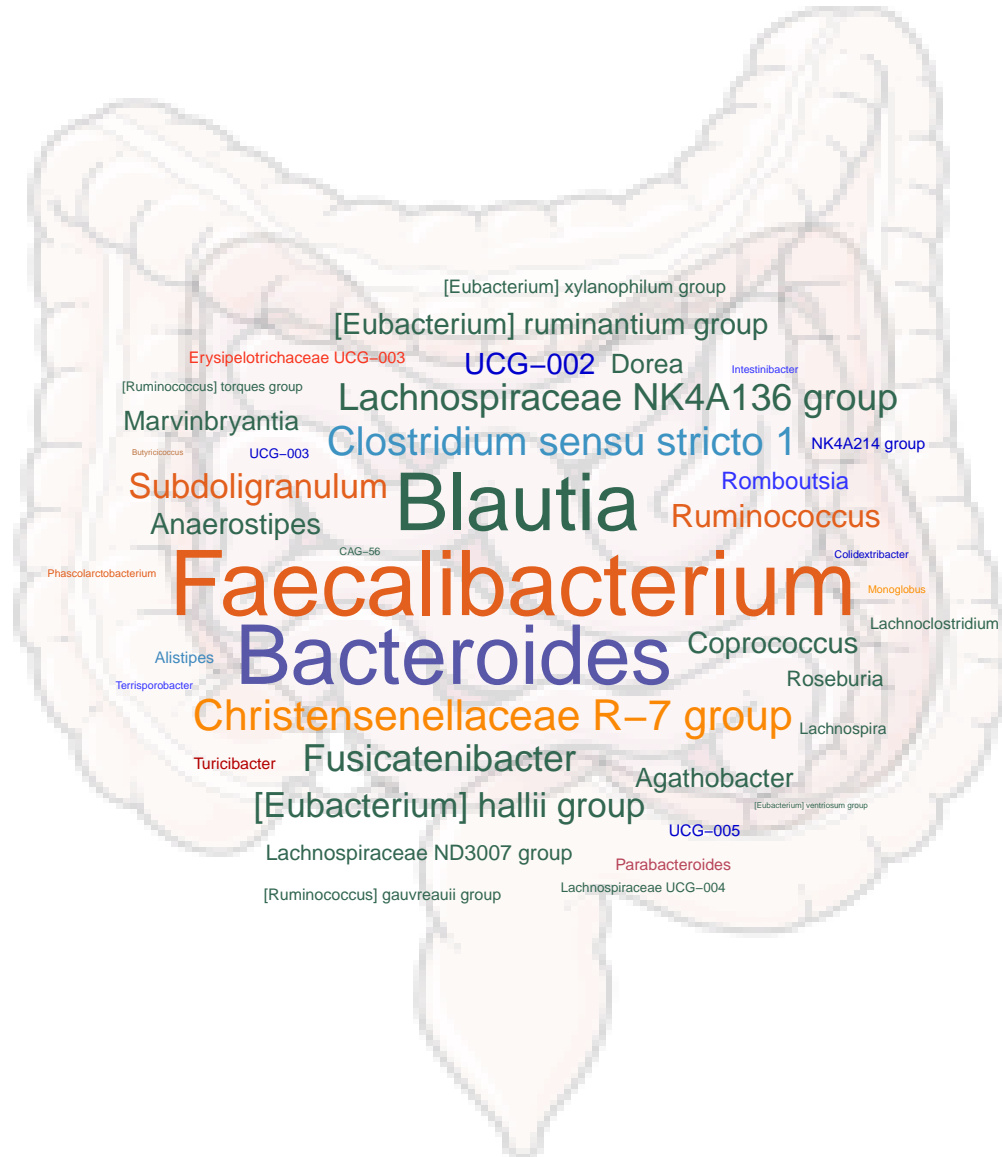


Inflammation, Microbiome & Alimentation  Gastro-Intestinal & Neuropsychiatric Effects

Welcome to Your Microbiome!



Welcome to your **MAGIC / IMAGINE** microbiome report! In this report, you will find an introduction to the human fecal microbiome, a description of your personal microbiome, and some more detailed information about the specific bacteria that were abundant in your sample.



The human gut is home to hundreds of species of microbes, mostly bacteria. In fact, your gut contains as many bacterial cells as there are human cells in your whole body! This microbial community is known as your 'gut microbiome'.

We are still very much at the beginning of understanding all the things the gut microbiome does, how our actions and environment affect it, and how we can use it to keep people healthier and living longer. The **MAGIC** study (a sub-study of the **IMAGINE** project that you are participating in) is an

The diagram illustrates the hierarchy of biological classification, showing the relationship between different taxonomic ranks. The ranks are represented by inverted cones of increasing size, with the number of organisms in each category indicated by the number of small circles at the base of each cone.

Taxonomic Rank	Number of Organisms (approximate)
Life	1
Domain	2
Kingdom	3
Phylum	4
Class	5
Order	6
Family	7
Genus	8
Species	9

A key component of the **MAGIC** study is generating microbiome profiles for each participant. So, how do we do that?

Each bacterial species has a unique genetic “barcode” that can be used to identify it. To determine the composition of each sample’s microbiome, we extract the DNA from your stool sample and then isolate and sequence these bacterial DNA barcodes. We don’t sequence any human DNA, just the bacterial barcodes. We generate



Inflammation, Microbiome & Alimentation  Gastro-Intestinal & Neuropsychiatric Effects

10,000 to 50,000 barcode sequences per sample. Each sequence is then labeled with its taxonomic identity (which species, genus, family, etc. it belongs to) and the number of bacteria present in each species is counted.

You can think of the bacteria in your gut like a jar of jelly beans. The barcode tells us what colour each jelly bean is, and the number of times we see that barcode in our sequences tells us how many jelly beans there are of that colour. This allows us to sort the bacteria into species and generate the “taxonomic bar chart” you’ll see in this document.



As there are hundreds of species in a sample, we quickly run out of colours! Therefore, we will use the categories at the genus or family level, and also only display the bacteria that are abundant enough to show up clearly on the chart.

These microbiome profiles are only the beginning. We use the information in them to compare profiles between healthy controls and people with IBD/IBS, and to investigate ways that a person’s microbiome changes with their health status. We also try to identify individual microbes that might be associated with specific illnesses. Understanding these associations between our microbes and our health will lead to new treatments that target the microbiome directly: increasing “good” bacteria and decreasing “bad” bacteria.



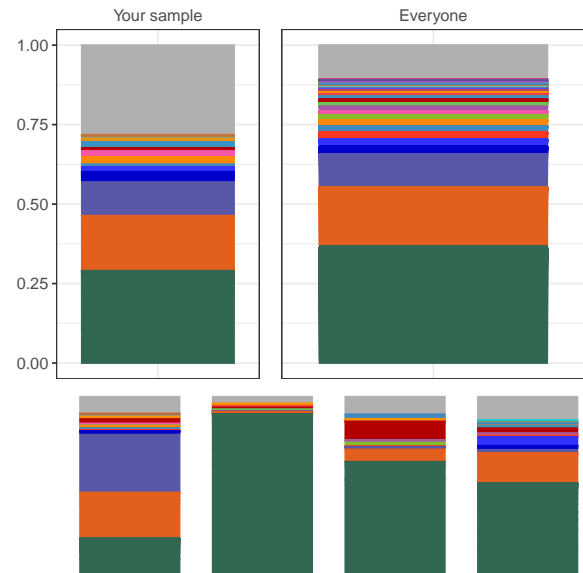
Inflammation, Microbiome & Alimentation  Gastro-Intestinal & Neuropsychiatric Effects

Your Sample


















This ****taxonomic bar chart**** shows your personal fecal bacterial community. Bacteria are grouped into **families** based on how closely related they are.

The bar chart is stacked from most abundant bacterial family on the bottom, to least abundant on the top, with very low-abundance bacteria grouped together as "Other". Next to it is a chart showing the average community of all the people who participated in the study, and across the bottom are four anonymous individuals chosen to show the range of variation in this study. As you can see, it's quite wide!

Below are the names of the most common bacterial families found in this study.



Family

	Lachnospiraceae		Rikenellaceae		Tannerellaceae
	Ruminococcaceae		Christensenellaceae		o_Clostridia UCG-014
	Bacteroidaceae		[Eubacterium] coprostanoligenes group		Butyricicoccaceae
	Oscillospiraceae		Erysipelotrichaceae		Acidaminococcaceae
	Peptostreptococcaceae		Clostridiaceae		Other
	Erysipelatoclostridiaceae		Monoglobaceae		



[Eubacterium] xylanophilum group

[Ruminococcus] gauvreauji group Marvinbryantia NK4A214 group

Erysipelotrichaceae UCG-003 Ruminococcus Alistipes

Lachnoclostridium Lachnospiraceae NK4A136 group

UCG-005 Dorea Clostridium sensu stricto 1 Butyrivibrio

Subdoligranulum Blautia Romboutsia

Colefesteribacter UCG-002 Agathobacter

Turicibacter UCG-003 Anaerostipes

Faecalibacterium Bacteroides Roseburia

Christensenellaceae R-7 group Terrisporibacter

Lachnospira Fusicatenibacter Coprococcus

Phascolarctobacterium [Eubacterium] hallii group Parabacteroides

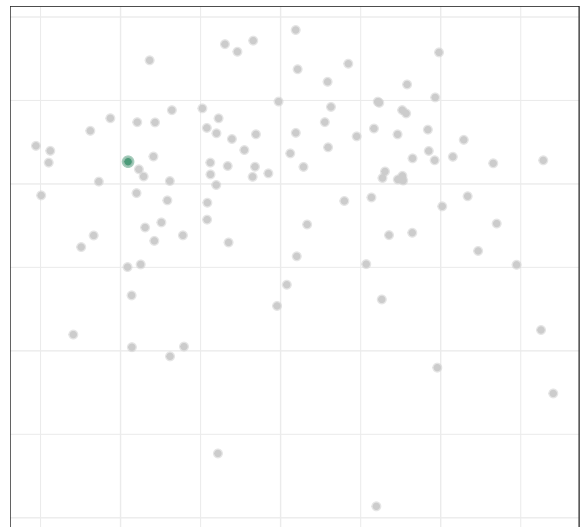
[Eubacterium] ruminantium group

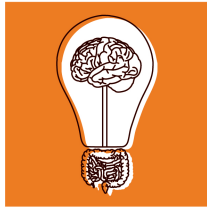
Lachnospiraceae ND3007 group Lachnospiraceae UCG-004

[Ruminococcus] torques group

This word cloud shows your personal bacterial community at a finer level of detail. Within each family, bacteria can be subdivided into several **genera** (singular, **genus**). The size of each word represents the relative abundance of that genus, and the colour shows which family that genus comes from.

There are nearly 4,000 people participating in this study so far! We have graphed everyone together based on how similar or different their gut microbiomes were. In the next graph, points that are closer together are more similar to each other, and points that are farther apart are more different. Your sample is shown in green. Remember that your position in this graph doesn't say anything about how healthy your gut microbiome is. As we've seen above, there is a wide range of normal variation in the human gut.





Inflammation, Microbiome & Alimentation  Gastro-Intestinal & Neuropsychiatric Effects

Your Bacterial Families

Everyone's microbiome is different. In your microbiome, the four most abundant bacterial families were *Lachnospiraceae*, *Ruminococcaceae*, *Bacteroidaceae*, and *Oscillospiraceae*. Here is a little bit of information about what functions these four families perform in the gut.

Lachnospiraceae

This family of bacteria is found in the gut and plays an important role in the breakdown of complex carbohydrates. Lachnospiraceae are known for their ability to ferment a variety of dietary fibers, producing short-chain fatty acids (SCFAs) such as butyrate, propionate, and acetate. These SCFAs provide an energy source for the body, improve gut health, and have anti-inflammatory properties. Research has also linked Lachnospiraceae to improved metabolic health and a reduced risk of obesity.

Ruminococcaceae

Ruminococcaceae are involved in the fermentation of dietary fiber and the production of SCFAs. These bacteria also play a role in regulating the immune system and maintaining gut health. Research has shown that reduced levels of Ruminococcaceae in the gut are associated with inflammatory bowel diseases such as Crohn's disease and ulcerative colitis.

Bacteroidaceae

Bacteroidaceae is a family of bacteria found in the gut that are involved in the breakdown of complex carbohydrates, such as dietary fibers and resistant starches. These bacteria produce enzymes that can break down plant-based foods, making the nutrients more accessible to the body. Bacteroidaceae also play a role in regulating the immune system and maintaining gut health, and their presence has been associated with a reduced risk of inflammatory bowel diseases.



Inflammation, Microbiome & Alimentation  Gastro-Intestinal & Neuropsychiatric Effects

Oscillospiraceae

Members of the Oscillospiraceae family of bacteria have been linked to improved glucose metabolism and may have a role in regulating blood sugar levels. These bacteria are involved in the breakdown of complex carbohydrates and the production of SCFAs such as butyrate, which have been shown to improve gut health and protect against inflammation.