> [17]	● Normal	
	<i>Anaerotruncus colihominis</i> [17,50]	● Low	⚠ Condition more likely
	<i>Barnesiella</i> [17]	● Normal	
	<i>Bifidobacterium</i> [45]	● Normal	
	<i>Butyrivibrio crossotus</i> [51,52]	● Low	⚠ Condition more likely
	<i>Butyricimonas</i> [53]	● Normal	
	<i>Dialister</i> [54]	● Low	⚠ Condition more likely
	<i>Methanobrevibacter smithii</i> [45,55]	● Low	⚠ Condition more likely
	<i>Ruminococcus flavefaciens</i> [45]	● Low	⚠ Condition more likely
	Microbial Diversity [46,51,52,56]	● Normal	

Prediabetes		How Your Results Compare: 30th 	
Association	Organism	Result	Out of Range
Associated	<i>Prevotella</i> [57]	● Normal	
	<i>Veillonella</i> [57]	● Normal	
Inversely associated	<i>Akkermansia muciniphila</i> [58]	● Low	⚠ Condition more likely
	<i>Bifidobacterium</i> [57]	● Normal	
	<i>Butyricimonas</i> [57]	● Normal	
	Microbial Diversity [51]	● Normal	

Metabolic Conditions (continued)

Type 2 Diabetes		How Your Results Compare: 10th	
Association	Organism	Result	Out of Range
Associated	<i>Akkermansia muciniphila</i> [59]	● Low	
	<i>Barnesiella</i> [60]	● Normal	
	<i>Collinsella</i> [61]	● Normal	
	<i>Prevotella</i> [62,63]	● Normal	
Inversely associated	<i>Lactobacillus</i> [64,65]	● Low	⚠ Condition more likely
	<i>Roseburia</i> [59,66]	● Normal	

Non-Alcoholic Fatty Liver Disease		How Your Results Compare: 80th	
Association	Organism	Result	Out of Range
Associated	<i>Escherichia/Shigella</i> [67]	● Negative	
	<i>Streptococcus</i> [67]	● Normal	
Inversely associated	<i>Alistipes</i> [67]	● Normal	
	<i>Flavonifractor</i> [67]	● Low	⚠ Condition more likely
	<i>Odoribacter</i> [67]	● Normal	
	<i>Oscillibacter</i> [67]	● Low	⚠ Condition more likely

Cardiovascular Conditions

Your microbiome may include microorganisms associated with cardiovascular conditions, including cardiovascular disease and atherosclerosis. Use this section below to find out more about the relationship between cardiovascular conditions and your microbiome. Please consult with your healthcare provider for follow-up regarding these results.

Atherosclerosis		How Your Results Compare: 0	
Association	Organism	Result	Out of Range
Associated	<i>Collinsella</i> [68]	● Normal	
Inversely associated	<i>Roseburia</i> [68]	● Normal	

Cardiovascular Disease		How Your Results Compare: 10th	
Association	Organism	Result	Out of Range
Associated	<i>Tyzzarella</i> [69]	● Normal	
Inversely associated	<i>Alloprevotella</i> [69]	● Low	Condition more likely
	<i>Catenibacterium</i> [69]	● Normal	
	Microbial Diversity [69]	● Normal	

Kidney Conditions

The composition of the gut microbiome has been linked with kidney conditions, including kidney stones and chronic kidney disease. Use this section to find out more about the relationship between kidney health and your microbiome. Please consult your healthcare provider for follow-up regarding these results.

Kidney Stones		How Your Results Compare: 30th	
Association	Organism	Result	Out of Range
Associated	<i>Bacteroides</i> [70]	● Normal	
Inversely associated	<i>Oxalobacter formigenes</i> [71]	● Low	⚠ Condition more likely
	<i>Prevotella</i> [70]	● Normal	

Chronic Kidney Disease		How Your Results Compare: 0	
Association	Organism	Result	Out of Range
Inversely associated	<i>Bacteroides fragilis</i> [72]	● Normal	
	<i>Bifidobacterium</i> [72]	● Normal	
	<i>Prevotella</i> [72]	● Normal	
	<i>Roseburia</i> [72]	● Normal	

Definitions

The reference range for each organism and the microbial diversity score were established using 865 samples from individuals who self-reported as healthy. For more information about the healthy cohort, visit <http://ubiome.com/gutpaper> to access the publication explaining uBiome's methods.

For these conditions and symptoms:

Infectious Diarrhea	Obesity
Irritable Bowel Syndrome	Prediabetes
Inflammatory Bowel Disease	Type 2 Diabetes
Crohn's Disease	Non-Alcoholic Fatty Liver Disease
Ulcerative Colitis	Atherosclerosis
Asymptomatic Diverticulosis	Cardiovascular Disease
Constipation	Kidney Stones
Chronic Kidney Disease	Abdominal Pain
Bloating	Flatulence

A microorganism is either:

Associated

These microorganisms have been found to be more abundant in people with the condition.

Inversely associated

These microorganisms have been found to be less abundant in people with the condition.

For the following microorganisms:

Campylobacter
Clostridium difficile
Escherichia/Shigella
Salmonella enterica
Vibrio cholerae

Results are displayed as:

● Negative ● Positive

Negative: Microorganism in the sample is within the 99th percentile of the reference range.

Positive: Microorganism in the sample exceeds the upper 99th percentile of the reference range.

For the the following microorganisms:

<i>Akkermansia muciniphila</i>	<i>Lactobacillus</i>
<i>Anaerotruncus colihominis</i>	<i>Methanobrevibacter smithii</i>
<i>Bacteroides</i>	<i>Paraprevotella</i>
<i>Bacteroides fragilis</i>	<i>Phascolarctobacterium</i>
<i>Barnesiella</i>	<i>Prevotella</i>
<i>Butyricimonas</i>	<i>Ruminococcus flavefaciens</i>
<i>Butyrivibrio crossotus</i>	

Results are displayed as:

● Low ● Normal ● High

Low: Microorganism in the sample is absent or below the lower 99th percentile of the reference range.

Normal: Microorganism in the sample is within the 99th percentile of the reference range.

High: Microorganism in the sample is above the 99th percentile of the reference range.

For the following microorganisms:

<i>Blautia</i>	<i>Gelria</i>
<i>Clostridium</i>	<i>Holdemania</i>
<i>Collinsella</i>	<i>Parabacteroides</i>
<i>Coprococcus</i>	<i>Ruminococcus albus</i>
<i>Desulfovibrio piger</i>	<i>Streptococcus</i>
<i>Faecalibacterium</i>	<i>Tyzzera</i>
<i>Fusobacterium</i>	<i>Veillonella</i>

Results are displayed as:

● Normal ● High

Normal: Microorganism in the sample is within the 99th percentile of the reference range.

High: Microorganism in the sample is above the 99th percentile of the reference range.

Definitions (continued)

For the following microorganisms:

<i>Alistipes</i>	<i>Flavonifractor</i>
<i>Alloprevotella</i>	<i>Odoribacter</i>
<i>Bifidobacterium</i>	<i>Oscillibacter</i>
<i>Catenibacterium</i>	<i>Oxalobacter formigenes</i>
<i>Collinsella aerofaciens</i>	<i>Roseburia</i>
<i>Dialister</i>	<i>Ruminococcus</i>
<i>Dialister invisus</i>	

Results are displayed as:

● Low ● Normal

Low: Microorganism in the sample is absent or below the lower 99th percentile of the reference range.

Normal: Microorganism in the sample is within the 99th percentile of the reference range.

For the microbial diversity score:

Results are displayed as:

● Low ● Normal ● High

Normal: Microorganism in the sample is within the 95th percentile of the reference range.

High: Microorganism in the sample is above the 95th percentile of the reference range.

Low: Microorganism in the sample is below the lower 95th percentile of the reference range.

For these sources of probiotics:

Cheese	Pickles
Kefir	Sauerkraut
Raw cow milk	Bee products
Yogurt	Kimchi
Probiotic supplements	

A microorganism is:

Associated: These microorganisms have been found in these food sources or Probiotic supplements.

For the following microorganisms:

<i>Bacillus coagulans</i>	<i>Lactobacillus kefiranofaciens</i>
<i>Bifidobacterium animalis</i>	<i>Lactobacillus rhamnosus</i>
<i>Bifidobacterium bifidum</i>	<i>Lactobacillus salivarius</i>
<i>Clostridium butyricum</i>	<i>Lactococcus lactis</i>
<i>Lactobacillus brevis</i>	<i>Leuconostoc kimchii</i>
<i>Lactobacillus delbrueckii</i>	<i>Pediococcus pentosaceus</i>
<i>Lactobacillus fermentum</i>	<i>Propionibacterium freudenreichii</i>
<i>Lactobacillus helveticus</i>	<i>Weissella koreensis</i>

Results are displayed as:

Normal Medium High

Normal: Microorganism was not detected in the sample.

Medium: Microorganism in the sample is within the 50th percentile of samples with detected taxa.

High: Microorganism in the sample is above the 50th percentile of samples with detected taxa.

For the following microorganisms:

<i>Enterococcus italicus</i>	<i>Lactobacillus coryniformis</i>
<i>Lactobacillus kunkeei</i>	

Results are displayed as:

Normal High

Normal: Microorganism was not detected in the sample.

High: Microorganism was detected in the sample.

Results outside of the healthy reference range are highlighted with an alert symbol:



References to scientific publications associating organisms with conditions are listed in brackets:

[1]

Methods & Limitations

In the SmartGut test, microbial DNA is extracted and marker genes are amplified by polymerase chain reaction (PCR) and then sequenced using the Illumina® NextSeq 500 sequencer. The sequence data is processed using a proprietary phylogenetic analysis algorithm. On average, the sensitivity, specificity, precision, and negative predictive value for the microorganisms on our target list are 97.7%, 99.9%, 98.0%, 100.0% for the species, and 97.2%, 99.9%, 99.1%, 99.9% for the genera, respectively.

This test detects the presence of the following microorganisms: *Alistipes*, *Alloprevotella*, *Bacteroides*, *Barnesiella*, *Bifidobacterium*, *Blautia*, *Butyricimonas*, *Campylobacter*, *Catenibacterium*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dialister*, *Escherichia/Shigella*, *Faecalibacterium*, *Flavonifractor*, *Fusobacterium*, *Gelria*, *Holdemania*, *Lactobacillus*, *Odoribacter*, *Oscillibacter*, *Oscillospira*, *Parabacteroides*, *Paraprevotella*, *Phascolarctobacterium*, *Prevotella*, *Roseburia*, *Ruminococcus*, *Streptococcus*, *Tyzzereella*, *Veillonella*, *Akkermansia muciniphila*, *Anaerotruncus colihominis*, *Bacillus coagulans*, *Bacteroides fragilis*, *Bifidobacterium animalis*, *Bifidobacterium bifidum*, *Butyrivibrio crossotus*, *Clostridium butyricum*, *Clostridium difficile*, *Collinsella aerofaciens*, *Desulfovibrio piger*, *Dialister invisus*, *Enterococcus italicus*, *Lactobacillus brevis*, *Lactobacillus coryniformis*, *Lactobacillus delbrueckii*, *Lactobacillus fermentum*, *Lactobacillus helveticus*, *Lactobacillus kefirifaciens*, *Lactobacillus kunzei*, *Lactobacillus rhamnosus*, *Lactobacillus salivarius*, *Lactococcus lactis*, *Leuconostoc kimchii*, *Methanobrevibacter smithii*, *Oxalobacter formigenes*, *Pediococcus pentosaceus*, *Propionibacterium freudenreichii*, *Ruminococcus albus*, *Ruminococcus flavefaciens*, *Salmonella enterica*, *Vibrio cholerae*, and *Weissella koreensis*.

Some of these microorganisms may not be considered pathogenic but are included as they reflect the state of the patient's microbiome. The microbiome and its clinical relevance is an area of active investigation. This sample has passed all laboratory and sample quality metrics.

About SmartGut

Detection of a microorganism by this test does not imply a diagnosis. Similarly, a lack of detection does not exclude the presence of a disease-causing microorganism or a diagnosis of disease. Please consult your healthcare provider to interpret the results provided in this report.

The SmartGut test was developed, and its performance characteristics were determined, by uBiome, Inc. For more information about the methods underlying uBiome's SmartGut test, please see Almonacid *et al.*, 2017 (<http://ubiome.com/gutpaper>). This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary. This test may be used for clinical purposes and should not be regarded as investigational or for research only. uBiome's clinical reference laboratory is accredited by the internationally recognized College of American Pathologists (CAP) and is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) as qualified to perform high complexity clinical laboratory testing.

This test is a next-generation sequencing-based assay that can identify 33 species and 32 genera of gastrointestinal microbiome related microorganisms from a stool swab sample, including 5 pathogenic organisms. The detection (or lack thereof) of microorganisms is reported to the medical professional in this report. The report should be considered in context with other clinical criteria (e.g. patient history, physical exam), as well as other studies (such as laboratory, pathology, and imaging) by a qualified medical professional prior to initiating or changing a patient diagnostic work-up or treatment plan.

Patient management decisions must be based on the independent medical judgment of the treating medical professional. The test and accompanying report are not intended to be used as the sole means for clinical diagnosis or patient management decisions.

The report may include information on the relevance of reported microorganisms. This information is derived from peer-reviewed studies and other publicly available databases and may include associations between the microorganism and a health condition. Careful consideration must be made by the medical professional when using this information, as it may or may not be relevant to this patient. Organisms not included in this test may also have an effect on the mentioned health conditions. The organisms on this test may affect additional health conditions not mentioned on this report.

SmartGut is a clinical test, successfully validated using samples collected from individuals of mainly adult age, with a subset of minors. When ordered for minors, the results may still provide valuable information about the minor's health; however, the accuracy of the results will differ from what was validated for the adult age range.

The reference range for each organism was established using 865 samples from self-reported healthy individuals.

References

- [1] B. Durmaz, M. Dalgalar, R. Durmaz, *Anaerobe* 11 (2005) 318-321.
- [2] J.I. Keenan, A. Aitchison, R.V. Purcell, R. Greenlees, J.F. Pearson, F.A. Frizelle, *Anaerobe* 40 (2016) 50-53.
- [3] J. Silva, D. Leite, M. Fernandes, C. Mena, P.A. Gibbs, P. Teixeira, *Front. Microbiol.* 2 (2011) 200.
- [4] S.W. Pawlowski, C.A. Warren, R. Guerrant, *Gastroenterology* 136 (2009) 1874-1886.
- [5] S. Brynestad, P.E. Granum, *Int. J. Food Microbiol.* 74 (2002) 195-202.
- [6] B.M. Lund, M.W. Peck, in: *Guide to Foodborne Pathogens*, John Wiley & Sons, Oxford, 2013, pp. 91-111.
- [7] Y.P. Hung, J.C. Lee, H.J. Lin, H.C. Liu, Y.H. Wu, P.J. Tsai, W.C. Ko, *J. Microbiol. Immunol.* 48 (2015) 241-248.
- [8] D.R. Hill, N.J. Beeching, *Current Opinion in Infectious Diseases* 23 (2010) 481-487.
- [9] J.B. Harris, R.C. LaRocque, F. Qadri, E.T. Ryan, S.B. Calderwood, *Lancet* 379 (2012) 2466-2476.
- [10] P.B. Kale-Pradhan, H.K. Jassal, S.M. Wilhelm, *Pharmacotherapy* 30 (2010) 119-126.
- [11] J.Y. Chang, D.A. Antonopoulos, A. Kalra, A. Tonelli, W.T. Khalife, T.M. Schmidt, V.B. Young, *J. Infect. Dis.* 197 (2008) 435-438.
- [12] V.C. Antharam, E.C. Li, A. Ishmael, A. Sharma, V. Mai, K.H. Rand, G.P. Wang, *J. Clin. Microbiol.* 51 (2013) 2884-2892.
- [13] R.C. Spiller, *J. Gastroenterol.* 42 Suppl 17 (2007) 41-47
- [14] U. Ghoshal, R. Shukla, D. Srivastava, U.C. Ghoshal, *Gut and Liver* 10 (2016) 932-938.
- [15] M.K. Tripathi, C.B. Pratap, V.K. Dixit, T.B. Singh, S.K. Shukla, A.K. Jain, G. Nath, *Interdiscip. Perspect. Infect. Dis.* 2016 (2016) 5854285
- [16] E. Malinen, T. Rinttila, K. Kajander, J. Matto, A. Kassinen, L. Kroggius, M. Saarela, R. Korpela, A. Palva, *Am J Gastroenterology* 100 (2005) 373-382.
- [17] A. Zhernakova, A. Kurilshikov, M.J. Bonder, E.F. Tigchelaar, M. Schirmer, T. Vatanen, Z. Mujagic, A.V. Vila, G. Falony, S. Vieira-Silva, J. Wang, F. Imhann, E. Brandsma, S.A. Jankipersadsing, M. Joossens, M.C. Cenit, P. Deelen, M.A. Swertz, L. cohort Study, R.K. Weersma, E.J.M. Feskens, M.G. Netea, D. Gevers, D. Jonkers, L. Franke, Y.S. Aulchenko, C. Huttenhower, J. Raes, M.H. Hofker, R.J. Xavier, C. Wijmenga, J. Fu, *Science* 352 (2016) 565-569.
- [18] A.P. Kerckhoffs, M. Samsom, M.E. van der Rest, J. de Vogel, J. Knol, K. Ben-Amor, L.M. Akkermans, *World J Gastroenterol* 15 (2009) 2887-2892.
- [19] E. Malinen, L. Kroggius-Kurikka, A. Lyra, J. Nikkilä, A. Jääskeläinen, T. Rinttila, T. Vilpponen-Salmela, A.J. von Wright, A. Palva, *World J. Gastroenterol.* 16 (2010) 4532-4540.
- [20] A. Kassinen, L. Kroggius-Kurikka, H. Mäkituokko, T. Rinttila, L. Paulin, J. Corander, E. Malinen, J. Apajalahti, A. Palva, *Gastroenterology* 133 (2007) 24-33.
- [21] J. Jalanka-Tuovinen, J. Salojärvi, A. Salonen, O. Immonen, K. Garsed, F.M. Kelly, A. Zaitoun, A. Palva, R.C. Spiller, W.M. de Vos, *Gut* 63 (2014) 1737-1745.
- [22] V. Mahendran, S.M. Riordan, M.C. Grimm, T.A.T. Tran, J. Major, N.O. Kaakoush, H. Mitchell, L. Zhang, *PLOS ONE* 6 (2011) e25417.
- [23] J. Loubinoux, J.-P. Bronowicki, I.A.C. Pereira, J.-L. Mougénel, L. Faou, A. E, *FEMS Microbiol. Ecol.* 40 (2002) 107-112.
- [24] J. Strauss, G.G. Kaplan, P.L. Beck, K. Rioux, R. Panaccione, R. [57] DeVinney, T. Lynch, E. Allen-Vercoe, *Inflamm. Bowel Dis.* 17 (2011) 1971-1978.
- [25] X.C. Morgan, T.L. Tickle, H. Sokol, D. Gevers, K.L. Devaney, D.V. Ward, J.A. Reyes, S.A. Shah, N. LeLeiko, S.B. Snapper, A. Bousvaros, J. Korzenik, B.E. Sands, R.J. Xavier, C. Huttenhower, *Genome Biology* 13 (2012) R79.
- [26] F. Imhann, A. Vich Vila, M.J. Bonder, J. Fu, D. Gevers, M.C. Visschedijk, L.M. Spekhorst, R. Alberts, L. Franke, H.M. van Dullemen, R.W.F. Ter Steege, C. Huttenhower, G. Dijkstra, R.J. Xavier, E.A.M. Festen, C. Wijmenga, A. Zhernakova, R.K. Weersma, *Gut* 67 (2018) 108-119.
- [27] Y.B. Gu, M.C. Zhang, J. Sun, K.Z. Lv, J. Zhong, *J. Dig. Dis.* 18 (2017) 207-211.
- [28] R. Verma, A.K. Verma, V. Ahuja, J. Paul, *J. Clin. Microbiol.* 48 (2010) 4279-4282.
- [29] C.W. Png, S.K. Lindén, K.S. Gilshenan, E.G. Zoetendal, C.S. McSweeney, L.I. Sly, M.A. McGuckin, T.H.J. Florin, *Am J Gastroenterology* 105 (2010) 2420-2428.
- [30] S. Sha, B. Xu, X. Wang, Y. Zhang, H. Wang, X. Kong, H. Zhu, K. Wu, *Diagn. Microbiol. Infect. Dis.* 75 (2013) 245-251.
- [31] M. Joossens, G. Huys, M. Cnockaert, V.D. Preter, K. Verbeke, P. Rutgeerts, P. Vandamme, S. Vermeire, *Gut* 60 (2011) 631-637.
- [32] C. Manichanh, *Gut* 55 (2006) 205-211.
- [33] I. Mukhopadhyay, J.M. Thomson, R. Hansen, S.H. Berry, E.M. El-Omar, G.L. Hold, *PLOS ONE* 6 (2011) e21490.
- [34] H. Sokol, V. Lalande, C. Landman, A. Bourrier, I. Nion-Larmurier, S. Rajca, J. Kirchgesner, P. Seksik, J. Cosnes, F. Barbut, L. Beaugerie, *Digestive and Liver Disease* 49 (2017) 643-646.
- [35] A. Fite, S. Macfarlane, E. Furrrie, B. Bahrami, J.H. Cummings, D.T. Steinke, G.T. Macfarlane, *J. Clin. Microbiol.* 51 (2013) 849-856.
- [36] P. Lepage, R. Häsler, M.E. Spehlmann, A. Rehman, A. Zvirbliene, A. Begun, S. Ott, L. Kupcinskas, J. Doré, A. Raedler, S. Schreiber, *Gastroenterology* 141 (2011) 227-236.
- [37] J. Jalanka-Tuovinen, A. Salonen, J. Nikkilä, O. Immonen, R. Kekkonen, L. Lahti, A. Palva, W.M. de Vos, *PLoS One* 6 (2011).
- [38] G.A. Weaver, J.A. Krause, T.L. Miller, M.J. Wolin, *Gut* 27 (1986) 698-704.
- [39] L. Mancabelli, C. Milani, G.A. Lugli, F. Turroni, M. Mangifesta, A. Viappiani, A. Ticinesi, A. Nouvenne, T. Meschi, D. van Sinderen, M. Ventura, *Sci Rep* 7 (2017).
- [40] G. Parthasarathy, J. Chen, X. Chen, N. Chia, H.M. O'Connor, P.G. Wolf, H.R. Gaskins, A.E. Bharucha, *Gastroenterology* 150 (2016) 367-379.e1.
- [41] M. Pimentel, A.G. Mayer, S. Park, E.J. Chow, A. Hasan, Y. Kong, *Dig. Dis. Sci.* 48 (2003) 86-92.
- [42] C. Chassard, M. Dapoigny, K.P. Scott, L. Crouzet, C. Delhomme, P. Marquet, J.C. Martin, G. Pickering, D. Ardid, A. Eschaliere, C. Dubray, H.J. Flint, A. Bernalier-Donadille, *Aliment. Pharmacol. Ther.* 35 (2012) 828-838.
- [43] C. Manichanh, A. Eck, E. Varela, J. Roca, J.C. Clemente, A. González, D. Knights, R. Knight, S. Estrella, C. Hernandez, D. Guyonnet, A. Accarino, J. Santos, J.-R. Malagelada, F. Guarner, F. Azpiroz, *Gut* 63 (2014) 401-408.
- [44] A. Tursi, P. Mastromarino, D. Capobianco, W. Elisei, A. Miccheli, G. Capuani, A. Tomassini, G. Campagna, M. Picchio, G. Giorgetti, F. Fabbicchi, G. Brandimarte, *J. Clin. Gastroenterol.* 50 Suppl 1 (2016) S9-S12.
- [45] A. Schwiertz, D. Taras, K. Schäfer, S. Beijer, N.A. Bos, C. Donus, P.D. Hardt, *Obesity* 18 (2010) 190-195.
- [46] A. Andoh, A. Nishida, K. Takahashi, O. Inatomi, H. Imaeda, S. Bamba, K. Kito, M. Sugimoto, T. Kobayashi, *J. Clin. Biochem. Nutr.* 59 (2016) 65-70.
- [47] F. Armougom, M. Henry, B. Vialettes, D. Raccach, D. Raoult, *PLoS ONE* 4 (2009) e7125-8.
- [48] A. Santacruz, M.C. Collado, L. García-Valdés, M.T. Segura, J.A. Martí-Lagos, T. Anjos, M. Martí-Romero, R.M. Lopez, J. Florido, C. Campoy, Y. Sanz, *Br J Nutr* 104 (2010) 83-92.
- [49] S.F. Clarke, E.F. Murphy, O. O'Sullivan, A.J. Lucey, M. Humphreys, A. Hogan, P. Hayes, M. O'Reilly, I.B. Jeffery, R. Wood-Martin, D.M. Kerins, E. Quigley, R.P. Ross, P.W. O'Toole, M.G. Molloy, E. Falvey, F. Shanahan, P.D. Cotter, *Gut* 63 (2014) 1913-1920.
- [50] M.L. Zupancic, B.L. Cantarel, Z. Liu, E.F. Drabek, K.A. Ryan, S. Cirimotich, C. Jones, R. Knight, W.A. Walters, D. Knights, E.F. Mongodin, R.B. Horenstein, B.D. Mitchell, N. Steinle, S. Snitker, A.R. Shuldiner, C.M. Fraser, *PLoS ONE* 7 (2012) e43052.
- [51] E. Le Chatelier, T. Nielsen, J. Qin, E. Prifti, F. Hildebrand, G. Falony, M. Almeida, M. Arumugam, J.-M. Batto, S. Kennedy, P. Leonard, J. Li, K. Burgdorf, N. Grarup, T. Jorgensen, I. Brandslund, H.B. Nielsen, A.S. Juncker, M. Bertalan, F. Levenez, N. Pons, S. Rasmussen, S. Sunagawa, J. Tap, S. Tims, E.G. Zoetendal, S. Brunak, K. Clement, J. Doré, M. Kleerebezem, K. Kristiansen, P. Renault, T. Sicheritz-Ponten, W.M. de Vos, J.-D. Zucker, J. Raes, T. Hansen, MetaHIT consortium, P. Bork, J. Wang, S.D. Ehrlich, O. Pedersen, *Nature* 500 (2013) 541-546.
- [52] M.A. Sze, P.D. Schloss, *mBio* 7 (2016) e01018-16-9.
- [53] C.-M. Chiu, W.-C. Huang, S.-L. Weng, H.-C. Tseng, C. Liang, W.-C. Wang, T. Yang, T.-L. Yang, C.-T. Weng, T.-H. Chang, H.-D. Huang, *Biomed Res Int* 2014 (2014) 906168.

References

- [54] C. Haro, O.A. Rangel-Zúñiga, J.F. Alcalá-Díaz, F. Gómez-Delgado, P. Pérez-Martínez, J. Delgado-Lista, G.M. Quintana-Navarro, B.B. Landa, J.A. Navas-Cortés, M. Tena-Sempere, J.C. Clemente, J. López-Miranda, F. Pérez-Jiménez, A. Camargo, *PLOS ONE* 11 (2016) e0154090.
- [55] M. Million, M. Maraninchi, M. Henry, F. Armougom, H. Richet, P. Carrieri, R. Valero, D. Raccach, B. Vialettes, D. Raoult, *Int J Obes (Lond)* 36 (2012) 817-825.
- [56] P.J. Turnbaugh, M. Hamady, T. Yatsuneneko, B.L. Cantarel, A. Duncan, R.E. Ley, M.L. Sogin, W.J. Jones, B.A. Roe, J.P. Affourtit, M. Egholm, B. Henrissat, A.C. Heath, R. Knight, J.I. Gordon, *Nature* 457 (2009) 480-484.
- [57] I. Moreno-Indias, L. Sánchez-Alcoholado, E. García-Fuentes, F. Cardona, M.I. Queipo-Ortuño, F.J. Tinahones, *Am J Transl Res* 8 (2016) 5672-5684.
- [58] M.C. Dao, A. Everard, J. Aron-Wisnewsky, N. Sokolovska, E. Prifti, E.O. Verger, B.D. Kayser, F. Levenez, J. Chilloux, L. Hoyles, M.-O. Consortium, M.-E. Dumas, S.W. Rizkalla, J. Doré, P.D. Cani, K. Clément, *Gut* 65 (2016) 426-436.
- [59] J. Qin, Y. Li, Z. Cai, S. Li, J. Zhu, F. Zhang, S. Liang, W. Zhang, Y. Guan, D. Shen, Y. Peng, D. Zhang, Z. Jie, W. Wu, Y. Qin, W. Xue, J. Li, L. Han, D. Lu, P. Wu, Y. Dai, X. Sun, Z. Li, A. Tang, S. Zhong, X. Li, W. Chen, R. Xu, M. Wang, Q. Feng, M. Gong, J. Yu, Y. Zhang, M. Zhang, T. Hansen, G. Sanchez, J. Raes, G. Falony, S. Okuda, M. Almeida, E. LeChatelier, P. Renault, N. Pons, J.-M. Batto, Z. Zhang, H. Chen, R. Yang, W. Zheng, S. Li, H. Yang, J. Wang, S.D. Ehrlich, R. Nielsen, O. Pedersen, K. Kristiansen, J. Wang, *Nature* 490 (2012) 55-60.
- [60] J. Xu, F. Lian, L. Zhao, Y. Zhao, X. Chen, X. Zhang, Y. Guo, C. Zhang, Q. Zhou, Z. Xue, X. Pang, L. Zhao, X. Tong, *ISME J* 9 (2015) 552-562.
- [61] S.M. Lambeth, T. Carson, J. Lowe, T. Ramaraj, J.W. Leff, L. Luo, C.J. Bell, V.O. Shah, *J Diabetes Obes* 2 (2015) 1-7.
- [62] J. de la Cuesta-Zuluaga, N.T. Mueller, V. Corrales-Agudelo, E.P. Velásquez-Mejía, J.A. Carmona, J.M. Abad, J.S. Escobar, *Diabetes Care* 40 (2017) 54-62.
- [63] S.S. Bhute, M.V. Suryavanshi, S.M. Joshi, C.S. Yajnik, Y.S. Shouche, S.S. Ghaskadbi, *Front Microbiol* 8 (2017) 214.
- [64] H.S. Ejtahed, J. Mohtadi-Nia, A. Homayouni-Rad, M. Niafar, M. Asghari-Jafarabadi, V. Mofid, *Nutrition* 28 (2012) 539-543.
- [65] L.B. Tonucci, K.M.O. dos Santos, L.L. de Oliveira, S.M.R. Ribeiro, H.S.D. Martino, *Clinical Nutrition* (2015) 1-8.
- [66] K. Forslund, F. Hildebrand, T. Nielsen, G. Falony, E. Le Chatelier, S. Sunagawa, E. Prifti, S. Vieira-Silva, V. Gudmundsdottir, H.K. Pedersen, M. Arumugam, K. Kristiansen, A.Y. Voigt, H. Vestergaard, R. Hercog, P.I. Costea, J.R. Kultima, J. Li, T. Jørgensen, F. Levenez, J. Doré, MetaHIT consortium, H.B. Nielsen, S. Brunak, J. Raes, T. Hansen, J. Wang, S.D. Ehrlich, P. Bork, O. Pedersen, *Nature* 528 (2015) 262-266.
- [67] W. Jiang, N. Wu, X. Wang, Y. Chi, Y. Zhang, X. Qiu, Y. Hu, J. Li, Y. Liu, *Sci Rep* 5 (2015) 8096.
- [68] F.H. Karlsson, V. Tremaroli, I. Nookaew, G. Bergström, C.J. Behre, B. Fagerberg, J. Nielsen, F. Bäckhed, *Nature* 498 (2013) 99.
- [69] T.N. Kelly, L.A. Bazzano, N.J. Ajami, H. He, J. Zhao, J.F. Petrosino, A. Correa, J. He, *Circ. Res.* 119 (2016) 956-964.
- [70] J.M. Stern, S. Moazami, Y. Qiu, I. Kurland, Z. Chen, I. Agalliu, R. Burk, K.P. Davies, *Urolithiasis* 44 (2016) 399-407.
- [71] D.W. Kaufman, J.P. Kelly, G.C. Curhan, T.E. Anderson, S.P. Dretler, G.M. Preminger, D.R. Cave, *JASN* 19 (2008) 1197-1203.
- [72] S. Jiang, S. Xie, D. Lv, P. Wang, H. He, T. Zhang, Y. Zhou, Q. Lin, H. Zhou, J. Jiang, J. Nie, F. Hou, Y. Chen, *Scientific Reports* 7 (2017) 2870.