

Patient		Sample		Order	
Name	Sam Sample	Type	Swab	Report Date	August 30, 2018
DOB	January 07, 1981	Source	Fecal	Provider	John Wick
Age	37	Collected	August 13, 2018	Provider NPI	1234567890
Gender	Male	Received	August 16, 2018	Order Date	August 10, 2018
Patient ID	ID patient				

## Results and interpretation of this test

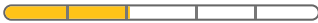


Your SmartGut test results indicate that your **microbial diversity score** is **normal**. This indicates that your gut microbiome is similar to that of individuals within the healthy reference range.

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

**Significance Index: Gut Conditions**

<p>Irritable Bowel Syndrome (IBS)</p>  <p><b>40</b></p>	<p>Inflammatory Bowel Disease (IBD): Crohn's Disease</p>  <p><b>18</b></p>	<p>Inflammatory Bowel Disease (IBD): Ulcerative Colitis</p>  <p><b>12</b></p>
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*SmartGut testing does not imply a diagnosis or lack of diagnosis. Please consult your medical professional 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>
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




















**Pathogenic Genera**

<p><i>Campylobacter</i></p> <p>● Negative</p>	<p><i>Escherichia/Shigella</i></p> <p>● Negative</p>
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## 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>	 Low	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 kefirifaciens</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

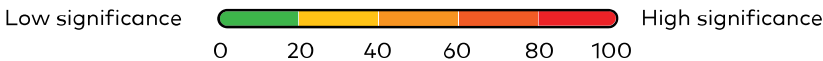
\*This result shows the amount of a probiotic group of bacteria at the genus level. The genus level result combines the amounts of all species within this group, including, but not limited to, the ones listed above. It is very normal to have **low** levels of the *Lactobacillus* and *Bifidobacterium*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




## Significance Index

The Significance Index provides information about your results, summarizing all the microbial associations found with a given health condition into a single value. The Significance Index is calculated using healthy ranges that have been determined for each microorganism using a cohort of self-reported healthy individuals. Results include microorganisms selected from scientific literature that are both associated with and inversely associated with a health condition.



The Significance Index is expressed as a numerical value from 0 to 100. A lower Significance Index indicates that your microbiome has a lower number of microorganisms outside the healthy range, while a higher Significance Index indicates that your microbiome has an increased number of microorganisms outside the healthy range.

The Significance Index 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	
Condition	Significance Index
Irritable Bowel Syndrome (IBS)	 40
Inflammatory Bowel Disease (IBD): Crohn's Disease	 18
Inflammatory Bowel Disease (IBD): Ulcerative Colitis	 12

## 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			
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)		Significance Index	40	
Association	Organism	Result	Out of Range	
Associated	<i>Campylobacter</i> [13]	● Negative		
	<i>Escherichia/Shigella</i> [13]	● Negative		
	<i>Methanobrevibacter smithii</i> [14]	● Normal		
	<i>Salmonella enterica</i> [15]	● Negative		
	<i>Veillonella</i> [16]	● Normal		
Inversely associated	<i>Alistipes</i> [17]	● Normal		
	<i>Bifidobacterium</i> [18]	● Low	⚠ Condition more likely	
	<i>Collinsella aerofaciens</i> [19-21]	● Low	⚠ Condition more likely	
	<i>Paraprevotella</i> [17]	● Low	⚠ Condition more likely	
	<i>Lactobacillus</i> [16]	● Low	⚠ Condition more likely	

## Gut Conditions (continued)

Inflammatory Bowel Disease (IBD)			
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	

Inflammatory Bowel Disease (IBD): Crohn's Disease			Significance Index	18
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]	● Normal		
	<i>Parabacteroides</i> [26]	● Normal		
Inversely associated	<i>Akkermansia muciniphila</i> [29]	● Normal		
	<i>Bacteroides</i> [28,30]	● Normal		
	<i>Bacteroides fragilis</i> [30]	● Normal		
	<i>Bifidobacterium</i> [26,28,30]	● Low	⚠ Condition more likely	
	<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)

Inflammatory Bowel Disease (IBD): Ulcerative Colitis		Significance Index	12	
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]	● Normal		
	<i>Ruminococcus albus</i> [35]	● Normal		
	<i>Salmonella enterica</i> [15]	● Negative		
Inversely associated	<i>Akkermansia muciniphila</i> [29]	● Normal		
	<i>Bacteroides</i> [28,30]	● Normal		
	<i>Bacteroides fragilis</i> [30]	● Normal		
	<i>Bifidobacterium</i> [28,30]	● 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 [36]	● Normal		

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

## 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			
Association	Organism	Result	Out of Range
Associated	<i>Ruminococcus flavefaciens</i> [37]	<span style="color: orange;">●</span> Low	
	<i>Methanobrevibacter smithii</i> [38]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Ruminococcus</i> [37]	<span style="color: green;">●</span> Normal	

Bloating			
Association	Organism	Result	Out of Range
Associated	<i>Anaerotruncus colihominis</i> [37]	<span style="color: green;">●</span> Normal	
	<i>Butyrivibrio crossotus</i> [37]	<span style="color: green;">●</span> Normal	
	<i>Ruminococcus flavefaciens</i> [37]	<span style="color: orange;">●</span> Low	

Constipation			
Association	Organism	Result	Out of Range
Associated	<i>Butyricimonas</i> [39,40]	<span style="color: green;">●</span> Normal	
	<i>Coproccoccus</i> [39,40]	<span style="color: green;">●</span> Normal	
	<i>Faecalibacterium</i> [40]	<span style="color: green;">●</span> Normal	
	<i>Gelria</i> [39]	<span style="color: green;">●</span> Normal	
	<i>Holdemania</i> [39]	<span style="color: green;">●</span> Normal	
	<i>Methanobrevibacter smithii</i> [41]	<span style="color: green;">●</span> Normal	
	<i>Paraprevotella</i> [39]	<span style="color: orange;">●</span> Low	
	<i>Phascolarctobacterium</i> [39]	<span style="color: green;">●</span> Normal	
	<i>Veillonella</i> [19]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Bifidobacterium</i> [42]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Roseburia</i> [39,40]	<span style="color: green;">●</span> Normal	

## Gut Symptoms (continued)

Flatulence			
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]	● Normal	



## 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			
Association	Organism	Result	Out of Range
Associated	<i>Bacteroides</i> [45]	<span style="color: green;">●</span> Normal	
	<i>Fusobacterium</i> [46]	<span style="color: green;">●</span> Normal	
	<i>Lactobacillus</i> [47]	<span style="color: orange;">●</span> Low	
Inversely associated	<i>Akkermansia muciniphila</i> [48,49]	<span style="color: green;">●</span> Normal	
	<i>Alistipes</i> [17]	<span style="color: green;">●</span> Normal	
	<i>Anaerotruncus colihominis</i> [17,50]	<span style="color: green;">●</span> Normal	
	<i>Barnesiella</i> [17]	<span style="color: green;">●</span> Normal	
	<i>Bifidobacterium</i> [45]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Butyrivibrio crossotus</i> [51,52]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Butyricimonas</i> [53]	<span style="color: green;">●</span> Normal	
	<i>Dialister</i> [54]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Methanobrevibacter smithii</i> [45,55]	<span style="color: green;">●</span> Normal	
	<i>Ruminococcus flavefaciens</i> [45]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	Microbial Diversity [46,51,52,56]	<span style="color: green;">●</span> Normal	

Prediabetes			
Association	Organism	Result	Out of Range
Associated	<i>Prevotella</i> [57]	<span style="color: green;">●</span> Normal	
	<i>Veillonella</i> [57]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Akkermansia muciniphila</i> [58]	<span style="color: green;">●</span> Normal	
	<i>Bifidobacterium</i> [57]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Butyricimonas</i> [57]	<span style="color: green;">●</span> Normal	
	Microbial Diversity [51]	<span style="color: green;">●</span> Normal	

## Metabolic Conditions (continued)

Type 2 Diabetes			
Association	Organism	Result	Out of Range
Associated	<i>Akkermansia muciniphila</i> [59]	<span style="color: green;">●</span> Normal	
	<i>Barnesiella</i> [60]	<span style="color: green;">●</span> Normal	
	<i>Collinsella</i> [61]	<span style="color: green;">●</span> Normal	
	<i>Prevotella</i> [62,63]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Lactobacillus</i> [64,65]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Roseburia</i> [59,66]	<span style="color: green;">●</span> Normal	

Non-Alcoholic Fatty Liver Disease			
Association	Organism	Result	Out of Range
Associated	<i>Escherichia/Shigella</i> [67]	<span style="color: green;">●</span> Negative	
	<i>Streptococcus</i> [67]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Alistipes</i> [67]	<span style="color: green;">●</span> Normal	
	<i>Flavonifractor</i> [67]	<span style="color: green;">●</span> Normal	
	<i>Odoribacter</i> [67]	<span style="color: green;">●</span> Normal	
	<i>Oscillibacter</i> [67]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> 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			
Association	Organism	Result	Out of Range
Associated	<i>Collinsella</i> [68]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Roseburia</i> [68]	<span style="color: green;">●</span> Normal	

Cardiovascular Disease			
Association	Organism	Result	Out of Range
Associated	<i>Tyzzarella</i> [69]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Alloprevotella</i> [69]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Catenibacterium</i> [69]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	Microbial Diversity [69]	<span style="color: green;">●</span> 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			
Association	Organism	Result	Out of Range
Associated	<i>Bacteroides</i> [70]	<span style="color: green;">●</span> Normal	
Inversely associated	<i>Oxalobacter formigenes</i> [71]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Prevotella</i> [70]	<span style="color: green;">●</span> Normal	

Chronic Kidney Disease			
Association	Organism	Result	Out of Range
Inversely associated	<i>Bacteroides fragilis</i> [72]	<span style="color: green;">●</span> Normal	
	<i>Bifidobacterium</i> [72]	<span style="color: orange;">●</span> Low	<span style="color: red;">⚠</span> Condition more likely
	<i>Prevotella</i> [72]	<span style="color: green;">●</span> Normal	
	<i>Roseburia</i> [72]	<span style="color: green;">●</span> 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 microbial diversity score and the following microorganisms:

*Akkermansia muciniphila*  
*Anaerotruncus colihominis*  
*Bacteroides*  
*Bacteroides fragilis*  
*Barnesiella*  
*Butyricimonas*  
*Butyrivibrio crossotus*  
*Lactobacillus*  
*Methanobrevibacter smithii*  
*Paraprevotella*  
*Phascolarctobacterium*  
*Prevotella*  
*Ruminococcus flavefaciens*

### 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.

\*95th percentile for the microbial diversity score

### 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 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 kefirifaciens</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*, *Butyrivimonas*, *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.

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