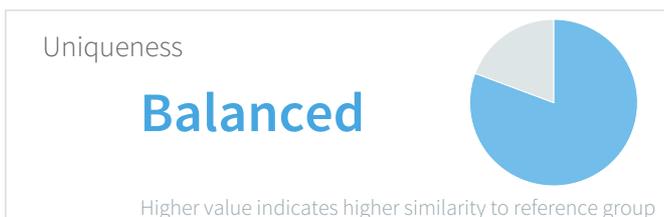


## Gut microbiome report

Client

17.10.2017



### Beneficial qualities of Your gut microbiome:

- The community structure is balanced and very similar to average healthy gut.
- The abundance of bacteria associated with protein and fat consumption is comparable to average.
- Levels of gut health supporting butyrogenic bacteria are average, which indicates sufficient fiber consumption.
- Weak indication of proinflammatory overgrowth of bacteria.

### Unfavorable qualities of Your gut microbiome:

- The diversity of microbiome is lower than average, which could indicate mild dysbiosis.
- The species richness is lower average.
- The levels of probiotic-like bifidobacteria are significantly lower than average.

# Your Gut microbiome

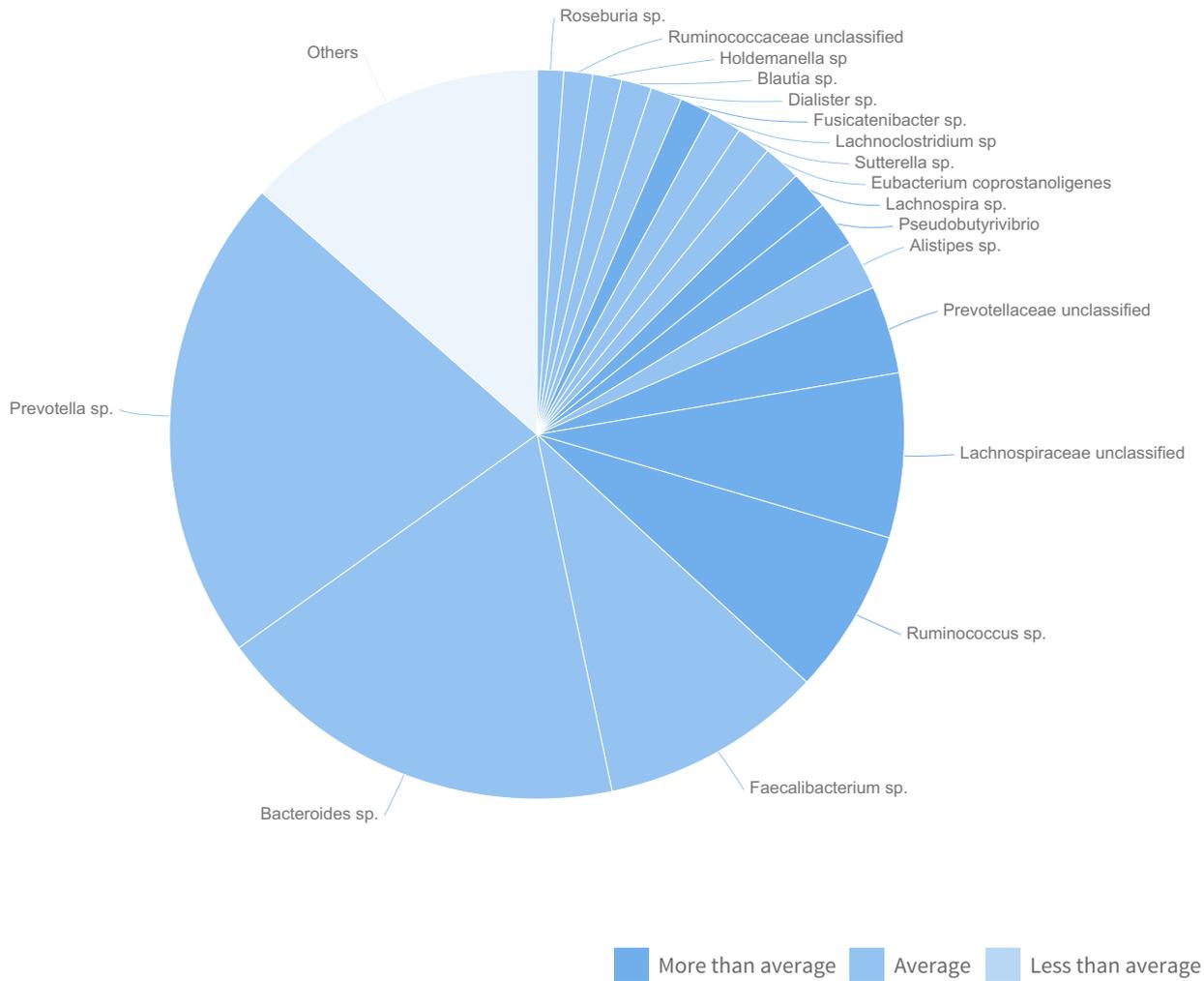


Figure shows gut microbiota abundances at genus level.

Bacterial genera are comprised of related bacterial species which harbor similar properties. Bacterial genera which consist of only one described species include Akkermansia, Faecalibacterium. Contrary to these, much more diverse genera exist, whose members are well defined and described. For example, Bacteroides combines tens of species with specific characteristics.

Is my gut community diverse?

**No, Your gut has low-diversity community.**

Microbiota diversity index characterizes gut community balance and indicates disease risk. Decreased diversity has been linked with modern diseases (diabetes, obesity, colorectal cancer, etc.). Microbiota diversity is evaluated by shannon index, which in Your sample is 3.38 and indicates low diversity (healthy score > 3.5-3.2). Diversity of Your gut is lower than in 76.2% of healthy reference.

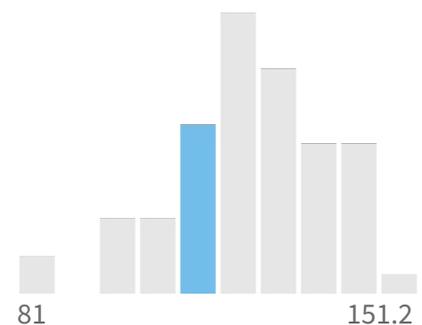


Diet enrichment with various fibre is recommended.

Is my gut community rich?

**No, Your gut community richness is low.**

Microbiota richness indicates gut community potential in adapting to changing conditions. Lower richness is accompanied by community structure changes (greater rick of proinflammatory overgrowth and reduction of anti-inflammatory species). In Your sample 116 different species were identified. Richness of Your gut is lower than in 77.8% of healthy reference.

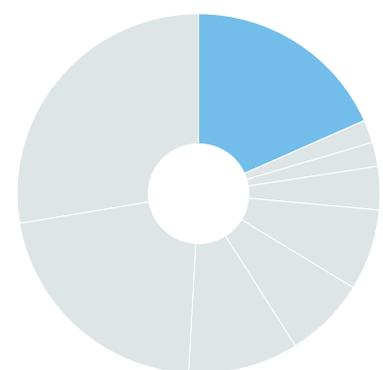


Diet enrichment with various fibre is recommended.

Could my diet be exceedingly rich in protein?

**No, Your gut community contains average amount of species associated with protein consumption.**

Proportional abundance of various species represents current diet and correlates with specific food consumption. High protein high fat diet enhances growth of epithelium-attaching species. Excess of such bacteria can be proinflammatory. Proteolytic fermentation can be carried out by species of Bacteroides (Your sample contains 18.3%).

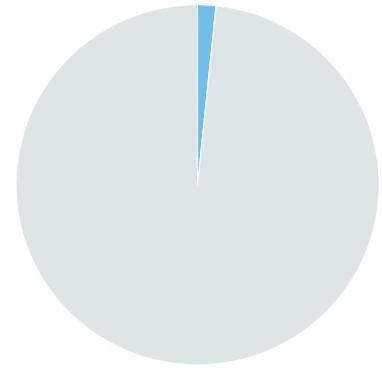


Consumption of additonal animal-based products could be limited.

Does my gut microbiota indicate overgrowth of proinflammatory bacteria?

**No, Your gut community contains average abundance of proinflammatory species.**

A major function of commensal microbiota is protection against overgrowth of proinflammatory bacteria, which is facilitated by metabolic interactions or induction of immune responses. Proinflammatory species also compete with commensal bacteria for gut niches and nutrients. Abundance of proinflammatory bacteria in Your sample is 1.63%, which is lower than in 69.0% of healthy reference.

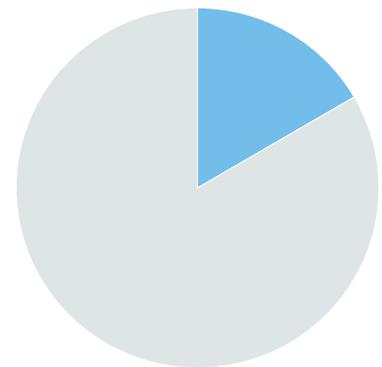


Specific suggestions cannot be made based on this score.

Does my gut microbiota contain sufficient levels of butyrate-producers?

**Yes, abundance of butyrate-producers is average.**

Butyrate, one of the gut microbiota produced metabolites, has major role in providing anti-inflammatory response. Butyrate is important as a primary energy resource for colonocytes enabling many beneficial features: reduction of toxin accumulation, increase of insulin sensitivity, reinforcement of gut barrier function (reproduction of mucin layer) and protection from diet induced obesity. Abundance of anti-inflammatory butyrogenic bacteria in Your sample is 16.6%, which is lower than in 67.5% of healthy reference.



Specific suggestions cannot be made based on this score.

# Extras

## Popular bacteria in Your sample

This table contains 30 most popular bacteria in Your gut. Levels of each bacteria are compared to the healthy group and assessed accordingly. This results with evaluation of relative amounts (depleted, medium, abundant). Bacteria which are depleted and considered as healthy could be enhanced while abundant bacteria could be closely investigated to identify their potential negative or positive effect. The table is sorted based on Your test - decreasing proportions from top to bottom.

**Percentage** specifies proportional abundance of bacteria

Bacterium	Percentage	Depleted Medium Abundant	Description
<i>Prevotella unclassified</i>	14.7%	 ✓	Digests wide range of carbohydrates and fibre. Dominant in native Africans. Also includes species which cause infections and inflammation. Binds collagen, degrades mucin. Correlations: IBS abdominal pain(↓), T2D(↓).
<i>Bacteroides plebeius</i>	9.7%	 ✓	Correlations: CRP(-), BMI(-), obesity(↓).
<i>Faecalibacterium prausnitzii</i>	9.4%	 ✓	Beneficial bacteria, major butyrate producer. Health state indicator. Correlations: IBD-CD(↓), cancer(↓), elderly with reduced immunity(↓), butyrate(+), gout(↓). Digests: pectin(fruits), inulin, AG, oligosaccharides.
<i>Lachnospiraceae unclassified</i>	7.3%	 ✓	Members of Lachnospiraceae family have been linked to obesity and protection from colon cancer in humans, mainly due to the association of many species within the group with the production of butyric acid, a substance that is important for both microbial and host epithelial cell growth.
<i>Ruminococcus unclassified</i>	6.9%	 ✓	Correlations: IBD(+), UC(+), active CD(+), CD(+), autism(+), bacterial gene richness(↓).
<i>Prevotella copri</i>	6.7%	 ✓	Prevalent in vegetarians and rheumatoid arthritis. Correlations: better glucose metabolism(↑), improved insulin response(↑), autistic children(↓). Diet: barley kernel-based bread(↑).
<i>Prevotellaceae unclassified</i>	3.9%	 ✓	NA
<i>Bacteroides vulgatus</i>	2.9%	 ✓	In high abundance can be pathogenic and attack gut epithelium. Correlations: IBS(↓), type(II) diabetes(↓), CRC(↑), CRP(+), Crohn's disease(CD)(↑). Diet: meat and fish consumption(↑), RS-rich diet(↓). Does not degrade starch.
<i>Bacteroides massiliensis</i>	2.2%	 ✓	Correlations: CRP(+), CRC(+). Diet: meat consumption(+), fruit consumption(-)

Bacterium	Percentage	Depleted Medium Abundant	Description
<i>Bacteroides unclassified</i>	2.3%		Bacteria belonging to this genus have ability to degrade wide range of food components(aminoacids, fiber), but are mainly focused on glucans. As Bacteroides species can degrade mucus-layer components, overgrowth can result with unfavourable consequences. Correlations: higher weight-loss(+), gut gene richness(-), obesity(↓), waist circumference(-), CRC(↓). Diet: long-term high-protein consumption(↑), wholegrain barley-brown rice diet(↓).
<i>Pseudobutyrvibrio unclassified</i>	2.1%		Non-spore forming, Gram-stain-negative, anaerobic rods. Ferment a variety of carbohydrates. Major end products of fermentation are formate, butyrate, and lactate.
<i>Eubacterium coprostanoligenes</i>	1.7%		Potential probiotic species as it can reduce plasma cholesterol levels.
<i>Lachnospira pectinoschiza</i>	1.6%		Pectin degrader and potentially antiinflammatory bacterium. Correlations: butyrate(+), but not a butyrate producer.
<i>Alistipes putredinis</i>	1.6%		Has been linked with abdominal abscesses and inflamed appendix tissue. Correlations: UC(↓).
<i>Sutterella unclassified</i>	1.5%		More abundant in feces of children with autism.
<i>Dialister succinatiphilus</i>	1.3%		Asaccharolytic.
<i>Fusicatenibacter saccharivorans</i>	1.3%		Correlations: active UC(↓).
<i>Holdemanella biformis</i>	1.3%		Correlations: unhealthy blood lipid profile(+).
<i>Ruminococcaceae unclassified</i>	1.3%		Members of this family have been associated with plant-based diet and many of them produce butyrate.
<i>Blautia unclassified</i>	1.3%		Correlations: CRC(↓), CD(↑). Diet: whole grain barley enriched diet(↑), brown rice enriched diet(↑), whole grains(↑).
<i>Ruminococcus bromii</i>	0.87%		Correlations: reduced insulin resistance(+), prevents CRC. Diet: RS enriched diet(↑). Digests: RS.
<i>Thalassospira unclassified</i>	0.78%		NA
<i>Ruminococcaceae unclassified</i>	0.77%		Members of this family have been associated with plant-based diet and many of them produce butyrate.
<i>Coprococcus eutactus</i>	0.75%		Butyrate producer. Correlations: bacterial gene richness(↑), IBS(↓) if accompanied with higher levels of Ruminococcus species.
<i>Anaeroplasma sp.</i>	0.74%		NA
<i>Ruminococcaceae unclassified</i>	0.68%		Members of this family have been associated with plant-based diet and many of them produce butyrate.
<i>Lachnospira unclassified</i>	0.66%		NA
<i>Lachnospiraceae unclassified</i>	0.6%		NA

Bacterium	Percentage	Depleted Medium Abundant	Description
<i>Roseburia intestinalis</i>	0.56%		Butyrate producer. Correlations: BMI(↑), BMI(+), CRP(+), whole grain barley enriched diet(↑).
<i>Erysipelotrichaceae unclassified</i>	0.53%		NA

# Extras

## Abundance of common bacteria in Your gut

This table is based on Your sample data. Only common bacterial taxa which are present in average gut are shown. Levels of each bacteria are compared to the healthy group and assessed accordingly. This results with evaluation of relative amounts (depleted, medium, abundant). Bacteria are classified in multiple levels. This table is sorted in alphabetical order, in which the general (higher) level is genus (bold) and the specific (lower) level is species (table: genus name + species name). If bacterial genera include lots of members, only the most common are shown.

**Percentage** specifies proportional abundance of bacteria

**Percentile** indicates proportional abundance compared to community data (>50% - above average; <50% - below average)

**Prevalence** indicates percentage of a population that accommodate this bacteria

(↑) – higher levels of specific bacteria associated with specific health condition.

(↓) – lower levels of specific bacteria associated with specific health condition.

(+) – specific bacteria correlates positively with mentioned health condition.

(-) – specific bacteria correlates negatively with mentioned health condition.

Bacterium	Percentage	Percentile	Prevalence	Depleted	Medium	Abundant	Description
<b>Akkermansia sp.</b>	0.07%	20%	68%	✓			Has been associated with healthy gut. Correlations: age(+), T2D(↓).
Akkermansia muciniphila	0.01%	-	62%	✓			Beneficial bacteria, which feeds on the intestinal mucus-layer. Correlations: richness(+), UC(↓), CD(↓), obesity(-), T1D(-), prediabetes(-), autism(-), appendicitis(-), pregnant weight(-), children weight(-), glucose levels during fasting(-), waist-hip ratio(-).
<b>Alistipes sp.</b>	2.2%	64%	98%		✓		Correlations: clinical depression(↑), CRP(-), BMI(-), obesity(↓), IBD(↓), CRC(↑), CRC(↓). Diet: animal-based diet(↑), cruciferous vegetables(cabbage, cauliflower, broccoli, brussels sprouts)-based diet(↑).
Alistipes finegoldii	-	-	59%				Correlations: CRC(↑), BMI(-). Diet: fruits and root vegetables(-).
Alistipes putredinis	1.6%	74%	81%		✓		Has been linked with abdominal abscesses and inflamed appendix tissue. Correlations: UC(↓).
Alistipes shahii	0.34%	65%	79%		✓		Correlations: TG(-), HDL(+); richness(+), higher fruit intake(+).
Bacteroides plebeius	9.7%	95%	46%			✓	Correlations: CRP(-), BMI(-), obesity(↓).
Blautia faecis	0.07%	23%	98%	✓			Butyrate producer. Correlations: CD(↓).

Bacterium	Percentage	Percentile	Prevalence	Depleted	Medium	Abundant	Description
<b>Bacteroides sp.</b>	18.3%	67%	100%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Bacteria belonging to this genus have ability to degrade wide range of food components(aminoacids, fiber), but are mainly focused on glucans. As Bacteroides species can degrade mucus-layer components, overgrowth can result with unfavourable consequences. Correlations: higher weight-loss(+), gut gene richness(-), obesity(↓), waist circumference(-), CRC(↓). Diet: long-term high-protein consumption(↑), wholegrain barley-brown rice diet(↓).
Bacteroides thetaiotaomicron	0.1%	23%	67%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Stimulates angiogenesis and protects from pathogenic invasions. Rare opportunistic pathogen in peritonitis. Correlations: metabolic syndrome(-), TG(-), HDL(+), waist circumference(-). diet: vegetarians(↑). Digests: glucans, pectin, AG, levan.
Bacteroides uniformis	0.29%	19%	94%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Correlations: TG and cholesterol(-), gut inflammation(-), BMI(-), obesity(↓);Crohn's disease(CD)(↓). Diet: lower values associated with legume consumption. Digests: B-glucans.
Bacteroides vulgatus	2.9%	59%	92%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	In high abundance can be pathogenic and attack gut epithelium. Correlations: IBS(↓), type(II) diabetes(↓), CRC(↑), CRP(+), Crohn's disease(CD)(↑). Diet: meat and fish consumption(↑), RS-rich diet(↓). Does not degrade starch.
<b>Bifidobacterium sp.</b>	0.08%	3%	94%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Reduced after weight-loss. Correlations: gut gene richness(+), IBD(↓), IBS(↓), IBS severity(+), T2D(↓), obesity(↑), BMI(+), CRC(↓).
Bifidobacterium adolescentis	-	-	81%	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	This bacteria has been associated with good health. One of the major starch-degraders in gut. Correlations: RS-rich diet(↑), weight-loss(↓), Crohn's disease(CD)(↓), metabolic syndrome(-), waist circumference(-), HDL(+), TG(-).
Bifidobacterium longum	0.08%	7%	76%	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Correlations: weight loss(↓), metabolic syndrome(-), waist circumference(-), HDL(+), TG(-), blood plasma glucose(-), systolic blood pressure(-).
<b>Blautia sp.</b>	1.3%	44%	100%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Correlations: CRC(↓), CD(↑). Diet: whole grain barley enriched diet(↑), brown rice enriched diet(↑), whole grains(↑).
Blautia luti	-	-	41%	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Digests: inulin, FOS, galactose, lactose.
<b>Christensenellaceae sp.</b>	-	-	60%	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Inheritable bacteria , prevalent in elderly. Correlations: BMI(↓), UC(↓), IBS(↓)
Christensenellaceae unclassified	-	-	60%	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Inheritable bacteria , prevalent in elderly. Correlations: BMI(↓), UC(↓), IBS(↓)
<b>Collinsella sp.</b>	0.49%	32%	97%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Correlations: T2D(↑), atherosclerosis(↑).
Collinsella aerofaciens	0.44%	35%	97%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Correlations: IBD(↑), CD(+).
<b>Dorea sp.</b>	0.59%	29%	100%	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Has been associated with inflammation, but can be also considered as commensal bacteria.

Bacterium	Percentage	Percentile	Prevalence	Depleted	Medium	Abundant	Description
Dorea formicigenerans	0.11%	27%	97%				Correlations: IBS(↑), UC(↑), BMI(+), obesity(↑).
Dorea longicatena	0.3%	34%	97%				Correlations: CD(↓).
<b>Eubacterium sp.</b>	0.53%	19%	97%				Correlations: T2D(↓), CRC(↓).
Eubacterium rectale	0.36%	19%	94%				Major butyrate producer. Correlations: obesity(statistically not significant), fecal calprotectin(+), whole grain barley enriched diet(↑), UC(↓), butyrate(+), metabolic syndrome(-).
<b>Faecalibacterium sp.</b>	9.8%	71%	100%				Only known species of this genus is F. prausnitzii. Major butyrate producer in the gut.
Faecalibacterium prausnitzii	9.4%	82%	100%				Beneficial bacteria, major butyrate producer. Health state indicator. Correlations: IBD-CD(↓), cancer(↓), elderly with reduced immunity(↓), butyrate(+), gout(↓). Digests: pectin(fruits), inulin, AG, oligosaccharides.
<b>Fusicatenibacter sp.</b>	1.4%	90%	98%				Digests: inulin.
Fusicatenibacter saccharivorans	1.3%	91%	98%				Correlations: active UC(↓).
<b>Lachnoclostridium sp</b>	1.5%	75%	100%				NA
Lachnoclostridium gnavus	-	-	14%				Known also as Ruminococcus gnavus. Degrades mucin. Predominant in mucosal samples of patients with CD. Correlations: BMI(+), Crohn's disease(CD)(↑)
<b>Prevotella sp.</b>	21.5%	55%	73%				Digests wide range of carbohydrates and fibre. Dominant in native Africans. Also includes species which cause infections and inflammation. Binds collagen, degrades mucin. Correlations: IBS abdominal pain(↓), T2D(↓).
Prevotella copri	6.7%	37%	49%				Prevalent in vegetarians and rheumatoid arthritis. Correlations: better glucose metabolism(↑), improved insulin response(↑), autistic children(↓). Diet: barley kernel-based bread(↑).
<b>Roseburia sp.</b>	1.2%	26%	100%				Correlations: bacterial richness(↑), IBS(↓), IBS-C(↓), T2D(↓), plasma glucose(-), UC(↓), CD(↓), CRC(↓), early rheumatoid arthritis(↓), whole grain barley enriched diet(↑), age(-).
Roseburia faecis	-	-	90%				Prevalent butyrate producer. Correlations: whole grain barley enriched diet(↑).
Roseburia intestinalis	0.56%	69%	70%				Butyrate producer. Correlations: BMI(↑), BMI(+), CRP(+), whole grain barley enriched diet(↑).
Roseburia inulinivorans	0.34%	64%	90%				Correlations: butyrate(+), CD(↓). Digests: starch and inulin.
<b>Ruminococcus sp.</b>	0.87%	63%	67%				Correlations: IBD(+), UC(+), active CD(+), CD(+), autism(+), bacterial gene richness(↓).

Bacterium	Percentage	Percentile	Prevalence	Depleted	Medium	Abundant	Description
Ruminococcus bromii	0.87%	65%	62%	<input checked="" type="checkbox"/>			Correlations: reduced insulin resistance(+), prevents CRC. Diet: RS enriched diet(↑). Digests: RS.

# Abbreviations

BMI - body mass index

CD - Crohn's disease, type of IBD

CRC - colorectal cancer

CRP - C-reactive protein

HDL - high-density lipoproteins, "good" cholesterol, high levels indicate good health

IBS - irritable bowel syndrome

IBS-C - IBS constipation

IBS-D - IBS diarrhea

IBS-M - IBS mixed/alternating

IBD - inflammatory bowel disease

LDL - low-density lipoproteins, "bad" cholesterol, high levels indicate bad health

TG - triglycerides, high levels may indicate metabolic syndrome

T1D - type 1 diabetes

T2D - type 2 diabetes

UC - ulcerative colitis, type of IBD