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Gut Health

Summary Report

REPORT CATEGORY

GUT HEALTH

Report date: 27 January 2026

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DISCLAIMER

This report does not diagnose this or any other health conditions. Please talk to a healthcare professional if this condition runs in your family, you think you might have this condition, or you have any concerns about your results.

Personal information

NAME

SEX AT BIRTH

Male

REPORT PROVIDED BY

Summary

Your gut is an amazingly complex system of organs, finely tuned to take in and process nutrients and then get rid of the waste. Besides supplying you with the energy you need, it is also a central hub for overall health, comprising about 70% of your immune system and having a direct connection to your brain.

Given its enormous importance to your health, it's crucial to keep your digestive system healthy. When the gut is out of balance various things can happen, from indigestion and constipation to inflammation and ulcers. The important thing is to understand the signs, what they might mean, and what you can do about it.

Everything from lifestyle to diet and exercise can impact gut health. **Importantly, your genetic predispositions play a major role.** This comprehensive report looks at your genetics in a number of major categories, including:

- Digestive issues
- Infections and inflammation
- Food intolerance
- Gut microbiome

This summary report contains:

65 **Genetic Results**

Overview of Your Results

Bowel Health

MORE LIKELY

Colorectal Cancer

More likely to get colorectal cancer

MORE LIKELY

Hemorrhoids

More likely to have hemorrhoids

TYPICAL LIKELIHOOD

Irritable Bowel (IBS)

Typical likelihood of IBS

TYPICAL LIKELIHOOD

Constipation

Typical likelihood of constipation

TYPICAL LIKELIHOOD

Flatulence (Gas)

Typical likelihood of having flatulence

TYPICAL LIKELIHOOD

Bloating

Typical likelihood of bloating

TYPICAL LIKELIHOOD

Bowel Incontinence

Typical likelihood of bowel incontinence

TYPICAL

Stool Frequency

Predisposed to typical stool frequency

TYPICAL

Leaky Gut

Likely typical intestinal permeability

LESS LIKELY

Colorectal Polyps

Less likely to have colorectal polyps

LESS LIKELY

Intestinal Obstruction

Less likely to have an intestinal obstruction

LESS LIKELY

Malabsorption

Less likely to have intestinal malabsorption

LESS LIKELY

Rectal Prolapse

Less likely to have rectal prolapse

LESS LIKELY

Anal Fissure

Less likely to have anal fissures

Stomach Health & Acid Production

MORE LIKELY

Peptic Ulcers

More likely to have peptic ulcers

MORE LIKELY

Nausea

More likely to have nausea

MORE LIKELY

Vomiting

More likely to vomit

TYPICAL LIKELIHOOD

Esophageal Cancer

Typical likelihood of esophageal cancer

TYPICAL LIKELIHOOD

Acid Reflux

Typical likelihood of GERD

TYPICAL LIKELIHOOD

H. pylori

Typical likelihood of H. pylori infection

TYPICAL LIKELIHOOD

Barrett's Esophagus

Typical likelihood of having Barrett’s esophagus

TYPICAL LIKELIHOOD

Esophageal Varices

Typical likelihood of esophageal varices

TYPICAL LIKELIHOOD

Low Stomach Acid

Typical likelihood of hypochlorhydria

TYPICAL LIKELIHOOD

Stomach Pain

Typical likelihood of having stomach pain

TYPICAL LIKELIHOOD

Stomach Inflammation

Typical likelihood of gastritis

LESS LIKELY

Stomach Cancer

Less likely to have stomach cancer

LESS LIKELY

Indigestion

Less likely to have indigestion

LESS LIKELY

Hiatus Hernia

Less likely to have hiatus hernia

Gut Infections

TYPICAL LIKELIHOOD

EBV Infection

Typical likelihood of getting EBV infection

TYPICAL LIKELIHOOD

Shigella Infection

Typical likelihood of shigellosis

TYPICAL LIKELIHOOD

Diarrhea

Typical likelihood of getting diarrhea

TYPICAL LIKELIHOOD

Stomach Bug

Typical likelihood of gastroenteritis

TYPICAL LIKELIHOOD

C. difficile Infection

Typical likelihood of a C. difficile infection

TYPICAL LIKELIHOOD

H. pylori

Typical likelihood of H. pylori infection

TYPICAL LIKELIHOOD

Gastrointestinal Infection

Typical likelihood of a GI infection

Gut Inflammation

MORE LIKELY

Pancreas Inflammation

More likely to get pancreas inflammation

TYPICAL LIKELIHOOD

Gut Inflammation

Typical likelihood of IBD

TYPICAL LIKELIHOOD

Appendicitis

Typical likelihood of appendicitis

TYPICAL LIKELIHOOD

Ulcerative Colitis

Typical likelihood of ulcerative colitis

TYPICAL LIKELIHOOD

Crohn’s Disease

Typical likelihood of Crohn's disease

TYPICAL LIKELIHOOD

Stomach Inflammation

Typical likelihood of gastritis

LESS LIKELY

Diverticular Disease

Less likely to have diverticular disease

Food Intolerance

MORE LIKELY

Histamine Intolerance

More likely to be histamine intolerant

TYPICAL

Gluten Sensitivity (Non-Celiac)

Predisposed to typical gluten sensitivity

TYPICAL LIKELIHOOD

Food Allergies

Typical likelihood of food allergies

TYPICAL

Alcohol Sensitivity

Likely typical sensitivity to alcohol

TYPICAL

Salt Sensitivity

Likely typical sensitivity to salt

TYPICAL LIKELIHOOD

Celiac Disease

Typical likelihood of celiac disease

LIKELY TOLERANT

Lactose Intolerance

Likely lactose tolerant

LOWER

Caffeine Sensitivity

Predisposed to lower caffeine sensitivity

Gut Microbiome

LOWER

Gut Microbiome Diversity

Predisposed to lower gut microbiome diversity

TYPICAL LEVELS

Bifidobacterium

Predisposed to typical Bifidobacterium levels

TYPICAL LEVELS

Bifidobacterium Longum

Predisposed to typical B. longum levels

TYPICAL LEVELS

Bifidobacterium Breve

Predisposed to typical B. breve levels

TYPICAL LEVELS

Bifidobacterium Bifidum

Predisposed to typical B. bifidum levels

Gut Health Genes

TYPICAL GENETICS

SLC2A14 (Gut Inflammation)

Likely typical SLC2A14 genetics

INTERMEDIATE ACTIVITY

HNF4A (Gut Inflammation)

Likely intermediate HNF4A activity

SECRETOR

FUT2 (Gut/ Vitamin B12)

Likely secretor

TYPICAL GENETICS

MUC1 (Immunity, Gut, Minerals)

Likely typical MUC1 genetics

TYPICAL ACTIVITY

NLRP3 (Gut Inflammation)

Likely typical NLRP3 activity

TYPICAL ACTIVITY

HRH2 (Gut Health)

Likely typical HRH2 activity

HIGHER ACTIVITY

IBD5 (Gut Inflammation)

Predisposed to higher IBD5 activity

LOWER ACTIVITY

JAK2 (Gut Inflammation)

Likely lower JAK2 activity

BETTER GENETICS

KIAA1109 (Gut Inflammation)

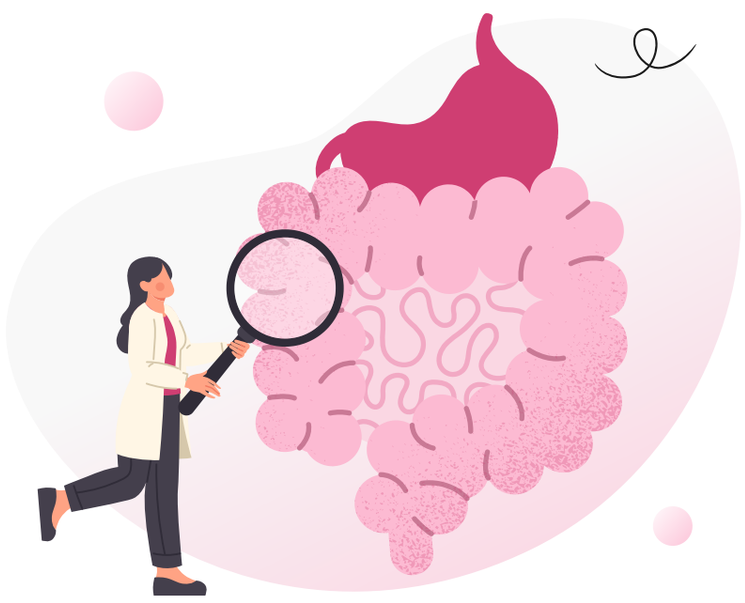
Likely better KIAA1109 genetics

BETTER GENETICS

SLC22A4 (Gut Inflammation)

Likely better SLC22A4 genetics

Your Results in Details



Bowel Health

Digestive issues related to bowel health are more common than you might think, with millions of people experiencing conditions like bloating, constipation, and irritable bowel syndrome (IBS). Modern life, filled with stressors, poor diet, and sedentary habits, can exacerbate these issues, leading to uncomfortable symptoms such as bloating, gas, constipation, or diarrhea that affect your quality of life.

Your genetics can play a significant role in how your body processes food, absorbs nutrients, and manages bowel function. This section covers key genetic factors that influence conditions like irritable bowel, constipation, flatulence, hemorrhoids, intestinal malabsorption, bowel incontinence, and more. By understanding your genetic predispositions, you can take a more personalized approach to manage your gut health and make informed decisions about diet and lifestyle.

MORE LIKELY

Colorectal Cancer

More likely to get colorectal cancer

MORE LIKELY

Hemorrhoids

More likely to have hemorrhoids

TYPICAL LIKELIHOOD

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Typical likelihood of IBS

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Leaky Gut

Likely typical intestinal permeability

LESS LIKELY

Colorectal Polyps

Less likely to have colorectal polyps

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Intestinal Obstruction

Less likely to have an intestinal obstruction

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Less likely to have intestinal malabsorption

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Rectal Prolapse

Less likely to have rectal prolapse

LESS LIKELY

Anal Fissure

Less likely to have anal fissures

Colorectal Cancer

While the exact cause of colorectal cancer is not fully understood, several factors increase the risk of developing this disease [R]:

- Age: The majority of cases occur in people aged 50 and older, though incidence rates are rising among younger populations.
- Family history: Having a family history of colorectal cancer or polyps increases one's risk.
- Personal history: Those with a history of inflammatory bowel disease (like Crohn's disease or ulcerative colitis), or who have had colorectal cancer or adenomatous polyps before are at higher risk.
- Genetic syndromes: Genetic mutations passed through generations, such as familial adenomatous polyposis (FAP) and hereditary non-polyposis colorectal cancer (Lynch syndrome), significantly increase the risk.
- Lifestyle factors: A diet high in red or processed meats, physical inactivity, obesity, smoking, and heavy alcohol use are known risk factors.
- Racial and ethnic background: African Americans have a higher incidence rate of colorectal cancer than other racial groups in the United States.

Treatment for colorectal cancer depends on the stage of the disease, the location of the tumor, and the patient's overall health [R]:

- Surgery: The primary treatment for localized cancer, surgery involves removing the tumor and surrounding tissue. For some cases, resection of part of the colon or rectum may be necessary.
- Chemotherapy: Used before or after surgery to shrink tumors and kill any cancer cells that may remain.
- Radiation therapy: Often used alongside chemotherapy, especially for rectal cancer, to reduce tumor size before surgery or eliminate remaining cells postoperatively.
- Targeted therapy: Drugs that target specific abnormalities in cancer cells. It's used for cancers that have specific gene mutations.
- Immunotherapy: Uses the body’s immune system to fight cancer. It’s typically reserved for advanced colorectal cancer.

Preventive measures include:

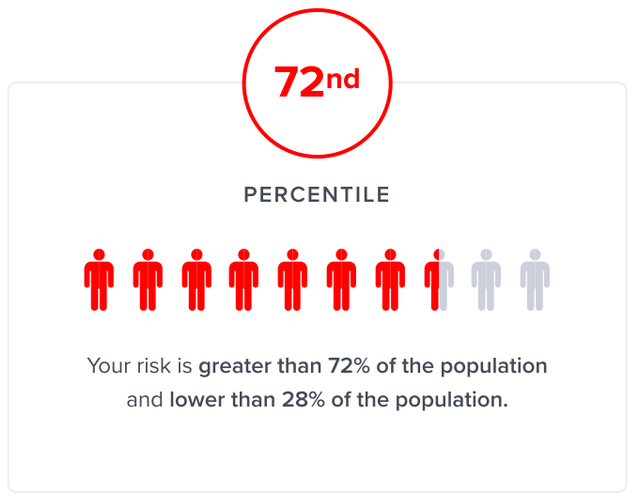
- Regular screening: Beginning at age 45 for average-risk adults, as recommended by the American Cancer Society.
- Diet and lifestyle: A diet rich in fruits, vegetables, and whole grains, limited red and processed meats, regular physical activity, maintaining a healthy weight, not smoking, and moderating alcohol intake can reduce risk.
- Genetic testing and counseling: Recommended for those with a family history indicative of genetic syndromes.

Colorectal cancer, when discovered early, is often treatable and frequently curable, highlighting the importance of regular screening and awareness of risk factors and symptoms.

Please note: This report is not diagnostic and can't be used to make any medical decisions. Most cancers are uncommon and have a strong environmental component. Even if your genetic predisposition is high, you will most likely not develop the disease. This report doesn’t test for hereditary cancer syndromes or ‘cancer genes’. These are usually caused by rare mutations that can’t be analyzed by our test. If you're concerned about your risk of hereditary cancer, consider getting a specialized test at a reference laboratory.

MORE LIKELY

More likely to get colorectal cancer based on 1,049,410 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
POU5F1B	rs6983267	GG
ZPLD1	rs116265807	GG
ACTL8	rs11203467	GG
UTP23	rs6469654	CC
RHPN2	rs10411210	CC
COX7A2L	rs13426988	GG
MAF	rs140851213	TT
MAF	rs9930005	CC
MYL2	rs17550549	CC
LRP1	rs7398375	CC
CCDC195	rs35413825	AA
GRM7	rs2163735	GG
CAMSAP1	rs74995296	CC
PITX1	rs7722513	GC
/	rs10795668	AG
SMAD7	rs4939827	TC
MYH3	rs1078643	AG
MAP2K5	rs7171219	AC
PRICKLE1	rs11610543	GA
NUDT2	rs62558833	TC
PTPN2	rs8083786	GA

GENE	SNP	GENOTYPE
SLC6A3	rs2735940	AG
CHRDL2	rs3824999	TG
COLCA2	rs3802842	AC
PARP11	rs12818766	GG
MICB	rs3830041	CC
BMP2	rs6085662	GG
PITX1	rs35917784	GG
TCF7L2	rs11196172	GG
TRAPPC4	rs11217091	TT
PLCB1	rs8117408	AA
PREX1	rs6066825	GG
BMP2	rs4813802	TT
VANGL1	rs2226738	TT
ETS2	rs2242936	TT
CDKN1A	rs1321311	CC
THSD4	rs4777372	TT
ABCC4	rs12855244	GG
UBQLN1	rs12235741	TT
USP44	rs11108175	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Hemorrhoids

Key Takeaways:

- Hemorrhoids are a very common condition. Your genetics can make you more susceptible to them.
- Mild cases can be managed with eating more fiber, drinking more water, topical creams or suppositories, soaking in a warm bath, and pain medication. Talk to your doctor if symptoms persist beyond a week.
- If your genetic risk is high, taking more precautions to avoid straining during bowel movements and constipation may prove beneficial.
- Click the **next steps** tab for relevant labs.

Hemorrhoids are swollen veins in the anus or lower rectum. They are also called *piles*. They can be [R, R, R, R]:

- **Internal** (on the walls of the rectum)
- **External** (under the skin around the anus)

Hemorrhoids are very common. **In fact, up to 3 out of 4 adults will have them at some point in their lives** [R].

The risk of hemorrhoids increases as the body ages. Hemorrhoids can also occur during pregnancy [R].

Symptoms can vary between different types of hemorrhoids. The symptoms of **external hemorrhoids** may include [R, R]:

- Itching
- Swelling
- Bleeding
- Pain

The symptoms of **internal hemorrhoids** may include [R, R]:

- Bleeding during bowel movements
- Pain and irritation if a hemorrhoid pushes through the anus

In rare cases, hemorrhoids may cause complications such as [R]:

- A lack of healthy red blood cells (*anemia*)
- Blood clots in the hemorrhoid
- Extreme pain if blood supply to the hemorrhoid is cut off

If you have rectal bleeding, don't assume that hemorrhoids are the cause. Rectal bleeding can occur as a result of other conditions, some of them more serious. Be sure to see your doctor if your bleeding lasts longer than a week or you bleed during bowel movements [R].

In most cases, hemorrhoids can be managed at home. Some options for mild cases include [R, R]:

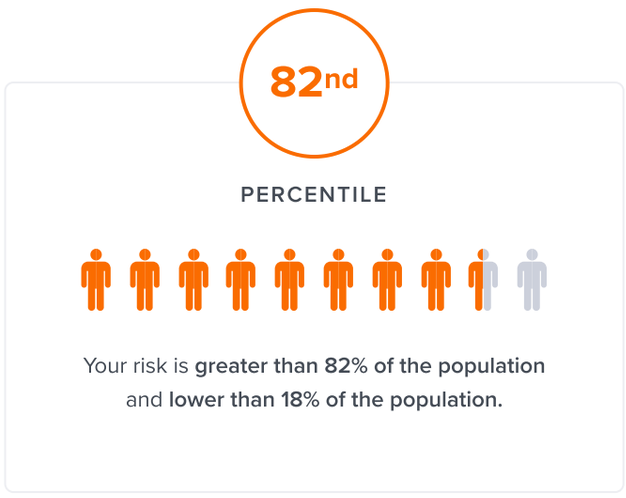
- Eating foods high in fiber
- Drinking more water
- Creams or suppositories
- Soaking in a warm bath
- Painkillers

If these strategies don't help within a week, a doctor may recommend [R, R]:

- Topical medication
- Injectable treatments (sclerotherapy)
- Surgical removal

MORE LIKELY

More likely to have hemorrhoids based on 640,366 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
MUC12	rs4556017	TT
SFMBT1	rs9847710	TT
PPIE	rs11585073	TA
PRKCA	rs4423457	GG
ATPAF2	rs854786	AA
ASPN	rs755209	AA
NLRC4	rs6723226	GG
ESR1	rs9322356	AG
AMPD3	rs2218793	CA
PLEC	rs58579887	CT
CCT8	rs2832279	AC
/	rs7183672	GA
GAS2L1	rs174767	GA
EVI2A	rs2525570	GA
PIAS1	rs12594232	GA
TBX5	rs2555004	AG
OTX1	rs4671051	AT
ATP1B1	rs145163454	TT
TP53	rs78378222	TT
LLPH	rs11176001	CC
/	rs676996	TT

Genetic differences may play a role in people's chances of developing hemorrhoids. Genes involved in hemorrhoids may influence the function of [R]:

- Muscles in the anus
- The gut
- Blood vessels

GENE	SNP	GENOTYPE
SMAD3	rs17293632	CC
ETAA1	rs2861709	AA
XKR9	rs1838392	GG
SLC40A1	rs16831319	TT
MYH11	rs6498573	CC
MYOCD	rs62061554	GG
CDKN2B	rs1333047	TT
/	rs12153515	CC
CAP2	rs10807610	AA
MERTK	rs57116599	GG
CDH26	rs35384758	AA
THBS2	rs3253	CC
KANK2	rs2421206	TT
CCAR2	rs13271626	CC
MTCH2	rs10838738	AA
/	rs7423637	AA
ISL1	rs4485884	TT
SPRY1	rs2060285	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Irritable Bowel (IBS)

Key Takeaways:

- Up to **60%** of IBS differences may be due to genetic factors.
- Other risk factors include young age, female sex, stress, and gut infections.
- IBS affects **1 in 10** people in the US. Symptoms include cramping, vomiting, rectal bleeding, diarrhea, and constipation.
- If you have high genetic risk or symptoms, look to improve modifiable factors like stress, sleep, and diet.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

There is no known cure for IBS. If you have IBS, **doctors can help you manage symptoms and prevent flare-ups** so that you can live a normal life [R, R].

The main IBS management strategies include [R]:

- Eating foods high in dietary fiber
- Drinking lots of water
- Regular exercise
- A healthy & regular sleep schedule
- Avoiding stress
- Avoiding triggering foods

The strategies most likely to work for you may be written into your genes. Up to 60% of IBS differences may be due to genetic factors [R].

Genes involved in IBS may play a role in [R, R]:

- Bile production and release (*KLB*)
- Gut movement (*HTR3E*)
- Pain perception (*HTR3E*)
- Immune system activity (*TLR9*)

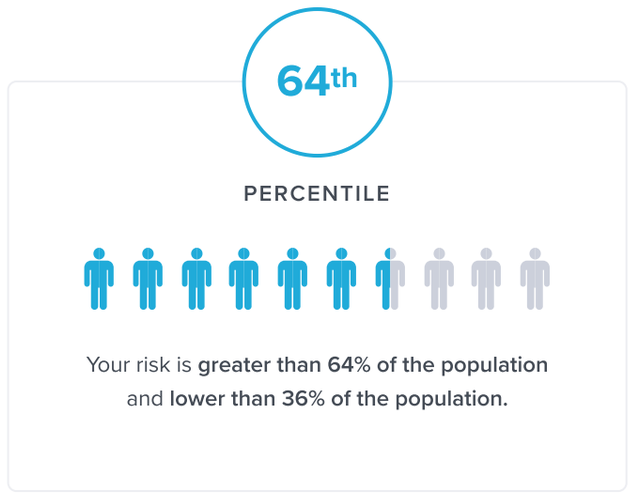
Moreover, genetically high betaine levels may be causally associated with a high risk of Crohn's disease [R].

It's important to remember that **genetics is only one piece of the puzzle.** You are also more likely to develop IBS if you are [R]:

- Under the age of 50
- Experiencing a lot of mental stress
- Female or taking estrogen
- Anxious or depressed
- Recovering from a gut infection
- Related to other people with IBS

TYPICAL LIKELIHOOD

Typical likelihood of IBS based on 1,671 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
MAPT	rs242924	GG
TRPM8	rs10166942	TT
TNFSF15	rs4263839	GG
NXPH1	rs2349775	AA
ZFP90	rs16260	CA
PPM1M	rs5743836	AG
TNFSF15	rs6478108	CT
FGFR4	rs1966265	GA
IL6	rs1800795	CG
EXTL2	rs72987295	AG
PCDH15	rs10825269	CT
MAPT	rs110402	GG
BDNF	rs6265	TC
/	rs2366846	AC
STK17A	rs7802995	AG
TGFBR2	rs7427882	AC
PON2	rs6973126	TC
KDELR2	rs12702514	TC
KLB	rs17618244	GG
PRRC2A	rs2736155	CC
CADM2	rs1248825	AC

GENE	SNP	GENOTYPE
PHF2	rs10156602	GA
NCAM1	rs7947502	CT
NCAM1	rs7106434	TC
DOCK9	rs9513519	AG
ABCC5	rs56109847	GG
NNMT	rs1062613	CC
MAPT	rs7209436	CC
TNFSF8	rs7848647	CC
TNFSF8	rs6478109	GG
TNF	rs1800629	GG
SPATA5	rs9999118	AA
SI	rs79717168	AA
SI	rs121912615	AA
SI	rs9290264	CC
LSR	rs10424110	AA
HES6	rs4663866	AA
/	rs17112758	GG
IL19	rs1800896	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Constipation

Key Takeaways:

- Genetic research indicates that genes involved in constipation are likely similar to those influencing IBS.
- Other risk factors include dehydration, a low-fiber diet, lack of exercise, intestinal blockages, certain nerve, muscle, or hormone issues, older age, being female, and certain medications.
- Constipation is very common, with about 1 in 4 people having it at any given time.
- If your genetic risk is high or you have symptoms, you may lower your overall risk by taking action on those factors that you can change.

Constipation is difficulty passing stools. It presents as few bowel movements a week, generally less than three. People with constipation may also have [R, R]:

- Difficult or painful bowel movements
- Stools that are hard, dry, or lumpy
- A feeling that more stool needs to be passed

Constipation is very common; **about 1 in 4 people may have it at any time** [R, R].

The following may contribute to constipation [R]:

- Dehydration
- A low-fiber diet
- A lack of exercise
- Something blocking the intestine
- Problems with certain nerves, muscles, or hormones
- Older age
- Female sex
- Some medications

To support healthy bowel movements, experts recommend [R]:

- Eating lots of fiber
- Drinking lots of water
- Staying active
- Managing stress
- Passing stool as soon as you feel the urge

Some people may need laxatives or other medications to help with constipation. In some cases, surgery may be required to remove a blockage [R].

Some of the differences in people's bowel movements may be attributed to genetics [R, R].

TYPICAL LIKELIHOOD

Typical likelihood of constipation based on 1,687 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
KATNIP	rs149014823	TC
MORC2	rs55694472	CC
FZD4	rs182200829	GG
/	rs574648890	AA
HORMAD1	rs150782165	GG
/	rs140085457	AA
MCUR1	rs562047350	AA
/	rs560797967	TT
TRAPPC9	rs116380351	CC
LRRC31	rs564587334	AA
SEC62	rs551839727	CC
/	rs13328995	TT
CXCR4	rs146493009	TT
CALM1	rs113878265	CC
PPP6R2	rs188272551	CC
ST18	rs144859003	CC
KCTD9	rs79700501	TT
SLITRK1	rs113428943	TT
MTRES1	rs116465542	GG
ATP8B2	rs144890977	CC
AP1M1	rs143695943	CC

GENE	SNP	GENOTYPE
/	rs537591474	CC
KLF2	rs561412363	CC
MCTP2	rs115350201	AA
CLSTN1	rs542394633	CC
AVL9	rs576185900	GG
CCNI	rs115310636	TT
GRK5	rs551434317	GG
GCFC2	rs568976510	GG
ESRRG	rs142704599	GG
JARID2	rs150597631	GG
DDR1	rs147082103	GG
MUC21	rs59236926	GG
GABRG3	rs112865614	CC
SLC35G1	rs138110766	AA
NAALADL2	rs144790287	GG
TMEM174	rs6872673	CC
MAP4K3	rs146245526	AA
VPS41	rs77233399	TT
ZNF764	rs147809573	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Flatulence (Gas)

Flatulence is the process of expelling intestinal gas through the rectum, more commonly known as farting.

There are a number of things that can cause flatulence, including [R]:

- Eating certain foods like beans, broccoli, cabbage, and onions
- Chewing gum, which can increase the amount of swallowed air
- Drinking carbonated beverages
- Having lactose intolerance or other food sensitivities
- Having a gut disorders like IBS or food intolerance

Flatulence is more common in adults and in men [R].

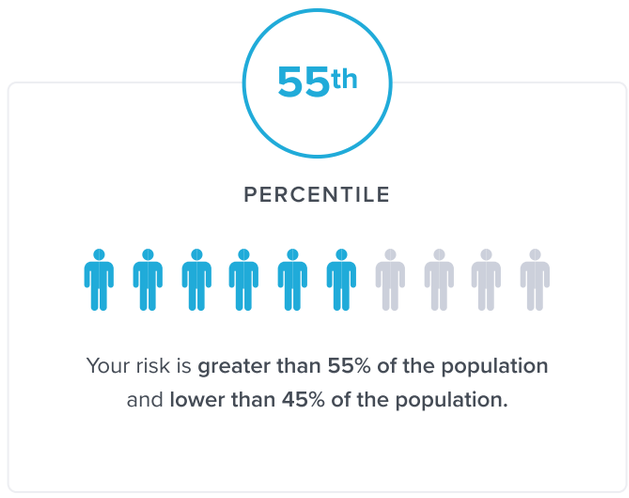
The following may help reduce flatulence [R]:

- Avoiding foods known to cause flatulence
- Chewing food thoroughly
- Avoiding carbonated beverages
- OTC gas-reducing medications and supplements
- Addressing medical conditions

If you have concerns about the amount or cause of intestinal gas, talk to your healthcare professional.

TYPICAL LIKELIHOOD

Typical likelihood of having flatulence based on 775,632 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
NSUN6	rs116878364	TC
MALRD1	rs75856818	GA
MALRD1	rs77713489	GT
NSUN6	rs117028789	CG
WDR37	rs201006450	TDEL(C)
/	rs12242510	TT
FAM171A1	rs138125072	TT
GTPBP4	rs143878742	TT
GTPBP4	rs552719354	GG
LARP4B	rs190038118	GG
/	rs192623360	CC
PRKCQ	rs17156356	GG
KIAA1217	rs147375660	TT
APBB1IP	rs17815108	CC
GTPBP4	rs184771055	CC
/	rs370926748	GG
PFKP	rs559503906	GG
CELF2	rs144660889	GG
CAMK1D	rs555448981	AA
FAM107B	rs140967718	CC
PIP4K2A	rs530904842	TT

GENE	SNP	GENOTYPE
KLF6	rs543494212	GG
/	rs188892049	AA
WDR37	rs186720474	GG
PFKP	rs539807663	GG
MYO3A	rs11014670	GG
IDI1	rs370234733	TT
NSUN6	rs182203275	AA
MLLT10	rs181729711	AA
PFKP	rs565546654	GG
SVIL	rs118089431	CC
MYO3A	rs10828937	AA
ADARB2	rs77306508	AA
NSUN6	rs77728096	TT
NSUN6	rs141100641	GG
MYO3A	rs563886464	AA
NEBL	rs182011742	GG
GATA3	rs17143403	GG
PTER	rs138238948	GG
FBH1	rs12246606	GG
PFKP	rs76705177	GG
UPF2	rs144877016	GG
GATA3	rs79528041	TT
GATA3	rs74650638	GG
UPF2	rs571930960	CC
BAMBI	rs188063739	CC
PFKP	rs7070002	CC
OPTN	rs79121055	TT
MALRD1	rs188294543	AA
PRPF18	rs12220538	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Bloating

Factors that might increase the risk or cause bloating include:

- Consuming high-fat foods, which can delay stomach emptying.
- Swallowing air while eating or drinking.
- Gastrointestinal infections or imbalances in gut bacteria.
- Food intolerances, such as lactose, fructose, or gluten intolerance.
- Digestive disorders like irritable bowel syndrome (IBS), inflammatory bowel disease, or gastroparesis.
- Constipation.
- Overgrowth of bacteria in the small intestine.
- Hormonal changes, especially in women during their menstrual cycles.
- Genetics

While bloating is primarily associated with lifestyle and dietary factors, genetics can play a role in an individual's predisposition to certain digestive conditions that result in bloating. Additionally, genetics can influence the makeup of gut bacteria and how the body responds to certain triggers, potentially affecting susceptibility to bloating.

TYPICAL LIKELIHOOD

Typical likelihood of bloating based on 1,662 genetic variants we looked at

32nd

PERCENTILE

Your risk is **greater than 32% of the population** and **lower than 68% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
GRIN3A	rs182276014	TT
GZMH	rs190749747	CC
FZD1	rs182267037	CC
/	rs72683482	GG
RALGPS2	rs6675656	TT
IGF1R	rs144880784	CC
/	rs56252721	AA
EPS8L3	rs190178166	CC
BTG1	rs141884556	GG
CWF19L2	rs79224501	AA
TMEM128	rs543096999	CC
MXRA8	rs112044473	GG
/	rs145439079	CC
AMN1	rs569208093	GG
PPM1F	rs34639823	CC
IGF1R	rs118021991	AA
COX7C	rs114575486	TT
PLPPR4	rs115008227	AA
EPS8L3	rs78018756	CC
CNTNAP5	rs78037681	CC
ARHGAP45	rs116305519	CC

GENE	SNP	GENOTYPE
GUCY1A2	rs117090859	AA
KCND2	rs191721892	AA
COL15A1	rs150185691	AA
SERPINB8	rs118084041	AA
LRRTM1	rs186057704	GG
FOXK1	rs118117357	TT
MKLN1	rs78522184	GG
TMEM131	rs142462181	GG
ANGPT1	rs12542882	TT
PRMT6	rs145009014	GG
/	rs146534400	TT
KIF21A	rs189504750	GG
C16ORF95	rs192095736	CC
CDIN1	rs113441091	GG
LRATD1	rs113707455	TT
/	rs76449150	GG
SMIM14	rs73240633	TT
NEBL	rs151118164	AA
VTI1A	rs148319443	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Bowel Incontinence

Managing fecal incontinence often involves a multifaceted approach that includes dietary changes, medication, and sometimes surgery. Dietary management may focus on the consistency of stools, either bulking up loose stools with fiber supplements or softening hard stools to reduce straining. Medications can help reduce diarrhea or constipation and enhance sphincter tone.

In cases where conservative treatments are ineffective, surgical options, such as sphincter repair or the installation of a sacral nerve stimulator, may be considered. Additionally, pelvic floor physical therapy can be beneficial to strengthen the muscles involved in bowel control.

TYPICAL LIKELIHOOD

Typical likelihood of bowel incontinence based on 365 genetic variants we looked at

73rd

PERCENTILE

Your risk is **greater than 73% of the population** and **lower than 27% of the population.**

Stool Frequency

The following factors can influence the frequency of bowel movements:

- Diet: Fiber intake plays a crucial role in bowel movements. Diets high in fiber can promote regular bowel movements, while low-fiber diets might lead to constipation.
- Hydration: Adequate water intake softens the stool and promotes regularity.
- Physical Activity: Regular exercise can stimulate bowel movements and help prevent constipation.
- Medications: Some medications, such as opioids, antacids containing calcium or aluminum, certain antihypertensives, and some antidepressants, can decrease stool frequency. In contrast, others like antibiotics or magnesium-containing products can increase it.
- Stress and Mental Health: Stress, anxiety, and depression can influence bowel habits, potentially altering stool frequency.
- Medical Conditions: Conditions like Irritable Bowel Syndrome (IBS), Inflammatory Bowel Disease (IBD), thyroid disorders, diabetes, and bowel obstruction can significantly affect stool frequency.
- Age: As people age, metabolic rates and muscle tone in the gastrointestinal tract can decrease, potentially leading to reduced stool frequency.
- Pregnancy: Hormonal changes during pregnancy can affect gastrointestinal motility, leading to changes in stool frequency.
- Genetics: Some studies have shown that families tend to have similar bowel habits, suggesting a potential genetic influence.

TYPICAL

Predisposed to typical stool frequency based on 14 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LIN7C	rs12273363	TT
LFNG	rs12700026	AA
MUC12	rs4556017	TT
STX16	rs6123818	AA
PPIC	rs39819	AA
/	rs10407548	TC
LRRC37A	rs2732706	TC
CALCB	rs6486216	TC
CDK18	rs11240503	GA
FAM227A	rs5757162	CT
/	rs3858648	AC
LLPH	rs11176001	CC
MOSPD3	rs62482222	GG
HEY2	rs1268068	CC
FAXDC2	rs13162291	GG
XKR9	rs10957534	GG
/	rs10492268	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Leaky Gut

Factors that might increase intestinal permeability include:

- Chronic stress.
- Poor diet, particularly high in sugar and low in fiber.
- Infections
- Bacteria imbalance in the gut (dysbiosis)
- Autoimmune diseases.
- Excessive alcohol consumption.
- Drugs (e.g., painkillers, antibiotics, chemotherapy).
- Radiation therapy

Genetics may also influence intestinal permeability. Certain individuals might have a genetic predisposition for a more susceptible gut lining. For example, conditions such as celiac disease, which has a clear genetic component, can increase the risk of a leaky gut [R].

TYPICAL

Likely typical intestinal permeability based on 16 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
BRD1	rs9616637	GG
RAB28	rs4834946	TT
/	rs75673924	TT
STAB2	rs1993919	AA
LYZL1	rs73596019	CC
ADAMTS1	rs9967959	GG
ASIC2	rs2346689	GG
KCNJ6	rs857958	GG
/	rs1907608	GG
/	rs7337023	TC
GRIN3A	rs10119861	GC
PID1	rs10179193	CT
GNMT	rs41274896	GA
BUD13	rs1784128	GA
COL6A1	rs1883048	TC
AATK	rs11650927	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Colorectal Polyps

The process of polyp formation is influenced by both lifestyle and hereditary factors, even though the exact causes of colorectal polyps are not fully understood. Diets high in red meat and fat and low in fiber, as well as obesity and smoking, have been linked with an increased risk of polyp development. Age is also a significant risk factor; individuals over the age of 50 are more likely to develop polyps.

Regular screening and removal of polyps are essential preventive strategies, as removing them can significantly reduce the risk of progression to colorectal cancer. Post-removal, patients are generally advised to undergo periodic surveillance to monitor for new polyp formation.

LESS LIKELY

Less likely to have colorectal polyps based on 1,670 genetic variants we looked at

4th

PERCENTILE

Your risk is **greater than 4% of the population** and **lower than 96% of the population.**

Intestinal Obstruction

Treatment for intestinal obstruction depends on the underlying cause and the severity of the obstruction. In some cases, a liquid diet and rest may be enough to allow the obstruction to clear on its own.

However, more serious obstructions may require hospitalization where intravenous fluids are administered to prevent dehydration, and medications may be given to reduce pain and vomiting. In cases where a complete blockage exists, or if the blood supply to the intestines is compromised, emergency surgery might be necessary to remove the obstruction and prevent more severe health issues such as tissue death or perforation of the intestinal wall, which can lead to peritonitis (an infection of the inner lining of the abdominal cavity).

LESS LIKELY

Less likely to have an intestinal obstruction based on 854,609 genetic variants we looked at

6th

PERCENTILE

Your risk is **greater than 6% of the population** and **lower than 94% of the population.**

Malabsorption

The effects of malabsorption extend beyond gastrointestinal distress; it can lead to malnutrition and the development of deficiencies in critical vitamins and minerals, such as vitamin B12, iron, calcium, and vitamin D. These deficiencies can have wide-ranging impacts on the body, including anemia, osteoporosis, and neurological disorders.

Diagnosing malabsorption typically involves a combination of medical history evaluation, physical examinations, and specialized tests to identify the specific nutrients that are not being properly absorbed and to determine the underlying cause of the malabsorption.

LESS LIKELY

Less likely to have intestinal malabsorption based on 38 genetic variants we looked at

6th

PERCENTILE

Your risk is **greater than 6% of the population** and **lower than 94% of the population.**

Rectal Prolapse

Symptoms of rectal prolapse include a sensation of a bulging from the anus, discharge of mucus or blood, anal pain, fecal incontinence, or an obstructed bowel movement. The causes are diverse, ranging from chronic constipation, straining during bowel movements, weakened pelvic floor muscles due to age, previous surgeries, or childbearing.

Treatment hinges on the severity and can vary from self-care techniques and exercises to strengthen the pelvic floor, to surgical interventions aimed at repairing and securing the rectum in its proper place.

LESS LIKELY

Less likely to have rectal prolapse based on 10,706 genetic variants we looked at

1st

PERCENTILE

Your risk is **greater than 1% of the population** and **lower than 99% of the population.**

Anal Fissure

Beyond pain and bleeding, an anal fissure may cause a visible crack in the skin around the anus. It may cause a small lump or skin tag on the skin near the anal fissure, often referred to as a sentinel pile.

Chronic anal fissures may need medical treatment, which can include topical creams to relax the muscle around the anus or surgery to prevent muscle spasms that prevent healing. Additionally, maintaining a healthy diet with ample fiber can soften stool and reduce straining, which is a preventative measure to minimize the risk of developing anal fissures.

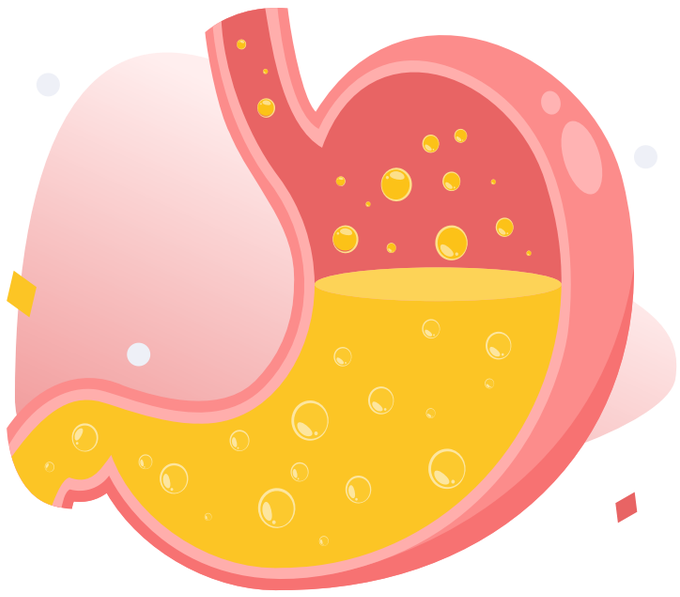
LESS LIKELY

Less likely to have anal fissures based on 19,798 genetic variants we looked at

1st

PERCENTILE

Your risk is **greater than 1% of the population** and **lower than 99% of the population.**



Stomach Health & Acid Production

We deal with digestive problems on a common basis. One look at store shelves and the number of products for digestive problems will tell you just how prevalent they are. Heartburn medications are the number three selling class of over-the-counter drugs. Digestive discomfort related to the stomach can range from mild indigestion to more severe conditions like acid reflux and peptic ulcers.

This section explores genetic factors related to conditions such as peptic ulcers, acid reflux, indigestion, or stomach inflammation. By gaining insight into your genetic predispositions, you can take proactive steps toward managing your stomach health and minimizing symptoms for better digestion and comfort.

MORE LIKELY

Peptic Ulcers

More likely to have peptic ulcers

MORE LIKELY

Nausea

More likely to have nausea

MORE LIKELY

Vomiting

More likely to vomit

TYPICAL LIKELIHOOD

Esophageal Cancer

Typical likelihood of esophageal cancer

TYPICAL LIKELIHOOD

Acid Reflux

Typical likelihood of GERD

TYPICAL LIKELIHOOD

H. pylori

Typical likelihood of H. pylori infection

TYPICAL LIKELIHOOD

Barrett's Esophagus

Typical likelihood of having Barrett’s esophagus

TYPICAL LIKELIHOOD

Esophageal Varices

Typical likelihood of esophageal varices

TYPICAL LIKELIHOOD

Low Stomach Acid

Typical likelihood of hypochlorhydria

TYPICAL LIKELIHOOD

Stomach Pain

Typical likelihood of having stomach pain

TYPICAL LIKELIHOOD

Stomach Inflammation

Typical likelihood of gastritis

LESS LIKELY

Stomach Cancer

Less likely to have stomach cancer

LESS LIKELY

Indigestion

Less likely to have indigestion

LESS LIKELY

Hiatus Hernia

Less likely to have hiatus hernia

Peptic Ulcers

Key Takeaways:

- Up to **30%** of differences in people's chances of developing peptic ulcers may be attributed to genetics.
- Risk factors include: stress, mental health issues, smoking, alcohol use, excessive NSAID use, H. Pylori, and genetics.
- If you have a high genetic risk, you may reduce overall risk by taking action on risk factors that you can change.
- Click the **next steps** tab for relevant labs and lifestyle factors.

Ulcers are open sores anywhere inside or on the body. **Peptic ulcers are a very common type**. Up to 1 in 10 people may develop them at some point in their life. These ulcers usually affect the lining of the stomach (*gastric ulcers*) or the upper part of the small intestine (*duodenal ulcers*) [R, R].

Many people with peptic ulcers don't have any symptoms. Those that do may experience [R]:

- Burning pain in the stomach
- Heartburn
- Nausea or vomiting

There are two main causes of peptic ulcers [R, R, R]:

- *H. pylori* infection
- Long-term use of anti-inflammatory drugs called NSAIDs (e.g., aspirin, ibuprofen)

Other risk factors include [R, R, R, R]:

- Stress and mental health issues
- Smoking
- Drinking alcohol
- **Genetics**

Treatment for peptic ulcers often includes medications that neutralize or reduce stomach acid. Other medications may be used to protect the stomach lining or kill *H. pylori* [R].

It's important to follow your doctor's instructions to treat peptic ulcers. Untreated, they may lead to [R]:

- Bleeding in the gut
- Holes in the gut wall
- Gut blockage
- Stomach cancer

About 30% of differences in people's chances of developing peptic ulcers may be attributed to genetics. Genes involved in peptic ulcers may influence [R, R, R]:

- Stomach acid levels (*IL1B*)
- Stomach lining (*PSCA*)
- Inflammation (*IL1B*, *TNF*)
- Drug metabolism (*CYP2C19*)

MORE LIKELY

More likely to have peptic ulcers based on 113,543 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LY6K	rs2976397	TG
CD151	rs78459074	AA
/	rs687621	AA
PSCA	rs2976388	AG
FUT2	rs681343	TC
JUP	rs34074411	TC
/	rs371481926	CC
FUT2	rs1047781	AA
MUC1	rs147048677	CC
GUCY2F	rs1205531	G
FAM160A2	rs10500661	TT
URAD	rs9581957	CC
EPB41L4A	rs112868245	AA
/	rs114480379	AA
SRBD1	rs112982103	TT
PAPLN	rs112556267	GG
/	rs114374460	AA
/	rs113280140	CC
VIPR2	rs113752094	AA
NAV2	rs113513948	AA
DDX1	rs113922859	CC

GENE	SNP	GENOTYPE
NRP1	rs114044637	CC
CD55	rs113651496	CC
ADGRL3	rs114424033	TT
RASEF	rs114371539	CC
MCL1	rs114488090	CC
CCDC59	rs113931357	GG
KATNAL1	rs114413563	CC
GGH	rs113434022	CC
CLYBL	rs114501577	CC
LHX3	rs113723545	GG
CFTR	rs114276290	CC
/	rs114478365	GG
PALD1	rs111311740	GG
PPP1R3D	rs112733784	CC
GLS	rs114366763	TT
DNM2	rs113192269	AA
TNFSF14	rs111410594	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Nausea

Common situations or conditions that can result in nausea include:

- Stomach flu or gastroenteritis.
- Pregnancy (morning sickness).
- Motion sickness or seasickness.
- Intense pain.
- Emotional stress, fear, or anxiety.
- Overeating or consuming spicy foods.
- Excessive alcohol consumption or substance misuse.
- Food poisoning.
- Certain medications or medical treatments, such as chemotherapy or radiation.
- Gallbladder disease.
- Gastroesophageal reflux disease (GERD).
- Gastroparesis or delayed stomach emptying.

While nausea is primarily a symptom resulting from various conditions or stimuli, genetics can play a role in an individual's susceptibility to certain triggers of nausea. For instance, there may be a genetic predisposition to conditions like motion sickness or migraines.

MORE LIKELY

More likely to have nausea based on 1,670 genetic variants we looked at

96th

PERCENTILE

Your risk is **greater than 96% of the population** and **lower than 4% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
KCND2	rs12706265	CC
GJB4	rs11589940	TT
FGF14	rs1927382	TT
/	rs62493919	GC
/	rs10928874	TA
PPP2R1A	rs8108607	TC
SLCO3A1	rs1568209	GA
MEIS2	rs2681320	TA
CPEB2	rs6848922	CT
NT5M	rs8082383	CC
/	rs1355625	GG
SLC5A8	rs7956620	AG
C9ORF50	rs10118527	CC
C9ORF50	rs10118507	CC
CLDN14	rs2071049	TT
SPATS2L	rs1561296	CT
MTNR1B	rs7118248	GT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Vomiting

Common causes of vomiting include:

- **Gastroenteritis (stomach flu)**
- Pregnancy-related sickness
- Migraine headaches
- Chemotherapy or radiation
- Food poisoning or contamination
- Overeating or drinking large amounts of alcohol
- Certain medications
- Vestibular disorders, like motion sickness
- Gallbladder disease

Factors that might increase the risk of vomiting include:

- Exposure to individuals with stomach viruses or infections
- Consuming contaminated food or water
- Traveling, especially to areas with different water or food sanitation standards
- A history of motion sickness or migraine
- Genetics

MORE LIKELY

More likely to vomit based on 1,675 genetic variants we looked at

88th

PERCENTILE

Your risk is **greater than 88% of the population** and **lower than 12% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
KCND2	rs12706265	CC
GJB4	rs11589940	TT
FGF14	rs1927382	TT
/	rs62493919	GC
/	rs10928874	TA
PPP2R1A	rs8108607	TC
SLCO3A1	rs1568209	GA
MEIS2	rs2681320	TA
CPEB2	rs6848922	CT
NT5M	rs8082383	CC
/	rs1355625	GG
SLC5A8	rs7956620	AG
C9ORF50	rs10118527	CC
C9ORF50	rs10118507	CC
CLDN14	rs2071049	TT
SPATS2L	rs1561296	CT
MTNR1B	rs7118248	GT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Esophageal Cancer

Risk factors for esophageal cancer include [R]:

- Chronic gastroesophageal reflux disease (GERD): Prolonged exposure to stomach acids can damage the lining of the esophagus and may lead to Barrett's esophagus.
- Barrett's esophagus: Increases the risk of adenocarcinoma.
- Smoking: A significant risk factor for squamous cell carcinoma.
- Heavy alcohol consumption: Especially increases the risk for squamous cell carcinoma.
- Obesity: Associated with a higher risk of adenocarcinoma.
- Diet: A diet low in fruits and vegetables may increase the risk.
- Achalasia: A rare disorder that makes it difficult for food and liquid to pass into the stomach, raising the risk of squamous cell carcinoma.
- Drinking hot liquids: Regularly consuming very hot beverages may irritate the lining of the esophagus, which can increase the risk.

Treatment depends on the stage of the cancer, the patient's overall health, and other factors. It may include [R]:

- Surgery: To remove the tumor and some surrounding healthy tissue, and possibly nearby lymph nodes. In advanced cases, part or all of the esophagus may be removed.
- Radiation therapy: Often used alongside chemotherapy before surgery to shrink the tumor or after surgery to eliminate any remaining cancer cells.
- Chemotherapy: Used to kill cancer cells, often in combination with radiation therapy either before surgery or as a standalone treatment in cases where surgery isn't an option.
- Targeted therapy: Uses drugs or other substances to precisely identify and attack cancer cells, usually while doing little damage to normal cells.

Please note: This report is not diagnostic and can't be used to make any medical decisions. Most cancers are uncommon and have a strong environmental component. Even if your genetic predisposition is high, you will most likely not develop the disease. This report doesn't test for hereditary cancer syndromes or 'cancer genes'. These are usually caused by rare mutations that can't be analyzed by our test. If you're concerned about your risk of hereditary cancer, consider getting a specialized test at a reference laboratory.

TYPICAL LIKELIHOOD

Typical likelihood of esophageal cancer based on 939,366 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CCDC71L	rs114448224	CC
/	rs10417850	GG
STAT4	rs113702517	TT
SLC16A14	rs35963873	TG
PPP4R1	rs78048962	GG
SALL4	rs16996300	CC
SCG2	rs714943	CC
ABHD11	rs7806956	AT
SPATA6	rs11205513	GC
ZFYVE16	rs79319332	GC
PPP3R1	rs1868403	CT
RBBP8	rs62093212	CT
CHRM3	rs10802794	CT
PTCH1	rs4744456	CT
CHST10	rs147274464	AA
MYO1B	rs142741123	TT
UBE3D	rs115648060	GG
AMTN	rs148725713	CC
TNFRSF10C	rs531841075	GG
PCM1	rs144188626	GG
CSTF2T	rs143380404	TT
/	rs73365656	CC
UBXN2B	rs114039795	CC
SALL1	rs115523423	CC
GINS2	rs112854191	TT
FAM120AOS	rs12379660	GG
/	rs9783765	AA
C15ORF48	rs73412484	AA
GPM6A	rs4532186	GG

GENE	SNP	GENOTYPE
CDCA2	rs1365016	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Acid Reflux

Key Takeaways:

- About **40%** of differences in people's chances of developing GERD may be attributed to genetics. It affects about **1 in 5** people in the U.S.
- GERD affects about **1 in 5** people in the U.S.
- Risk factors include: obesity, smoking, pregnancy, slow stomach emptying, hiatal hernia, certain foods, and genetics.
- If you have a high genetic risk, you may reduce overall risk by taking action on risk factors that you can change.
- Click the **next steps** tab for relevant labs and lifestyle factors.

Have you ever had heartburn after a meal? If so, you're already familiar with **acid reflux**.

The stomach is full of acid that helps it digest food. Normally, a muscle (sphincter) above the stomach keeps the acid from moving up into the esophagus. If the muscle relaxes at the wrong time or becomes weak, it can allow stomach acid to flow up. This is called acid reflux [R].

In addition to heartburn, other signs and symptoms of acid reflux include [R]:

- A sour taste
- A constant cough or hiccups
- A hoarse voice
- Bad breath
- Bloating

Factors that can trigger or worsen these symptoms include [R]:

- Eating large meals
- Eating late at night
- Lying down or bending over after eating
- Consuming certain foods or drinks (e.g., fried or spicy foods, chocolate, coffee, and alcohol)

Many people have occasional acid reflux. However, if it is frequent, severe, or long-term, it may be a sign of gastroesophageal reflux disease (GERD). GERD is one of the most common gut disorders in the US. It affects about 1 in 5 people in North America [R, R, R, R].

Risk factors for GERD include [R, R]:

- Obesity
- Smoking
- Pregnancy
- Slow stomach emptying
- Hiatal hernia (bulging of stomach tissue into the chest)
- **Genetics**

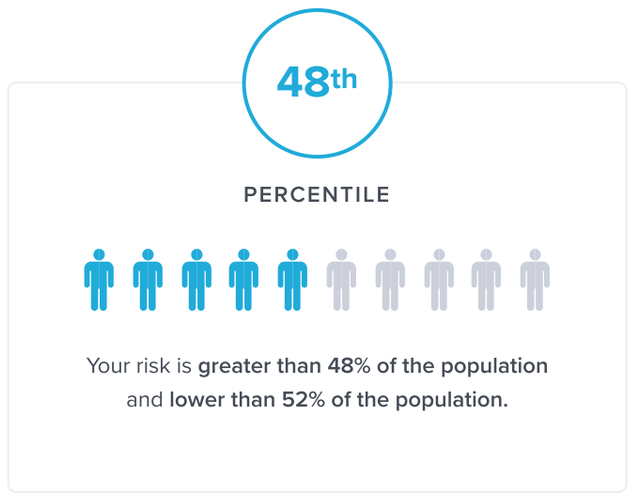
GERD is commonly treated with medications that help neutralize stomach acid or reduce its production [R].

If left untreated, GERD may lead to chronic inflammation in the esophagus. This may cause [R, R]:

- Difficulty swallowing
- Open sores (ulcers) in the esophagus
- Changes in the lining of the esophagus (Barrett's esophagus)
- Cancer of the esophagus

TYPICAL LIKELIHOOD

Typical likelihood of GERD based on 222,102 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
GNB3	rs5443	TT
MRM2	rs11762636	CC
/	rs9372625	GG
REX1BD	rs2023878	CC
PGPEP1	rs9636202	GG
TSKU	rs7942368	CC
HIVEP2	rs9373363	AA
/	rs324769	CC
ETAA1	rs4362541	AA
PPP3CA	rs920559	CG
CELF4	rs12967855	AG
MAD1L1	rs4721096	CC
VCAN	rs72771256	GG
BTN2A2	rs2145318	TA
PPP1R17	rs215614	GA
MAML3	rs809955	GG
REX1BD	rs12974777	CC
SORCS3	rs1021363	GA
MLN	rs4713692	TC
SNRK	rs74652506	TC
HLA-B	rs9266237	CG

About 40% of differences in people's chances of developing GERD may be attributed to genetics. Genes involved in GERD may influence [R, R, R, R, R, R]:

- Detoxification (*DPYD*)
- Inflammation (*MST1R*, *PDE4B*)
- Muscle function (*LAMA2*)

GENE	SNP	GENOTYPE
BTN3A2	rs7763910	AG
/	rs10940767	TA
PGPEP1	rs1363119	GA
OLIG1	rs7282609	GA
SLC39A8	rs13107325	CC
GRM8	rs2106353	GG
KNDC1	rs761777	AA
AFF3	rs4851239	TT
ANO10	rs6441814	AA
ADARB1	rs2838771	CC
DPYD	rs7552188	CC
/	rs4676893	TT
CA10	rs34796998	CC
FAM160A2	rs12792379	GG
AFF3	rs7609078	AA
SDK1	rs10242223	GG
GRM8	rs12706746	GG
APOB	rs11901649	AA
SH2B3	rs597808	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

H. Pylori

Key Takeaways:

- Genes involved in H. Pylori affect stomach acid production and the stomach's mucous barrier.
- Risk factors include an unsanitary environment, poverty, eating at restaurants, eating meat, and smoking.
- If you have a high genetic risk, you may reduce overall risk by taking action on risk factors that you can change.
- Click the **next steps** tab for relevant labs and lifestyle factors.

Helicobacter pylori (*H. pylori*) is a type of bacteria that can live in the stomach. About half of all people may be infected with *H. pylori*. Developing countries have higher infection rates [R, R, R].

Most people don't have any symptoms of infection. In some, however, the bacteria can start to break down the protective mucous barrier of the stomach wall. This can cause serious problems [R, R, R].

H. pylori may contribute to [R, R]:

- Gastritis (stomach inflammation)
- Peptic ulcers (sores in the stomach or upper small intestine lining)
- Stomach cancer

Symptoms arise when a person develops gastritis or ulcers. These can include [R, R, R]:

- Nausea
- Stomach pain
- Vomiting
- Low appetite
- Weight loss
- Indigestion

People usually become infected with *H. pylori* in childhood. Growing up around a lot of people or in unsanitary conditions may play a large role. Other risk factors for *H. pylori* infection include [R, R]:

- Lower socioeconomic status
- Eating out at restaurants
- Eating meat
- Smoking cigarettes

Medications for *H. pylori* help kill the bacteria and heal the stomach. They are usually prescribed in different combinations [R, R, R].

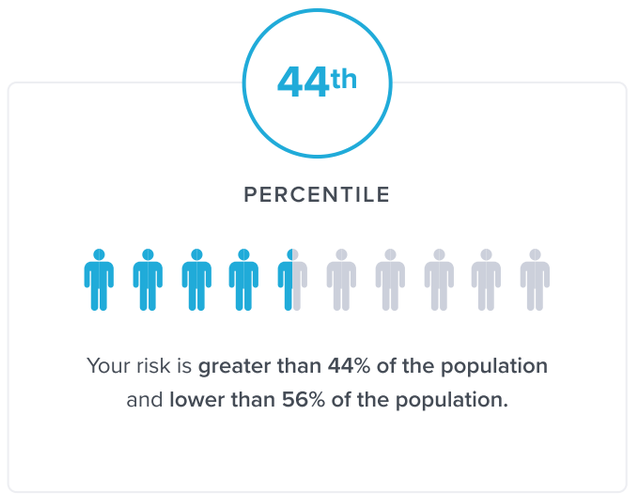
Some strains of *H. pylori* are becoming more difficult to kill with antibiotics. This makes them harder to treat [R, R].

Genetics seems to play a role in the risk of ulcers due to *H. pylori*. Genes involved in *H. pylori* infection and related diseases may influence [R, R]:

- Stomach acid production (*GAST*)
- The mucous barrier in the stomach (*MUC1*, *FUT2*, *ABO*)

TYPICAL LIKELIHOOD

Typical likelihood of H. pylori infection based on 86,987 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
DOCK10	rs10201967	CC
IKZF2	rs10194411	GG
AKR1E2	rs112501331	CC
VMP1	rs111821451	GG
FBXO21	rs111576798	GG
RAP2B	rs112013042	CC
SIPA1L3	rs113428378	AA
NFE2	rs11170954	CC
HPCAL1	rs10929658	AA
METTL14	rs112991781	TT
PCDH15	rs11004038	TT
FGD4	rs11052023	TT
LGSN	rs1020805	GG
PCDH15	rs11004387	TT
/	rs10008115	GG
HEBP1	rs111707992	AA
CLEC2B	rs1088309	GG
PTCHD4	rs1150811	AA
ADAMTSL4	rs10888382	CC
PDSS1	rs112022787	AG
PDZD2	rs10472790	TC

GENE	SNP	GENOTYPE
/	rs11059054	AC
TCF7L1	rs113194344	AG
GAREM2	rs1019972	CT
TLE1	rs11139024	TC
LRRTM3	rs10762128	TA
KLHL31	rs113924095	AA
FIGLA	rs115235891	CC
RBP7	rs112432872	GG
TFPI	rs10497687	CC
ZNF91	rs112713994	GG
ASAH2	rs10508925	GG
TP53INP1	rs112904682	GG
CLMP	rs11219074	CC
MRPS33	rs113513883	GG
RDH14	rs10181477	AA
SYT13	rs11038374	TT
GULP1	rs112821517	CC
LILRA4	rs112985797	GG
PLCL1	rs113784795	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Barrett's Esophagus

Factors that increase your risk of Barrett's esophagus include [R]:

- **Chronic GERD**
- Age: more common in adults over 50.
- Gender: more common in men.
- Current or past smoking
- Obesity, particularly abdominal obesity.
- Family history. Your odds of having Barrett's esophagus increase if you have a family history of Barrett's esophagus or esophageal cancer.

While the primary risk factor for Barrett's esophagus is chronic GERD, genetic factors might also play a role. A family history of the condition can indicate a predisposition. However, the exact nature of the genetic influence is not fully understood and appears to be complex.

Treatment of Barrett's esophagus depends on the extent of abnormal cell growth in your esophagus and your overall health, and may include [R]:

- Medications to reduce acid production and manage GERD symptoms.
- Periodic endoscopy to monitor the cells in your esophagus.
- In severe cases, surgical procedures like fundoplication, or endoscopic procedures like radiofrequency ablation, may be recommended.

In addition, the following lifestyle changes can ease the symptoms of GERD [R]:

- Maintaining a healthy weight
- Avoiding food triggers
- Giving up smoking
- Raising the head of your bed

TYPICAL LIKELIHOOD

Typical likelihood of having Barrett's esophagus based on 1,674 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
ETAA1	rs2861695	AA
OR2H2	rs9257809	AA
TBX5	rs1247942	GG
REX1BD	rs7258722	TT
CTTNBP2	rs17451754	GG
BARX1	rs11789015	AA
REX1BD	rs2003476	TT
FAM167A	rs10108511	TC
/	rs9918259	CT
LDAH	rs7255	TC
FAM167A	rs2409797	TC
FOXF1	rs1979654	CG
IKBIP	rs9668109	GG
HMCN2	rs763936875	TT
PNMA2	rs17321041	CC
GOLIM4	rs7632500	GG
/	rs2597301	GG
TMOD1	rs10982622	GG
MIB1	rs4800353	AA
MSRA	rs17749155	GG
DPP6	rs11771429	CC
/	rs2880866	CC
CEP72	rs4957081	GG
/	rs2687201	CC
REX1BD	rs10419226	TG
AQP9	rs3784262	CT
GRID1	rs7904985	GG
/	rs62423175	GG
ISL1	rs6449586	TT

GENE	SNP	GENOTYPE
NECTIN2	rs2927438	GG
/	rs2342002	CC
CEP72	rs11955068	CC
TMOD1	rs7852462	TT
FOXF1	rs9936833	TT
FOXF1	rs2178146	CT
/	rs2687202	CC
ALDH1A2	rs2464469	AA
/	rs139606545	CC
MAP7D1	rs491603	TC
IQCK	rs1548445	AA
SLFN12	rs2671828	CC
SLC12A6	rs11631094	TG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Esophageal Varices

The rupture of esophageal varices is a life-threatening emergency that requires immediate medical attention. Warning signs may include vomiting blood, black or tarry stools, and a drop in blood pressure, which can lead to shock.

Due to the risk of bleeding, preventative measures are often taken, such as periodic surveillance endoscopies and medications to reduce portal pressure. For individuals with known esophageal varices, lifestyle changes such as avoiding alcohol and monitoring the use of medications that can affect bleeding risks are also recommended to minimize the chance of rupture.

TYPICAL LIKELIHOOD

Typical likelihood of esophageal varices based on 18,935 genetic variants we looked at

69th

PERCENTILE

Your risk is **greater than 69% of the population** and **lower than 31% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
TRAF3IP2	rs9487666	CA
PNPLA3	rs738409	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Low Stomach Acid

The main risk factors for hypochlorhydria include [R]:

- Atrophic gastritis: Chronic inflammation in the stomach can make the cells that secrete stomach juices atrophy and stop working. It can be caused by alcoholism, bacterial infections, and autoimmune conditions.
- *H. pylori* infection: although it causes no symptoms in some people, it can take over, fighting and eventually decreasing stomach acid. Ironically, low stomach acid can also allow for *H. pylori* to take over.
- Chronic use of acid-suppressing medications like proton pump inhibitors (PPIs) and H2 blockers.
- Gastric surgery or certain medical conditions that affect the stomach.
- Chronic stress, which can alter stomach acid production.
- Age: hypochlorhydria is typically diagnosed after the age of 65 because stomach acid production tends to decrease with age.

There is limited direct evidence linking genetics to hypochlorhydria, though genetics may play a role in predisposing individuals to conditions associated with low stomach acid, such as *H. pylori* infections or autoimmune gastritis.

The most important step in hypochlorhydria treatment involves identifying and addressing the underlying causes, such as discontinuing long-term acid suppressants, treating *H. pylori* infection, or managing stress. Other management strategies include [R]:

- Supplementation with hydrochloric acid (HCl), often combined with the enzyme pepsin, to treat the hydrochloric acid deficiency itself.
- Ensuring adequate intake of key nutrients such as iron, calcium, or vitamin B12, possibly through supplementation.
- Mindful eating practices, such as including smaller, more frequent meals, avoiding fatty and processed foods, or finishing the last meal of the day 2-3 hours before bedtime.

TYPICAL LIKELIHOOD

Typical likelihood of hypochlorhydria based on the genetic variants we looked at

77%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **77% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
TLR4	rs4986790	AA
IL1B	rs16944	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Stomach Pain

The cause of stomach pain can be attributed to a wide variety of conditions, from digestive issues like indigestion or gastroenteritis to more serious conditions like appendicitis or kidney stones.

Risk factors for recurrent or chronic stomach pain include:

- Dietary choices: Consuming spicy, fatty, or acidic foods
- Overeating or eating too quickly
- Chronic conditions such as gastritis, ulcers, or gallstones
- Infections or viruses affecting the digestive system
- Physical or emotional stress
- Certain medications that can irritate the stomach lining

TYPICAL LIKELIHOOD

Typical likelihood of having stomach pain based on 1,673 genetic variants we looked at

46th

PERCENTILE

Your risk is **greater than 46% of the population** and **lower than 54% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
GRIN3A	rs182276014	TT
GZMH	rs190749747	CC
FZD1	rs182267037	CC
/	rs72683482	GG
RALGPS2	rs6675656	TT
IGF1R	rs144880784	CC
/	rs56252721	AA
EPS8L3	rs190178166	CC
BTG1	rs141884556	GG
CWF19L2	rs79224501	AA
TMEM128	rs543096999	CC
MXRA8	rs112044473	GG
/	rs145439079	CC
AMN1	rs569208093	GG
PPM1F	rs34639823	CC
IGF1R	rs118021991	AA
COX7C	rs114575486	TT
PLPPR4	rs115008227	AA
EPS8L3	rs78018756	CC
CNTNAP5	rs78037681	CC
ARHGAP45	rs116305519	CC

GENE	SNP	GENOTYPE
GUCY1A2	rs117090859	AA
KCND2	rs191721892	AA
COL15A1	rs150185691	AA
SERPINB8	rs118084041	AA
LRRTM1	rs186057704	GG
FOXK1	rs118117357	TT
MKLN1	rs78522184	GG
TMEM131	rs142462181	GG
ANGPT1	rs12542882	TT
PRMT6	rs145009014	GG
/	rs146534400	TT
KIF21A	rs189504750	GG
C16ORF95	rs192095736	CC
CDIN1	rs113441091	GG
LRATD1	rs113707455	TT
/	rs76449150	GG
SMIM14	rs73240633	TT
NEBL	rs151118164	AA
VTI1A	rs148319443	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Stomach Inflammation

Symptoms of gastritis vary among individuals and can range from mild discomfort to severe pain. Common symptoms include upper abdominal pain or burning, nausea, vomiting, bloating, and a feeling of fullness in the upper abdomen after eating. If left untreated, gastritis can lead to stomach ulcers and an increased risk of stomach bleeding, which may be life-threatening.

In some cases, chronic gastritis may increase the risk of developing stomach polyps or stomach tumors. Treatment for gastritis generally involves a combination of medications to reduce stomach acid and a change in diet or lifestyle habits that may be contributing to the inflammation.

TYPICAL LIKELIHOOD

Typical likelihood of gastritis based on 9,903 genetic variants we looked at

PERCENTILE

Your risk is **greater than 44% of the population** and **lower than 56% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CCDC66	rs6445797	GC
MRPL13	rs7826906	GA
TCP10L	rs11088226	CG
MTBP	rs10955971	AG
CDC37	rs8112449	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Stomach Cancer

Risk factors for stomach cancer include [R]:

- *Helicobacter pylori* infection: This bacterium is a major risk factor for stomach cancer.
- Diet: A diet high in red meat, processed meats, and salty foods may increase the risk of stomach cancer.
- Smoking
- Family history
- Other factors: Certain medical conditions, such as anemia and pernicious anemia, may also increase the risk of stomach cancer.

Treatment depends on the stage of the cancer and the patient's overall health [R]:

- Surgery: removing part or all of the stomach, sometimes along with nearby lymph nodes.
- Chemotherapy: uses drugs to kill cancer cells or stop them from growing.
- Radiation therapy: uses high-energy rays to target and kill cancer cells.
- Targeted therapy: drugs that specifically target cancer cells without affecting normal cells.
- Immunotherapy: boosts the body's immune system to fight cancer cells.

The prognosis for stomach cancer depends on several factors, including the stage at diagnosis, the patient's overall health, and how well the cancer responds to treatment. Early detection improves the chances of successful treatment.

Please note: This report is not diagnostic and can't be used to make any medical decisions. Most cancers are uncommon and have a strong environmental component. Even if your genetic predisposition is high, you will most likely not develop the disease. This report doesn't test for hereditary cancer syndromes or 'cancer genes'. These are usually caused by rare mutations that can't be analyzed by our test. If you're concerned about your risk of hereditary cancer, consider getting a specialized test at a reference laboratory.

LESS LIKELY

Less likely to have stomach cancer based on 16,655 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LMNA	rs138554234	GG
PRKAA1	rs10074991	GG
OR10C1	rs77454196	CC
VPS35L	rs117430025	GG
THBS3	rs7366775	AG
KIAA2026	rs343471	TT
ANKRD50	rs11937064	GG
LYPD2	rs10105842	CC
HLA-A	rs28749114	AA
KCNU1	rs11775036	CC
BRMS1L	rs11851309	CC
SNX13	rs11560253	AA
IRF2	rs793885	CC
ZSCAN26	rs2799081	TT
/	rs10202299	TT
ZNF248	rs2475206	GG
ANKEF1	rs6039695	AG
CLPTM1L	rs2853669	GA
SMARCA2	rs10491697	GA
IRAK2	rs2544001	TT
NOC3L	rs10509670	AA
SPRY2	rs61291112	CC
CCDC32	rs999197	CC
C7	rs2675982	CC
PTGER4	rs114080964	GG
H2BC12	rs9461366	GG
ZSCAN9	rs16893741	TT
LRIG3	rs11172733	TT
UNC5CL	rs9381024	GG

GENE	SNP	GENOTYPE
ZFP36L2	rs12471190	TT
MICA	rs3128983	TT
TUBB	rs2267637	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Indigestion

Key Takeaways:

- Genes affecting indigestion may influence nerve function, gut muscle movements, and pain sensitivity.
- Risk factors: age, overweight, smoking, stress, poor diet, gut conditions, medications, and lying down after eating.
- Up to 40% of people in Western countries may experience indigestion.
- If you are at high genetic risk, take action now to lower your overall risk. If your risk is low and you have symptoms, take action now to improve symptoms.

Indigestion (also called dyspepsia) is pain or discomfort in the upper abdomen. Other symptoms may include [R, R]:

- Bloating
- Feeling full after only eating a small amount
- Feeling full for a long time after eating
- Nausea
- Hot or burning feeling

Up to 40% of people in Western countries may experience indigestion. Contributing factors include [R, R, R, R, R, R]:

- Older age
- Being overweight
- Smoking
- Stress and anxiety
- Certain medications (e.g., NSAIDs)
- Other gut conditions (e.g., ulcers, chronic acid reflux, *H. pylori* infection)
- Poor food choices and eating habits
- Lying down after eating
- Wearing tight clothes
- **Genetics**

Indigestion usually doesn't have serious complications. However, if left untreated, it can progress to serious medical problems. Contact a doctor if you have severe or ongoing symptoms [R, R].

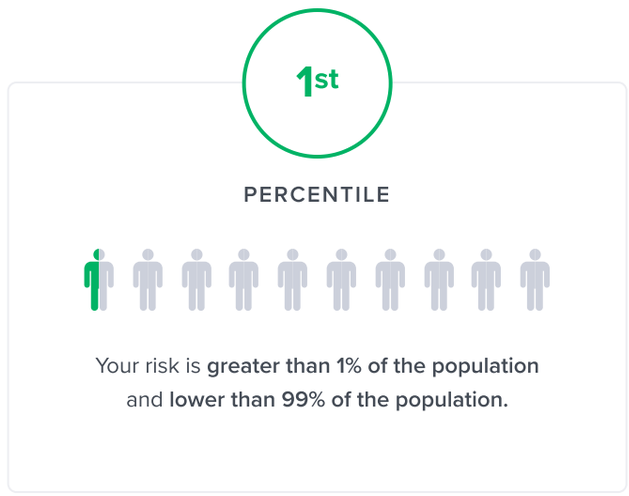
Indigestion may be treated with medication and diet changes [R].

Genetics seems to play a role in indigestion. Genes involved in indigestion may influence [R, R, R]:

- Nerve function (*NFASC*, *CNTN2*, *NXPH1*)
- Gut muscle movements (*ADRB2*)
- Pain sensitivity (*SCN10A*)

LESS LIKELY

Less likely to have indigestion based on 226 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
FBXO21	rs2682826	GA
GRIN3A	rs182276014	TT
GZMH	rs190749747	CC
FZD1	rs182267037	CC
/	rs72683482	GG
RALGPS2	rs6675656	TT
IGF1R	rs144880784	CC
/	rs56252721	AA
EPS8L3	rs190178166	CC
BTG1	rs141884556	GG
CWF19L2	rs79224501	AA
TMEM128	rs543096999	CC
MXRA8	rs112044473	GG
/	rs145439079	CC
AMN1	rs569208093	GG
PPM1F	rs34639823	CC
IGF1R	rs118021991	AA
COX7C	rs114575486	TT
PLPPR4	rs115008227	AA
EPS8L3	rs78018756	CC
CNTNAP5	rs78037681	CC

GENE	SNP	GENOTYPE
ARHGAP45	rs116305519	CC
GUCY1A2	rs117090859	AA
KCND2	rs191721892	AA
COL15A1	rs150185691	AA
SERPINB8	rs118084041	AA
LRRTM1	rs186057704	GG
FOXK1	rs118117357	TT
MKLN1	rs78522184	GG
TMEM131	rs142462181	GG
ANGPT1	rs12542882	TT
PRMT6	rs145009014	GG
/	rs146534400	TT
KIF21A	rs189504750	GG
C16ORF95	rs192095736	CC
CDIN1	rs113441091	GG
LRATD1	rs113707455	TT
/	rs76449150	GG
SMIM14	rs73240633	TT
NEBL	rs151118164	AA
VTI1A	rs148319443	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Hiatus Hernia

Hiatus hernia is commonly categorized into two types: sliding and paraesophageal. The more prevalent type (sliding) occurs when the stomach and part of the esophagus slide up into the chest.

On the other hand, a paraesophageal hernia happens when part of the stomach squeezes through the hiatus, positioning itself next to the esophagus. While sliding hernias can be managed with lifestyle changes and medication, paraesophageal hernias might require surgical intervention due to the risk of the stomach becoming strangulated—cut off from blood supply—which is a medical emergency.

LESS LIKELY

Less likely to have hiatus hernia based on 640,581 genetic variants we looked at

1st

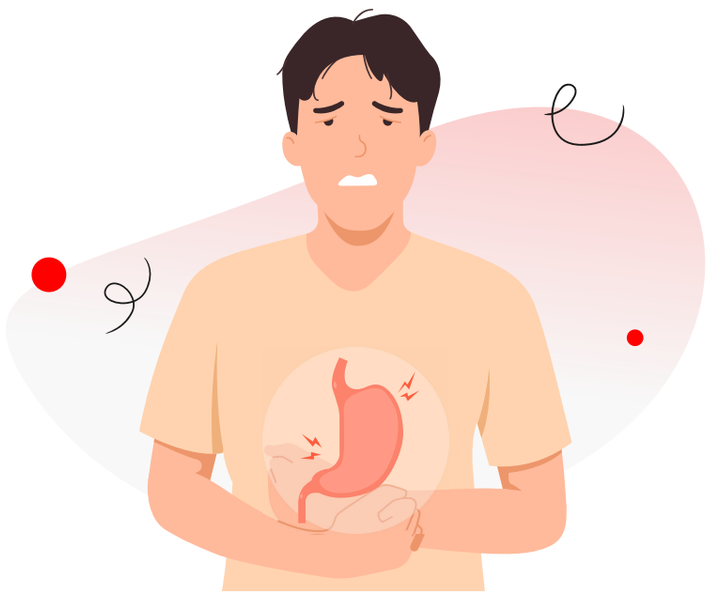
PERCENTILE

Your risk is **greater than 1% of the population** and **lower than 99% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
EFEMP1	rs10207635	AA
BTN3A2	rs9393735	AA
WT1	rs11031796	AG
REX1BD	rs2891698	GA
CALD1	rs4728341	CT
BARX1	rs4075733	TC
ADAMTS16	rs42202	GG
/	rs4499560	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.



Gut Infections

Foreign microbes invade our gut all of the time, from viruses to parasites to bacteria. Anyone who has had stomach flu or eaten bad seafood will tell just how bad the effects can be. Some infections like *H. pylori* can have chronic unpleasant symptoms and even lead to ulcers and other complications.

This section delves into your genetic predisposition to various gut infections such as C. difficile, H. pylori, EBV, shigellosis, and others. Understanding how your genetics influence your immune response to these infections can help you take preventive measures and choose the most effective treatment options.

TYPICAL LIKELIHOOD

EBV Infection

Typical likelihood of getting EBV infection

TYPICAL LIKELIHOOD

Shigella Infection

Typical likelihood of shigellosis

TYPICAL LIKELIHOOD

Diarrhea

Typical likelihood of getting diarrhea

TYPICAL LIKELIHOOD

Stomach Bug

Typical likelihood of gastroenteritis

TYPICAL LIKELIHOOD

C. difficile Infection

Typical likelihood of a C. difficile infection

TYPICAL LIKELIHOOD

H. pylori

Typical likelihood of H. pylori infection

TYPICAL LIKELIHOOD

Gastrointestinal Infection

Typical likelihood of a GI infection

EBV Infection

Epstein-Barr virus (EBV) is one of the most common human viruses. It mainly spreads via saliva and may cause mononucleosis or “the kissing disease”.

Although almost everyone will come into contact with the virus, only a fraction of people will develop EBV infection. Risk factors for EBV infection include [R]:

- Contact with infected person or objects
- Spending time in unventilated, crowded spaces
- Compromised immune system
- **Genetics**

Genetics also seems to play a role in mononucleosis, the main condition caused by EBV [R].

TYPICAL LIKELIHOOD

Typical likelihood of getting EBV infection based on 1,667 genetic variants we looked at

50th

PERCENTILE

Your risk is **greater than 50% of the population** and **lower than 50% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HLA-DQA1	rs6927022	AA
PHF14	rs73067509	CC
SUGCT	rs186721582	GG
H3C12	rs34034915	TINS(G)
BTN3A2	rs9379862	CT
P2RY12	rs67886110	GT
RHBDD3	rs138870856	CC
SLC24A4	rs4900130	GG
UTP20	rs78440807	GG
S1PR4	rs61731111	CC
PHKB	rs56257827	GG
SIDT1	rs34023543	AA
GCNT1	rs11546569	CC
SVEP1	rs74597491	TT
GBE1	rs28763904	AA
SPATA6	rs77303590	CC
CPXM1	rs41310169	CC
MS4A13	rs55756397	GG
MST1	rs142690032	GG
CEP63	rs114108011	GG
FANCI	rs117125761	CC

GENE	SNP	GENOTYPE
HLA-DRB1	rs9271536	TT
IRF4	rs2316515	GG
DCAF4	rs117449182	AA
KRT83	rs2857667	GA
CC2D2A	rs144439937	AA
C1QBP	rs56014026	GG
EXOG	rs1141223	GG
RAB11FIP1	rs61746628	GG
RELN	rs55689103	CC
COQ2	rs112033303	TT
CGRRF1	rs34839928	CC
MFSD12	rs34878396	CC
CFAP206	rs35438647	GG
FILIP1	rs62415695	GG
SDF2L1	rs73166641	GG
FAM81A	rs111778770	GG
ASCC1	rs11000217	GG
BBS10	rs142863601	CC
LIPI	rs61740029	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Shigella Infection

Individuals with shigellosis often experience symptoms within one to two days after exposure to the bacteria, and the illness usually resolves within five to seven days. Some cases, however, can be more severe and require medical treatment.

Complications can include dehydration due to severe diarrhea, rectal bleeding, and in rare instances, the bacteria can enter the bloodstream leading to bacteremia or other severe infections. Prevention of shigella infection is largely centered around proper sanitation practices, including thorough handwashing with soap and avoiding consumption of potentially contaminated food or water.

TYPICAL LIKELIHOOD

Typical likelihood of shigellosis based on 6 genetic variants we looked at

53rd

PERCENTILE

Your risk is **greater than 53% of the population** and **lower than 47% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
TMEM218	rs147975801	AA
CYTH3	rs10266841	CG
MPP7	rs2801847	AA
TMEM218	rs653552	AA
TMEM218	rs582240	CC
TNKS	rs12550437	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Diarrhea

Diarrhea is a common condition that affects the digestive system. It involves loose, watery stools that are passed more often than usual.

While genetics plays a role in diarrhea, environmental and lifestyle factors have the largest impact. They include [R]:

- Being a young child or older adult
- Traveling to or living in a developing country
- Having a weakened immune system
- Having chronic digestive conditions like IBS or celiac disease
- Taking certain medications such as antibiotics

If you experience diarrhea, **it is important to stay hydrated**. Drink plenty of fluids, such as water, clear broth, or sports drinks.

TYPICAL LIKELIHOOD

Typical likelihood of getting diarrhea based on 1,670 genetic variants we looked at

66th

PERCENTILE

Your risk is **greater than 66% of the population** and **lower than 34% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
MANF	rs61570769	GG
LAMA1	rs140718292	TC
ST7L	rs114199731	TT
KRT83	rs2857667	GA
VIT	rs140104536	CC
SDCBP2	rs35367003	CC
EMID1	rs76367973	CC
COL6A6	rs114511272	CC
CGRRF1	rs34839928	CC
CDKL2	rs56229013	CC
THEMIS2	rs41284294	TT
TM9SF1	rs62621251	TT
ZBP1	rs45521631	CC
IGDCC4	rs75405617	TT
MCM10	rs35114749	CC
IRAK4	rs55944915	GG
PALM2AKAP2	rs72757010	GG
RBL2	rs76818213	GG
GANC	rs35285091	CC
WDR35	rs56395266	GG
NPHP3	rs41272317	CC

GENE	SNP	GENOTYPE
SNX25	rs34120554	CC
FANCI	rs117125761	CC
EBLN2	rs2231925	TT
MRPS34	rs11552434	CC
LAMA4	rs41289902	CC
UNC80	rs78846221	CC
VWA2	rs62623671	CC
FAM162B	rs41306045	CC
STK32A	rs35852718	AA
TTC21A	rs80238762	GG
RPGRIP1L	rs139974543	GG
SREBF1	rs36215896	CC
IL17RC	rs148575246	GG
SIDT1	rs34023543	AA
C1QTNF6	rs17812681	CC
FLNC	rs181067717	CC
ABCB6	rs57467915	GG
RAB21	rs61754230	CC
RELN	rs78008536	GG
ASH2L	rs193080501	GG
CBR1	rs61759823	TT
ERCC4	rs1800124	AA
GC	rs76781122	CC
S1PR4	rs61731111	CC
CACNA1S	rs142356235	CC
UMODL1	rs114358105	CC
FAM81A	rs111778770	GG
ZNF703	rs79707182	CC
DNAJC13	rs61748102	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Stomach Bug

Treatment for gastroenteritis is usually focused on hydration and electrolyte balance, as the risk of dehydration from fluid loss due to diarrhea and vomiting can be significant, especially in young children and the elderly. Over-the-counter anti-diarrheal medications can help reduce the length of the illness and improve symptoms, but they are generally not recommended for use in severe cases or in children.

Probiotics and a bland diet can aid in the recovery of the gastrointestinal tract. Prevention efforts are centered on good hygiene practices, such as frequent hand-washing, and careful preparation and handling of food to avoid contamination.

TYPICAL LIKELIHOOD

Typical likelihood of gastroenteritis based on 282,527 genetic variants we looked at

39th

PERCENTILE

Your risk is **greater than 39% of the population** and **lower than 61% of the population.**

C. Difficile Infection

***C. difficile* is a type of bacteria that may cause colitis**, meaning inflammation of the large intestine or colon. It can be found in **contaminated** [R, R, R]:

- Water
- Food (e.g., retail meat, vegetables)
- Human and animal feces
- Hospital surfaces

Recent antibiotic use is the main risk factor for *C. difficile* infection. Antibiotics alter the gut microbiome and make it susceptible to infection. Other risk factors include [R, R, R, R]:

- **Hospital or nursing home stay**
- Malnutrition
- Being 65 or older
- Drugs to reduce stomach acid (e.g., omeprazole)
- Inflammatory diseases (e.g., inflammatory bowel disease)
- Chronic kidney or liver disease
- Chemotherapy
- Previous *C. difficile* infection
- **Genetics**

***C. difficile* produces toxins**, which contribute to the following infection symptoms [R, R, R]:

- Diarrhea
- Belly pain and cramps
- Nausea and vomiting
- Fever

C. difficile infection may cause severe colon inflammation and even death if left untreated [R].

On the other hand, some people may not have symptoms at all, but they may still pass *C. difficile* on to others [R, R].

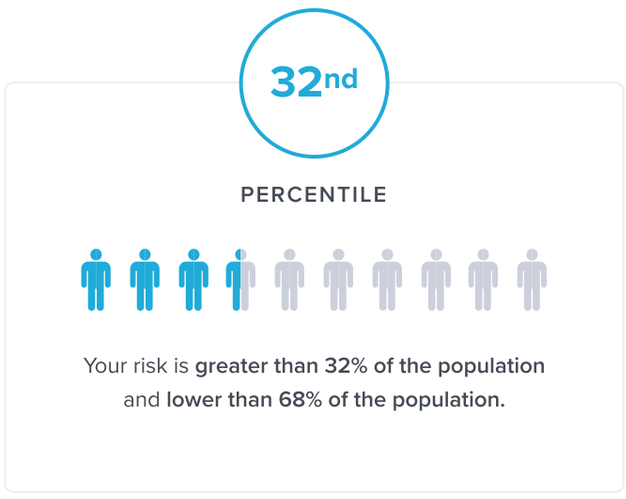
Medications for *C. difficile* help kill the bacteria. To prevent *C. difficile* infections, doctors also recommend [R, R, R]:

- Hand hygiene with soap and water
- Avoiding antibiotic misuse
- Taking probiotics

Some strains of *C. difficile* are becoming more difficult to kill with antibiotics. This makes them harder to treat and calls for new treatment approaches. One such treatment is *fecal microbiota transplantation* (FMT), or the transfer of a healthy person's feces into a patient's colon [R, R, R, R].

TYPICAL LIKELIHOOD

Typical likelihood of a C. difficile infection based on 2,751 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
KCNJ15	rs62222030	TC
/	rs1434351	GT
/	rs11617974	AC
CDH8	rs141932469	CC
PRSS37	rs17719655	CC
CNOT4	rs117373257	GG
NWD2	rs116838950	TT
TRIM37	rs73321289	CC
DAP	rs13181507	GG
CSMD3	rs80176672	AA
USP25	rs192418381	TT
KCTD1	rs57118264	CC
CSMD1	rs890001	GG
NECTIN2	rs138769755	GG
C6ORF47	rs115062572	CC
LRRN1	rs139959052	GG
ASCL2	rs117600357	GG
/	rs35294279	TT
TCF19	rs149917912	TT
GALNT5	rs13409177	CC
PDE5A	rs72672568	TT

GENE	SNP	GENOTYPE
SORCS2	rs12641357	AA
PCDH9	rs1982305	AA
/	rs867720	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

H. Pylori

Key Takeaways:

- Genes involved in H. Pylori affect stomach acid production and the stomach's mucous barrier.
- Risk factors include an unsanitary environment, poverty, eating at restaurants, eating meat, and smoking.
- If you have a high genetic risk, you may reduce overall risk by taking action on risk factors that you can change.
- Click the **next steps** tab for relevant labs and lifestyle factors.

Helicobacter pylori (*H. pylori*) is a type of bacteria that can live in the stomach. About half of all people may be infected with *H. pylori*. Developing countries have higher infection rates [R, R, R].

Most people don't have any symptoms of infection. In some, however, the bacteria can start to break down the protective mucous barrier of the stomach wall. This can cause serious problems [R, R, R].

H. pylori may contribute to [R, R]:

- Gastritis (stomach inflammation)
- Peptic ulcers (sores in the stomach or upper small intestine lining)
- Stomach cancer

Symptoms arise when a person develops gastritis or ulcers. These can include [R, R, R]:

- Nausea
- Stomach pain
- Vomiting
- Low appetite
- Weight loss
- Indigestion

People usually become infected with *H. pylori* in childhood. Growing up around a lot of people or in unsanitary conditions may play a large role. Other risk factors for *H. pylori* infection include [R, R]:

- Lower socioeconomic status
- Eating out at restaurants
- Eating meat
- Smoking cigarettes

Medications for *H. pylori* help kill the bacteria and heal the stomach. They are usually prescribed in different combinations [R, R, R].

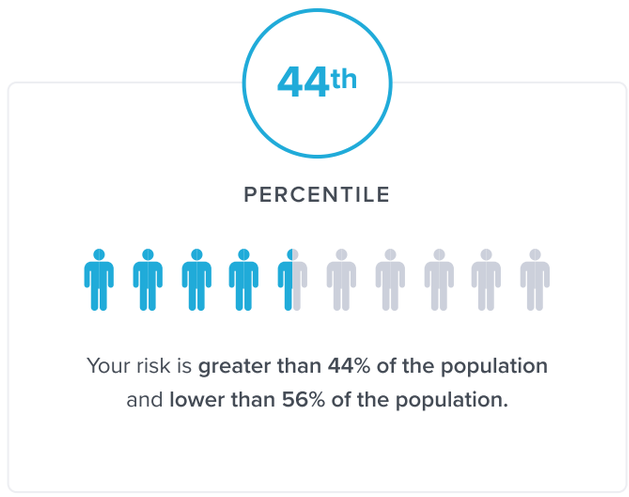
Some strains of *H. pylori* are becoming more difficult to kill with antibiotics. This makes them harder to treat [R, R].

Genetics seems to play a role in the risk of ulcers due to *H. pylori*. Genes involved in *H. pylori* infection and related diseases may influence [R, R]:

- Stomach acid production (*GAST*)
- The mucous barrier in the stomach (*MUC1*, *FUT2*, *ABO*)

TYPICAL LIKELIHOOD

Typical likelihood of H. pylori infection based on 86,987 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
DOCK10	rs10201967	CC
IKZF2	rs10194411	GG
AKR1E2	rs112501331	CC
VMP1	rs111821451	GG
FBXO21	rs111576798	GG
RAP2B	rs112013042	CC
SIPA1L3	rs113428378	AA
NFE2	rs11170954	CC
HPCAL1	rs10929658	AA
METTL14	rs112991781	TT
PCDH15	rs11004038	TT
FGD4	rs11052023	TT
LGSN	rs1020805	GG
PCDH15	rs11004387	TT
/	rs10008115	GG
HEBP1	rs111707992	AA
CLEC2B	rs1088309	GG
PTCHD4	rs1150811	AA
ADAMTSL4	rs10888382	CC
PDSS1	rs112022787	AG
PDZD2	rs10472790	TC

GENE	SNP	GENOTYPE
/	rs11059054	AC
TCF7L1	rs113194344	AG
GAREM2	rs1019972	CT
TLE1	rs11139024	TC
LRRTM3	rs10762128	TA
KLHL31	rs113924095	AA
FIGLA	rs115235891	CC
RBP7	rs112432872	GG
TFPI	rs10497687	CC
ZNF91	rs112713994	GG
ASAH2	rs10508925	GG
TP53INP1	rs112904682	GG
CLMP	rs11219074	CC
MRPS33	rs113513883	GG
RDH14	rs10181477	AA
SYT13	rs11038374	TT
GULP1	rs112821517	CC
LILRA4	rs112985797	GG
PLCL1	rs113784795	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Gastrointestinal Infection

Gastrointestinal (GI) infections are diseases of the digestive system. They are caused by the invasion of microbes that do not usually live there.

Many different microbes may cause GI infections. Some examples are [R, R, R]:

- Parasites (e.g., *Giardia lamblia*)
- Bacteria (e.g., *Salmonella, Shigella, Campylobacter, E. coli*)
- Virus (e.g., rotavirus, norovirus)

In developed countries, most cases are due to viruses [R].

The main sources of infection include [R]:

- Person-to-person contact
- Consumption of contaminated food (e.g., undercooked or poorly stored meat, raw milk)
- Consumption of contaminated water (e.g., river or swimming pool water)
- Contact with contaminated objects (e.g., soil, work tools)
- Contact with animals or their feces (e.g., contact with farm animals and pets, visiting petting zoos)

Risk factors for GI infections include [R, R, R, R, R, R].

- Malnutrition
- A recent visit to an endemic area
- Recent use of antibiotics
- Drugs to reduce stomach acid (e.g., omeprazole)
- Chronic stress
- Weakened immunity
- Recent abdominal surgeries
- **Genetics**

The symptoms of GI infections depend on the causing microbe. They usually include [R, R]:

- Diarrhea
- Fever
- Belly cramps
- Nausea and vomiting
- Headache
- Muscle pain
- Dehydration (weakness, confusion, dizziness)

In most cases, the symptoms will disappear within 7 days. In rare cases, the GI infection can last more than 30 days and turn chronic [R, R].

Mild cases usually don’t require treatment. Proper hydration and rest are crucial for recovery. Make sure to seek medical care if your symptoms are severe [R].

TYPICAL LIKELIHOOD

Typical likelihood of a GI infection based on 49,910 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
MFHAS1	rs11995244	TT
FCHO2	rs3010256	TT
NPC1	rs1652362	TT
BHLHE41	rs3825165	TT
SESN3	rs75887387	GG
CNTN5	rs7112253	AG
ATXN1	rs3793102	CA
/	rs143538360	TT
RBMS3	rs115249766	TT
/	rs376479926	AA
FLNB	rs1866164	CC
PRICKLE1	rs117347473	CC
ABO	rs41302673	TT
PIK3R1	rs12517727	GG
ABO	rs635634	CC
MGA	rs7183231	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Gut Inflammation

Inflammatory conditions of the gut can range from mild discomfort to chronic, debilitating diseases. Conditions like IBD, appendicitis, pancreatitis, and gastritis are often tied to an imbalance in the gut's immune response. The link between gut inflammation and the microbiome is strong, with disruptions in microbial balance playing a significant role in how your immune system reacts.

This section explores genetic factors that contribute to gut inflammation, including predispositions to these and other conditions. By understanding your genetic profile, you can gain insights into your risks for these conditions and how best to manage or prevent them.

MORE LIKELY

Pancreas Inflammation

More likely to get pancreas inflammation

TYPICAL LIKELIHOOD

Gut Inflammation

Typical likelihood of IBD

TYPICAL LIKELIHOOD

Appendicitis

Typical likelihood of appendicitis

TYPICAL LIKELIHOOD

Ulcerative Colitis

Typical likelihood of ulcerative colitis

TYPICAL LIKELIHOOD

Crohn’s Disease

Typical likelihood of Crohn's disease

TYPICAL LIKELIHOOD

Stomach Inflammation

Typical likelihood of gastritis

LESS LIKELY

Diverticular Disease

Less likely to have diverticular disease

Pancreas Inflammation

The pancreas is an organ located behind the stomach that releases crucial enzymes for carbs and fats digestion. **Pancreatitis** is inflammation of the pancreas, which can be acute or chronic.

Potential risk factors for pancreatitis include [R, R, R]:

- **Alcohol**
- Cigarette smoking
- Obesity
- High blood lipids
- Certain medications
- Genetics

Genetically predicted higher fasting insulin may be associated with acute and chronic pancreas inflammation. In contrast, genetically high testosterone levels may be causally associated with a lower risk of pancreas inflammation [R, R].

Health conditions that may contribute to pancreas inflammation include [R, R]:

- Gallstones
- Diabetes
- Infections
- Injury or trauma

MORE LIKELY

More likely to get pancreas inflammation based on 1,669 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SLC25A34	rs60816621	GC
TWIST2	rs4663946	TT
RNF128	rs66491909	A
JAKMIP2	rs17107296	AA
JAKMIP2	rs150261364	CC
SPINK5	rs112861203	TT
STK32A	rs148849032	CC
MORC4	rs12688220	C
JAKMIP2	rs146303903	AA
CTRC	rs497078	CC
STK32A	rs142623619	AA
/	rs150176211	GG
ADRB2	rs17640347	GG
ABCG5	rs75331444	GG
PRSS1	rs10273639	TT
COLEC10	rs11988997	CC
NUP62CL	rs12688091	G
TBC1D8B	rs12689287	G
JCAD	rs2995271	CC
PWWP3B	rs379742	G
RADX	rs5916761	A

GENE	SNP	GENOTYPE
PWWP3B	rs67184230	G
IGDCC4	rs75405617	TT
SYNJ1	rs61750217	CC
GBE1	rs28763904	AA
C4ORF50	rs138928790	CC
PLEKHH3	rs200210041	GG
NAA38	rs144163075	CC
PDLIM5	rs76352571	AA
FLNC	rs181067717	CC
SNRK	rs56104180	CC
FAM81A	rs111778770	GG
PCDHB1	rs17208383	CC
RAP1B	rs141697489	GG
TMEM222	rs150461998	CC
CAPG	rs62623452	CC
KRT76	rs149868801	CC
TMC3	rs150843673	GG
CFAP61	rs115175415	CC
RAD51C	rs28363317	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Gut Inflammation

Key Takeaways:

- Up to **75%** of differences in people's chances of developing IBD may be due to genetics.
- Risk factors include being under age 30, European ancestry, and smoking.
- IBD may cause: diarrhea, fatigue, abdominal pain, bloody stool, weight loss, inflammation, liver damage, and colon cancer.
- IBD only affects about **3 in 1000** people worldwide. So, even with high genetic risk, your overall risk is actually low.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

Our intestines do much more than absorb food. They can impact our immune system, mood, and more [R]!

Inflammatory bowel disease (IBD) is a group of gut diseases affecting **about 0.3% of people worldwide.** It's most common in North America, Europe, and Australia [R].

The exact causes of IBD are unknown. Possible risk factors include [R]:

- Age (most people develop IBD before the age of 30)
- European ancestry
- Cigarette smoking
- **Genetics**

There are two major types of IBD: ulcerative colitis and Crohn's disease. Ulcerative colitis involves inflammation in the large intestine, while Crohn's disease often affects both the large and small intestines [R, R, R].

In both types of IBD, the immune system reacts to normal gut bacteria as if they're dangerous. These immune reactions cause inflammation and damage to the gut lining [R].

This gut damage can cause signs and symptoms like [R, R, R]:

- Diarrhea
- Fatigue
- Abdominal pain and cramping
- Blood in the stool
- Low appetite
- Weight loss

Untreated IBD can have serious complications, including [R]:

- Skin, eye, and joint inflammation
- Bile duct and liver damage
- Blood clots
- Colon cancer

People with IBD typically need anti-inflammatory medications to control their disease [R, R].

Many people with IBD take supplements because their damaged guts have trouble absorbing certain nutrients. Some people may need to adhere to special diets as well [R, R].

IBD can be a disabling condition, and many turn to alternative and complementary strategies to help them manage their symptoms. Your DNA may help determine which of these strategies is likely to work best for you.

TYPICAL LIKELIHOOD

Typical likelihood of IBD based on 1,671 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HLA-DQA2	rs2395185	GG
FCGR2A	rs1801274	AG
IL23R	rs11465804	TT
NOD2	rs2066845	CG
IL23R	rs11209026	GG
ATG16L1	rs2241880	GA
IL23R	rs10889677	AC
TNFSF15	rs6478108	CT
IL23R	rs76418789	GG
IRGM	rs10065172	CT
TNFSF8	rs6478109	GG
HNF4A	rs6017342	AC
TNF	rs1799724	TC
TNFSF8	rs6478106	TT
NOD2	rs17221417	GC
IL23R	rs11805303	TC
TNFSF15	rs4263839	GG
ATG16L1	rs10210302	TC
BSN	rs9858542	GA
PPM1M	rs5743836	AG
TNFSF15	rs3810936	CC

Up to 75% of differences in people's chances of developing IBD may be attributed to genetics. Genes involved in IBD may influence [R, R, R, R]:

- Inflammation (*JAK2*, *TNFSF15*, *SLAMF8*)
- Immune response (*TLR9*, *UBE2L3*, *BCL3*)

Moreover, genetically high betaine levels may be causally associated with a high risk of Crohn's disease. In contrast, genetically high levels of omega-3s may be causally associated with a lower risk [R, R, R, R].

GENE	SNP	GENOTYPE
PTPN22	rs2476601	GG
NKX2-3	rs10883365	AG
NOD2	rs2076756	GA
IRGM	rs4958847	GA
IL23R	rs1004819	AG
IRGM	rs13361189	TC
AGT	rs5051	TC
IL23R	rs7517847	TT
NOD2	rs2066843	TC
DLD	rs2158836	AA
STAT3	rs4796793	GC
IL19	rs1800872	GG
NKX2-3	rs4409764	TT
ETS2	rs2836878	GG
ZNF365	rs7076156	GA
INAVA	rs7554511	CC
TNFSF8	rs7848647	CC
JAK2	rs1830610	TC
NRIP1	rs2823286	GG
IRF8	rs10521318	CC
CIITA	rs4781011	TT
RORC	rs4845604	GG
TNFSF15	rs4246905	CC
HLA-DQB1	rs9469220	AA
ICAM5	rs11879191	GG
IKZF3	rs2872507	AA
PHACTR2	rs12199775	AA
TNFSF15	rs7869487	TT
GLYCTK	rs352140	CT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Appendicitis

Key Takeaways:

- Up to **56%** of differences in people's chances of developing appendicitis may be due to genetics.
- Other risk factors include being young and male.
- Appendicitis is not rare, happening to about 7-8% of people in their lifetime.
- If your genetic risk is high, know the symptoms and seek medical attention if you have them.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

The **appendix** is a small, finger-shaped pouch near the beginning of the large intestine. It is in the lower right of your abdomen [R, R].

The function of the appendix has been debated for many years. More recent studies suggest that the appendix is a safe house for good bacteria that live in the gut. If an illness wipes out large numbers of these bacteria in the gut, the ones from the appendix can help replace them [R].

Appendicitis is inflammation of the appendix. It is likely caused by something blocking the lining of the appendix, leading to an infection. If left untreated, the appendix can rupture and the infection can spread. This can be life-threatening [R].

Although anyone can develop appendicitis, it most often occurs in people between 10 and 30 years old. Men are slightly more likely to experience it than women [R, R].

The symptoms of appendicitis include [R]:

- Sudden pain in the lower right abdomen
- Sudden pain around the belly button that shifts to the lower right abdomen
- Pain that worsens if you move suddenly
- Nausea and vomiting
- Loss of appetite
- Fever
- Gut issues

The standard treatment for appendicitis is surgery to remove the appendix [R].

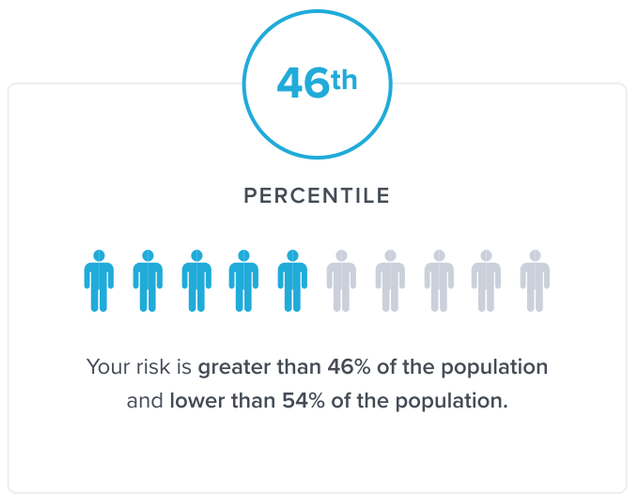
Up to 56% of differences in people's chances of developing appendicitis may be attributed to genetics. Involved genes may influence [R, R]:

- Gut development
- Gut function
- Inflammation

Genetically predicted higher levels of fasting insulin may be associated with appendicitis [R].

TYPICAL LIKELIHOOD

Typical likelihood of appendicitis based on 809,853 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
ENPEP	rs2129979	GT
PITX2	rs7697491	AA
PITX2	rs13121924	AA
KRT73	rs146783619	TA
MTARC1	rs3738182	GG
LTBR	rs10849448	GA
DLEU7	rs201768	CT
/	rs77114860	TT
TUB	rs72848490	CC
OSR1	rs56259011	CC
NKX2-3	rs41290504	CC
NKX2-3	rs7095491	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Ulcerative Colitis

The exact cause of ulcerative colitis is not fully understood, but it is believed to be the result of an overactive immune system response that leads to inflammation in the colon. It can affect individuals at any age, though it often begins during adolescence and early adulthood.

The impact of the disease can range from mild to severe, with some patients experiencing life-threatening complications. Managing ulcerative colitis often requires a combination of medication, lifestyle changes, and potentially surgery to control symptoms and improve quality of life.

TYPICAL LIKELIHOOD

Typical likelihood of ulcerative colitis based on 1,049,227 genetic variants we looked at

49th

PERCENTILE

Your risk is **greater than 49% of the population** and **lower than 51% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HLA-DQA2	rs2395185	GG
IL23R	rs76418789	GG
HNF4A	rs6017342	AC
IL23R	rs11805303	TC
/	rs113653754	CC
OTUD3	rs6426833	AA
ETS2	rs2836878	GG
DLD	rs2158836	AA
MFSD4B	rs3851228	AA
NR5A2	rs2816958	GG
IL19	rs1800872	GG
INAVA	rs7554511	CC
RORC	rs4845604	GG
MDM1	rs7134472	AA
JAK2	rs1830610	TC
CIITA	rs4781011	TT
MST1	rs3197999	GA
FCGR2A	rs1801274	AG
IL23R	rs2201841	GA
IL12B	rs56167332	CA
CARD9	rs13300218	AG

GENE	SNP	GENOTYPE
CARD9	rs10781499	GA
PRKAB1	rs11064881	GA
SLC39A11	rs17780256	CA
IL23R	rs1343151	GA
STAT3	rs744166	GG
NCR3	rs3749946	CC
IL23R	rs80174646	GG
TLR4	rs4986790	AA
IL19	rs1800896	CC
IRF5	rs4728142	GG
IL19	rs3024505	GG
LRRK2	rs12422544	TT
TMCO4	rs3806308	TT
NKX2-3	rs4409764	TT
TYK2	rs12720356	AA
TNFAIP3	rs6920220	GG
CELSR3	rs9868809	CC
GPR35	rs3749171	CT
TNFSF15	rs11554257	TT
PDGFB	rs2413583	TC
PARK7	rs3766606	GG
GPR12	rs17085007	TT
IKZF3	rs12946510	CT
DLD	rs4380874	CT
GALC	rs8005161	CC
HSPG2	rs12568930	TT
KIAA1841	rs7608910	AA
CCR1	rs113010081	TT
NXPE4	rs561722	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Crohn’s Disease

Aside from gastrointestinal symptoms, Crohn's Disease can also have systemic effects on the body, leading to issues such as anemia, skin rashes, arthritis, and eye inflammation. The cause of Crohn's Disease is not fully understood, but it involves an abnormal immune response to the microorganisms in the intestine, in genetically susceptible individuals.

There's no known cure for Crohn's Disease, but therapies can greatly reduce its signs and symptoms and even bring about long-term remission and healing of inflammation.

TYPICAL LIKELIHOOD

Typical likelihood of Crohn's disease based on 1,031,499 genetic variants we looked at

55th

PERCENTILE

Your risk is **greater than 55% of the population** and **lower than 45% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SLC23A1	rs10063949	CC
IL23R	rs11465804	TT
NOD2	rs2066845	CG
ATG16L1	rs2241880	GA
IL23R	rs11805303	TC
BSN	rs9858542	GA
PPM1M	rs5743836	AG
PTPN22	rs2476601	GG
NKX2-3	rs10883365	AG
NOD2	rs2076756	GA
IRGM	rs4958847	GA
IL23R	rs1004819	AG
IRGM	rs13361189	TC
AGT	rs5051	TC
NOD2	rs2066843	TC
BTBD8	rs34856868	GG
IRF8	rs2361755	GG
CACNA1S	rs11584383	TT
INAVA	rs7554511	CC
ICAM5	rs11879191	GG
NRIP1	rs2823286	GG

GENE	SNP	GENOTYPE
HLA-DQB1	rs9469220	AA
MFSD4B	rs3851228	AA
IKZF3	rs2872507	AA
ATG16L1	rs3828309	GA
IRGM	rs11747270	AG
CDKAL1	rs6908425	CC
NKX2-3	rs11190140	CT
IL12B	rs56167332	CA
CARD9	rs13300218	AG
CARD9	rs10781499	GA
MST1	rs3197999	GA
TRIB1	rs1551398	AA
FOXO1	rs17061048	TA
ZEB2	rs11681525	CG
CCL13	rs3091315	AG
TNFSF18	rs9286879	GA
CUL2	rs11010067	GC
PRDM1	rs7746082	GC
ITLN1	rs2274910	TC
UBLCP1	rs10045431	AC
NOD2	rs2066844	CC
JAK2	rs10758669	AA
IRGM	rs1000113	CC
STAT3	rs744166	GG
SLC22A5	rs12521868	GG
SEH1L	rs2542151	TT
LRRK2	rs11175593	CC
LRRK2	rs12422544	TT
PTGER4	rs1992660	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Stomach Inflammation

Symptoms of gastritis vary among individuals and can range from mild discomfort to severe pain. Common symptoms include upper abdominal pain or burning, nausea, vomiting, bloating, and a feeling of fullness in the upper abdomen after eating. If left untreated, gastritis can lead to stomach ulcers and an increased risk of stomach bleeding, which may be life-threatening.

In some cases, chronic gastritis may increase the risk of developing stomach polyps or stomach tumors. Treatment for gastritis generally involves a combination of medications to reduce stomach acid and a change in diet or lifestyle habits that may be contributing to the inflammation.

TYPICAL LIKELIHOOD

Typical likelihood of gastritis based on 9,903 genetic variants we looked at

PERCENTILE

Your risk is **greater than 44% of the population** and **lower than 56% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CCDC66	rs6445797	GC
MRPL13	rs7826906	GA
TCP10L	rs11088226	CG
MTBP	rs10955971	AG
CDC37	rs8112449	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Diverticular Disease

When diverticula become inflamed or infected, the condition can cause more severe symptoms. These include severe abdominal pain, fever, nausea, and a marked change in bowel habits. Complications of diverticular disease include abscesses, perforation of the colon, peritonitis, fistulas, and intestinal obstruction.

Treatment typically involves a combination of antibiotics for infection and a liquid or low-fiber diet to allow the colon to heal. In some severe cases, surgery may be necessary to remove the affected portion of the colon. Lifestyle changes, such as increasing the intake of fiber, drinking plenty of fluids, and exercising regularly can help to manage symptoms and prevent future episodes.

LESS LIKELY

Less likely to have diverticular disease based on 996,903 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
POLR3A	rs139044580	GG
TBX5	rs2551395	TT
UPF2	rs78114187	CC
LYPLAL1	rs61823192	CC
SHANK1	rs113101273	GG
SOCS6	rs79586998	CC
TMEM270	rs3823878	GA
YARS2	rs191699548	GG
/	rs190502327	CC
MGAT4A	rs148376933	CC
BHLHE23	rs6011570	GG
OMG	rs150700179	AA
SPDYE21	rs189921337	CC
FIBCD1	rs182799903	CC
INSIG1	rs138074947	TT
UBL4B	rs115490395	TT
NOC4L	rs73486316	GG
IFNAR2	rs138262539	AA
DIRAS2	rs78628486	GG
ROBO1	rs183318239	AA
ARHGAP15	rs6734367	GG
VAPA	rs80261783	CC
EPB41L3	rs141727959	GG
SLCO5A1	rs117969400	GG
FAM180A	rs113477191	CC
MPP7	rs12219062	CC
ZNF28	rs140094156	CC
CIB4	rs74887298	GG
SLC35F3	rs4333882	AA

GENE	SNP	GENOTYPE
TMEM101	rs71371957	AA
EFEMP1	rs1802575	GG
COL6A1	rs75434097	GG
/	rs12814314	AA
IVD	rs71472433	AA
LHFPL3	rs6980251	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Food Intolerance

There are some people, quite a few in fact, who have difficulty processing certain food products like gluten and lactose. In Western diets at least, having to limit gluten and lactose products can create some diet hardships.

This level of sensitivity, while potentially impacted by something like an infection, is heavily influenced by your DNA. Knowing your genetic predispositions can help you make smart diet choices or recognize a potential problem you didn't know that you had!

MORE LIKELY

Histamine Intolerance

More likely to be histamine intolerant

TYPICAL

Gluten Sensitivity (Non-Celiac)

Predisposed to typical gluten sensitivity

TYPICAL LIKELIHOOD

Food Allergies

Typical likelihood of food allergies

TYPICAL

Alcohol Sensitivity

Likely typical sensitivity to alcohol

TYPICAL

Salt Sensitivity

Likely typical sensitivity to salt

TYPICAL LIKELIHOOD

Celiac Disease

Typical likelihood of celiac disease

LIKELY TOLERANT

Lactose Intolerance

Likely lactose tolerant

LOWER

Caffeine Sensitivity

Predisposed to lower caffeine sensitivity

Histamine Intolerance

Histamine is broken down by two enzymes called **DAO** and **HNMT**. DAO is the main enzyme that breaks down histamine in the gut. HNMT deactivates histamine within cells [R, R].

Scientists currently think that DAO deficiency likely plays a more significant role in histamine intolerance related to dietary histamine. The gene that helps make DAO is called ***AOC1*** [R, R].

On the other hand, HNMT is more responsible for breaking down the histamine created by our body. Different *HNMT* gene variants have been linked to histamine-related conditions, such as [R, R, R, R, R]:

- Allergies
- Asthma
- Eczema
- Migraines
- ADHD

While genetic variants can influence histamine levels, research suggests that variants alone are probably **not sufficient** to cause full-blown histamine intolerance. Various environmental factors also play a key role [R].

Some of the factors that may contribute to histamine intolerance include [R, R, R, R, R, R, R, R]:

- Gut damage and inflammation (e.g., due to inflammatory bowel disease (IBD), gluten sensitivity, lactose intolerance, chemotherapy, etc.)
- Alcohol consumption
- Certain medications, such as some antibiotics and stomach acid blockers
- Underlying imbalances in the gut bacteria
- Consumption of foods containing high levels of biological *amines*, chemicals similar to histamine

MORE LIKELY

More likely to be histamine intolerant based on 11 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
AOC1	rs10156191	TT
AOC1	rs2268999	TT
AOC1	rs1049793	GG
AOC1	rs2071517	GG
AOC1	rs2071514	GG
AOC1	rs1049748	CT
HNMT	rs1050891	AG
HNMT	rs2071048	TC
AOC1	rs2052129	GG
HNMT	rs11558538	CC
AOC1	rs1049742	CC
HNMT	rs16840064	GG
HRH4	rs11662595	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Gluten Sensitivity (Non-Celiac)

People with gluten sensitivity may develop antibodies to gluten. These antibodies recognize and attack gluten proteins like *gliadin*.

Genetics plays a major role in gluten sensitivity. It may account for **50%** of differences in anti-gliadin antibodies [R].

Certain variants near the *HLA-DRA* gene are linked to higher amounts of these antibodies. The one with the strongest effect is rs3135350-C. The *HLA* genes affect the immune response and have a well-known role in gluten sensitivity [R].

Interestingly, most genetic variants linked to celiac disease don't seem to affect these antibodies. Scientists suggest that celiac disease and non-celiac gluten sensitivity may have different genetic backgrounds [R].

Keep in mind that other gene variants, your diet, and your environment can also influence gluten sensitivity. Consult your doctor or dietitian before making any major dietary changes.

TYPICAL

Predisposed to typical gluten sensitivity based on the genetic variants we looked at

79%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **79% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HLA-DQB1	rs3135350	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Food Allergies

Key Takeaways:

- Up to 80% of differences in people's chances of having food allergies may be attributed to genetics.
- Many allergies come and go through childhood, but common ones that linger into adulthood include nuts, seafood, milk, and eggs.
- Reducing risk for allergies involves avoiding the various food triggers.
- Click the **Recommendations** tab for potential dietary and lifestyle changes.

An *allergy* is an immune reaction to a trigger that is normally harmless. This allergy trigger is called an *allergen*. Food allergies are allergies triggered by foods. The best-known food allergens are peanuts. However, people can be allergic to just about anything [R, R].

Up to 80% of differences in people's chances of having food allergies may be attributed to genetics [R].

Many of the genes that influence food allergies affect the immune system [R, R].

TYPICAL LIKELIHOOD

Typical likelihood of food allergies based on 16,808 genetic variants we looked at

1st

PERCENTILE

Your risk is **greater than 1% of the population** and **lower than 99% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SPINK6	rs9325071	GA
RBFOX1	rs59325236	GA
SERPINB10	rs1243064	TA
LRRC32	rs7936434	CG
LRRC32	rs2212434	TC
SLC22A5	rs2243250	TC
TLR1	rs2101521	AG
FHIT	rs142617341	CC
STAT6	rs4759044	CC
GSTP1	rs1871042	CC
TMEM243	rs6942407	AA
FLG	rs1933064	AG
HLA-DPA1	rs9277630	CC
LINGO4	rs12123821	CC
HLA-DQA1	rs2187668	CC
HLA-DQA2	rs9271588	CT
KIZ	rs17664036	TT
SERPINB10	rs12964116	AA
HLA-DQA2	rs9275596	TT
HLA-DRA	rs7192	GG
BMPR1B	rs17023017	TT

GENE	SNP	GENOTYPE
SLC22A5	rs1295686	CT
GVQW3	rs11236809	TT
DIPK2A	rs115529815	TT
TSC22D1	rs147507729	AA
DIPK2A	rs147539730	TT
CTSO	rs147666089	CC
DIPK2A	rs187491414	GG
OR52I2	rs145735233	AA
SREK1IP1	rs72756857	TT
NRSN1	rs77470907	GG
CFAP300	rs149958938	TT
/	rs146702717	TT
RCHY1	rs138784094	AA
ENPP6	rs139241737	AA
RPRD2	rs191802974	GG
IQCE	rs1036504	TT
/	rs572847817	AA
FLG	rs61816761	GG
IL19	rs1800872	GG
STAT6	rs12307379	CC
STAT6	rs324015	CC
MS4A2	rs556917	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Alcohol Sensitivity

There are two enzymes involved in clearing alcohol from the body. They are coded by genes called *ADH1B* and *ALDH2*. The first enzyme breaks down alcohol to toxic acetaldehyde, while the second one breaks down acetaldehyde into a less harmful substance [R].

Genetic variants that speed up the first enzyme or slow down the second enzyme contribute to the buildup of acetaldehyde and increase alcohol sensitivity [R].

Variants that increase the buildup of acetaldehyde are common in East Asian populations but rare in other parts of the world [R].

TYPICAL

Likely typical sensitivity to alcohol based on the genetic variants we looked at

93%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **93% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
ALDH2	rs671	GG
ADH1B	rs1229984	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Salt Sensitivity

People who are salt sensitive will experience a bump in blood pressure when they eat salty foods. This happens because their kidneys function a bit differently [R, R, R].

Salt sensitivity is partly determined by the genes we carry. Genes involved in salt sensitivity may influence [R, R, R, R, R, R]:

- Sodium levels in the blood and kidney
- Blood vessel function
- Blood pressure

However, other genes and environmental factors may also influence your salt needs. It is important to get the right amount of salt for you.

TYPICAL

Likely typical sensitivity to salt based on 68 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
NR2F2	rs2398162	AA
SGK1	rs9389154	GG
PRKG1	rs7905063	TT
FGF5	rs16998073	AA
ACE2	rs184874220	T
GSKIP	rs11847625	GC
AGT	rs699	GA
PRKG1	rs7897633	CA
SCNN1G	rs4299163	GG
CLGN	rs2567241	CC
RAD52	rs2301880	CT
WNK1	rs12828016	GT
SLC8A1	rs11893826	GA
SLC4A4	rs10022637	CT
SCNN1G	rs7404408	CT
SCNN1G	rs5735	TC
GC	rs4254735	TC
SCNN1G	rs4073930	TC
SCNN1G	rs4073291	AC
BCAT1	rs7961152	CC
RENBP	rs78377269	G
ACE2	rs714205	C
ACE	rs4343	AA
SLC24A3	rs3790261	AA
POC1B	rs2681472	AA
ACE2	rs2285666	C
SGK1	rs9376026	CC
RAD52	rs880054	TC
SLC4A5	rs7571842	AA

GENE	SNP	GENOTYPE
CPA3	rs75367686	AA
SLC8A1	rs434082	CC
CSTF2T	rs12414562	GG
CSTF2T	rs10997916	GG
HYAL1	rs10510755	CC
ADRB2	rs1042714	CC
SLC4A5	rs10177833	AA
KL	rs9536314	TT
SCNN1A	rs4764586	CC
SCNN1G	rs4499238	CC
SCNN1A	rs3741914	CC
TNFRSF1A	rs11614164	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Celiac Disease

Key Takeaways:

- It's estimated that 1-2% of the population has gluten sensitivity. The most likely risk factor is genetics.
- If you have symptoms, diet restriction may indicate whether you have the sensitivity or not. You should speak to a healthcare professional if symptoms persist.
- Symptoms include diarrhea/constipation, fatigue, weight loss, gut pain/bloating, and nausea.
- Celiac disease is rare, so even with high genetic risk, your overall risk is still low.
- Click the **next steps** tab for relevant labs.

Gluten is a protein found in grains such as wheat, rye, spelt, barley, and triticale. Some people cannot properly digest gluten. In fact, their immune systems may react to gluten as if it is dangerous. To make matters worse, gluten is similar to a normal protein in the intestine. Sometimes, the immune system will attack both. People with this type of reaction have celiac disease [R, R, R].

Researchers aren't completely sure why some people are sensitive to gluten. Infections in the gut may play a role. However, a major risk factor is probably genetic [R, R, R].

The most important genes involved in celiac disease are *HLA* genes. These genes help make HLA proteins, which sit on the surface of white blood cells. They help the immune system attack and remove dangerous invaders like bacteria and viruses. In people with celiac disease, HLA proteins may attack gluten by mistake and damage the gut barrier [R, R].

Moreover, genetically high testosterone levels may be causally associated with a lower risk of celiac disease in men [R].

TYPICAL LIKELIHOOD

Typical likelihood of celiac disease based on 1,019,187 genetic variants we looked at

19th

PERCENTILE

Your risk is **greater than 19% of the population** and **lower than 81% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HLA-DQA2	rs7454108	TT
HLA-DQA1	rs2187668	CC
HLA-DRB5	rs2395182	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Lactose Intolerance

Lactose intolerance means a person cannot digest lactose, a sugar found in dairy. To be able to digest lactose, you need an enzyme called *lactase*. People with lactose intolerance may experience symptoms such as diarrhea, stomach cramps, nausea, bloating, and gas after eating dairy [R, R].

In people who are lactose intolerant, the gene that makes the enzyme lactase—*LCT*—gets "turned off" in adulthood. Without this enzyme, people may have trouble digesting dairy as adults [R, R].

A common variant near the *LCT* gene (rs4988235 'A') is responsible for keeping the lactase enzyme “turned on.” This variant is responsible for lactose tolerance in most people who are able to digest milk as adults. The 'T' allele of rs182549 has the same effect. Because these variants are usually inherited together, you will most likely have both variants or neither of them [R, R].

It's important to note that there are also other less common variants linked to lactose tolerance that we are not including in this report [R, R]. In addition, the way people respond to dairy may also depend on factors like diet, gut bacteria, and certain health conditions.

LIKELY TOLERANT

Likely lactose tolerant based on the genetic variants we looked at

66%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **66% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LCT	rs4988235	GA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Caffeine Sensitivity

Genetic variants may explain about **70%** of the difference in caffeine sensitivity [R, R]. Genes associated with caffeine sensitivity impact how quickly caffeine is broken down and the strength of its effects in different parts of the body.

The **CYP1A2 gene** is a **key enzyme responsible for caffeine breakdown**. The **rs762551** variant (-163 A>C) determines whether someone is a “fast” or “slow” caffeine metabolizer. Carriers of the “C” allele are slow metabolisers. This means they caffeine stays in their body for a longer time, increasing their caffeine sensitivity [R, R, R, R].

Other notable genes and variants include:

- **AHR (rs4410790)**: The AHR gene regulates the expression of **CYP1A2**, mentioned above. Certain variants at AHR slow down caffeine metabolism, prolonging the effects caffeine has on the body [R].
- **ADORA2A (rs5751876)**: This ADORA2A gene encodes the adenosine A2A receptor, a primary target of caffeine in the brain. Caffeine may make those with the “T” variant more anxious, especially women. Interestingly, this variant seems to have the opposite effects on sleep problems (“C” carriers may be more affected) [R, R, R, R].
- **COMT (rs4680)**: The COMT gene is involved in the breakdown of the neurotransmitter dopamine. The rs4680 variant (Val158Met G>A) may increase sensitivity to both positive and negative effects of caffeine [R].
- **NAT2 (R/S, rs1495741)**: NAT2 helps break down various substances, including caffeine. Individuals with a “slow” acetylator status in the NAT2 gene may break down caffeine more slowly, leading to prolonged effects and increased sensitivity [R].

These genetic variations collectively influence individual sensitivity to caffeine, determining both the intensity and duration of the response to caffeine in the body. Understanding these genetic factors can help tailor caffeine intake to avoid adverse effects and optimize performance and well-being.

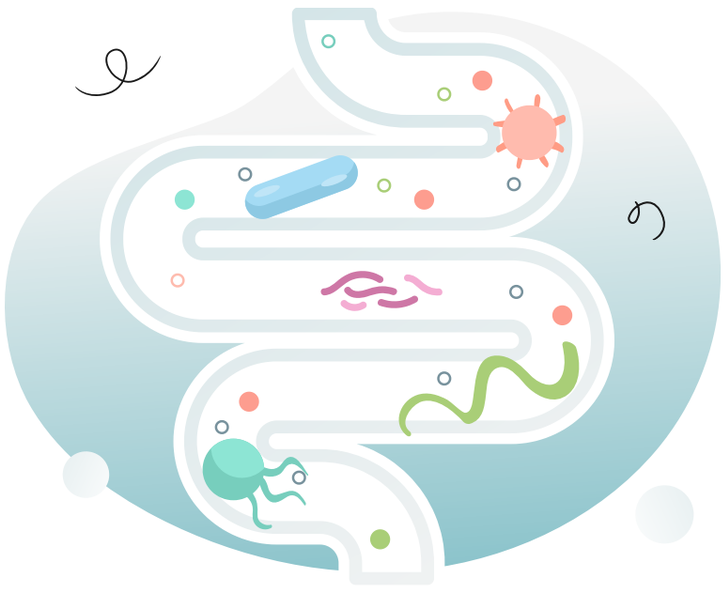
LOWER

Predisposed to lower caffeine sensitivity based on 5 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
NAT2	rs1495741	AA
AHR	rs4410790	TC
COMT	rs4680	AG
CYP1A2	rs762551	AA
ADORA2A	rs5751876	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.



Gut Microbiome

Your gut houses somewhere between 10 and 30 trillion microbes! It is its own little world, working diligently 24-7 to keep you protected and healthy, help digest food, support brain health, and more. That's how crucial your gut microbiome is to your health!

Your genetics may affect the composition of the microbes in your gut, making you more susceptible to gut and mood disorders, allergic conditions, and more. Knowing your predisposition may help you make more informed decisions to keep your microbiome in balance.

LOWER

Gut Microbiome Diversity

Predisposed to lower gut microbiome diversity

TYPICAL LEVELS

Bifidobacterium

Predisposed to typical Bifidobacterium levels

TYPICAL LEVELS

Bifidobacterium Longum

Predisposed to typical B. longum levels

TYPICAL LEVELS

Bifidobacterium Breve

Predisposed to typical B. breve levels

TYPICAL LEVELS

Bifidobacterium Bifidum

Predisposed to typical B. bifidum levels

Gut Microbiome Diversity

Key Takeaways:

- Genes that affect our gut bacteria are involved in nutrition, blood type, and metabolism.
- Other risk factors for reduced gut microbiome diversity include age, diet, and certain medications.
- A lack of diversity may be linked to diabetes, obesity, mood disorders, allergic conditions, IBS, and IBD. A diverse gut microbiome may improve the immune system, cognitive abilities, and mood.
- If your genetic risk is high or believe your gut microbiome may be out of balance, take action now on factors you can change.

We share our bodies with our gut microbes. They may make us thin or fat, healthy or sick, happy or depressed. The entire community of microbes (bacteria, fungi, viruses) living in your gut is called the 'gut microbiome' [R].

Gut microbes play many beneficial roles in our bodies. They [R, R, R]:

- Help harvest more energy from food
- Provide nutrients such as vitamins B12 and K
- Strengthen the gut barrier and the immune system
- Protect from harmful microbes
- Degrade toxins and cancer-causing chemicals
- Impact our mood and cognitive ability

While in perfect harmony, the gut microbiome is beneficial to our health. Off balance, these microbes can contribute to a range of issues, including [R]:

- Gut disorders (e.g., inflammatory bowel disease)
- Mood disorders (e.g., anxiety and depression)
- Allergic conditions (e.g., eczema and asthma)

Genetics influences our microbiome composition. Genes that affect our gut bacteria are involved in [R, R, R]:

- Nutrition
- Blood type
- Metabolism

LOWER

Predisposed to lower gut microbiome diversity based on 497 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
GPR158	rs71495423	CC
BRSK2	rs574686237	GG
SORCS3	rs184389714	AA
NIPSNAP3A	rs12348106	CC
NR2F2	rs6496140	TT
UBR5	rs9773443	AA
/	rs144477852	CC
MACF1	rs74786007	GG
AGPAT5	rs2928601	CC
CACNA1D	rs188274086	AA
/	rs139795364	AA
INHBC	rs145837154	GG
ISCA2	rs72730160	TT
CHL1	rs6442427	TT
GP2	rs73546249	CC
CCBE1	rs111870840	AA
RASEF	rs13284654	CC
NSG1	rs7693922	AA
OAT	rs74160914	GG
/	rs75113042	TT
FUT2	rs1047781	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Bifidobacterium

The following factors play a role in *Bifidobacterium* abundance in your gut flora:

- **Diet**: Foods rich in fiber, like fruits, vegetables, and whole grains, can increase Bifidobacterium. On the other hand, diets high in sugar and processed foods might reduce their numbers.
- **Age**: As we get older, *Bifidobacterium* levels in our gut can decrease.
- **Medications**: Some medicines, especially antibiotics, can reduce the number of these bacteria in our gut.
- **Illnesses**: Certain gut-related diseases, like irritable bowel syndrome (IBS), can change the levels of *Bifidobacterium*.
- **Probiotics**: These are supplements that contain live beneficial bacteria, often including *Bifidobacterium*. Taking them can increase the number of these bacteria in the gut.
- **Birth Method**: Babies born through natural birth tend to have more *Bifidobacterium* compared to those born through C-section. This is because they get exposed to their mother's beneficial bacteria during birth.
- **Genetics**: Some people may be genetically prone to a higher or lower abundance of *Bifidobacterium* in their gut flora.

TYPICAL LEVELS

Predisposed to typical Bifidobacterium levels based on 11,526 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
ZRANB3	rs7605229	CC
SOX1	rs7322849	CC
LCT	rs182549	CT
LCT	rs7570971	AC
LCT	rs1375131	CT
LCT	rs12465802	AG
LCT	rs687670	CT
LCT	rs1561277	AC
LCT	rs71348714	GA
CCNT2	rs1979033	AG
TMEM163	rs6723108	TG
DARS1	rs2680880	AT
TMEM163	rs35564151	GA
THSD7B	rs1961273	CT
MCM6	rs72847650	CA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Bifidobacterium Longum

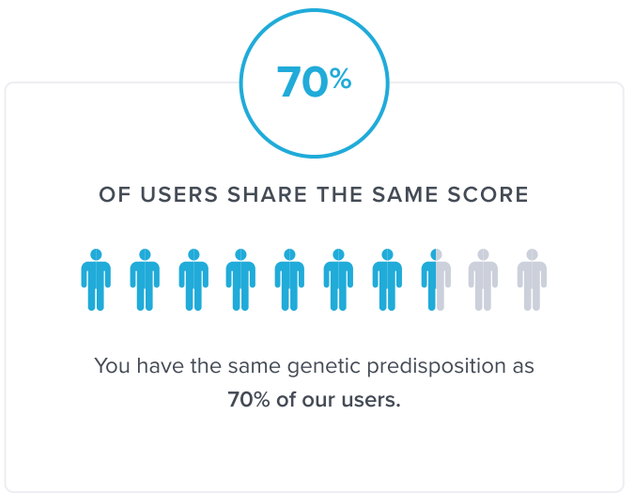
The following factors play a role in *B. longum* abundance in your gut flora [R]:

- **Diet**: Foods rich in fiber, like fruits, vegetables, and whole grains, can increase *B. longum*. On the other hand, diets high in sugar and processed foods might reduce their numbers.
- **Feeding method:** *B. longum ssp. longum* is more commonly found in bottle-fed babies, while *B. longum ssp. infantis* is more common in breast-fed babies.
- **Age**: As we get older, *B. longum* levels in our gut can decrease.
- **Stress:** High levels of stress can alter the balance of our gut bacteria.
- **Medications**: Some medicines, especially antibiotics, can reduce the number of these bacteria in our gut.
- **Illnesses**: Certain gut-related diseases, like irritable bowel syndrome (IBS), can change the levels of *B. longum*.
- **Probiotics**: Taking probiotic supplements containing *B. longum* can increase the number of these bacteria in the gut.
- **Birth Method**: Babies born through natural birth tend to have more *B. longum* compared to those born through C-section. This is because they get exposed to their mother's beneficial bacteria during birth.

Genetics may also play a role. A few variants have been associated with higher or lower abundance of *B. longum* in the gut flora [R, R].

TYPICAL LEVELS

Predisposed to typical B. longum levels based on the genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LCT	rs3940549	GA
R3HDM1	rs1446585	GA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Bifidobacterium Breve

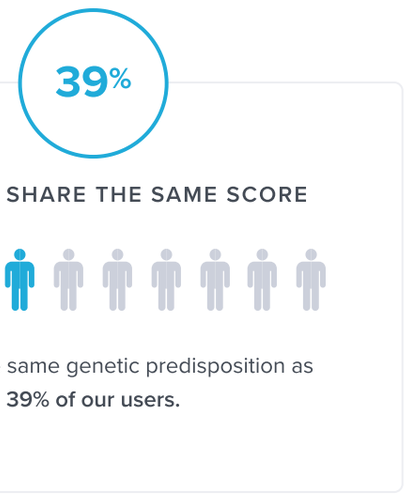
The following factors play a role in *B. breve* abundance in your gut flora [R]:

- **Diet**: Foods rich in fiber, like fruits, vegetables, and whole grains, can increase *B. breve*. On the other hand, diets high in sugar and processed foods might reduce their numbers.
- **Age**: As we get older, *B. breve* levels in our gut can decrease.
- **Stress:** High levels of stress can alter the balance of our gut bacteria.
- **Medications**: Some medicines, especially antibiotics, can reduce the number of these bacteria in our gut.
- **Illnesses**: Certain gut-related diseases, like irritable bowel syndrome (IBS), can change the levels of *B. breve*.
- **Probiotics**: Taking probiotic supplements containing *B. breve* can increase the number of these bacteria in the gut.
- **Birth Method**: Babies born through natural birth tend to have more *B. breve* compared to those born through C-section. This is because they get exposed to their mother's beneficial bacteria during birth.

Genetics may also play a role. A genetic variant has been associated with higher abundance of *B. breve* in the gut flora [R].

TYPICAL LEVELS

Predisposed to typical B. breve levels based on the genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LCT	rs3940549	GA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Bifidobacterium Bifidum

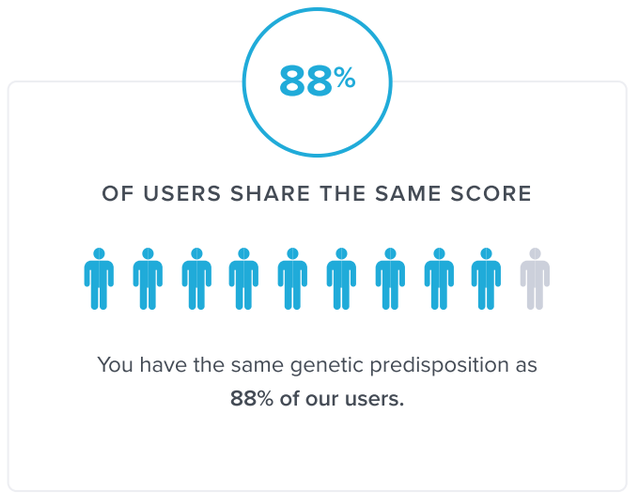
The following factors play a role in *B. bifidum* abundance in your gut flora [R]:

- **Diet**: Foods rich in fiber, like fruits, vegetables, and whole grains, can increase *B. bifidum*. On the other hand, diets high in sugar and processed foods might reduce their numbers.
- **Age**: As we get older, *B. bifidum* levels in our gut can decrease.
- **Stress:** High levels of stress can alter the balance of our gut bacteria.
- **Medications**: Some medicines, especially antibiotics, can reduce the number of these bacteria in our gut.
- **Illnesses**: Certain gut-related diseases, like irritable bowel syndrome (IBS), can change the levels of *B. bifidum*.
- **Probiotics**: Taking probiotic supplements containing *B. bifidum* can increase the number of these bacteria in the gut.
- **Birth Method**: Babies born through natural birth tend to have more *B. bifidum* compared to those born through C-section. This is because they get exposed to their mother's beneficial bacteria during birth.

Genetics may also play a role. A few variants have been associated with higher or lower abundance of *B. bifidum* in the gut flora [R, R].

TYPICAL LEVELS

Predisposed to typical B. bifidum levels based on the genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
LCT	rs4988235	GA
/	rs8176645	TT

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

Gut Health Genes

Your gut health is influenced by a variety of factors, including your diet, lifestyle, and, importantly, your genetics. Specific genes play a crucial role in maintaining a healthy gut microbiome, regulating immune responses, and protecting the gut lining from harmful substances. Genetic variations can impact how your body responds to infections, inflammation, and other gut-related conditions.

This section examines key gut health genes such as **HNF4A**, **FUT2**, **MUC1**, **JAK2**, and **NLRP3**, which are involved in processes like nutrient absorption, immune regulation, and gut barrier function. Understanding these genetic predispositions can provide valuable insights into how your gut functions and help you make informed decisions to support overall digestive health.

TYPICAL GENETICS

SLC2A14 (Gut Inflammation)

Likely typical SLC2A14 genetics

INTERMEDIATE ACTIVITY

HNF4A (Gut Inflammation)

Likely intermediate HNF4A activity

SECRETOR

FUT2 (Gut/ Vitamin B12)

Likely secretor

TYPICAL GENETICS

MUC1 (Immunity, Gut, Minerals)

Likely typical MUC1 genetics

TYPICAL ACTIVITY

NLRP3 (Gut Inflammation)

Likely typical NLRP3 activity

TYPICAL ACTIVITY

HRH2 (Gut Health)

Likely typical HRH2 activity

HIGHER ACTIVITY

IBD5 (Gut Inflammation)

Predisposed to higher IBD5 activity

LOWER ACTIVITY

JAK2 (Gut Inflammation)

Likely lower JAK2 activity

BETTER GENETICS

KIAA1109 (Gut Inflammation)

Likely better KIAA1109 genetics

BETTER GENETICS

SLC22A4 (Gut Inflammation)

Likely better SLC22A4 genetics

SLC2A14 (Gut Inflammation)

A study of 388 participants identified the following SLC2A14 variants as increasing the risk of both Crohn's disease and ulcerative colitis by 2- to 5-fold [R]:

- 'A' of **rs2889504**
- 'G' of **rs10846086**
- 'T' of **rs12815313**

The authors speculated that vitamin C imbalances caused by these variants may increase oxidative damage to the gut lining and reduce its barrier function.

TYPICAL GENETICS

Likely typical SLC2A14 genetics based on 3 genetic variants we looked at

33rd

PERCENTILE

Your risk is **greater than 33% of the population** and **lower than 67% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SLC2A14	rs2889504	AC
SLC2A14	rs12815313	CC
SLC2A3	rs10846086	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

HNF4A (Gut Inflammation)

Several studies suggest that certain genetic variants of *HNF4A* may increase the risk of developing ulcerative colitis (UC) [R, R, R].

A genome study including over 7,000 people with European ancestry found that **the 'C' allele in rs6017342 is associated with greater rates of UC** [R].

Likewise, two more studies of over 2,000 Dutch and 1,900 Korean patients also found that those carrying a 'C' allele were significantly more likely to have UC [R, R].

The HNF4A protein helps maintain the mucosal barrier in the intestines. This barrier is responsible for protecting the lining of the intestines while allowing nutrients to be absorbed. Variants resulting in lower levels of this protein may disrupt this mucosal barrier [R, R, R].

INTERMEDIATE ACTIVITY

Likely intermediate HNF4A activity based on the genetic variants we looked at

53%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **53% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HNF4A	rs6017342	AC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

FUT2 (Gut/ Vitamin B12)

The ‘AA’ (non-secretor) genotype of rs601338 has been associated with higher vitamin B12 absorption in comparison to secretor genotypes in European and West African populations. In European populations, this variant has been associated with a greater risk of developing celiac disease but may protect against the development of Crohn’s disease and ulcerative colitis [R].

The same goes for rs602662-A and rs492602-G, which are almost always inherited with rs601338-A [R, R].

Non-secretors (AA) lack histo-blood group antigens in the gut lining, preventing certain pathogens like norovirus from attaching and causing disease. However, this also limits beneficial bacteria (e.g., bifidobacteria), potentially reducing their immune-supporting and protective effects against harmful species [R, R].

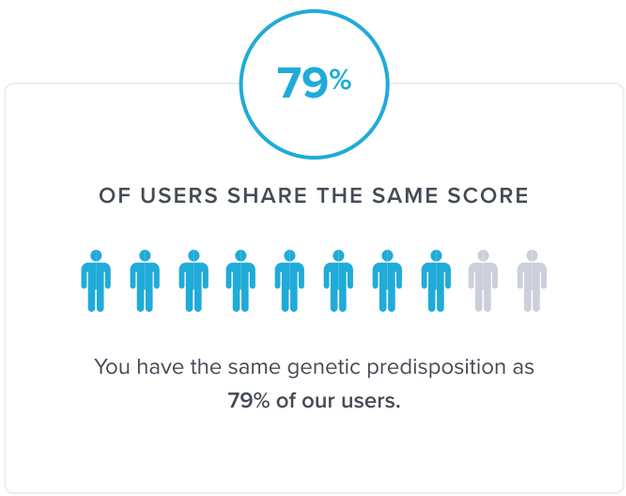
The minor ‘T’ allele of another variant, rs1047781, has been associated with higher vitamin B12 absorption but a greater risk of developing Crohn’s disease. This allele has also been associated with a reduced amount and diversity of gut bacteria [R, R, R].

The rs1047781 is closely associated with rs601338 in all individuals but those of East Asian (Japanese) descent. In individuals of Japanese descent, only rs1047781 determines secretor status. People with the ‘TT’ genotype are non-secretors [R].

FUT2 status is significant for **methylation** because FUT2 influences B12 absorption and availability, which is crucial for the methylation cycle. "Secretors" may have reduced B12 absorption, which can impact the methylation cycle since B12 is required as a cofactor for methionine synthase, a key enzyme in the methylation pathway that helps convert homocysteine to methionine.

SECRETOR

Likely secretor based on the genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
FUT2	rs601338	AG
FUT2	rs492602	GA
FUT2	rs602662	AG
FUT2	rs1047781	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

MUC1 (Immunity, Gut, Minerals)

The main MUC1 variant is **rs4072037**. Its **“C” allele** is linked to [R, R]:

- Stomach cancer
- Lung conditions
- IBD
- Weaker bones and lower calcium levels
- Lower magnesium levels

Scientists are unsure about the mechanisms behind these associations. They may reflect the protective role of MUC1 in mucous membranes, but on the other hand, some studies also linked higher MUC1 activity in cancer tissue [R].

Its link to weaker bones stems from calcium and magnesium loss. On the bright side, the variant is also linked to **lower uric acid levels** and thus lower odds of gout [R, R].

TYPICAL GENETICS

Likely typical MUC1 genetics based on the genetic variants we looked at

50%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **50% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
THBS3	rs4072037	TC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

NLRP3 (Gut Inflammation)

One of the main *NLRP3* variants is **rs10754558**. People with the "**GG**" **genotype** were about **2.5 times** more likely to have **ulcerative colitis** in one study. Interestingly, this variant has also been linked to severe food allergies [R, R, R].

Another well-researched variant is **rs35829419**. Its **"C" allele** is linked to higher odds of **IBD** and other inflammatory conditions like rheumatoid arthritis and eczema [R, R].

Other *NLRP3* variants linked to higher odds of IBD (Crohn's) include [R]:

- rs3806265-C
- rs4925648-T
- rs3738447-G

These variants likely increase *NLRP3* activity, contributing to excess inflammation [R, R].

TYPICAL ACTIVITY

Likely typical NLRP3 activity based on 5 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
NLRP3	rs35829419	CC
NLRP3	rs3806265	CC
NLRP3	rs3738447	AG
NLRP3	rs10754558	CC
NLRP3	rs4925648	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

HRH2 (Gut Health)

The most widely-investigated *HRH2* polymorphism is **rs2067474** (-1018 G>A). Its minor 'A' allele may **reduce** gene expression. This variant has been associated with:

- Decreased risk of stomach lining atrophy [R, R]
- Decreased risk of stomach cancer [R]

TYPICAL ACTIVITY

Likely typical HRH2 activity based on the genetic variants we looked at

91%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **91% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HRH2	rs2067474	GG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

IBD5 (Gut Inflammation)

A large meta-analysis of over 75,000 subjects found 16% higher disease rates per “T” allele of the **rs2188962** polymorphism. In another meta-analysis of over 15,000 participants, this variant was associated with 25% higher odds of Crohn’s disease. However, a review with nearly 10,000 people didn’t find a link between rs2188962-T and ulcerative colitis. This variant belongs to a gene called *C5ORF56*. Interestingly, the study on Crohn’s disease patients found that all *IBD5* variants were associated with decreased expression of another gene, *SLC22A5* [R, R, R].

A study of 158 families with Crohn's disease-affected members also suggested *SLC22A5* as a causal genetic factor. More precisely, the authors suggested two SNPs that may play a role in IBD development [R]:

- **rs1050152**-T in the *SLC22A4 (*OCTN1*)* gene
- **rs2631367**-C in the *SLC22A5 (*OCTN2*)* gene

These variants are almost always inherited together, along with other ones from the *IBD5* region. *SLC22* genes enable the uptake of the amino acid carnitine in the gut lining.

A meta-analysis of 26 studies confirmed the link between the above two variants and IBD. They correlated with 20-23% higher rates of both Crohn's disease and ulcerative colitis. This paper identified another significant *IBD5* SNP, **rs12521868**, associated with 36% higher IBD rates [R].

The *SLC22A4* and *SLC22A5* genes encode transport proteins (OCTN1 and OCTN2) that supply the gut lining with carnitine and other essential components. Mice lacking OCTN2 develop gut inflammation, ulcers, and perforations due to carnitine deficiency [R, R].

A study of 944 participants found that people with *SLC22A4* and *SLC22A5* variants have reduced gene expression in the blood and gut tissue, making them prone to inflammation. This confirms the mentioned link between *IBD5* SNPs and lower *SLC22A5* expression [R].

HIGHER ACTIVITY

Predisposed to higher IBD5 activity based on 4 genetic variants we looked at

99th

PERCENTILE

Your risk is **greater than 99% of the population** and **lower than 1% of the population.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SLC22A5	rs12521868	GG
SLC22A4	rs1050152	CC
SLC22A4	rs2631367	GG
SLC22A5	rs2188962	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

JAK2 (Gut Inflammation)

The most widely-studied *JAK2* polymorphism is **rs10758669**. **Its minor variant "C" increases the production and activity of the JAK2 protein**, leading to an enhanced immune response and inflammation [R].

As a result, it's linked to higher odds of **IBD — both Crohn's disease and ulcerative colitis**. The link may be stronger for Crohn's disease, especially in people of European ancestry [R, R, R, R, R, R, R, R].

Another important JAK2 variant, **rs12340895-G,** has shown similar associations. It's often inherited with rs10758669-C, meaning that many people will either have none or both of them [R, R, R].

LOWER ACTIVITY

Likely lower JAK2 activity based on the genetic variants we looked at

60%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **60% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
JAK2	rs10758669	AA
JAK2	rs12340895	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

KIAA1109 (Gut Inflammation)

The main *KIAA1109* polymorphism is **rs13151961**. Its minor 'G' allele has been associated with a decreased risk of celiac disease and ulcerative colitis. However, the association of this variant with the activity of *KIAA1109* or any other, nearby genes remains unknown [R, R, R, R, R].

BETTER GENETICS

Likely better KIAA1109 genetics based on the genetic variants we looked at

27%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **27% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
KIAA1109	rs13151961	AG

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

SLC22A4 (Gut Inflammation)

The main SLC22A4 variant is **rs1050152**. Its **“T” allele** is linked to **higher odds of IBD**, especially Crohn’s disease [R].

An interesting aspect of SLC22A4's function involves transporting **ergothioneine**, a compound abundant in **mushrooms**. A study has revealed that this variant can increase ergothioneine transport by approximately 50%. While ergothioneine typically acts as an antioxidant, this increased absorption may **exacerbate IBD symptoms** in people with this variant [R].

This interaction represents a clear example of how genetic variations can affect dietary tolerances and potentially impact disease management strategies.

Evolutionary perspective: Early farming communities ate fewer mushrooms than hunter-gatherers. The SLC22A4 variant may have helped European farmers adapt by absorbing more nutrients from the limited mushrooms in their diet.

BETTER GENETICS

Likely better SLC22A4 genetics based on the genetic variants we looked at

37%

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **37% of our users.**

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SLC22A4	rs1050152	CC

The number of "risk" variants in this table doesn't necessarily reflect your overall result.