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# Bluegrass Precision Wellness Report

## Health Report

REPORT CATEGORIES

- MENTAL HEALTH
- NUTRITION
- FOOD SENSITIVITIES
- HEART & BLOOD VESSELS
- SLEEP
- DETOX
- FITNESS
- SKIN & BEAUTY

## Sample Client

Report date: 30 April 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.

Viewing this medical test requires a medical doctor or use one of our contracted genetic counselors. By accessing these results, you acknowledge and agree that you will consult with a licensed physician or one of our contracted genetic counselors to review and interpret the results, and you agree not to rely on this information as a substitute for professional medical advice, diagnosis, or treatment.

# Personal information

NAME

**Sample Client**

SEX AT BIRTH

**Male**

HEIGHT

**5ft 10"** 178cm

WEIGHT

**215lb** 97.5kg


REPORT PROVIDED BY

UGenome

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# Summary

Welcome to your personalized genetic health analysis, a comprehensive exploration of how your unique DNA influences virtually every aspect of your health and well-being. This report examines the fundamental genetic variations that shape your body's responses to everything from the foods you eat to the way you sleep, exercise, and age.

Your genetic code serves as a blueprint that influences countless biological processes—from how quickly you metabolize caffeine and absorb vitamins to your susceptibility to certain health conditions and your body's ability to recover from exercise. Understanding these genetic predispositions empowers you to make informed decisions about your lifestyle, nutrition, fitness routines, and health monitoring strategies.

This analysis covers nine key areas of your genetic health profile. The Foundational Genomics section explores essential genetic variants, including **APOE and MTHFR**, that affect metabolism and disease risk. Sleep genetics reveal how your genes influence rest quality and caffeine sensitivity. Diet & Nutrition examines your body's unique responses to macronutrients, vitamins, and food sensitivities.

Your genetic profile also influences detoxification capacity (Phase 1 Detox), skin health and aging, fitness performance and injury risk, brain health and cognitive function, cardiovascular disease susceptibility, and more.

Rather than viewing genetics as destiny, this report presents your genetic information as valuable insights that can guide personalized health strategies. By understanding your genetic strengths and vulnerabilities, you can optimize your approach to nutrition, exercise, sleep, and preventive care, ultimately supporting your long-term health and vitality.

## This summary report contains:

- **64** Genetic Results
- **15** Recommendations
- **4** Lifestyle Assessments

# Overview of Your Results

## Foundational Genomics

LOWER ACTIVITY

### MTHFR

Likely lower MTHFR activity

E3/E3

### APOE

You carry two APOE ε3 variants

HIGHER ACTIVITY

### CYP1A2 (Detox)

Likely higher CYP1A2 activity

## Sleep

LOWER LEVELS

### Melatonin

Predisposed to lower melatonin levels

TYPICAL

### Sleep Quality

Predisposed to typical sleep quality

TYPICAL

### Sleep Duration

Predisposed to typical sleep duration

TYPICAL LIKELIHOOD

### Restless Legs

Typical likelihood of restless legs syndrome

TYPICAL LIKELIHOOD

### Sleep Movement

Typical likelihood of sleep movement

TYPICAL LIKELIHOOD

### Caffeine-Related Sleep Problems

Typical likelihood of caffeine-related sleep problems

DEEP

### Deep Sleep (ADA)

Likely a deep sleeper

LOWER

### Sleep Latency

Predisposed to lower sleep latency

LOWER

### Caffeine Sensitivity

Predisposed to lower caffeine sensitivity

LESS LIKELY

### Daytime Sleepiness

Less likely to experience daytime sleepiness

# Diet & Nutrition

HIGHER

## Alcohol Sensitivity

Likely higher sensitivity to alcohol

WORSE RESPONSE

## Protein Metabolism

Predisposed to worse protein metabolism

INCREASED NEED

## Folate (Vitamin B9)

Likely increased need for folate

INCREASED NEED

## Vitamin B6 (Pyridoxine)

Likely increased need for vitamin B6

TYPICAL LIKELIHOOD

## Tendency to Overeat

Typical likelihood of overeating

TYPICAL GENETICS

## HLA-DQ (Gluten)

Likely typical HLA-DQ genetics

TYPICAL

## Carbohydrate Metabolism

Predisposed to typical carbohydrate metabolism

TYPICAL RESPONSE

## Saturated Fat

Predisposed to typical saturated fat response

TYPICAL NEED

## Vitamin B12

Likely typical need for vitamin B12

TYPICAL NEED

## Biotin

Likely typical need for biotin

TYPICAL

## Salt Sensitivity

Likely typical sensitivity to salt

TYPICAL NEED

## Potassium

Likely typical need for potassium

TYPICAL NEED

## Magnesium

Likely typical need for magnesium

LIKELY TOLERANT

## Lactose Intolerance

Likely lactose tolerant

LESS LIKELY

## Binge Eating

Less likely to binge eat

BETTER

## Fat Metabolism

Predisposed to better fat metabolism

# Phase I Detox

TYPICAL METABOLIZER

## CYP2C9 (Detox)

Likely a typical metabolizer

TYPICAL

## Sensitivity to Foodborne Mold

Likely typical sensitivity to foodborne mold

TYPICAL ACTIVITY

## CYP2D6 (Mental Health, Detox)

Predisposed to a typical CYP2D6 activity

TYPICAL ACTIVITY

## CYP2B6 (Drug Metabolism)

Predisposed to a typical CYP2B6 activity

# Skin Health

MORE LIKELY

## Melanoma

More likely to get melanoma

TYPICAL

## Glycation

Predisposed to typical glycation

TYPICAL LIKELIHOOD

## Basal Cell Carcinoma

Typical likelihood of basal cell carcinoma

TYPICAL ACTIVITY

## MC1R (Pigmentation & Skin Damage)

Likely typical MC1R activity

TYPICAL

## Facial Wrinkles

Predisposed to a typical amount of facial wrinkles

# Fitness

LOWER

## Muscle Mass

Predisposed to lower muscle mass

TYPICAL

## Muscle Recovery

Predisposed to typical muscle recovery

TYPICAL

## Strength

Predisposed to typical strength

TYPICAL ACTIVITY

### COL5A1 (Collagen)

Likely typical COL5A1 activity

TYPICAL LIKELIHOOD

### Achilles Tendon Injury

Typical likelihood of Achilles tendon injury

HIGHER

### Endurance

Predisposed to higher endurance

HIGHER ACTIVITY

### COL1A1 (Collagen)

Predisposed to higher COL1A1 activity

LESS LIKELY

### Tendon Injury

Less likely to have tendinopathy

## Brain Health

WORSE

### GAD1 (Glutamate/GABA)

Likely worse GAD1 genetics

MORE LIKELY

### THC and Psychosis

More likely to experience psychotic symptoms from cannabis use

INCREASED

### Psychedelic Effects of THC (Functional)

Predisposed to increased psychedelic effects of THC

TYPICAL LIKELIHOOD

### Anxiety

Typical likelihood of anxiety

TYPICAL

### Cognitive Function

Predisposed to typical cognition

TYPICAL

### Attention

Typical likelihood of ADHD

TYPICAL

### Memory Performance

Predisposed to typical memory performance

TYPICAL LIKELIHOOD

### Alzheimer's Disease

Typical likelihood of Alzheimer's disease

E3/E3

### APOE

You carry two APOE ε3 variants

LESS LIKELY

### Cognitive Decline

Less likely to have cognitive decline

# Heart & Blood Vessels

MORE LIKELY

## Coronary Artery Disease

More likely to have coronary artery disease

TYPICAL ACTIVITY

## NOS3 (Cardiovascular)

Likely typical NOS3 activity

TYPICAL LEVELS

## Lipoprotein(a)

Predisposed to typical Lipoprotein(a) levels

TYPICAL LIKELIHOOD

## Atrial Fibrillation

Typical likelihood of atrial fibrillation

# Miscellaneous

MORE LIKELY

## Asthma

More likely to get asthma

TYPICAL

## Insulin Resistance

Predisposed to typical insulin resistance

TYPICAL LIKELIHOOD

## Hashimoto's Disease

Typical likelihood of Hashimoto's disease

LESS LIKELY

## Graves' Disease

Less likely to have Graves' disease

# Recommendations Overview

Your recommendations are prioritized according to the likelihood of it having an impact for you based on your genetics, along with the amount of scientific evidence supporting the recommendation.

You'll likely find common healthy recommendations at the top of the list because they are often the most impactful and most researched.

| | | DOSAGE |
|---|---|---|
| 1 | Aerobic Exercise (Cardio) | 1 hour |
| 2 | Strength Training | 1 hour |
| 3 | Omega-3 (Fish Oil) | 500 mg |
| 4 | Vitamin C | 500 mg |
| 5 | Music Therapy | 30 minutes |
| 6 | Mediterranean Diet | |
| 7 | Yoga | 30 minutes |
| 8 | Ginkgo | 120 mg |
| 9 | Relaxation Techniques | 30 minutes |
| 10 | Magnesium | 250 mg |
| 11 | Tai Chi | 1 hour |
| 12 | Avoid Air Pollution | |
| 13 | Meditation | 30 minutes |
| 14 | Methylfolate | 400 mcg |
| 15 | Walking | 30 minutes |

# Your Results in Details

## Foundational Genomics

This Foundational Genomics section examines the genetic factors that shape how our bodies respond to everyday compounds and biological processes, with particular attention to **caffeine and melatonin metabolism, APOE status, and MTHFR genetic variants**.

Understanding these genetic influences can reveal how individual variations affect our capacity to process caffeine, how effectively melatonin functions in our sleep regulation, APOE's contribution to cholesterol processing and Alzheimer's disease susceptibility, and the ways MTHFR genetic differences influence folate metabolism and general health outcomes.

This genetic information plays a crucial role in recognizing personal variations in nutritional requirements, sleep patterns, health risks, and how our bodies utilize nutrients. This foundational genomics exploration aims to be both informative and empowering, offering valuable insights into how our distinct genetic profiles influence our health and well-being.

LOWER ACTIVITY

### MTHFR

Likely lower MTHFR activity

E3/E3

### APOE

You carry two APOE ε3 variants

HIGHER ACTIVITY

### CYP1A2 (Detox)

Likely higher CYP1A2 activity

# MTHFR

**Key Takeaways:**

- MTHFR is an enzyme that helps your body process folate, an important nutrient for many body functions and processes.
- If you have lower MTHFR activity due to genetics, make sure you include folate-rich foods in your diet, like fruits and vegetables or other fortified foods. This is even more important with pregnancy.

The most common *MTHFR* SNP is **rs1801133** (C677T). The **'A' variant** of this SNP decreases the activity of the MTHFR enzyme. People with two 'A' variants may have about 16% lower blood folate levels ('A' equals 'T' on the opposite DNA strand) [R].

The **'G' variant*** of another SNP, **rs1801131** (A1298C), also decreases MTHFR enzyme activity, but less so than rs1801133. The effects of this variant may only be meaningful in people who also have the other low-activity variant, rs1801133-AA ('G' equals 'C' on the opposite DNA strand) [R, R, R, R, R].

Read this blog post for more details about MTHFR variants and potential ways to reduce their impact.

If you carry a lower-activity variant, make sure your diet is healthy, well-balanced, and contains plenty of folate-rich food sources. These include [R, R, R]:

- Spinach
- Black-eyed and green peas
- Asparagus
- Lettuce
- Avocado
- Broccoli
- Citrus fruits
- Fortified rice, bread, and pasta

Some sources recommend methylfolate supplements instead of folic acid. Methylfolate supplements would in theory bypass the MTHFR enzyme, which converts folic acid to methylfolate. However, even if you have lower-activity *MTHFR* variants, experts say you can still process folic acid without any issues [R].

Importantly, CDC notes that folic acid is the only folate supplement proven to reduce neural tube defects. Methylfolate supplements have not been properly studied [R].

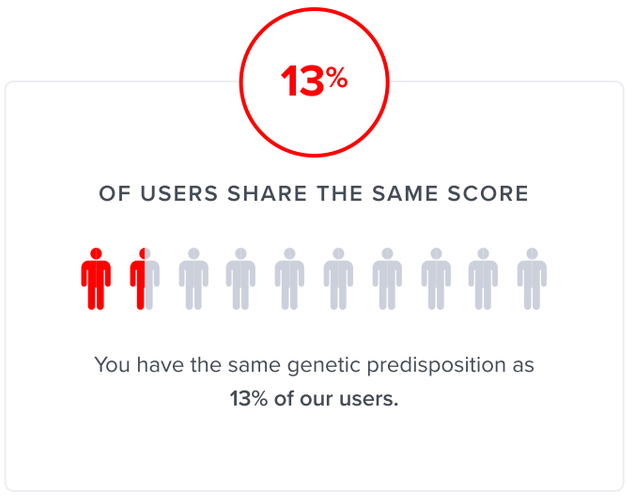
In addition to folate, there is some evidence that people with *MTHFR* variants may do better if they get more riboflavin (vitamin B2). This vitamin helps MTHFR work properly [R, R, R, R, R, R, R, R].

Good sources of riboflavin include [R, R]:

- Eggs
- Dairy (milk, cheese, yogurt)
- Lean and organ meats
- Green vegetables
- Fortified cereals
- Mushrooms
- Almonds

LOWER ACTIVITY

**Likely lower MTHFR activity based on the genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| MTHFR | rs1801133 | AA |
| MTHFR | rs1801131 | TT |

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

# APOE

**Key Takeaways:**

- If you carry one or both **ε4** variants, your risk for Alzheimer's disease may be higher.
- The risk is greatest for late onset (after age 65) Alzheimer's disease.
- Even if your risk is higher due to the **ε4** variants, numerous other factors from your environment to lifestyle to other genetic variants impact overall risk.
- People with both variants may never get Alzheimer's, and some who have neither variant can get the disease.

There are three major forms (variants) of the *APOE* gene. These are called ε2, ε3, and ε4. You can have two copies of the same variant or two different variants [R, R].

ε2, ε3, and ε4 change the shape of the ApoE protein. This can impact how well ApoE functions [R, R].

**ε3** is the most common variant. It makes a protein that is good at clearing plaque from the brain and fats from the blood. Most people have two ε3 variants and a typical risk of Alzheimer's disease [R].

**ε4** is less common. It makes a protein that is not as good at clearing plaque from the brain and fats from the blood. ε4 has been linked to a higher risk of Alzheimer's disease and artery hardening [R, R].

**ε2** is another less common variant. It makes a protein that is better than ε3 at removing plaque from the brain, but not as good at removing fats from the blood. ε2 has been linked to a lower risk of Alzheimer's disease [R, R, R].

However, it has also been linked to a higher risk of artery hardening in people with two ε2 variants and an underlying chronic health condition, such as obesity or diabetes [R, R, R].

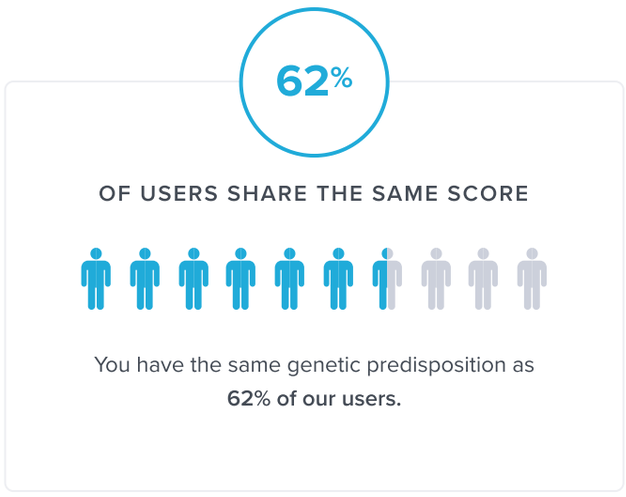
***Did you know?*** The **ε4** variant was much more common among ancient hunter-gatherers. Scientists suggest this variant might have improved their [R]:

- Inflammatory response to germs in the wilderness
- Vitamin D status in less sunny European areas
- Aerobic endurance, crucial for a hunter-gatherer lifestyle

As humans largely switched to farming, some effects of this variant became useless or even harmful. For this reason, evolution strongly favored the **ε3** variant in ancient farmers and their modern descendants [R].

E3/E3

**You carry two APOE ε3 variants based on the genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| APOE | rs7412 | CC |
| APOE | rs429358 | TT |

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

# CYP1A2 (Detox)

CYP1A2 is an enzyme that helps break down caffeine, drugs, and certain toxins like mold. Variants in the *CYP1A2* gene affect how fast people break down those substances [R, R, R].

The "slow metabolizer" variants make a less efficient enzyme. People who carry these variants may be more **sensitive to caffeine**. Accordingly, they may be more likely to experience negative effects when drinking coffee [R, R, R].

In terms of detox, they may be more susceptible to the adverse effects of certain drugs and toxins. However, the link between CYP1A2 variants and environmental toxins is more complex and requires further investigation [R, R].

The "fast metabolizer" variant makes a protein that breaks down caffeine. People with these variants may be less sensitive to its effects [R, R, R, R].

Nevertheless, "fast metabolizers" may experience the benefits of caffeine supplementation on athletic performance after a short time while "slow metabolizers" may need a longer ingestion period [R, R].

The following factors and substances may **increase** CYP1A2 activity:

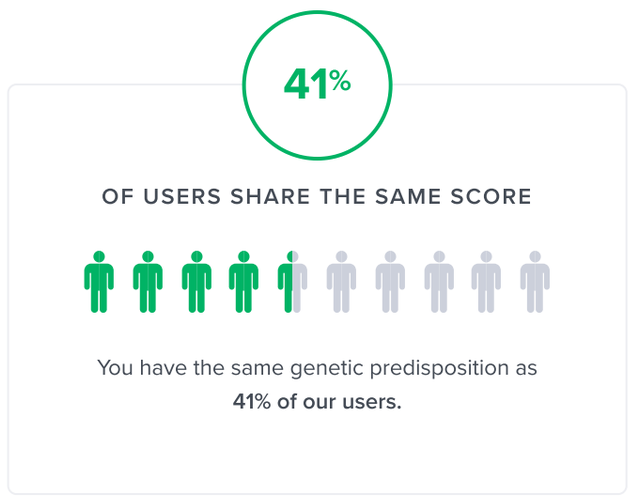
- Cigarette smoke: 1.72-fold for >20 cigarettes per day [R, R]
- Coffee consumption: 1.45-fold per liter of coffee drunk daily [R, R]
- Meat pan-fried at high temperatures: 1.4-fold [R]
- Chargrilled meat: 1.89-fold [R]
- Cruciferous vegetables [R, R, R]
- Green and black tea [R]
- Insulin [R]
- Being female: 0.90-fold [R]
- Heavy exercise [R]
- Omeprazole [R]
- Evodioa
- Reishi
- Andrographis,
- Modafinil
- Glycyrrhizin (liquorice)

The following factors and substances may **decrease** CYP1A2 activity:

- Apiaceous vegetables (carrots, parsnips, celery, and parsley) [R]
- Curcumin [R]
- Grapefruit juice and its component naringenin [R]
- Echinacea [R]
- Quercetin [R]
- Antibiotic fluoroquinolones [R]
- Fluvoxamine, an antidepressant [R]
- Peppermint, chamomile, and dandelion tea [R]
- Garlic
- Berberine
- Chamomile
- Lactoferrin
- Hops
- Galangin (galangal root)
- Scutellaria baicalensis,
- Tangeritin
- Trans-resveratrol

HIGHER ACTIVITY

**Likely higher CYP1A2 activity based on the genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CYP1A2 | rs762551 | AA |
| LMAN1L | rs2069514 | GG |

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

# Sleep

This section explores the complex genetic factors that influence your sleep patterns, quality, and overall sleep health. Understanding these genetic variations provides insights into individual differences in sleep architecture, caffeine sensitivity, and circadian rhythm regulation.

Your genetic makeup plays a significant role in determining how long you sleep, how well you sleep, and how external factors like caffeine affect your rest. This analysis examines various aspects of sleep biology, from basic sleep metrics to specific genetic variants that influence your body's response to stimulants and sleep-regulating hormones.

This comprehensive sleep assessment is designed to help you understand your unique sleep profile, empowering you to make informed decisions about sleep hygiene, caffeine consumption timing, and lifestyle choices that support optimal rest and recovery.

**Topics include:**

- Time in Bed
- Sleep Sensitivity to Caffeine
- Excessive Sleepiness
- Sleep Movement
- Melatonin

LOWER LEVELS

## Melatonin

Predisposed to lower melatonin levels

TYPICAL

## Sleep Quality

Predisposed to typical sleep quality

TYPICAL

## Sleep Duration

Predisposed to typical sleep duration

TYPICAL LIKELIHOOD

## Restless Legs

Typical likelihood of restless legs syndrome

TYPICAL LIKELIHOOD

## Sleep Movement

Typical likelihood of sleep movement

TYPICAL LIKELIHOOD

## Caffeine-Related Sleep Problems

Typical likelihood of caffeine-related sleep problems

DEEP

## Deep Sleep (ADA)

Likely a deep sleeper

LOWER

## Sleep Latency

Predisposed to lower sleep latency

LOWER

## Caffeine Sensitivity

Predisposed to lower caffeine sensitivity

LESS LIKELY

## Daytime Sleepiness

Less likely to experience daytime sleepiness

# Melatonin

**Key takeaways:**

- Up to **80%** of differences in people's melatonin levels may be due to genetics.
- Low melatonin is a common issue. It may disrupt sleep and cause tiredness.
- Artificial light, stress, caffeine, alcohol, and tobacco may reduce melatonin levels.
- Lack of sunlight, liver issues, and some supplements and drugs may increase melatonin levels too much.

**Up to 80% of differences in people's melatonin levels may be due to genetics** [R].

Genes involved in melatonin levels may influence [R, R]:

- Light sensitivity
- Sleep-wake cycle
- Brain development and health
- Mental health

Factors linked to **low melatonin levels** include [R, R, R]:

- Artificial light, including your phone and TV
- Long daylight in the summer
- Stress
- Caffeine, alcohol, tobacco
- Late-night physical activity
- Some drugs (e.g., beta-blockers)
- Aging

**Excessive melatonin levels** may result from [R, R]:

- Colder and darker winter months
- Liver issues
- Supplements (e.g., 5-HTP, tryptophan, vitamin B3 or B6)
- Some antidepressants

LOWER LEVELS

## Predisposed to lower melatonin levels based on 5 genetic variants we looked at

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| GALNT13 | rs7571016 | GG |
| GALNT15 | rs142037747 | GG |
| LDLRAD3 | rs9645614 | AA |
| ANXA2R | rs6451653 | GG |
| ZFHX3 | rs17681554 | AA |

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

# Sleep Quality

The quality of your sleep can have a big impact on how much energy you have during the day [R, R].

Many genetic variants influence sleep [R]. However, your environment and your habits also affect sleep quality.

Some strategies that may improve sleep quality include [R]:

- Reducing your bright light exposure (screen time) in the evenings
- Sticking to a regular sleep schedule
- Avoiding hunger or large meals before bed
- Avoiding nicotine, caffeine, and alcohol before bed
- Maintaining a sleep area that's cool, dark, and quiet

TYPICAL

**Predisposed to typical sleep quality based on 576,285 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| / | rs71365296 | AA |
| KANSL1 | rs1107820 | TT |
| VGLL2 | rs4946246 | TG |
| RALYL | rs118149821 | CC |
| CHRM2 | rs146885652 | GG |
| FOXO6 | rs2226263 | TT |
| / | rs184060364 | GG |
| TENM4 | rs117191802 | AA |
| TCF21 | rs13201465 | AA |
| RALYL | rs191939331 | GG |
| FBN2 | rs115375165 | GG |
| TJP2 | rs7030480 | AA |
| COQ8A | rs113207574 | CT |
| PRICKLE1 | rs11829548 | GT |
| ADCY1 | rs79209880 | CC |
| CHRM2 | rs74757156 | CC |
| / | rs111921861 | AA |
| / | rs140707667 | GG |
| FUT9 | rs142123475 | CC |
| UFL1 | rs75842709 | CC |
| COX7C | rs2964898 | CC |
| ERCC4 | rs74321030 | TT |
| VRK1 | rs78807545 | GG |
| / | rs147738873 | CC |
| MSX2 | rs28450080 | CC |
| RFX4 | rs11610873 | GG |
| CDH13 | rs111702115 | GG |
| CASP3 | rs7695597 | AA |
| TNF | rs1800629 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| NREP | rs140529718 | GG |
| EPB41L4A | rs146128029 | TT |
| RBMS3 | rs17023449 | TT |
| SASH1 | rs112390069 | GG |
| FAM107B | rs74122981 | AA |
| PLK2 | rs76395602 | GG |
| RGS6 | rs36032616 | AA |
| PIGZ | rs4916588 | CC |
| PLK2 | rs170741 | TT |
| ENC1 | rs76768179 | TT |
| ZNF626 | rs6511152 | CC |
| CD36 | rs4437584 | TT |
| LAMA2 | rs11962701 | CC |

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

# Sleep Duration

**The amount of sleep you need** depends on many factors, such as your age. Adults typically need 7-9 hours of sleep per night [R, R, R].

**How much sleep you actually get** may depend both on your genes and the environment. Around 50% of the differences in sleep duration between people may be due to genetics [R].

Many of the genes that affect sleep duration are involved in the circadian clock. This is our internal clock that helps control and adjust the sleep-wake cycle to the 24-hour cycle of the Earth's day [R, R, R, R].

Strategies that may help you get the recommended amount of sleep include [R]:

- Sticking to a regular sleep schedule
- Maintaining a sleep area that's cool, dark, and quiet
- Reducing your bright light exposure (screen time) in the evenings
- Avoiding hunger or large meals before bed
- Avoiding nicotine, caffeine, and alcohol before bed

TYPICAL

**Predisposed to typical sleep duration based on 7,192,262 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| IGKV1OR2-108 | rs62158206 | TT |
| MBOAT2 | rs79512144 | AA |
| ZCCHC7 | rs10973207 | GG |
| RBFOX1 | rs77684884 | AA |
| TTC21B | rs12463754 | CC |
| COG5 | rs6979198 | TT |
| LPCAT1 | rs365663 | GG |
| DAB1 | rs540431 | GG |
| / | rs12791153 | AT |
| VRK2 | rs116219610 | TC |
| CLOCK | rs12649507 | AG |
| SEMA6D | rs13329140 | GA |
| TCF4 | rs12607679 | CT |
| PAM | rs6889592 | GA |
| FOXP2 | rs1668331 | TG |
| ANKK1 | rs17601612 | GC |
| PAX8 | rs2863244 | AG |
| BUD13 | rs1263056 | GA |
| BANK1 | rs13109404 | TT |
| ERC2 | rs112230981 | AA |
| NRXN3 | rs11621908 | CC |
| ACTR1A | rs144625846 | AA |
| CLOCK | rs2070062 | AC |
| MRM2 | rs3823624 | CC |
| ZSCAN23 | rs34388845 | AA |
| VRK2 | rs11682175 | CC |
| H2BC12 | rs12215241 | GG |
| MAPT | rs62061734 | TT |
| FTO | rs8047587 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| ZFP57 | rs1633063 | CC |
| PM20D2 | rs9451146 | CC |
| PRKG2 | rs41501452 | AA |
| GPD2 | rs11883686 | AA |
| COG5 | rs7778250 | AA |
| / | rs9362971 | TT |
| / | rs4688116 | TT |

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

# Restless Legs

**Key Takeaways:**

- Around **60%** of the differences in people's risk of developing RLS may be due to genetics.
- Other risk factors include iron deficiency, pregnancy, toxicurea levels, and certain medical conditions.
- RLS is fairly common, occurring in about **1 in 10 people**.
- If you have a high genetic risk, your overall risk may be lowered by taking action on risk factors that you can change.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

Restless legs syndrome (RLS) is a condition that causes an uncontrollable urge to move the legs. It is relatively common - around **1 in 10 people** have it [R].

Experts aren't sure what causes RLS. There is evidence that it may have to do with iron or dopamine levels in the brain [R, R].

RLS occurs in all age groups. Factors that may raise the risk for RLS include [R, R]:

- Iron deficiency
- Pregnancy
- Toxic buildup of urea in the blood (often found in people with kidney disease)
- Other chronic medical conditions
- **Genetics**

The feelings associated with RLS are described as pulling, creeping, and tugging. Typically, RLS symptoms [R]:

- Begin with rest, such as driving or sitting at a movie theater
- Relieve with movement, such as stretching, jiggling the legs, or walking
- Worsen in the evening
- May be associated with limb twitching

If left untreated, RLS may disrupt sleep. This can lead to daytime sleepiness, irritability, or problems at work.

The following lifestyle changes can help improve symptoms [R, R]:

- Exercise
- Massage
- Applying heat using a heating pad or a warm bath
- Avoiding or limiting caffeine, alcohol, and tobacco

Some supplements, like iron, may help people with RLS who have low iron. For severe cases, a doctor may prescribe medications.

Around 60% of the differences in people's risk of developing RLS may be due to genetics. Genes involved with RLS may influence [R, R, R, R]:

- Iron metabolism
- Nerve function
- Dopamine activity

TYPICAL LIKELIHOOD

**Typical likelihood of restless legs syndrome based on 34 genetic variants we looked at**


**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| GLO1 | rs9296249 | TT |
| GLO1 | rs9357271 | TT |
| GLO1 | rs3923809 | GA |
| MEIS1 | rs2300478 | GT |
| SEMA6D | rs111652004 | GG |
| TOX3 | rs3104767 | GT |
| CCDC167 | rs17636328 | AA |
| MEIS1 | rs6747972 | AG |
| HOXB2 | rs12450895 | AA |
| PTPRD | rs62535767 | CC |
| PRMT6 | rs12046503 | CT |
| ZNF804B | rs10952927 | AG |
| C1D | rs1820989 | AC |
| PIK3R4 | rs35987657 | GA |
| PKP4 | rs80319144 | TC |
| OPRL1 | rs365032 | AG |
| RANBP17 | rs10068599 | CT |
| CRBN | rs1848460 | AT |
| SLC40A1 | rs10188680 | TA |
| PMAIP1 | rs58127855 | CC |
| MEIS1 | rs113851554 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| MAP2K5 | rs12593813 | AA |
| PTPRD | rs4626664 | GG |
| PTPRD | rs1975197 | GG |
| MICALL2 | rs112716420 | CC |
| DPH6 | rs996064 | AA |
| DCDC2C | rs10208712 | GG |
| DACH1 | rs340561 | GG |
| SETBP1 | rs12962305 | CC |

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

# Sleep Movement

Have you ever been told you move while you sleep? Sleep movements are common. They don't usually disturb the mover's sleep. However, when they do disrupt sleep, they can make a person sleepy during the day [R, R].

People may be more likely to experience periodic limb movements as they age. About 1 in 3 people over the age of 60 experience sleep movements [R, R]

Other factors that may influence sleep movement include [R, R]:

- **Sex** – men tend to move more in their sleep
- **Diet** – a lack of iron in the diet may make sleep movements worse
- **Genetics**

Scientists have linked several genes to increased sleep movement. For example:

- *MEIS1* gene, which influences the iron metabolism in the brain [R, R, R, R, R].
- *BTBD9* gene, which may influence the brain dopamine metabolism [R, R, R, R, R].
- *TOX3* gene, which may play an important role in nerve cell activity [R, R, R].

TYPICAL LIKELIHOOD

**Typical likelihood of sleep movement based on 7,138,059 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| MEIS1 | rs2300478 | GT |
| GLO1 | rs3923809 | GA |
| TOX3 | rs3104788 | TC |
| MEIS1 | rs113851554 | GG |

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

# Caffeine-Related Sleep Problems

**Caffeine is a well-known stimulant**. It can promote wakefulness and interrupt sleep by reducing the activity of adenosine, a sleep-promoting compound that builds up while we are awake and decreases while we sleep. **Caffeine's effects on sleep tend to be strongest in the evening, before bedtime.** Older people and those who sleep less may be more sensitive to caffeine [R, R, R, R].

Up to **40%** of differences in caffeine-related sleep problems may be due to genetics. Interestingly, the majority of these genetic factors are specific to caffeine, and they don't affect sleep in general [R].

A gene called *ADORA2A* helps make a receptor for adenosine. Caffeine promotes wakefulness and interrupts sleep by blocking this receptor. Unsurprisingly, a variant belonging to this gene, rs5751876, is linked to caffeine-related sleep problems [R, R, R, R].

What's surprising is the opposite effect of this variant on caffeine-related anxiety. **People carrying the "T" allele may be less prone to sleep problems but more prone to anxiety due to caffeine intake** [R, R, R].

Other gene variants linked to caffeine-related sleep problems may affect:

- Melatonin (*MTNR1B*)
- Compounds similar to adenosine (*GBP1*, *GBP4*)
- Brain function (*ADGRL2*)
- Heart function (*NEBL*)

**Please note:** Your other gene variants, lifestyle, and environment may also affect caffeine-related sleep problems.

TYPICAL LIKELIHOOD

**Typical likelihood of caffeine-related sleep problems based on 18 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ADORA2A | rs5751876 | CT |
| NEBL | rs9665295 | CC |
| ALDH7A1 | rs13172305 | GG |
| FCHSD2 | rs1791933 | TC |
| KCTD15 | rs11878836 | TT |
| MDFIC2 | rs7628219 | CC |
| GBP7 | rs521704 | CA |
| ADGRL2 | rs12725617 | CT |
| COMT | rs4680 | GA |
| PRIMA1 | rs6575353 | AG |
| PRIMA1 | rs12895096 | GT |
| / | rs16905439 | CC |
| TMEM51 | rs2103117 | GG |
| GBP3 | rs12407812 | CC |
| ADRA2A | rs2065779 | GG |
| SLC7A1 | rs2388082 | CC |
| MTNR1B | rs10830964 | CC |
| LRTM1 | rs11706236 | AA |
| NEDD4L | rs158856 | CC |

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

# Deep Sleep (ADA)

Deep sleep is one of the stages of non-REM sleep. It is also called *slow-wave sleep* or *delta-wave sleep* because the brain emits slow (delta) waves during this stage [R, R, R].

A compound called adenosine builds up in the brain while we are awake and peaks at bedtime, causing us to feel sleepy. The longer we stay awake, the sleepier we get. Adenosine decreases while we sleep, so we feel rested when we wake up [R].

The *ADA* gene helps make an enzyme that breaks down adenosine. Scientists suggest that one variant in this gene reduces the enzyme's activity. This variant is linked to a faster buildup of adenosine [R].

People with at least one copy of this variant tend to [R, R, R]:

- Be sleepier
- Awaken less often during the night
- Have longer deep sleep
- Have stronger slow (delta) waves

Caffeine can promote wakefulness and interrupt sleep by reducing adenosine activity. However, it's still not clear if the effects of caffeine on sleep depend on this gene variant [R].

DEEP

**Likely a deep sleeper based on the genetic variants we looked at**

**11%**

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **11% of our users.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ADA | rs73598374 | TC |

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

# Sleep Latency

How long does it take for you to fall asleep? Do you pass out as soon as your head hits the pillow? Or do you toss and turn for what seems like hours, before you drift asleep? The time it takes for you to fall asleep is referred to as **sleep latency** [R].

Many factors can affect your sleep latency, including your genes. About **20-45% of differences in sleep latency are due to genetics**. Scientists identified several genes that play a key role in sleep latency by influencing the release of neurotransmitters such as GABA or by affecting the setting of the body's internal clock [R, R, R].

If you are struggling to fall asleep at night, these may improve your sleep latency [R, R, R, R, R, R]:

- Sticking to a regular sleep schedule and having a consistent sleep routine
- Maintaining a sleep area that's cool, dark, and quiet
- Avoiding hunger or large meals before bed
- Avoiding nicotine, caffeine, and alcohol before bed
- Getting enough daytime exposure to natural light
- Getting regular physical activity
- Addressing stress and anxiety, e.g. by mindfulness and relaxation techniques

LOWER

**Predisposed to lower sleep latency based on 7,281,604 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| MDFIC2 | rs147786325 | TT |
| SLC26A7 | rs77942316 | GA |
| SLC26A7 | rs61134957 | AC |
| NDUFA4 | rs73678284 | CC |
| IL21 | rs62324204 | TC |
| SP140L | rs17273810 | AC |
| MCTP2 | rs11074250 | AT |
| PMP22 | rs9907309 | GA |
| CSNK2A1 | rs112815007 | AA |
| CSNK2A1 | rs74448913 | TT |
| CSMD1 | rs62480124 | GG |
| FRAS1 | rs6842385 | GG |
| / | rs62217115 | TT |
| GRM7 | rs185934952 | GG |
| RANBP3L | rs114965806 | CC |
| ERCC4 | rs12934187 | CC |
| CDC42EP3 | rs144261420 | AA |
| HLF | rs79692461 | AA |
| KLHL29 | rs62126824 | AA |
| RANBP3L | rs74541420 | CC |
| MALRD1 | rs2686656 | AA |
| NAT1 | rs7845127 | CC |
| VAV3 | rs17556028 | CC |

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 |
|---|---|---|
| AHR | rs4410790 | CT |
| ADORA2A | rs5751876 | CT |
| NAT2 | rs1495741 | AG |
| COMT | rs4680 | GA |
| CYP1A2 | rs762551 | AA |

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

# Daytime Sleepiness

Daytime sleepiness is the feeling of excessive sleepiness during the day. People with excessive daytime sleepiness often complain of not feeling well-rested, having difficulty waking up, or accidentally falling asleep during the day, among others [R, R, R].

Daytime sleepiness is usually a consequence of poor sleep duration or quality. Other risk factors include [R]:

- Shift work [R]
- Sleep disorders (obstructive sleep apnea, narcolepsy) [R, R]
- Mood disorders (depression, bipolar disorder) [R]
- Allergies (asthma, hay fever) [R, R]
- GERD [R]
- Parkinson's disease [R]
- Epilepsy [R]
- Obesity [R]
- **Genetics**

Up to 40% of differences in people's chances of experiencing daytime sleepiness may be due to genetics. Genes involved may influence the sleep/wake cycle and sleep duration or quality [R, R, R, R].

Interventions aimed at improving sleep duration and quality may also reduce daytime sleepiness. These include [R, R, R, R]:

- Reducing your bright light exposure (screen time) in the evenings
- Maintaining a sleep area that's cool, dark, and quiet
- Sticking to a regular sleep schedule
- Avoiding hunger or large meals before bed
- Avoiding nicotine, caffeine, and alcohol before bed

LESS LIKELY

**Less likely to experience daytime sleepiness based on 993,458 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ASB3 | rs76645968 | GG |
| PATJ | rs12140153 | GG |
| / | rs920065 | CC |
| AP3B2 | rs17507216 | AG |
| TMEM144 | rs115320831 | AG |
| FGGY | rs371398972 | AA |
| AR | rs73536079 | G |
| / | rs573716401 | GG |
| / | rs553962214 | TT |
| SLC24A3 | rs565444861 | GG |
| PTPRM | rs558006880 | GG |
| LBP | rs6099524 | CC |
| SLC2A9 | rs543431433 | TT |
| TENT5A | rs189689339 | CC |
| FGGY | rs192315283 | TT |
| TMEM132B | rs142261172 | GG |
| / | rs182765975 | GG |

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

# Diet & Nutrition

This section examines the genetic factors that influence how your body processes foods, nutrients, and dietary compounds. Understanding these genetic variations provides insights into individual differences in hunger regulation, macronutrient metabolism, vitamin absorption, and food sensitivities.

Your genetic profile affects everything from how you experience hunger and satiety to how efficiently you metabolize carbohydrates, fats, and proteins. This analysis explores your body's unique responses to different foods and nutrients, including potential sensitivities and optimal dietary approaches based on your genetic makeup.

This comprehensive nutritional genetics assessment empowers you to make personalized dietary choices that align with your genetic predispositions, supporting optimal health, energy levels, and overall well-being through targeted nutrition strategies.

**Topics include:**

- Hunger and Fullness
- Response to Macros - Optimal Diet
- Food Sensitivity
- Alcohol Sensitivity
- B Vitamins
- Electrolytes

HIGHER

## Alcohol Sensitivity

Likely higher sensitivity to alcohol

WORSE RESPONSE

## Protein Metabolism

Predisposed to worse protein metabolism

INCREASED NEED

## Folate (Vitamin B9)

Likely increased need for folate

INCREASED NEED

## Vitamin B6 (Pyridoxine)

Likely increased need for vitamin B6

TYPICAL LIKELIHOOD

## Tendency to Overeat

Typical likelihood of overeating

TYPICAL GENETICS

## HLA-DQ (Gluten)

Likely typical HLA-DQ genetics

TYPICAL

## Carbohydrate Metabolism

Predisposed to typical carbohydrate metabolism

TYPICAL RESPONSE

## Saturated Fat

Predisposed to typical saturated fat response

TYPICAL NEED

## Vitamin B12

Likely typical need for vitamin B12

TYPICAL NEED

## Biotin

Likely typical need for biotin

TYPICAL

## Salt Sensitivity

Likely typical sensitivity to salt

TYPICAL NEED

## Potassium

Likely typical need for potassium

TYPICAL NEED

## Magnesium

Likely typical need for magnesium

LIKELY TOLERANT

## Lactose Intolerance

Likely lactose tolerant

LESS LIKELY

## Binge Eating

Less likely to binge eat

BETTER

## Fat Metabolism

Predisposed to better fat metabolism

# 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].

HIGHER

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

**7%**

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **7% of our users.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ADH1B | rs1229984 | CT |
| ALDH2 | rs671 | GG |

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

# Protein Metabolism

Some people do better on low- and others on high-protein diets. Your genes may affect your response to protein. Specifically, genes that affect your response to protein may also influence [R, R, R, R]:

- Body weight
- Food preference
- Metabolism

In people with a better response to dietary protein, higher amounts of protein in a diet may improve weight control and metabolism. On the other hand, high-protein diets may have adverse metabolic effects in people with a worse response [R, R, R, R].

However, other variants and environmental factors may also influence your dietary protein response. Try to get most of your protein from healthy sources such as legumes, poultry, and fish.

WORSE RESPONSE

**Predisposed to worse protein metabolism based on 17 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| FTO | rs9939609 | TT |
| FTO | rs1558902 | TT |
| GLP1R | rs6923761 | GG |
| ST6GAL1 | rs1501299 | GG |
| CNDP2 | rs4891558 | TT |
| NADSYN1 | rs12785878 | GG |
| MTNR1B | rs10830963 | CG |
| APOA1 | rs670 | CC |
| FUCA1 | rs3123554 | GA |
| NTN5 | rs838147 | GA |
| CLOCK | rs3749474 | TC |
| UCP3 | rs1800849 | GG |
| ADRB3 | rs4994 | AA |
| FABP2 | rs1799883 | CC |
| TFAP2B | rs987237 | AA |
| CNDP1 | rs7244647 | TT |
| TNF | rs1800629 | GG |

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

# Folate (Vitamin B9)

**Key Takeaways:**

- Folate is an essential vitamin. It is particularly important for pregnant women.
- Folate is needed for brain and heart health, gene signaling, and to protect DNA. It is readily available in citrus fruits, green vegetables, and fortified foods.
- Your diet, smoking, heavy drinking, gut issues, and genes may impact folate levels.
- Click the **next steps** tab for relevant labs.

Vitamin B9, also known as folate or folic acid, is an essential nutrient. Most adults should get **400 micrograms (mcg)** of folate per day. Among other functions, folate helps the body make red blood cells [R, R, R, R].

Low levels of folate are not common. However, women may be at a higher risk than men [R, R].

Additional risk factors and causes of low folate levels include:

- **Low intake of fruits and vegetables [R, R]**
- Heavy drinking [R, R]
- Smoking [R, R]
- Gut issues such as inflammatory bowel disease (IBD) or celiac disease [R, R, R]
- Certain medications [R]

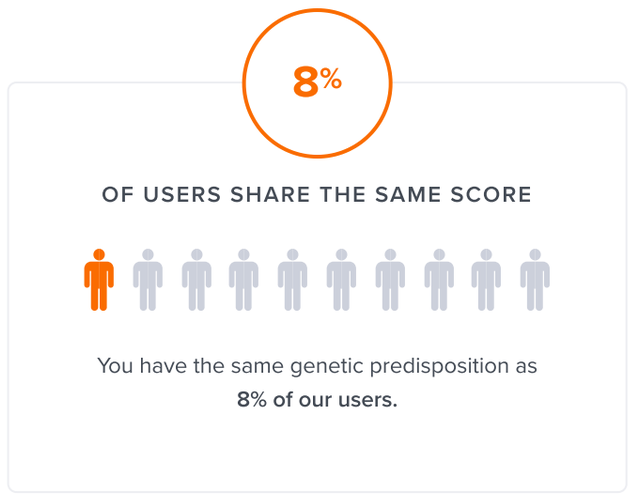
A variant in a gene called *MTHFR* is linked to slightly lower folate levels. People who carry two copies of this variant may have about 16% lower blood folate [R].
Genetically higher folate levels may be causally associated with [R, R, R, R, R, R, R, R]:

- IgE levels
- Fatty liver
- Vitiligo
- Joint pain
- HDL cholesterol
- Heart health (lower CHD)
- Stroke
- Gut inflammation (lower UC)

Read this blog post for more details about MTHFR variants and potential ways to reduce their impact.

INCREASED NEED

## Likely increased need for folate based on the genetic variants we looked at




## Your top variants that most likely impact your genetic predisposition:

| GENE | SNP | GENOTYPE |
|---|---|---|
| MTHFR | rs1801133 | AA |

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

# Vitamin B6 (Pyridoxine)

Some people may have genetically higher vitamin B6 levels than others. Genes involved may influence vitamin B6 metabolism [R, R, R].

INCREASED NEED

## Likely increased need for vitamin B6 based on 5 genetic variants we looked at

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| NBPF3 | rs4654748 | CC |
| ALPL | rs1256341 | TT |
| NBPF3 | rs1697421 | CT |
| CBS | rs234706 | GA |
| MTHFR | rs1801133 | AA |
| PDXK | rs2010795 | AG |
| ALPL | rs1772719 | CA |
| PDXK | rs147242481 | GG |
| ALPL | rs1256335 | AA |

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

# Tendency To Overeat

Several genetic variants are associated with overeating behaviors, appetite control, and sensitivity to hunger and satiety signals. These variants influence hormonal regulation, reward pathways, and metabolic processes that can contribute to individual differences in eating behavior.

**FTO (rs9939609, 87653 T>A)**: The *FTO* gene is strongly associated with appetite and obesity risk. The rs9939609 variant (T>A) can influence hunger and satiety, with the A allele linked to increased appetite and a higher likelihood of overeating and weight gain [R].

**FTO (rs6713532, A>G)**: Another *FTO* variant, rs6713532 (A>G), has been linked to increased risk of obesity and a tendency toward overeating. Individuals with the G allele may have a higher susceptibility to weight gain due to increased appetite and reduced satiety signals.

**LEPR (rs1805094, Lys656Asn G>C)**: *LEPR* encodes the leptin receptor, which is crucial for regulating hunger and satiety. The rs1805094 variant (Lys656Asn G>C) may impact leptin sensitivity, potentially affecting how full one feels after eating, influencing portion sizes and eating frequency.

**LEPR (rs1137101, Gln223Arg A>G)**: Another variant in the *LEPR* gene, rs1137101 (Gln223Arg A>G), affects leptin signaling. The G allele is associated with a reduced feeling of fullness, which may lead to larger meal sizes and frequent hunger cues [R, R, R].

**TAS2R38 (rs713598, Ala262Val C>T)**: *TAS2R38* is a taste receptor gene that affects taste sensitivity, particularly to bitter flavors. The rs713598 variant (Ala262Val C>T) can influence food preferences and eating behavior, potentially impacting overeating tendencies, especially in response to sweet or fatty foods [R, R, R].

**TAS2R38 (rs1726866, Ala49Pro G>A)**: Another *TAS2R38* variant, rs1726866 (Ala49Pro G>A), affects bitter taste perception. Individuals with the A allele may have a preference for bitter-tasting vegetables like cruciferous greens. This variant can influence dietary choices and eating behaviors, indirectly impacting overall nutrition and weight management.

**APOA2 (rs5082, -492 T>C)**: APOA2 is involved in lipid metabolism and satiety regulation. The rs5082 variant (-492 T>C) has been associated with higher intake of saturated fats and a tendency to overeat, especially in individuals with the CC genotype.

**CLOCK (rs1801260, 3111 T>C)**: The *CLOCK* gene influences circadian rhythms, which affect eating patterns and metabolism. The rs1801260 variant (3111 T>C) can disrupt regular eating schedules, potentially leading to increased food intake during irregular hours and contributing to overeating [R, R, R].

**DRD2 (rs1800497, Taq1A C>T)**: *DRD2* encodes a dopamine receptor, which is involved in reward and pleasure pathways in the brain. The rs1800497 variant (Taq1A C>T) can affect dopamine sensitivity, potentially leading to increased cravings and reward-seeking behaviors related to food [R, R, R, R].

**FAAH (rs324420, Pro129Thr C>A)**: FAAH is involved in endocannabinoid signaling, which influences appetite and pleasure from eating. The rs324420 variant (Pro129Thr C>A) can increase the tendency to snack and overeat, particularly high-fat foods, due to heightened pleasure responses to food.

**MC4R (rs17782313, T>C)**: The *MC4R* gene is associated with energy balance and appetite control. The rs17782313 variant (T>C) has been linked to increased appetite and a higher risk of

TYPICAL LIKELIHOOD

**Typical likelihood of overeating based on 20 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| POMC | rs6713532 | TT |
| NPY | rs16147 | TT |
| ANKK1 | rs1800497 | GA |
| CLOCK | rs1801260 | AG |
| CNR1 | rs1049353 | TT |
| LEPR | rs1805096 | GG |
| LEPR | rs1137101 | AG |
| TAS2R38 | rs713598 | GC |
| LEP | rs7799039 | GG |
| COMT | rs4680 | GA |
| FAAH | rs324420 | AC |
| TAS2R38 | rs1726866 | GA |
| LEPR | rs1137100 | AG |
| TCF7L2 | rs7903146 | TC |
| FTO | rs9939609 | TT |
| MC4R | rs17782313 | TT |
| MC4R | rs12970134 | GG |
| SLC2A2 | rs5400 | GG |
| FCER1G | rs5082 | AA |
| NPY | rs16139 | TT |
| POMC | rs1042571 | GG |

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

obesity, as individuals with the C allele may feel less satiated after eating [R, R, R, R].
**MC4R (rs12970134, G>A)**: The rs12970134 variant (G>A) near the *MC4R* gene has been linked to increased hunger and a reduced feeling of fullness. Individuals with the A allele may be more prone to overeating and weight gain due to a diminished satiety response, making appetite control more challenging [R].
**SLC2A2 (rs5400, Thr110Ile C>T)**: SLC2A2 plays a role in glucose transport and blood sugar regulation. The rs5400 variant (Thr110Ile C>T) can influence carbohydrate cravings and eating patterns, with certain alleles associated with a preference for high-carb foods.

**HADH (rs1042571, C>T)**: The *HADH* gene encodes hydroxyacyl-CoA dehydrogenase, an enzyme involved in fatty acid metabolism and energy regulation. The rs1042571 variant (C>T) has been associated with differences in metabolic efficiency and energy utilization.

**NPY (rs16147, A>G)**: The *NPY* gene encodes the neuropeptide Y, which is involved in regulating stress response, appetite, and arousal. The rs16147 variant (A>G) has been associated with differences in appetite control and stress-induced eating behaviors. Individuals with the G allele may be more prone to overeating, especially in response to stress [R].

**CNR1 (rs1049353, C>T)**: The *CNR1* gene encodes the cannabinoid receptor 1, which is involved in the endocannabinoid system that regulates appetite, mood, and reward pathways. Individuals with the T allele of rs1049353 may have an increased tendency to cravings and overeating, particularly for high-calorie or "comfort" foods, due to heightened activity in the brain's reward centers.

**COMT (rs4680, Val158Met G>A)**: The *COMT* gene encodes an enzyme that breaks down dopamine in the brain, affecting mood, reward sensitivity, and impulse control. The rs4680 variant (Val158Met G>A) influences dopamine levels, with the A allele (Met) associated with slower dopamine breakdown.. Individuals with the A allele may have heightened sensitivity to rewards, which can increase susceptibility to cravings and overeating.

**ADRB3 (rs1805096, Trp64Arg T>C)**: The *ADRB3* gene encodes the beta-3 adrenergic receptor, which is involved in regulating fat breakdown and energy expenditure. The rs1805096 variant (Trp64Arg T>C) has been associated with reduced receptor function, leading to decreased fat metabolism and an increased risk of weight gain.

# HLA-DQ (Gluten)

Different alleles in these genes can produce different types of HLA-DQ structures. The **DQ2** type (especially the DQ2.5 subtype) is present in up to 98% of celiac disease patients, depending on the population. That is among the strongest known links to autoimmunity in the entire HLA system [R, R].

Two alleles — DQA1*0501 and DQB1*0201 — form the DQ2.5 haplotype, which codes for the DQ2.5 receptor on white blood cells. The DQ2.5 receptor binds gluten and presents it to T-helper cells, initiating widespread gut inflammation [R, R].

The ‘T’ variant of rs2187668 serves as a genetic marker — it tags the DQ2.5 haplotype with high precision. In other words, the vast majority of people with this allele will have this haplotype. A study of over 27,000 subjects identified this SNP as the primary genetic factor for celiac disease. People carrying the ‘T’ allele had over six times higher chances of being diagnosed with celiac disease. A smaller trial of 889 participants came to a similar conclusion [R, R].

The 'C' variant of rs74541084 tags the DQ8 haplotype, an additional marker for gluten sensitivity in people who don't carry DQ2.5.

**Please note: this report only analyzes the HLA-DQ gene. Variants in many other genes have shown associations with gluten sensitivity.**

TYPICAL GENETICS

## Likely typical HLA-DQ genetics based on the genetic variants we looked at

**75%**

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **75% of our users.**

## Your top variants that most likely impact your genetic predisposition:

| GENE | SNP | GENOTYPE |
|---|---|---|
| HLA-DQB1 | rs2858331 | AA |
| HLA-DQA1 | rs2187668 | CC |
| HLA-DQA2 | rs7454108 | TT |

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

# Carbohydrate Metabolism

**For much of our history, we were all nomadic hunter-gatherers**. We ate what we could find: roots, plants, berries, nuts, fish, and meat. This varied by location, climate, and season. At this point in time, the way the body processed and responded to complex carbs wasn't very relevant [R, R].

**About 12,000 years ago, farming changed that.** Suddenly, there were more starchy foods such as grains in our diets. More carbs meant more readily available energy. But this also meant more blood sugar spikes and a higher risk of metabolic disorders. Luckily, variants in genes like *TCF7L2* allowed us to process these new food sources in a more productive, less harmful way [R].

**The *TCF7L2* gene affects insulin release after eating foods like grains.** It is one of the genes most strongly associated with **diabetes.** Depending on which variant of this gene you carry, your body may respond differently to carbs [R].

The "farmer" variant (rs7903146-C) is linked to a better response to carbs. **In people with this variant, carbs don't tend to spike blood sugar.** The "hunter-gatherer" variant (rs7903146-T) is linked to a worse response to carbs [R, R, R].

Other variants also shape our genetic predisposition to carbohydrate metabolism. They include:

- ***PPARG* rs1801282-G**: linked to better metabolism and longevity markers on a low-carb diet [R, R, R]
- ***FTO* rs9939609-A**: linked to obesity, especially on a high-carb diet [R, R]
- ***IRS1* rs2943641-C**: linked to better carb metabolism (mixed evidence) [R, R, R]
- ***CETP* rs5883-T and rs3764261-C**: linked to lower obesity rates and better metabolic profiles on a low-carb/high-fat diet [R, R]

Additional variants that may have a smaller or indirect impact on carb metabolism include:

- **ADIPOQ -11391 G>A** (rs17300539): Associated with alterations in adiponectin levels, which can influence glucose and carbohydrate metabolism.
- **ADRB2 Gln27Glu C>G** (rs1042714): Linked to differences in β2-adrenergic receptor function, which may affect glucose uptake and metabolism.
- **DRD2 C>T** (rs1800497): Linked to dopamine receptor function, which may influence eating behaviors (sugar and carb cravings) and glucose regulation.
- **TAS1R2 Ile191Val G>A** (rs35874116)**:** Impacts the sweet taste receptor, potentially influencing sugar intake and carbohydrate metabolism.
- **SLC2A2 Thr110Ile C>T** (rs5400): Affects glucose transporter 2 (GLUT2), which is key in glucose sensing and carbohydrate metabolism (linked to higher sugar intake but better metabolism!)

TYPICAL

**Predisposed to typical carbohydrate metabolism based on 16 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| TCF7L2 | rs7903146 | TC |
| AMY2B | rs4244372 | TA |
| IRS1 | rs2943641 | TC |
| TAS1R2 | rs35874116 | TT |
| SLC2A2 | rs5400 | GG |
| FTO | rs1121980 | GG |
| ADRB2 | rs1042714 | CG |
| ANKK1 | rs1800497 | GA |
| LEPR | rs1137101 | AG |
| FTO | rs9939609 | TT |
| PPARG | rs1801282 | CC |
| CETP | rs5883 | CC |
| NLRC5 | rs3764261 | AA |
| FABP2 | rs1799883 | CC |
| ADRB3 | rs4994 | AA |
| PPARG | rs3856806 | CC |
| RFC4 | rs17300539 | GG |

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

# Saturated Fat

Some people may tolerate more saturated fat than others. This difference may be genetic. If they eat a lot of saturated fats, people who are sensitive to saturated fat may have a higher risk of [R, R, R]:

- Elevated cholesterol
- Weight gain
- Reduced bone strength

TYPICAL RESPONSE

**Predisposed to typical saturated fat response based on 42 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| TLR4 | rs5030728 | GG |
| PPARA | rs135549 | TT |
| APOA1 | rs670 | CC |
| ABCA1 | rs2230806 | CC |
| TCF7L2 | rs7903146 | TC |
| SIDT2 | rs5070 | GG |
| FTO | rs1121980 | GG |
| SIDT2 | rs2854117 | CC |
| APOE | rs429358 | TT |
| ADAM10 | rs2070895 | GG |
| STAT6 | rs1799986 | CT |
| CETP | rs5882 | GA |
| APOB | rs693 | AG |
| FTO | rs1558902 | TT |
| FTO | rs1421085 | TT |
| FTO | rs17817449 | TT |
| STAT3 | rs2293152 | CG |
| LPL | rs13702 | CT |
| AHSG | rs4917 | CT |
| CD36 | rs1984112 | GA |
| CLOCK | rs1801260 | AG |
| CLOCK | rs4580704 | CC |
| PKDREJ | rs4253778 | CG |
| PEX11A | rs894160 | CT |
| FCER1G | rs5082 | AA |
| PPARG | rs1801282 | CC |
| PCSK7 | rs662799 | AA |
| FTO | rs9939609 | TT |
| AGT | rs699 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| ACE | rs4343 | AA |
| APOC1 | rs405509 | GG |
| ADAM10 | rs1800588 | CC |
| PPARA | rs1800206 | CC |
| MED24 | rs1568400 | TT |
| PPARG | rs10865710 | GG |
| SIDT2 | rs964184 | CC |
| STAT3 | rs8069645 | AA |
| STAT3 | rs744166 | AA |
| APOE | rs7412 | CC |
| PPARG | rs3856806 | CC |
| LPL | rs328 | CC |
| MC4R | rs12970134 | GG |
| LPL | rs1121923 | GG |
| STAT3 | rs1053005 | TT |

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

# Vitamin B12

**Key Takeaways:**

- Vitamin B12 is important for making energy and red blood cells, building DNA, and nerve function.
- It is most easily obtained via animal products like meat, eggs, dairy, and fortified foods.
- If you have an increased need or you tested as deficient, you may want to examine your current diet. You should talk to your doctor before taking B12 supplements.
- Click the **next steps** tab for relevant labs.

People more prone to low levels of vitamin B12 include [R]:

- Vegetarians and vegans
- Older adults
- People with gut disorders (e.g., Crohn's disease, celiac disease)

A hallmark of vitamin B12 deficiency is a lack of healthy red blood cells (anemia). Anemia can cause symptoms like weakness and fatigue. A sign of long-term vitamin B12 deficiency is nerve damage [R, R, R, R].

Vitamin B12 deficiency can be detected with a blood test. After it is diagnosed, you may need to work with your doctor to figure out the cause. Your doctor may recommend oral supplements or injections of vitamin B12 to help correct the deficiency [R, R].

**If you are not deficient, it is best to get vitamin B12 from food. Talk to your doctor before taking vitamin B12 supplements** [R].

TYPICAL NEED

**Likely typical need for vitamin B12 based on 1,018,082 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| TCN2 | rs1801198 | GG |
| FUT2 | rs1047781 | AA |
| FUT2 | rs602662 | GA |
| CUBN | rs11254363 | GG |
| ADGRE1 | rs62123070 | CC |
| FUT2 | rs601338 | GA |
| MTRR | rs1801394 | GA |
| ABCD4 | rs4148077 | CC |
| TCN1 | rs526934 | AG |
| FUT5 | rs3760775 | GT |
| FUT3 | rs708686 | CT |
| FUT2 | rs516246 | CT |
| CBS | rs234706 | GA |
| MMAB | rs7134594 | CT |
| CUBN | rs1801222 | GG |
| TCN1 | rs34324219 | CC |
| RGS7 | rs7544372 | TT |
| / | rs1990193 | AA |
| / | rs1513859 | AA |
| FAM240C | rs12478296 | CC |
| SLC25A2 | rs3749779 | AA |
| FOXK1 | rs314590 | AA |
| CFAP299 | rs1385890 | AA |
| LAMA4 | rs76190642 | GG |
| CHODL | rs34988353 | AA |
| ARAP2 | rs142554771 | TT |
| LAMA4 | rs144505878 | GG |
| C1QL3 | rs79770840 | GG |
| RGS18 | rs114973754 | CC |

| GENE | SNP | GENOTYPE |
|---|---|---|
| ADGRL3 | rs545255284 | TT |
| C16ORF82 | rs139645308 | CC |
| POU3F3 | rs188141458 | GG |
| KCNK2 | rs72761546 | TT |
| KCNK2 | rs189754522 | AA |
| PCSK2 | rs141477158 | GG |
| TMEM179 | rs79885401 | CC |
| LRRC6 | rs117429467 | AA |
| STT3B | rs188968123 | AA |
| SPATA18 | rs142766122 | CC |
| SRRM4 | rs73215576 | CC |
| MICA | rs556990455 | GG |
| CADM2 | rs188586547 | AA |
| CENPF | rs72759663 | GG |
| SMYD3 | rs148487271 | TT |
| HSPB7 | rs144839376 | AA |
| AKAIN1 | rs7239302 | CC |
| ST8SIA6 | rs188363440 | AA |
| DACT1 | rs118119041 | GG |
| MMUT | rs9473555 | GG |
| TCN2 | rs9606756 | AA |

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

# Biotin

A crucial gene affecting biotin levels is *BTD*. It helps make an enzyme called *biotinidase*. This enzyme helps release biotin from dietary protein and 'recycle' it from proteins in our body [R].

One *BTD* variant, **rs13078881-C**, may reduce enzyme activity by up to 50%. People with this variant might need more dietary biotin to compensate [R].

**Important:** this variant may be detrimental only when combined with other rare variants, such as **rs71627145-G** and **rs34885143-A**. People carrying single copies of these variants may have higher biotin needs, but they are **not likely to have biotinidase deficiency** [R].

Please also note that other factors, especially your diet, can greatly affect your biotin needs.

TYPICAL NEED

**Likely typical need for biotin based on 3 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| BTD | rs34885143 | GG |
| BTD | rs13078881 | GG |
| ANKRD28 | rs71627145 | AA |

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 |
|---|---|---|
| BCAT1 | rs7961152 | AA |
| SGK1 | rs9389154 | GG |
| POC1B | rs2681472 | AG |
| NR2F2 | rs2398162 | GA |
| ACE2 | rs184874220 | T |
| PRKG1 | rs7905063 | TC |
| PRKG1 | rs7897633 | AC |
| SLC4A5 | rs7571842 | GA |
| SCNN1A | rs4764586 | AA |
| SCNN1G | rs4299163 | GG |
| GC | rs4254735 | TT |
| CLGN | rs2567241 | CC |
| RAD52 | rs2301880 | TC |
| FGF5 | rs16998073 | TA |
| WNK1 | rs12828016 | TG |
| CSTF2T | rs12414562 | GA |
| HYAL1 | rs10510755 | TC |
| ADRB2 | rs1042714 | CG |
| SCNN1G | rs7404408 | TC |
| SCNN1G | rs5735 | CT |
| SCNN1G | rs4073930 | CT |
| SCNN1G | rs4073291 | CA |
| RENBP | rs78377269 | G |
| ACE2 | rs714205 | C |
| AGT | rs699 | GG |
| ACE | rs4343 | AA |
| SLC24A3 | rs3790261 | AA |
| ACE2 | rs2285666 | C |
| GSKIP | rs11847625 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| SGK1 | rs9376026 | CC |
| RAD52 | rs880054 | CT |
| CPA3 | rs75367686 | AA |
| SLC8A1 | rs434082 | CC |
| SLC8A1 | rs11893826 | GG |
| CSTF2T | rs10997916 | GG |
| SLC4A5 | rs10177833 | AA |
| SLC4A4 | rs10022637 | TT |
| KL | rs9536314 | TT |
| SCNN1G | rs4499238 | CC |
| SCNN1A | rs3741914 | CC |
| TNFRSF1A | rs11614164 | AA |

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

# Potassium

**Key Takeaways:**

- Up to **60%** of differences in people's potassium levels may be due to genetics.
- Other risk factors for potassium deficiency include poor diet, dehydration, magnesium deficiency, and certain medications and health conditions.
- The rate of potassium deficiency in the U.S. has risen from **4% to 11%** in the past two decades.
- If you are at high genetic risk, you may lower overall risk by taking action on factors that you can change.
- Click the **next steps** tab for relevant labs.

Up to **60%** of differences in people's potassium levels may be due to genetics. Involved genes may play a role in [R, R, R]:

- Potassium transport
- Electrolyte balance
- Kidney function

**Keep in mind that your diet and the environment may also influence your potassium levels. A blood test is the only reliable way to determine your potassium levels.**

TYPICAL NEED

**Likely typical need for potassium based on 152,421 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| RGS7 | rs183294212 | CC |
| LURAP1 | rs111512785 | AA |
| PRG4 | rs141261421 | GG |
| NVL | rs78473436 | AA |
| HMCN1 | rs138057810 | AA |
| CASQ2 | rs117999962 | GG |
| FMO2 | rs184768578 | AA |
| SSBP3 | rs182561930 | CC |
| PTPRC | rs141793725 | TT |
| ETV3 | rs75349367 | GG |
| OLFM3 | rs140864890 | AA |
| GALNT2 | rs80258856 | CC |
| BEND5 | rs139642127 | GG |
| FYB2 | rs143507390 | GG |
| SSBP3 | rs117932658 | TT |
| RRAGC | rs144130357 | CC |
| DMBX1 | rs78451089 | GG |
| / | rs80302144 | CC |
| / | rs7548119 | GG |
| RGS13 | rs12071444 | GG |
| HMCN1 | rs61829629 | GG |
| PLPP3 | rs139123937 | GG |
| PLPP3 | rs12075340 | AA |
| ATP1A1 | rs10924092 | GG |
| KCNT2 | rs77824746 | GG |
| SEC16B | rs75022918 | TT |
| LY9 | rs73017956 | GG |
| KCNT2 | rs76559586 | GG |
| KCNT2 | rs59729886 | CC |

| GENE | SNP | GENOTYPE |
|---|---|---|
| PRKAA2 | rs138876064 | GG |
| PLPP3 | rs146657061 | GG |
| PRKAA2 | rs184786990 | GG |
| RNF186 | rs7516526 | GG |
| CACHD1 | rs185466715 | AA |
| GNAI3 | rs76531483 | GG |
| C1ORF174 | rs74643023 | GG |
| MTARC1 | rs3849284 | GG |
| LRRC52 | rs17471444 | TT |
| C1ORF21 | rs139777178 | AA |
| LYPLAL1 | rs79278760 | GG |

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

# Magnesium

Some people may have higher magnesium levels than others. This may be partly due to genetics. Genes involved may influence:

- Magnesium transport in and out of cells [R, R, R, R]
- Magnesium metabolism [R, R]

Genetically higher magnesium levels may be causally associated with:

- Stroke [R]
- Bone health [R]
- Gout [R, R]
- Uric acid [R]
- Cataracts. [R]
- Mood Swings [R]
- Joint Inflammation [R]
- Atrial fibrillation [R]
- Heart Health [R]

TYPICAL NEED

**Likely typical need for magnesium based on 31 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| TRPM6 | rs11144134 | TT |
| MTMR7 | rs3764796 | TT |
| CSTA | rs1801725 | GG |
| FGFR2 | rs1219515 | GG |
| RTL1 | rs915364 | CC |
| PAPSS2 | rs1969821 | GG |
| VIPR1 | rs11718502 | TC |
| THBS3 | rs4072037 | CT |
| PAPSS2 | rs791888 | GG |
| RALGDS | rs7032317 | CT |
| CDKL2 | rs6838240 | CT |
| ALPK1 | rs2074379 | GA |
| C8ORF48 | rs10888073 | TC |
| CANT1 | rs11891 | GA |
| THBS3 | rs4971100 | GA |
| BORCS7 | rs3740393 | GC |
| CDKL2 | rs6852678 | TC |
| TRPM6 | rs113607577 | GG |
| HDHD2 | rs117060920 | GG |
| MPPED2 | rs3925584 | CC |
| SHROOM3 | rs13146355 | GG |
| SHROOM3 | rs9993810 | GA |
| MECOM | rs448378 | AG |
| TRPM6 | rs2274924 | TT |
| ASAP1 | rs72728275 | AA |
| CAMK1D | rs2648708 | CC |
| FGFR2 | rs3135758 | CC |
| CCDC136 | rs1472147 | TT |
| METTL21C | rs603894 | CC |

| GENE | SNP | GENOTYPE |
|---|---|---|
| PHACTR2 | rs2073214 | CC |
| DLK1 | rs4905994 | CC |
| OR5BS1P | rs193153567 | CC |
| PRMT7 | rs7197653 | GG |
| ATP2B1 | rs7965584 | AA |

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.

# Binge Eating

Binge eating can be associated with:

- Psychological issues: Low self-esteem, body dissatisfaction, and significant stress can trigger binge eating.
- Biological factors: Genetic mutations may affect hunger and satiety, through alterations in brain chemistry that can predispose individuals to eating disorders.
- Social and cultural factors: Dysfunctional family dynamics, professions and activities that focus on appearance and dieting, and traumatic situations such as bullying or abuse can increase the risk of BED.
- Dieting: Some people with binge eating disorder have a history of dieting or restrictive eating, which may trigger an urge to binge eat.

Treatment of binge eating disorder may involve:

- Psychotherapy: Cognitive-behavioral therapy (CBT) is considered effective for treating BED. It involves teaching individuals to regulate their eating patterns and to replace unhealthy thoughts and behaviors with healthier ones.
- Medications: Antidepressants, antiepileptic drugs, and certain stimulants such as lisdexamfetamine are sometimes prescribed to help control symptoms of binge eating.
- Nutritional counseling: Working with a nutritionist can help create healthier eating habits and mend one's relationship with food.
- Support groups: These can provide a network of support and an environment to share experiences and coping strategies.

Moreover, the following lifestyle interventions may help:

- Regular eating schedules: Eating regular meals and avoiding skipping meals can prevent extreme hunger that might trigger a binge.
- Mindfulness practices: Techniques such as mindful eating can help improve awareness of hunger cues and feelings of fullness.
- Stress management: Learning and implementing stress reduction techniques can help manage the emotional component often associated with binge eating.

LESS LIKELY

**Less likely to binge eat based on 13,449 genetic variants we looked at**

**7th**

PERCENTILE

Your risk is **greater than 7% of the population** and **lower than 93% of the population.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| NUP35 | rs1950038 | CT |
| CUBN | rs7904579 | GC |
| BCKDHB | rs17810023 | CC |
| MMADHC | rs182107583 | AA |
| RGPD4 | rs111940429 | CC |
| SYNDIG1 | rs76087671 | CC |
| SLC25A26 | rs145763646 | GG |
| FTO | rs9939609 | TT |
| / | rs73057489 | AA |
| MC4R | rs17782313 | TT |
| ARHGAP8 | rs726170 | CC |
| / | rs7337127 | CC |

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

# Fat Metabolism

Your genes may affect your response to different levels of fat in a diet. Some people do better on a high-fat diet, and others on a low-fat diet, in terms of weight control and cholesterol levels [R, R].

Some of the genes responsible may also influence [R, R, R]:

- Fat metabolism
- Sugar metabolism
- Inflammation

Talk to your doctor before making big changes to your diet. Keto and other high-fat diets may increase the risk of some nutrient deficiencies. They may also affect the body's response to medication [R].

BETTER

**Predisposed to better fat metabolism based on 53 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ADRB3 | rs4994 | AA |
| TCF7L2 | rs7903146 | TC |
| PPARA | rs135549 | TT |
| APOA1 | rs670 | CC |
| ABCA1 | rs2230806 | CC |
| MC4R | rs2229616 | CC |
| GIPR | rs2287019 | CC |
| ACSL5 | rs2419621 | CC |
| STAT3 | rs2293152 | CG |
| STAT6 | rs1799986 | CT |
| CETP | rs5882 | GA |
| MTTP | rs1800591 | GT |
| AHSG | rs4917 | CT |
| CD36 | rs1984112 | GA |
| CLOCK | rs1801260 | AG |
| PEX11A | rs894160 | CT |
| APOB | rs693 | AG |
| IRS1 | rs2943641 | TC |
| CLOCK | rs3749474 | TC |
| LPL | rs328 | CC |
| LPL | rs1121923 | GG |
| TLR4 | rs5030728 | GG |
| CLOCK | rs4580704 | CC |
| APOA4 | rs5110 | CC |
| SIDT2 | rs5070 | GG |
| FABP1 | rs2241883 | TT |
| UCP3 | rs1800849 | GG |
| TCF7L2 | rs12255372 | TG |
| LPL | rs13702 | CT |

| GENE | SNP | GENOTYPE |
|---|---|---|
| FCER1G | rs5082 | AA |
| PPARG | rs1801282 | CC |
| FTO | rs9939609 | TT |
| PCSK7 | rs662799 | AA |
| FABP2 | rs1799883 | CC |
| RFC4 | rs17300539 | GG |
| APOC1 | rs405509 | GG |
| SIDT2 | rs964184 | CC |
| STAT3 | rs8069645 | AA |
| STAT3 | rs744166 | AA |
| APOE | rs7412 | CC |
| CETP | rs708272 | AA |
| AGT | rs699 | GG |
| APOE | rs429358 | TT |
| PPARG | rs3856806 | CC |
| NSMAF | rs3808607 | TT |
| MICB | rs361525 | GG |
| ADAM10 | rs2070895 | GG |
| TNF | rs1800629 | GG |
| ADAM10 | rs1800588 | CC |
| PPARA | rs1800206 | CC |

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

# Phase I Detox

This section explores the genetic factors that influence your body's initial detoxification processes. Phase 1 detoxification involves enzymes that begin breaking down toxins, medications, and other foreign substances in your body, primarily in the liver.

Your genetic variations in key detoxification enzymes affect how efficiently your body processes everything from environmental toxins to common medications like acetaminophen. Understanding these genetic differences provides insights into your detoxification capacity and potential vulnerabilities to certain substances.

This analysis examines your unique genetic profile for Phase 1 detoxification pathways, helping you understand how your body handles toxin processing and what steps you can take to support optimal detoxification function based on your individual genetic makeup.

**Topics include:**

- CYP2D6
- CYP2C9
- CYP2B6
- Mold Sensitivity
- Acetaminophen Toxicity

TYPICAL METABOLIZER

## CYP2C9 (Detox)

Likely a typical metabolizer

TYPICAL

## Sensitivity to Foodborne Mold

Likely typical sensitivity to foodborne mold

TYPICAL ACTIVITY

## CYP2D6 (Mental Health, Detox)

Predisposed to a typical CYP2D6 activity

TYPICAL ACTIVITY

## CYP2B6 (Drug Metabolism)

Predisposed to a typical CYP2B6 activity

# CYP2C9 (Detox)

The CYP2C9 gene is highly polymorphic, with more than 50 known alleles affecting its metabolic activity compared to the wild-type CYP2C9*1 allele [R].

The two most common CYP2C9 gene polymorphisms decreasing enzyme activity are known as CYP2C9*2 and CYP2C9*3. Individuals with one copy of any of these alleles or two copies of the CYP2C9*2 allele are considered intermediate metabolizers, while those with one copy of each one or two copies of the CYP2C9*3 allele are considered poor metabolizers.

CYP2C9*2 ('T' at rs1799853) consists of the change of the amino acid arginine with the amino acid cysteine at position 144 while CYP2C9*3 ('C' at rs1057910) consists of the change of the amino acid isoleucine with the amino acid leucine at position 359. **THC metabolism is especially impaired in people with two copies of the CYP2C9*3 variant** [R, R].

The CYP2C9*5 allele ('G' at rs28371686) consists of the change of the amino acid aspartic acid with the amino acid glutamic acid at position 360 and is believed to decrease enzyme activity [R, R].

The CYP2C9*8 allele ('A' at rs7900194) consists of the change from an arginine to a histidine at position 150 and also encodes an enzyme with decreased activity. This variant is especially common in African Americans [R, R, R].

Finally, the CYP2C9*11 allele ('T' at rs28371685) consists of the change from an arginine to a tryptophan at position 335 and also encodes a protein with decreased enzyme activity [R, R].

TYPICAL METABOLIZER

**Likely a typical metabolizer based on 5 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CYP2C9 | rs1057910 | AA |
| CYP2C9 | rs7900194 | GG |
| CYP2C9 | rs28371686 | CC |
| CYP2C9 | rs28371685 | CC |
| CYP2C9 | rs1799853 | CC |

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

# Sensitivity To Foodborne Mold

Mycotoxins are the most dangerous aspect of foodborne mold. Exposure to higher amounts of these toxins can damage the organs and promote cancer growth [R, R, R].

The ability of our bodies to deal with mycotoxins partly depends on genetics. Involved genes play a role in [R, R, R, R, R]:

- Mycotoxin metabolism and detox (*CYP1A2*)
- DNA repair (*XPC*, *XRCC4*, *ATXN3*)
- Cancer protection (ADAMTS5)
- Mycotoxin transport (*SLCO1B1*)
- Glutathione function (*GSTA1*)

People with certain variants in these genes may be more prone to negative effects of mycotoxins, including [R, R, R, R, R]:

- Liver cancer
- Liver damage
- Kidney damage

**Remember that your other gene variants, diet, and environment also influence your sensitivity to foodborne mold.**

TYPICAL

**Likely typical sensitivity to foodborne mold based on 14 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| XPC | rs2228001 | GT |
| PRKDC | rs7003908 | CA |
| ADAMTS5 | rs2830581 | AG |
| GSTA1 | rs3957357 | AA |
| SLCO1B1 | rs4149056 | TC |
| XRCC3 | rs861539 | GG |
| XRCC4 | rs28383151 | GG |
| CYP1A2 | rs762551 | AA |
| XRCC4 | rs3734091 | GG |
| XRCC1 | rs25487 | CC |
| ERCC2 | rs13181 | TT |
| ATXN3 | rs8021276 | AA |
| SCAMP5 | rs2069526 | TT |
| LMAN1L | rs2069514 | GG |

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

# CYP2D6 (Mental Health, Detox)

**PLEASE NOTE:** This test did not evaluate for CYP2D6 copy number variations, such as gene deletions or duplications. CNVs are a primary factor influencing CYP2D6 enzyme activity and are essential for a complete assessment of metabolizer status. The results presented should be interpreted with this significant limitation in mind [R].

The *CYP2D6* gene has more than 100 known variants. These include [R, R]:

- Normal enzyme function variants (e.g., *1 and *2) [R, R]
- Reduced function variants (e.g., *9, *10, *17, and *41) [R, R]
- Non-functional variants (e.g., ▯3, ▯4, ▯5, ▯6, and *7) [R, R]

*CYP2D6*1* is the wild-type variant. The change from an 'A' to a 'G' at **rs16947** encodes *CYP2D6*2*. Although its activity is indistinguishable from that of CYP2D6*1, having several copies of this variant can result in an ultrafast phenotype. This variant has been associated with tyramine intolerance, suggesting a slightly lower metabolic efficiency for this substrate [R, R].

The 'T' allele of **rs3892097** corresponds to *CYP2D6*4*. This is the most frequent non-functional variant in Europeans and North Americans (18.0%), accounting for 70-90% of cases [R].

Another non-functional variant is *CYP2D6*6*, consisting of the deletion of an 'A' at **rs5030655**. This variant is generally rare, but may be slightly more common in Europeans (around 1%) [R, R, R].

Finally, the 'G' allele of **rs5030867** encodes the non-functional *CYP2D6*7* variant. This allele is very rare but may be slightly more common in South East Asians (around 1%) [R].

The 'A' allele of **rs1065852** encodes the intermediate-activity *CYP2D6*10* variant. This variant is especially common in Thai (50%) and East Asians (42%) [R, R].

Another intermediate-activity variant is *CYP2D6*17*, encoded by the 'A' allele of **rs28371706**. This variant is most common in Africans (20%-35%) [R, R].

Studies suggest that people with low CYP2D6 enzyme activity may be more prone to anxiety and less successful at socializing than extensive metabolizers. Reduced activity has also been associated with impulsivity or novelty seeking [R, R, R].

Alternatively, poor metabolizers may perform better in cognitive tasks that demand sustained attention or vigilance and spatial working memory. They may also have higher conscientiousness, responsibility, orderliness, and perseverance [R, R, R].

Low-activity variants have been associated with an increased risk of developing the following conditions:

- Alzheimer's disease [R]
- Parkinson's disease [R]
- Systemic sclerosis [R, R]
- Lupus [R]
- Ankylosing spondylitis [R]
- Pesticide toxicity [R]
- Adverse effects from antidepressants [R]

In contrast, they have been linked to a reduced risk of:

- Schizophrenia [R]
- Bulimia [R]

TYPICAL ACTIVITY

## Predisposed to a typical CYP2D6 activity based on 4 genetic variants we looked at

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CYP2D6 | rs5030867 | TT |
| CYP2D6 | rs5030655 | CC |
| CYP2D6 | rs3892097 | CC |
| CYP2D6 | rs28371706 | GG |
| CYP2D6 | rs1065852 | GG |
| CYP2D6 | rs16947 | AG |

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

- Heavy smoking [R]
- Adverse effects from codeine and tramadol [R]

# CYP2B6 (Drug Metabolism)

There are over 100 known *CYP2B6* polymorphisms, with numerous complex haplotypes and distinct ethnic frequencies, making *CYP2B6* one of the most polymorphic cytochrome p450 genes in humans [R].

The change from a ‘G’ to a ‘T’ at **rs3745274** encodes the *CYP2B6*6* variant, which has **markedly reduced enzyme activity**. This variant is very common (especially in Africans, Asians, and Hispanics), and has been associated with slower metabolism of multiple drugs such as methadone, efavirenz, bupropion, cyclophosphamide, sertraline, ketamine, and nicotine [R, R, R, R, R, R, R].

Another low-function variant is the rare ‘C’ allele of **rs28399499**, which encodes the *CYP2B6*18* variant. This variant has been associated with slower efavirenz and nevirapine metabolism, resulting in higher blood levels of these drugs [R, R].

*CYP2B6*1* is the wild-type variant. The change from a ‘C’ to a ‘T’ at **rs8192709** encodes the *CYP2B6*2* variant. Although considered a normal-function variant, carriers may have slightly slower efavirenz and prasugrel metabolism [R, R, R].

Another polymorphism considered a normal-function variant is the ‘T’ allele of **rs3211371** (*CYP2B6*5*). Research on its effects on methadone metabolism has produced mixed results. Moreover, this variant has been associated with an increased risk of gastrointestinal cancer and relapse after autologous hematopoietic cell transplantation for lymphoma [R, R, R, R, R].

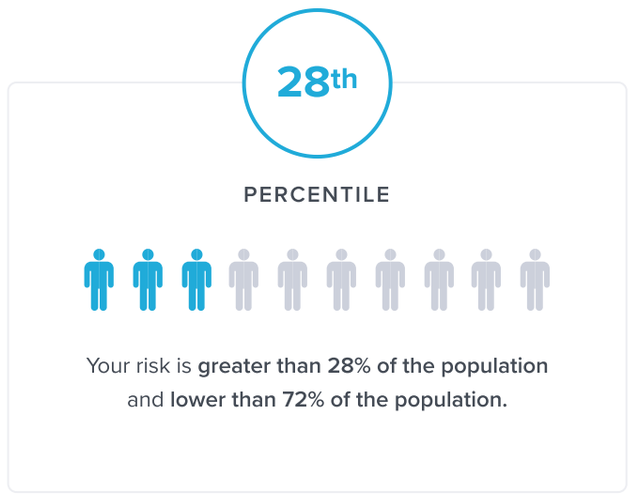
Finally, the ‘G’ allele of **rs2279343** encodes the *CYP2B6*4* variant. This polymorphism has been associated with slower metabolism of efavirenz. However, it has also been linked to faster metabolism of bupropion (and thus lower success rate of smoking cessation therapy with bupropion) and methadone [R, R, R, R].

The CYP2B6 gene affects how you metabolize ketamine via the liver. Between 10 and 20% of people have a variant that causes them to clear the drug from their system half as fast as others.

These "slow metabolizers" should be extra cautious about taking ketamine, since they're more likely to have a long or intense trip, according to some resources. They also have a higher risk for adverse reactions to the drug — such as drowsiness, unpleasant hallucinations, and confusion — especially if they inject it rather than taking it orally or nasally.

TYPICAL ACTIVITY

**Predisposed to a typical CYP2B6 activity based on 4 genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CYP2B6 | rs3745274 | GT |
| / | rs2279343 | AG |
| CYP2B6 | rs28399499 | TT |
| CYP2B6 | rs8192709 | CC |
| CYP2B6 | rs3211371 | CC |

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

# Skin Health

This section examines the genetic factors that influence your skin's aging process, elasticity, and susceptibility to various skin conditions. Understanding these genetic variations provides insights into how your skin responds to environmental factors, sun exposure, and the natural aging process.

Your genetic profile affects fundamental aspects of skin health, from collagen production and glycation processes to melanin formation and cellular repair mechanisms. This analysis explores your predisposition to skin aging, elasticity changes, and specific skin conditions based on your unique genetic makeup.

This comprehensive skin genetics assessment empowers you to make informed decisions about skincare routines, sun protection strategies, and lifestyle choices that support optimal skin health throughout your lifetime, tailored to your individual genetic predispositions.

**Topics include:**

- Skin Aging
- Skin Conditions

MORE LIKELY

## Melanoma

More likely to get melanoma

TYPICAL

## Glycation

Predisposed to typical glycation

TYPICAL LIKELIHOOD

## Basal Cell Carcinoma

Typical likelihood of basal cell carcinoma

TYPICAL ACTIVITY

## MC1R (Pigmentation & Skin Damage)

Likely typical MC1R activity

TYPICAL

## Facial Wrinkles

Predisposed to a typical amount of facial wrinkles

# Melanoma

Factors that may increase the risk of melanoma include [R]:

- High exposure to UV radiation: Exposure to UV radiation from the sun or tanning beds is the primary risk factor for melanoma.
- Fair skin: melanoma is most common in people with fair skin, hair, and eyes.
- History of sunburns: Severe, blistering sunburns, particularly in childhood, increase the risk.
- Multiple atypical moles:  Having a large number of moles or atypical (dysplastic) moles increases the risk.
- Weakened immune system: Individuals with weakened immune systems, such as those who have had organ transplants, are at higher risk.
- Living closer to the Earth's equator or at high elevation
- Family history

Treatment options vary depending on the stage and may include [R]:

- Surgery: The primary treatment for early-stage melanoma, which involves removing the tumor along with a margin of healthy tissue.
- Lymph node dissection: If the melanoma has spread to nearby lymph nodes, these may be surgically removed.
- Immunotherapy: Drugs like pembrolizumab (Keytruda) or nivolumab (Opdivo) boost the body's immune system to fight the cancer.
- Targeted therapy: For melanomas with specific genetic mutations, drugs that target those mutations (e.g., BRAF inhibitors like vemurafenib) can be effective.
- Radiation therapy: May be used in cases where surgery is not possible or if the melanoma has spread.
- Chemotherapy: Less commonly used for melanoma, but may be considered in certain advanced cases.

The prognosis for melanoma depends on the stage at diagnosis. Early-stage melanomas that are detected and treated before they spread have a very high cure rate. However, once melanoma has spread to other parts of the body, it becomes more challenging to treat. Advances in immunotherapy and targeted therapy have improved outcomes for many patients with advanced melanoma.

**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 melanoma based on 1,049,396 genetic variants we looked at**

92nd

PERCENTILE

Your risk is **greater than 92% of the population** and **lower than 8% of the population.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| SLC45A2 | rs35407 | GG |
| TERT | rs139996880 | AG |
| TYR | rs1393350 | AG |
| FLACC1 | rs13016963 | GA |
| MX2 | rs45430 | TC |
| CCND1 | rs498136 | AC |
| AGR2 | rs1636744 | CT |
| SOX4 | rs6914598 | CT |
| LINC02218 | rs187843643 | CC |
| ASIP | rs910873 | GG |
| SPATA2L | rs258322 | GG |
| ASIP | rs1885120 | GG |
| MC1R | rs1805007 | CC |
| ASIP | rs6059655 | GG |
| DBNDD1 | rs4785763 | CC |
| IRF4 | rs62389423 | GG |
| SLK | rs2995264 | AA |
| IRX3 | rs16953002 | GG |
| CTSS | rs7412746 | CC |
| / | rs10739221 | CC |
| CYP1B1 | rs6750047 | GG |

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

# Glycation

A genetic study identified five variants (SNPs) associated with skin autofluorescence in non-diabetic individuals. These SNPs are located in or near genes such as ***FANCA***, ***MMP27***, ***CYP1A1/2***, ***ZNF276***, and ***NAT2***, each with distinct potential roles in glycation mechanisms [R].

1. **rs12931267 (*FANCA*, Chr16)**: This SNP lies in an intronic region of the *FANCA* gene, which is involved in DNA repair. The G allele is associated with higher SAF. This locus also includes the ***MC1R*** gene, known for its role in skin pigmentation. This suggests a potential interplay between pigmentation and glycation levels.
2. **rs2846707 (*MMP27*, Chr11)**: Located in the *MMP27* gene, this SNP encodes a missense variant (Met30Val) affecting matrix metalloproteinase activity. The T allele correlates with lower SAF, suggesting a protective role potentially linked to extracellular matrix remodeling.
3. **rs2470893 (*CYP1A1/2*, Chr15)**: This SNP lies between *CYP1A1* and *CYP1A2*, genes involved in xenobiotic metabolism. The T allele is linked to higher SAF, with attenuation of the SNP effect when adjusted for **coffee consumption**, indicating environmental interactions.
4. **rs3764257 (*ZNF276*, Chr16)**: Found upstream of *FANCA*, this SNP is associated with lower *SAF*. *ZNF276* encodes a zinc finger protein that may influence gene regulation in response to glycation stress.
5. **rs576201050 (*NAT2*, Chr8)**: Located near *NAT2*, a gene encoding N-acetyltransferase, this SNP affects acetylator status (detox ability). The minor allele A is associated with lower SAF, highlighting its role in metabolic processing of AGEs.

Overall, the authors estimated about **20%** of the differences in glycation may be due to genetics. These findings demonstrate that SAF levels are influenced by complex genetic and environmental interactions [R].

TYPICAL

**Predisposed to typical glycation based on 5 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| NAT2 | rs576201050 | GG |
| ZNF276 | rs3764257 | CC |
| MMP27 | rs2846707 | TC |
| CSK | rs2470893 | TC |
| FANCA | rs12931267 | CC |

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

# Basal Cell Carcinoma

Unlike other forms of skin cancer, basal cell carcinoma rarely spreads (metastasizes) beyond the original tumor site. However, it can be disfiguring if not treated promptly and can cause considerable destruction and disfigurement by invading surrounding tissues.

It's important to monitor changes in the skin and seek medical advice if any suspicious growths or new lesions appear, especially in areas that receive a lot of sun exposure. Treatment options vary depending on the severity and can include surgical excision, topical medications, cryotherapy, laser therapy, or radiation, with the aim to remove or destroy the cancerous cells.

TYPICAL LIKELIHOOD

**Typical likelihood of basal cell carcinoma based on 33,751 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| SLC45A2 | rs16891982 | GG |
| RHOU | rs61824911 | GA |
| LPP | rs2049218 | TT |
| PADI6 | rs12122129 | AG |
| EDN2 | rs2781249 | CC |
| TYR | rs1126809 | AG |
| FOXP1 | rs35768603 | CT |
| BNC2 | rs10810657 | TA |
| CTLA4 | rs1427676 | CT |
| RNASET2 | rs4710154 | TA |
| KANK1 | rs1323262 | CG |
| IRF4 | rs62389423 | GG |
| FANCA | rs12931267 | CC |
| ASIP | rs56238684 | GG |
| KRT5 | rs11170164 | CC |
| ASIP | rs17401449 | AA |
| HLA-F | rs29243 | GG |
| NDRG3 | rs55804368 | CC |
| EXO1 | rs4149909 | AA |
| CTSS | rs41271951 | AA |
| NEK9 | rs7145468 | AA |
| OCA2 | rs1800407 | CC |
| NCR3 | rs61447909 | GG |
| HLA-DQB1 | rs9268847 | AA |
| / | rs2572140 | GG |
| SOX4 | rs55775505 | CC |
| TICAM1 | rs10425559 | AA |
| CTSH | rs2289702 | CC |
| CCDC88B | rs663743 | GG |

| GENE | SNP | GENOTYPE |
| --- | --- | --- |
| GRHL1 | rs6741117 | GG |

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

# MC1R (Pigmentation & Skin Damage)

A variant of *MC1R* has been associated with hair and skin color. Carriers of the minor 'T' allele of **rs1805007** are more likely to [R]:

- Have red or blonde hair
- Have lighter skin
- Get sunburns

Unsurprisingly, this variant has also been associated with skin cancer, including melanoma [R, R].

This variant likely reduces the production and activity of MC1R, leading to lower eumelanin and higher pheomelanin levels [R].

TYPICAL ACTIVITY

**Likely typical MC1R activity based on the genetic variants we looked at**

**86%**

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **86% of our users.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| MC1R | rs1805007 | CC |

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

# Facial Wrinkles

**Wrinkles are small but visible folds in the skin**. Wrinkles appear with age and develop over several decades. They are more evident in areas of the body that are usually exposed, such as the face, neck, forearms, and hands. **The most noticeable wrinkles are facial** [R, R, R].

Up to **55%** of differences in people's facial wrinkling may be due to genetics. Involved genes may influence **skin color and health** [R, R, R].

**UV radiation also contributes to facial wrinkling.** Excessive sunbathing or use of tanning beds exposes the skin to unhealthy levels of UV radiation and leads to premature aging. Hence, experts recommend wearing sunscreen [R, R, R].

**Make sure to find the right balance**. Sunlight or bright light during the day can benefit your body (by increasing vitamin D levels) and mind (by boosting mood) [R, R].

**The color of your skin also influences facial wrinkling.** Wrinkles appear more rapidly in people sensitive to UV radiation. Hence, white skin may wrinkle earlier than other skin types [R, R].

Others factors that may also contribute to facial wrinkling include [R, R, R]:

- Aging
- Smoking
- Very low weight
- Health conditions (e.g., depression)

TYPICAL

**Predisposed to a typical amount of facial wrinkles based on 20 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| SIK2 | rs11213999 | CC |
| TPGS2 | rs78569750 | GG |
| LRRC3B | rs116248825 | CC |
| NUDT12 | rs113322056 | AA |
| HACD4 | rs116873518 | GG |
| SYNDIG1 | rs184605088 | CC |
| NUDT12 | rs112608607 | TT |
| LINGO2 | rs117828793 | CC |
| BBX | rs1283106 | AC |
| BMP6 | rs1225927 | GT |
| / | rs11711327 | AG |
| BMP6 | rs382029 | AT |
| MON1B | rs62047859 | TT |
| DCSTAMP | rs147672305 | TT |
| GLIS1 | rs702491 | CC |
| RESF1 | rs1150997 | AA |
| CA3 | rs184880542 | GG |
| / | rs72811030 | GG |

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

# Fitness

This section explores the genetic factors that influence your athletic performance, recovery capacity, and injury susceptibility. Understanding these genetic variations provides insights into your body's natural strengths, optimal training approaches, and areas where you may need additional support or caution.

Your genetic profile affects key aspects of fitness including muscle fiber composition, cardiovascular endurance, recovery speed, and connective tissue integrity. This analysis examines how your genes influence your response to different types of exercise, your risk for specific injuries, and your body's ability to adapt to training stress.

This comprehensive fitness genetics assessment helps you optimize your training program, recovery strategies, and injury prevention approaches based on your unique genetic predispositions, enabling you to achieve better results while minimizing risk.

**Topics include:**

- Strength & Muscle
- Fatigue & Recovery
- Injuries

LOWER

## Muscle Mass

Predisposed to lower muscle mass

TYPICAL

## Muscle Recovery

Predisposed to typical muscle recovery

TYPICAL

## Strength

Predisposed to typical strength

TYPICAL ACTIVITY

## COL5A1 (Collagen)

Likely typical COL5A1 activity

TYPICAL LIKELIHOOD

## Achilles Tendon Injury

Typical likelihood of Achilles tendon injury

HIGHER

## Endurance

Predisposed to higher endurance

HIGHER ACTIVITY

## COL1A1 (Collagen)

Predisposed to higher COL1A1 activity

LESS LIKELY

## Tendon Injury

Less likely to have tendinopathy

# Muscle Mass

Muscle mass is the total amount of all the muscles in your body [R, R].

Your **physical activity and diet** have a great impact on your muscle mass. But some of it is also due to your genetics. Twin studies suggest **about 50-80% of people's differences in muscle mass are due to genes** [R, R, R].

Genes associated with muscle mass affect processes such as [R, R]:

- Muscle growth
- Growth and sex hormone levels
- Energy metabolism

Other factors that affect muscle mass include aging and certain health conditions [R, R, R].

To maintain and build your muscle mass:

- **Do regular resistance training,** such as weightlifting or bodyweight exercises (e.g. push-ups or squats). Aim for 2 or more sessions of strength training per week.
- **Get enough protein.** Make sure you get enough protein in your diet to support muscle growth and repair.
- **Be physically active.** Staying active throughout the day helps maintain muscle mass, beyond resistance training. Walking, cycling and other activities contribute to overall muscle health.
- **Get sufficient rest.** Muscles grow while you are resting. Getting enough sleep and recovery time between workouts supports muscle growth and repair.

LOWER

**Predisposed to lower muscle mass based on 7,086,143 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| IL1B | rs1143634 | GG |
| RPN1 | rs111804884 | TT |
| GJB2 | rs73442383 | TT |
| STEAP1B | rs10242595 | GA |
| MTCH2 | rs4752856 | GA |
| RASSF10 | rs543716802 | GG |
| LDB2 | rs573762110 | GG |
| NDUFA12 | rs529529785 | GG |
| PPARGC1A | rs752744147 | TT |
| AOAH | rs78185366 | TT |
| LEO1 | rs190878891 | AA |
| USP34 | rs183237934 | TT |
| MARCHF1 | rs150541056 | TT |
| CCDC171 | rs117635839 | AA |
| ZMAT4 | rs184622626 | AA |
| AQP6 | rs706798 | AA |
| FTO | rs9939609 | TT |
| ZNF648 | rs190210789 | AA |
| / | rs557373392 | CC |
| / | rs774160312 | GG |
| / | rs758954781 | CC |
| PRELID2 | rs574519712 | CC |
| / | rs758566456 | TT |
| DOCK3 | rs551736560 | GG |
| ATG7 | rs193172711 | GG |
| TSC22D1 | rs554766983 | GG |
| MYL12B | rs141372016 | GG |
| DRD5 | rs182591441 | TT |
| ACTR3B | rs138921315 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| LMX1B | rs144076261 | CC |
| DLG2 | rs558729974 | TT |
| KCNH7 | rs74698413 | GG |
| FTO | rs9972653 | GG |
| EPHA3 | rs72913870 | GG |
| METTL21A | rs111556242 | CC |
| ZDHHC14 | rs749547 | GG |
| SVBP | rs111455041 | CC |
| PRUNE2 | rs11145045 | CC |

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

# Muscle Recovery

Muscle recovery is when the **body repairs the muscle fibers damaged or strained during exercise.** It is during this time that muscles grow and become stronger.

The exact **genetic influences** on muscle recovery are still being researched. Several genes play a role in this process (e.g. ACTN3, CKM, IL6), through their effects on muscle growth, muscle repair and inflammation [R, R].

Other factors that affect muscle recovery, include [R, R]:

- Intensity and type of exercise
- Nutrition and hydration
- Sleep quality
- Stress
- Aging

Popular methods to aid muscle recovery include [R, R, R, R]:

- Light stretching
- Massage
- Applying heat or cold to the muscle
- Compression

Adequate nutrition and hydration are important for muscle health. Our bodies need enough protein to repair and build new muscle, and enough carbs to restore depleted energy stores [R, R, R].

Interestingly, drinking cherry juice several days before exercise may help improve muscle recovery [R].

TYPICAL

**Predisposed to typical muscle recovery based on 15 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ACTN3 | rs1815739 | CT |
| CCR2 | rs1799865 | TT |
| IGF2 | rs2230949 | GG |
| SLC30A8 | rs13266634 | CC |
| IGF2 | rs680 | TC |
| IGF2 | rs3213221 | CG |
| COL2A1 | rs2070739 | TC |
| COL5A1 | rs12722 | TC |
| TRIM63 | rs2275950 | TC |
| SOD2 | rs4880 | GG |
| CCR2 | rs3918358 | AA |
| CCL2 | rs3917878 | CC |
| TNF | rs1800629 | GG |
| IGF2 | rs7924316 | GG |
| IGF2 | rs4244808 | GG |

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

# Strength

**Strength is the maximum force applied in one movement (e.g., in a single weight lift)** [R].

Some people are stronger than others. Up to **85% of people's differences in muscle strength may be due to genetics**. Genes associated with strength affect [R, R, R, R, R, R]:

- Muscle composition (fast-twitch vs. slow-twitch muscle fibers)
- Muscle repair and regeneration
- Hormones and growth factors
- Energy metabolism

However, other factors, such as **fitness, diet and age**, also strongly affect your muscle power [R, R].

Strength training is important not just for your muscles, but also for your bones, cognition, and your overall health. Muscle strength is a predictor of healthy aging and longevity [R, R].

Some tips that may help you build stronger muscles include [R]:

- Resistance training. You can train with weights or do bodyweight exercises (e.g., pushups, planks). Aim for 2 or more sessions of strength training per week.
- Using a weight or resistance level that is heavy enough to tire your muscles after 12-15 repetitions. As your strength bulbs over time, you should be able to slowly increase the weight you are lifting.
- Eating a protein-rich diet to support muscle growth and repair
- Allowing plenty of rest for each muscle group to maximize strength gains.

TYPICAL

**Predisposed to typical strength based on 7,133,253 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| MTHFR | rs1801131 | TT |
| SLC16A1 | rs1049434 | TT |
| LRPPRC | rs10186876 | GG |
| PPARG | rs1801282 | CC |
| LEMD2 | rs12055409 | GG |
| IL11RA | rs41274853 | GG |
| BDNF | rs10501089 | CC |
| HIF1A | rs11549465 | CC |
| FTO | rs9939609 | TT |
| VEGFA | rs2010963 | GG |
| GABPB1 | rs7181866 | AA |
| / | rs9320823 | TC |
| PITX3 | rs2273555 | AG |
| IGF2 | rs680 | TC |
| ACTN3 | rs1815739 | CT |
| ADRB2 | rs1042713 | AG |
| ADRB2 | rs1042714 | CG |
| BDKRB2 | rs1799722 | TC |
| AGT | rs699 | GG |
| TBC1D7 | rs6905419 | CC |
| ZNF608 | rs4626333 | CC |
| ACVR1B | rs2854464 | AA |
| AMPD1 | rs17602729 | GG |
| TRHR | rs16892496 | AA |

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

# COL5A1 (Collagen)

Variants resulting in reduced type V collagen may increase the risk of injuries. This may be because carriers of these variants may have weaker ligaments, tendons, and muscles. One of such variants is **rs12722**. Its minor 'T' allele has been associated with an increased risk of:

- Achilles tendon injury [R, R]
- Anterior cruciate ligament injury [R, R]
- Tennis elbow [R, R]
- Carpal tunnel syndrome [R]
- Muscle cramps [R]

People with the 'TT' genotype may also have more severe (but not more frequent) muscle injuries. Probably due to the association of this variant with soft tissue injuries, carriers may have lower odds of elite rugby status [R, R].

On the bright side, this genotype has also been associated with improved endurance performance in runners. Moreover, the 'T' variant may reduce the risk of rotator cuff injury [R, R].

TYPICAL ACTIVITY

**Likely typical COL5A1 activity based on the genetic variants we looked at**

**46%**

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **46% of our users.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| COL5A1 | rs12722 | TC |

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

# Achilles Tendon Injury

The **Achilles tendon** is a cord made of strong tissue. It is found in the lower back leg and connects the calf muscles to the heel bone. The Achilles tendon helps you move around. Some common injuries to this tendon include **tendonitis** (inflammation of the tendon, usually due to overuse or damage) and **rupture** (partial or complete tear of the tendon) [R, R, R].

Some people may be more prone to Achilles tendon injuries than others. Risk factors include [R, R, R, R, R]:

- A “weekend warrior” exercise pattern (i.e. taking part in physical activity intermittently)
- Age (the risk tends to increase between age 30 and 40)
- Male sex
- Taking part in activities that include a lot of running, jumping, or sudden changes in movement (e.g., soccer, basketball, and tennis)
- Wearing improper shoes
- Lack of a warmup or cooldown
- Some medications
- Obesity
- **Genetics**

In fact, about 50% of differences in people’s chances of developing an Achilles tendon injury may be attributed to genetics [R].

Tips to help prevent an Achilles tendon injury include [R, R]:

- Stretching and strengthening your calf muscles
- Alternating high-impact sports with low-impact ones (e.g., alternating running with walking)
- Avoiding running on hard, uneven, or slippery surfaces
- Using proper equipment (e.g., well-fitting, cushioned running shoes)
- Slowly increasing the intensity of the activity

TYPICAL LIKELIHOOD

**Typical likelihood of Achilles tendon injury based on 23 genetic variants we looked at**


**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| MMP1 | rs650108 | AA |
| COL1A1 | rs1800012 | AC |
| MMP1 | rs591058 | CC |
| CPNE1 | rs143383 | AA |
| VEGFA | rs699947 | AC |
| SOAT1 | rs113435565 | CA |
| FCN2 | rs1134170 | TT |
| COL5A1 | rs12722 | TC |
| MPP7 | rs6481512 | TT |
| MPP7 | rs1249269 | TT |
| MRPL43 | rs4919510 | CG |
| TNF | rs1800629 | GG |
| CEP295NL | rs4789932 | GG |
| TMEM158 | rs183364169 | CC |
| DPP6 | rs4067493 | CC |
| / | rs11960097 | TT |
| TRIML1 | rs60713544 | GG |
| ZNF648 | rs57104447 | TT |
| MPP7 | rs1937810 | TT |
| SOX21 | rs4454832 | GG |

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

# Endurance

**Endurance is the ability to produce low-intensity movements for a long period of time (e.g., cycling, running, swimming).** It is made up of **cardiorespiratory endurance** (the ability of the heart and lungs to deliver enough oxygen to muscles during prolonged activity) and **muscular endurance** (the ability of muscles to contract over an extended period of time without fatigue) [R, R, R].

Some people have greater endurance than others. **Up to 70% of people's differences in endurance may be due to genetics.** Genes associated with endurance affect [R, R, R, R, R, R, R, R]:

- Muscle composition and efficiency (slow-twitch vs. fast-twitch muscle fibers)
- The body's ability to use oxygen
- Heart function

Some tips that may help you build endurance include:

- Getting at least 150 min of cardio per week
- Doing the same exercise regularly and letting your body adapt to it over time
- Slowly increasing the amount and intensity of your workouts over time
- Switching between periods of high-intensity training and resting. This is called high-intensity interval training (HIIT).

Great news is that **endurance can actually improve as we age**! For example, peak endurance age for ultra-marathoners often occurs in the late 30s and 40s, potentially even the 50s [R, R, R, R].

HIGHER

**Predisposed to higher endurance based on 36 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| HFE | rs1799945 | CC |
| GABPB1 | rs7181866 | AA |
| GABPB1 | rs8031031 | CC |
| ACTN3 | rs1815739 | CT |
| SLC16A1 | rs1049434 | TT |
| TTN | rs10497520 | CC |
| KDR | rs1870377 | TT |
| PRDM1 | rs10499043 | CC |
| ADRB3 | rs4994 | AA |
| CHRNB3 | rs4950 | AA |
| GSTP1 | rs1695 | AA |
| HIF1A | rs11549465 | CC |
| TSHR | rs7144481 | TT |
| NFE2L2 | rs35652124 | TT |
| DES | rs7564856 | GA |
| SATB1 | rs4973706 | TC |
| PPARGC1A | rs8192678 | CT |
| GALNTL6 | rs558129 | GA |
| ADRB2 | rs1042713 | AG |
| ADRB2 | rs1042714 | CG |
| COL5A1 | rs12722 | TC |
| GNB3 | rs5443 | CT |
| BDKRB2 | rs1799722 | TC |
| RBFOX1 | rs7191721 | GA |
| CNDP2 | rs6566810 | TA |
| PKDREJ | rs4253778 | CG |
| AGTR2 | rs11091046 | C |
| CKM | rs8111989 | TC |
| DEF6 | rs2016520 | CT |

| GENE | SNP | GENOTYPE |
|---|---|---|
| PPARGC1A | rs7665116 | CT |
| PPARGC1A | rs2970869 | CT |
| NR1H3 | rs7120118 | TT |
| ACE | rs4343 | AA |
| GABPB1 | rs12594956 | AA |
| MYBPC3 | rs1052373 | CC |
| CYFIP1 | rs8029108 | AA |
| NFIA | rs1572312 | GG |
| TTC23 | rs1464430 | AA |
| KCNA4 | rs1323860 | GG |
| PPARA | rs1800206 | CC |
| PPARGC1A | rs3774923 | CC |
| HIF1A | rs2301113 | AA |

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

# COL1A1 (Collagen)

The most well-researched *COL1A1* polymorphism is **rs1800012**. Its minor 'A' allele promotes the expression of an alternative version of the protein with increased pro-α1 chain levels, potentially increasing its mechanical strength and stability [R].

This variant has been associated with a decreased risk of:

- Sports-related tendon and ligament injuries [R]
- Musculoskeletal soft tissue injuries [R]
- Cervical insufficiency [R]
- Pelvic organ prolapse [R]

In contrast, it may increase the risk of osteoporosis and bone fractures [R, R].

The 'A' allele may also affect athletic performance and has been found more commonly in competitive runners [R].

HIGHER ACTIVITY

**Predisposed to higher COL1A1 activity based on the genetic variants we looked at**

**33%**

OF USERS SHARE THE SAME SCORE

You have the same genetic predisposition as **33% of our users.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| COL1A1 | rs1800012 | AC |

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

# Tendon Injury

**Key Takeaways:**

- Up to **40%** of the differences in people's chances of developing tendinopathy may be due to genetics.
- Other risk factors include intense physical activity or certain sports, using improper training technique or equipment, doing repetitive tasks, age (over 40), being female, some chronic health conditions and medications.
- About 16 million tendon and ligament injuries occur in the U.S. each year.
- If you have a high genetic risk, you may lower your overall risk by taking action on those factors that you can change.

**Tendons** are cords made of strong tissue. They attach muscle to bone. There are many tendons throughout the body. Conditions in which tendons become inflamed and painful are called **tendinopathies** [R, R].

Risk factors for tendinopathies include [R, R, R, R]:

- Taking part in intense physical activity or certain sports (e.g., baseball, golf)
- Using improper training technique or equipment
- Doing repetitive tasks (e.g., gardening, painting, typing)
- Age (over 40)
- Gender (women may be at a higher risk)
- Some chronic health conditions (e.g., obesity, diabetes)
- Some medications
- **Genetics**

Up to **40%** of the differences in people's chances of developing tendinopathy may be due to genetics. Involved genes may influence tendon function [R, R, R, R, R].

Interestingly, one study that examined the impact of genetics on tendon injuries was conducted on elite athletes from FC Barcelona [R].

Tips to help prevent a tendon injury include [R, R]:

- Stretching and strengthening your muscles
- Alternating high-impact sports with low-impact ones (e.g., alternating running with walking)
- Avoiding running on hard, uneven, or slippery surfaces
- Using proper equipment (e.g., protective gloves, well-fitting shoes)
- Slowly increasing the intensity of the activity

LESS LIKELY

**Less likely to have tendinopathy based on 6 genetic variants we looked at**


**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| POLE2 | rs3218791 | TG |
| / | rs11232681 | AG |
| GJA1 | rs11154027 | CC |
| KLHL1 | rs59988404 | GG |
| TRIML1 | rs60713544 | GG |
| CERS5 | rs57224706 | AA |

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

# Brain Health

This section examines the genetic factors that influence cognitive function, mental health, and neurological well-being. Understanding these genetic variations provides insights into your brain's unique characteristics, including cognitive strengths, potential vulnerabilities, and responses to various substances and conditions.

Your genetic profile affects critical aspects of brain health from neurotransmitter function and cognitive processing to susceptibility to neurological conditions and mental health disorders. This analysis explores how your genes influence attention, memory, cognitive decline risk, and your brain's response to different compounds and stressors.

This comprehensive brain health genetics assessment empowers you to make informed decisions about cognitive enhancement strategies, mental health support, and lifestyle choices that promote optimal brain function throughout your lifetime, tailored to your individual genetic predispositions.

**Topics include:**

- Mental Effects of THC
- ADHD
- Cognition
- Cognitive Impairment and Decline
- Anxiety

WORSE

## GAD1 (Glutamate/GABA)

Likely worse GAD1 genetics

MORE LIKELY

## THC and Psychosis

More likely to experience psychotic symptoms from cannabis use

INCREASED

## Psychedelic Effects of THC (Functional)

Predisposed to increased psychedelic effects of THC

TYPICAL LIKELIHOOD

## Anxiety

Typical likelihood of anxiety

TYPICAL

## Cognitive Function

Predisposed to typical cognition

TYPICAL

## Attention

Typical likelihood of ADHD

TYPICAL

## Memory Performance

Predisposed to typical memory performance

TYPICAL LIKELIHOOD

## Alzheimer's Disease

Typical likelihood of Alzheimer's disease

E3/E3

## APOE

You carry two APOE ε3 variants

LESS LIKELY

## Cognitive Decline

Less likely to have cognitive decline

# GAD1 (Glutamate/GABA)

The most well-researched *GAD1* polymorphism is rs3749034. Its major 'G' allele has been shown to reduce GAD1 activity, resulting in lower GABA levels in the brain. In addition, this variant has been associated with an increased risk of [R]:

- Schizophrenia [R, R, R]
- Hyperactive and impulsive symptoms in ADHD [R]

However, this variant has also been linked to lower odds of bipolar disorder and fewer respiratory symptoms in people with panic disorder [R, R].

Another variant associated with schizophrenia is the minor 'A' allele at rs1978340. Surprisingly, this variant has been shown to reduce GABA levels. The fact that GABA acts as an inhibitory neurotransmitter in the mature brain but has the opposite activity during brain development may explain the complex effects of GABA levels on conditions such as schizophrenia and ADHD [R, R, R, R].

This variant has also been linked to:

- Cocaine dependence [R]
- Panic disorder and respiratory symptoms in this condition [R, R]
- Earlier onset of alcohol dependence [R]

However, this allele was associated with a reduced risk of heroin addiction [R].

WORSE

**Likely worse GAD1 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 |
|---|---|---|
| GAD1 | rs3749034 | GG |
| GAD1 | rs1978340 | AG |

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

# THC And Psychosis

Certain genetic variants may affect the risk and severity of THC-related psychosis. Carriers of several risk variants may want to consider avoiding cannabis use.

The *CNR1* gene encodes the type-1 cannabinoid receptor (CB1), whose activation improves mood and anxiety. The most studied SNP in this gene is rs1049353 or 1359G/A. Its minor 'T' allele doesn't change the CB1 receptor structure but is believed to impair gene expression and receptor activity. This variant has been linked to worse psychotic symptoms in cannabis smokers and greater size reduction in a region of the brain (the caudate nucleus) after the first episode [R, R].

Another *CNR1* variant, 'T' at rs12720071, has been associated with psychotic symptoms in cannabis users. However, the 'C' variant has been linked to greater white matter reduction in the brain from marijuana misuse [R, R].

The *FAAH* gene helps create an enzyme that breaks down certain compounds in the body, including endocannabinoids. The 'G' allele of rs2295633, associated with increased FAAH activity, has been linked to reduced odds of requiring treatment with antipsychotics in cannabis users [R, R].

The *COMT* gene encodes an enzyme that helps break down neurotransmitters such as dopamine, norepinephrine, and epinephrine. The major 'G' variant of its main polymorphism rs4680 has been associated with increased risk, earlier onset, and worse symptoms of psychosis and schizophrenia from cannabis use [R, R, R, R, R, R, R].

The *DRD2* gene helps make dopamine D2 receptors. Those are proteins on the surface of brain cells that bind dopamine. The minor 'A' allele of rs1076560 has been associated with increased DRD2 signaling and a 3- to 5-fold higher risk of psychosis in cannabis users [R, R].

Finally, the *AKT1* gene encodes an enzyme involved in many cellular processes, whose dysregulation may promote schizophrenia. The 'C' allele of rs2494732 has been associated with a 7-fold higher risk of psychosis in daily cannabis smokers [R, R].

MORE LIKELY

**More likely to experience psychotic symptoms from cannabis use based on 6 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CNR1 | rs1049353 | TT |
| FAAH | rs2295633 | AA |
| CNR1 | rs12720071 | TT |
| COMT | rs4680 | GA |
| TTC12 | rs1076560 | CA |
| AKT1 | rs2494732 | TT |

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

# Psychedelic Effects Of THC (Functional)

The genetic predisposition to THC's psychedelic effects is shaped by variations in specific genes involved in the endocannabinoid system and neurotransmitter regulation.

Among these, the ***CNR1*** gene (**rs1049353, rs12720071**) plays a critical role. This gene encodes cannabinoid receptor CB1. Variants in this gene influence receptor functionality and density, which modulate how THC interacts with the endocannabinoid system to produce psychedelic effects [R, R].

Additionally, the ***AKT1*** gene (particularly the SNP **rs2494732**) is linked to an increased risk of experiencing psychosis-like effects from THC. AKT1 is involved in dopamine signaling pathways, which THC impacts, potentially enhancing susceptibility to altered perceptions [R].

Another key gene is ***DRD2***, associated with the dopamine D2 receptor. The SNP **rs1076560** is linked to altered dopamine receptor activity, potentially influencing THC-induced euphoria and cognitive effects. Variants in this gene may also affect the likelihood of experiencing addiction or dependency on cannabis [R].

The ***FAAH*** gene, represented by SNP **rs324420**, is responsible for the breakdown of anandamide, a natural cannabinoid. Reduced FAAH activity leads to increased levels of anandamide, which may enhance THC's effects [R, R].

Finally, ***COMT*** is responsible for the breakdown of neurotransmitters such as dopamine, epinephrine, and norepinephrine in the brain. Its **rs4680** SNP may increase the risk of psychosis in cannabis users [R, R, R, R, R, R, R].

Understanding these genetic markers can provide valuable insights into personalized cannabis use, highlighting who might benefit from THC's therapeutic potential and who might be at risk for adverse effects.

INCREASED

**Predisposed to increased psychedelic effects of THC based on 7 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CNR1 | rs1049353 | TT |
| FAAH | rs2295633 | AA |
| COMT | rs4680 | GA |
| TTC12 | rs1076560 | CA |
| CNR1 | rs12720071 | TT |
| FAAH | rs324420 | AC |
| AKT1 | rs2494732 | TT |

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

# Anxiety

**Key Takeaways:**

- Up to **65%** of the differences in people's risk of getting anxiety may be due to genetics.
- Other risk factors include traumatic and stressful events, thyroid problems, heart problems, and substance use problems.
- If your genetic risk is high, managing stress and substance use may help reduce overall risk.
- Anxiety can cause issues with sleep, fatigue, the gut, stress, focus, and mood.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

**It's completely normal to feel anxious about things from time to time.** Occasional anxiety can help us solve problems and make better life decisions. However, people with *anxiety disorders* often worry about normal activities, which impacts their daily life [R, R].

Two parts of your brain process threats [R, R, R]:

- The *amygdala* helps activate the "fight or flight" response
- Frontal areas of your brain override the amygdala and help you respond logically

People experience anxiety when they have too much activity in their amygdala or too little in frontal brain areas [R, R].

If you're anxious, you may experience [R]:

- Restlessness
- Fatigue
- Problems concentrating
- Short temper
- Muscle tension
- Heavy sweating
- Trembling
- Gut problems
- Heart rate changes
- Sleep problems

People are more likely to have these symptoms if they experience [R]:

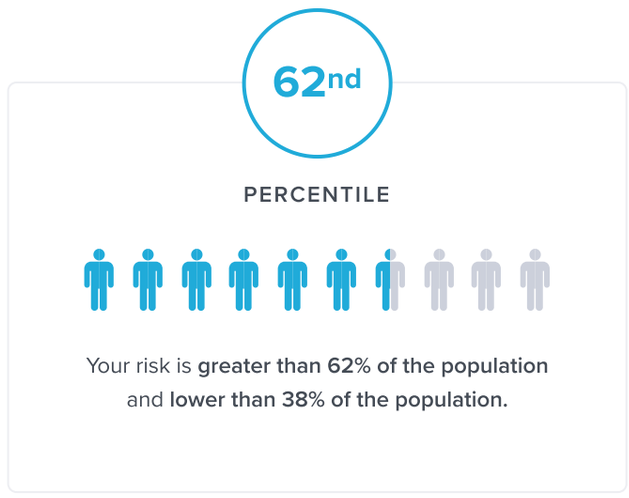
- Traumatic or stressful events
- Thyroid problems
- Heart problems
- Substance use problems

**Another important risk factor for anxiety is genetics.** About 30-65% of the differences in people's chances of getting anxiety can be attributed to genetics. Genes linked to anxiety may influence the levels and activity of different brain chemicals, such as [R, R, R, R, R, R, R]:

- Serotonin and dopamine, which make you feel happy (*SLC6A4*, *HTR1A*, *TPH2*, *MAOA*)
- GABA, which calms the mind (*GABRG2*)
- Stress hormones such as cortisol (*MC4R*, *MAOA*)
- Substances that promote new brain cell growth (*BDNF*, *NGF*)

TYPICAL LIKELIHOOD

**Typical likelihood of anxiety based on 806,651 genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| ATP8B4 | rs2413998 | AA |
| / | rs16838980 | GG |
| DNAH8 | rs4714177 | AA |
| NUP107 | rs11177321 | GG |
| FKBP4 | rs2302729 | CC |
| PREPL | rs1067327 | CC |
| RNF180 | rs6295 | GG |
| IL20RB | rs17374749 | GG |
| PID1 | rs10498237 | GG |
| / | rs10092548 | AA |
| C6ORF118 | rs9295300 | AA |
| NOX4 | rs17221829 | CC |
| NOX4 | rs10830352 | GG |
| GABRG2 | rs211037 | TT |
| MARCHF4 | rs955816 | GG |
| IRX6 | rs2397376 | TT |
| HTR2A | rs12584920 | GG |
| COMT | rs4680 | GA |
| ERCC6L2 | rs7867155 | CC |
| COMT | rs4633 | CT |
| SLC6A2 | rs3785151 | GC |

| GENE | SNP | GENOTYPE |
|---|---|---|
| CES1 | rs1566652 | TG |
| GAD1 | rs3828275 | CT |
| GAD1 | rs701492 | TC |
| GAD1 | rs769407 | CG |
| GAD1 | rs3791878 | TG |
| IL18R1 | rs2058622 | AG |
| GAD1 | rs3791851 | CT |
| ZPLD1 | rs1709393 | CT |
| DMD | rs921896 | C |
| CAMTA1 | rs11120917 | TC |
| OR5P3 | rs7112002 | AC |
| SRBD1 | rs2344662 | CA |
| ADRB1 | rs1034258 | AG |
| SSH2 | rs6354 | TT |
| ESR1 | rs9340799 | AG |
| ESR1 | rs2234693 | TC |
| AKAP6 | rs17406568 | GG |
| OSCP1 | rs906228 | CA |
| AGPAT4 | rs3798943 | CC |
| CCNY | rs2086153 | CT |
| COX7B2 | rs6447514 | TT |
| DDT | rs755622 | GG |
| TULP1 | rs3800373 | AA |
| RGS2 | rs10801153 | GG |
| RNF220 | rs12138940 | GA |
| MC4R | rs10871777 | AA |
| TBL1X | rs5934574 | T |
| TACR1 | rs3771841 | GA |
| DSCAM | rs1040315 | AG |

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

# Cognitive Function

Some people are really good at math, but bad at memorizing facts. Others excel at learning languages, but lack spatial awareness and get easily lost. Everyone's brain works differently.

Your strengths and your weaknesses depend on your education, your life experiences and your genes. Up to **50-80%** of differences in cognitive ability may be due to **genetics**. Genes that affect our cognitive function tend to influence **brain development, structure and function** [R, R, R, R, R].

Other factors that affect our cognitive function include [R, R, R, R, R, R]:

- Lifestyle (e.g. physical activity, sleep quality)
- Education
- Physical and mental health
- Sensory loss (e.g. vision or hearing loss)
- Aging
- Social connectedness
- Environment (e.g. air pollution)
- Being cognitively active (e.g. reading, having intellectual-stimulating jobs)

To improve cognitive function focus on:

- Staying physically active [R, R, R]
- Getting enough good quality sleep [R, R]
- Staying social (in person) [R, R, R]
- Eating a healthy, balanced diet [R, R]
- Keeping the mind active (e.g., with puzzles, games of strategy or learning new skills) [R, R, R, R]

TYPICAL

**Predisposed to typical cognition based on 7,159,700 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| SNAP25 | rs363043 | CC |
| ARMC2 | rs9384679 | TT |
| CHRM2 | rs8191992 | TT |
| MAPRE1 | rs406193 | CC |
| CABP5 | rs3936340 | TT |
| PAM | rs35658696 | AA |
| MTHFR | rs1801133 | AA |
| GYPC | rs1550404 | TT |
| PRMT6 | rs12125971 | CC |
| / | rs17813294 | CC |
| TET2 | rs2454205 | TT |
| NEGR1 | rs7531118 | TT |
| / | rs2478286 | CC |
| SCMH1 | rs12035012 | AA |
| UBA7 | rs7613360 | TT |
| CNR1 | rs1049353 | TT |
| UBA7 | rs9855505 | TT |
| BCL2 | rs956572 | GG |
| / | rs9388349 | TT |
| ST8SIA6 | rs7897269 | TT |
| CHRM2 | rs7799047 | GG |
| REC114 | rs7171755 | GA |
| CLSTN2 | rs6439886 | AA |
| NR2F2 | rs4984541 | AA |
| SNAP25 | rs363016 | TC |
| CHRM2 | rs2350786 | AA |
| DPP4 | rs1913808 | GG |
| ST8SIA6 | rs17141089 | GG |
| PKN2 | rs17130578 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| DPYD | rs1702294 | CC |
| SLC10A7 | rs11737630 | CC |
| SBNO1 | rs1060105 | CC |
| PPA2 | rs2726491 | AG |
| / | rs9320747 | GT |
| AKR1C3 | rs9423406 | GA |
| BDNF | rs6265 | CT |
| COMT | rs4680 | GA |
| SNAP25 | rs363050 | AG |
| SNAP25 | rs363039 | GA |
| PLXNB2 | rs28379706 | TC |
| CHRM2 | rs2350780 | AG |
| TFAM | rs1937 | GC |
| ARVCF | rs165599 | GA |
| SCN2A | rs10174400 | CT |
| NEGR1 | rs12128707 | AG |
| RBM6 | rs13100903 | CT |
| / | rs12211582 | GT |
| NR1D2 | rs6550835 | AG |
| NEGR1 | rs1486091 | TC |
| ELAVL2 | rs10733389 | GA |

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

# Attention

**Key Takeaways:**

- Up to **80%** of differences in people's chances of developing ADHD may be due to genetics.
- About **6.4 million** American children aged 4-17 have ADHD, along with **4% of adults**.
- Risk factors include: smoking, drug or alcohol use during pregnancy, toxins, brain injuries, and being male.
- ADHD can lead to substance abuse and money problems in adults.
- Since the condition is rare in adults, a high genetic risk is not necessarily a reason to worry.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

We've all struggled to stay focused on an important task. However, some people have more trouble paying attention than others.

The most important part of the brain for attention and focus is the *prefrontal cortex*. This region also helps you plan and solve problems [R].

Other parts of the brain help to filter important information without having to think about it. This allows you to avoid distractions [R].

**Problems in these brain regions may make it harder to stay focused**. Some people have so much difficulty focusing that it interferes with their daily lives. This is a sign of *attention-deficit/hyperactivity disorder* (ADHD) [R].

**ADHD affects millions of children and teenagers in the US.** More boys are diagnosed with ADHD than girls [R].

Children and teens with ADHD tend to have trouble with school. They might also experience problems with relationships [R, R, R, R].

**Attention problems often continue into adulthood.** Adults with ADHD are more likely to experience [R]:

- Substance abuse
- Car accidents
- Money problems

Treatment for ADHD usually includes talk therapy and medication [R].

The cause of ADHD is unknown. Risk factors include [R]:

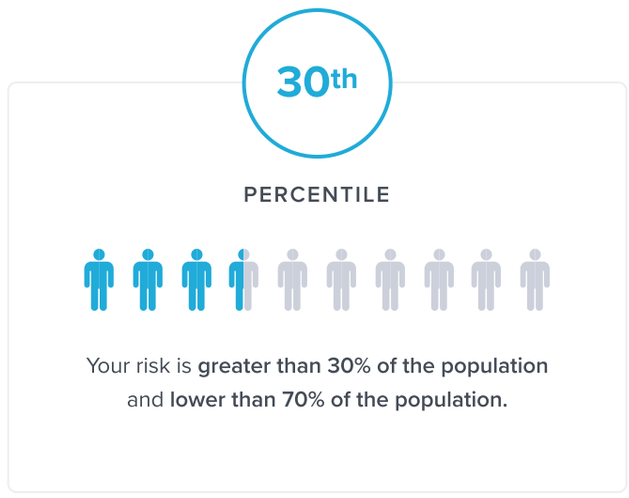
- Maternal use of cigarettes, drugs, or alcohol during pregnancy
- Environmental toxins
- Brain injuries
- Genetics

**Up to 80% of differences in people's chances of developing ADHD may be attributed to genetics.** Genes involved in ADHD may influence [R, R, R, R, R, R, R]:

- Dopamine (*DRD4*, *DRD5*, *COMT*)
- Serotonin (*HTR1B*, *SLC6A4*, *SNAP25*)
- Brain cell growth (*BAIAP2*)

TYPICAL

**Typical likelihood of ADHD based on 261,702 genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| LPCAT1 | rs27072 | CC |
| DLC1 | rs2410116 | GG |
| COMT | rs4680 | GA |
| TPH2 | rs1843809 | TT |
| MFHAS1 | rs13439086 | CT |
| AXIN2 | rs8074751 | AA |
| MUC15 | rs10767556 | AG |
| ANAPC4 | rs28612433 | CT |
| FBN3 | rs35624673 | CT |
| BDNF | rs56164415 | GG |
| / | rs9545903 | TC |
| CHRNA4 | rs1044396 | GG |
| CLPTM1L | rs11564750 | GG |
| SLC26A5 | rs144525 | CC |
| PLXDC2 | rs10828015 | CT |
| BLOC1S2 | rs35835615 | CC |
| TPH2 | rs1386497 | AA |
| LGR4 | rs11030104 | AA |
| HTR2C | rs3813929 | C |
| BDNF | rs6265 | CT |
| ANKK1 | rs1800497 | GA |

| GENE | SNP | GENOTYPE |
|---|---|---|
| MAOA | rs6323 | G |
| COMT | rs4633 | CT |
| SLC6A2 | rs3785151 | GC |
| CES1 | rs1566652 | TG |
| DRD1 | rs265981 | AG |
| SFXN1 | rs5326 | CT |
| DRD1 | rs686 | GA |
| KCTD3 | rs6540899 | GA |
| PFKP | rs1537617 | GA |
| SNAP25 | rs362987 | AC |
| CNTLN | rs10962864 | TC |
| SNAP25 | rs3746544 | GT |
| EXOC1L | rs895614 | AG |
| CNTLN | rs6475111 | TC |
| ZNF584 | rs35782676 | CT |
| DTNBP1 | rs760761 | AG |
| ADA | rs73598374 | TC |
| HTR1B | rs6296 | CG |
| DTNBP1 | rs2619528 | TC |
| DTNBP1 | rs2619522 | CA |
| DTNBP1 | rs1018381 | AG |
| SNAP25 | rs363039 | GA |
| ESD | rs7984966 | TT |
| IL10RB | rs77224013 | GG |
| SLC6A2 | rs3785143 | CC |
| C21ORF62 | rs112686226 | AA |
| TNR | rs6686722 | CC |
| SPATA7 | rs61975260 | CC |
| HERC2 | rs4778174 | GG |

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

# Memory Performance

**Memory performance** refers to how good your brain is at storing and recalling information [R, R, R].

About 30-70% of differences in people's memory performance may be due to genetics. Genes involved in memory may influence [R, R, R, R]:

- The way brain cells grow and develop
- Brain cell communication

Ways to boost your memory performance include [R, R, R, R]:

- Being physically active
- Getting 7-9 hours of good-quality sleep every night
- Eating a healthy diet
- Spending time with family and friends
- Engaging your mind (e.g, reading, solving puzzles, learning new skills)

If you want to go the extra mile, there are specific techniques you can use to train your memory (e.g. mind palace). There is even a world memory championship!

TYPICAL

**Predisposed to typical memory performance based on 7,166,380 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| HDGFL1 | rs9466427 | GG |
| HDGFL1 | rs9348530 | AA |
| HDGFL1 | rs9358578 | GG |
| HTATIP2 | rs10741845 | AT |
| / | rs9345419 | TT |
| TMEM63A | rs6426075 | AG |
| NT5DC2 | rs4687625 | CT |
| NT5DC2 | rs2015971 | CT |
| NT5DC2 | rs11711421 | CT |
| ITIH1 | rs3774354 | GA |
| ITIH1 | rs1961958 | AG |
| ITIH1 | rs3774355 | GA |
| ITIH1 | rs6778844 | TC |
| ITIH1 | rs12487445 | AC |
| ITIH1 | rs6798246 | GA |
| ITIH1 | rs1961959 | GC |
| PBRM1 | rs17264436 | TA |
| ITIH1 | rs2289249 | GA |
| GNL3 | rs11177 | GA |
| ITIH1 | rs10865973 | AT |
| ITIH1 | rs2118540 | TC |
| ITIH1 | rs11717836 | AG |
| ITIH1 | rs6976 | CT |
| ITIH1 | rs2268027 | GA |
| ITIH1 | rs2239551 | GA |
| CGGBP1 | rs12492805 | GT |
| ITIH1 | rs2268025 | AT |
| NEK4 | rs1029871 | GC |
| ITIH1 | rs2286798 | AC |

| GENE | SNP | GENOTYPE |
|---|---|---|
| TDRD3 | rs4886229 | TC |
| TEK | rs10757641 | TC |
| TEK | rs633903 | TG |
| TEK | rs581724 | GT |
| MAT1A | rs4933327 | GG |
| ZNF804A | rs1344706 | CA |
| STARD3 | rs879606 | GG |
| COMT | rs4680 | GA |
| DTNBP1 | rs2619522 | CA |
| TTC12 | rs1076560 | CA |
| SLC19A1 | rs1051266 | TC |
| SYNJ2 | rs10945973 | AG |
| LMX1A | rs4657412 | AG |
| SYNJ2 | rs2502601 | AG |
| MAT1A | rs3851059 | AG |
| SYNJ2 | rs9356200 | CT |
| SORL1 | rs3824968 | AT |
| COL4A2 | rs4773144 | AA |
| SYNJ2 | rs10455935 | GA |
| UBE2Z | rs15563 | AA |
| WWC1 | rs17070145 | TT |

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

# Alzheimer's Disease

**Key Takeaways:**

- About **60-80%** of differences in people's chances of getting Alzheimer's disease may be due to genetics.
- Alzheimer's disease can wipe out cognitive abilities.
- **5.8 million** Americans have Alzheimer's disease, the vast majority of them being over 75 years of age.
- Other risk factors include old age, female sex, air pollution, alcohol abuse, and obesity.
- **This report doesn't take into account the APOE-e4 variant.**

Some of the risk factors for Alzheimer's include [R]:

- Being over the age of 75
- Being female
- High exposure to air pollution
- Poor sleep patterns
- Alcohol abuse
- Sedentary lifestyle
- Low social interaction
- Low involvement in mentally stimulating activities

The following conditions may contribute to Alzheimer's disease [R]:

- Mild cognitive impairment
- Head trauma
- Obesity
- Diabetes
- High cholesterol
- Down syndrome

About **60-80%** of differences in people's chances of getting Alzheimer's disease may be due to genetics [R].

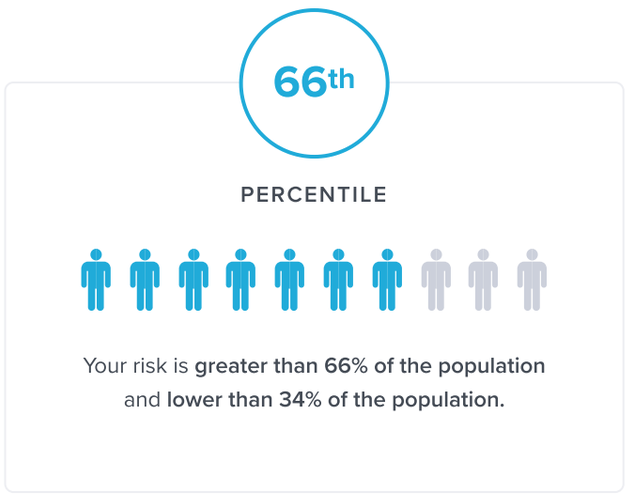
Genetically high fasting insulin, ApoB, and neutrophil levels may be causally associated with a higher risk of Alzheimer's disease [R, R, R, R].

In contrast, genetic predisposition to high total testosterone and glucosamine supplement use may be causally associated with a lower risk [R, R].

**Please note:** Genetic models analyzing a lot of variants (PRS models) usually don't take into account variants with large effects, such as **APOE-e4**. This variant is by far the strongest genetic factor for Alzheimer's disease. If you carry it, your predisposition to Alzheimer's disease is higher, regardless of your result for this report.

TYPICAL LIKELIHOOD

**Typical likelihood of Alzheimer's disease based on 1,049,157 genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CHRM2 | rs6962027 | TT |
| PICALM | rs3851179 | TT |
| GSK3B | rs334558 | GA |
| CD55 | rs3818361 | GA |
| POLR2E | rs12151021 | AA |
| HLA-DRB1 | rs9271192 | CA |
| CD55 | rs679515 | CT |
| ECHDC3 | rs7912495 | GG |
| SORT1 | rs11102972 | CT |
| CLNK | rs6846529 | CT |
| COX7C | rs62374257 | CT |
| CPSF3 | rs72777026 | AG |
| WDR81 | rs35048651 | DEL(GAG)T |
| IGHG3 | rs7157106 | GA |
| LILRB5 | rs587709 | CT |
| SNX1 | rs3848143 | AG |
| GC | rs2282679 | GT |
| CLU | rs11136000 | CC |
| APOE | rs429358 | TT |
| TREM2 | rs75932628 | CC |
| PTGS2 | rs20417 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| RELN | rs528528 | CC |
| SETD7 | rs535347112 | CC |
| BDNF | rs56164415 | GG |
| SYPL2 | rs17646665 | AA |
| NGFR | rs2072446 | CC |
| SLC20A1 | rs1800587 | GG |
| TREML1 | rs60755019 | AA |
| SORL1 | rs11218343 | TT |
| NCK2 | rs143080277 | TT |
| TREM2 | rs143332484 | CC |
| SORT1 | rs141749679 | TT |
| GPX4 | rs3764650 | TT |
| ABI3 | rs616338 | CC |
| WWC1 | rs17070145 | TT |
| ATP8B4 | rs138799625 | CC |
| PILRB | rs1476679 | TT |
| BIN1 | rs744373 | AA |
| SORL1 | rs74685827 | TT |
| BIN1 | rs6733839 | CC |
| MME | rs61762319 | AA |
| SHARPIN | rs34173062 | GG |
| FOXF1 | rs16941239 | TT |
| C1QTNF4 | rs10838725 | TT |
| DBNDD1 | rs56407236 | GG |
| APH1B | rs117618017 | CC |
| CD2AP | rs9349407 | GG |
| STYX | rs17125924 | AA |
| RASGEF1C | rs113706587 | GG |
| OTULIN | rs112403360 | TT |

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

# APOE

**Key Takeaways:**

- If you carry one or both **ε4** variants, your risk for Alzheimer's disease may be higher.
- The risk is greatest for late onset (after age 65) Alzheimer's disease.
- Even if your risk is higher due to the **ε4** variants, numerous other factors from your environment to lifestyle to other genetic variants impact overall risk.
- People with both variants may never get Alzheimer's, and some who have neither variant can get the disease.

There are three major forms (variants) of the *APOE* gene. These are called ε2, ε3, and ε4. You can have two copies of the same variant or two different variants [R, R].

ε2, ε3, and ε4 change the shape of the ApoE protein. This can impact how well ApoE functions [R, R].

**ε3** is the most common variant. It makes a protein that is good at clearing plaque from the brain and fats from the blood. Most people have two ε3 variants and a typical risk of Alzheimer's disease [R].

**ε4** is less common. It makes a protein that is not as good at clearing plaque from the brain and fats from the blood. ε4 has been linked to a higher risk of Alzheimer's disease and artery hardening [R, R].

**ε2** is another less common variant. It makes a protein that is better than ε3 at removing plaque from the brain, but not as good at removing fats from the blood. ε2 has been linked to a lower risk of Alzheimer's disease [R, R, R].

However, it has also been linked to a higher risk of artery hardening in people with two ε2 variants and an underlying chronic health condition, such as obesity or diabetes [R, R, R].

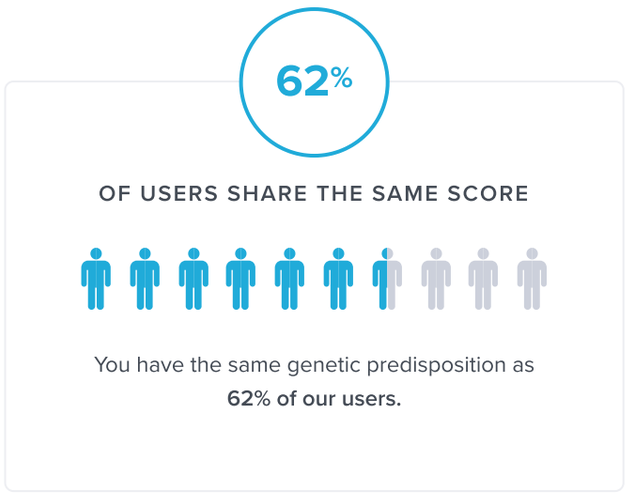
***Did you know?*** The **ε4** variant was much more common among ancient hunter-gatherers. Scientists suggest this variant might have improved their [R]:

- Inflammatory response to germs in the wilderness
- Vitamin D status in less sunny European areas
- Aerobic endurance, crucial for a hunter-gatherer lifestyle

As humans largely switched to farming, some effects of this variant became useless or even harmful. For this reason, evolution strongly favored the **ε3** variant in ancient farmers and their modern descendants [R].

E3/E3

**You carry two APOE ε3 variants based on the genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| APOE | rs7412 | CC |
| APOE | rs429358 | TT |

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

# Cognitive Decline

Mild cognitive decline is a normal part of aging that can affect cognitive functions such as memory, attention, and problem-solving.

About **60-70%** of the differences in people's cognitive decline may come from genetics. For example, genetically high total and bioavailable testosterone may be causally associated with larger gray matter volume in men [R, R, R].

Other risk factors for cognitive decline include [R]:

- Older age
- Female sex
- Lifestyle factors like smoking and being inactive
- Lower education level

Different health conditions may play a role in cognitive decline, including high cholesterol and blood pressure [R].

LESS LIKELY

**Less likely to have cognitive decline based on 272,168 genetic variants we looked at**

**2nd**

PERCENTILE



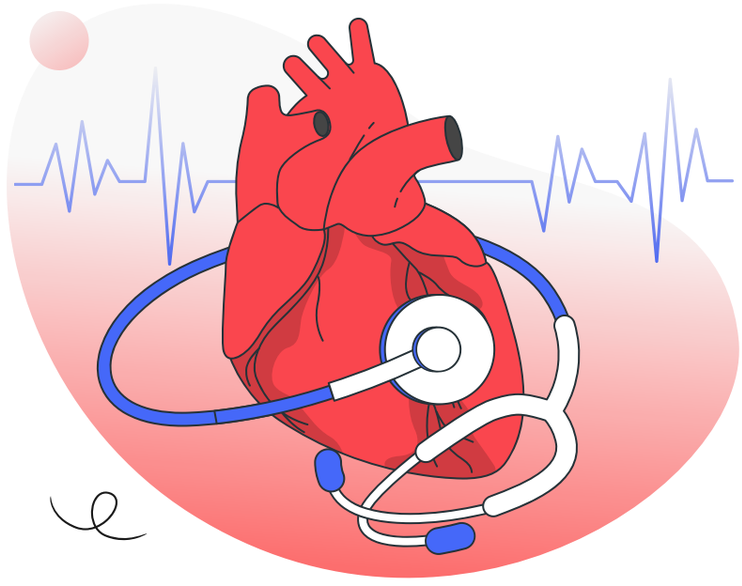
Your risk is **greater than 2% of the population** and **lower than 98% of the population.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CDCA7 | rs182734936 | CC |
| ANXA5 | rs141005242 | CC |
| / | rs200668351 | GG |
| TEK | rs147486058 | AA |
| DUSP15 | rs6089150 | CC |
| CTBP2 | rs61869228 | CC |
| HHEX | rs60320343 | AA |
| CRP | rs1205 | CC |
| FOXO3 | rs4946936 | CC |
| APOE | rs7412 | CC |
| CLU | rs11136000 | CC |
| KIF11 | rs6583817 | CC |
| MS4A6A | rs610932 | GG |
| TRIM32 | rs7852872 | CC |
| LHFPL6 | rs9315702 | AA |
| DPP4 | rs6741949 | GG |
| / | rs11706133 | TT |
| WDFY2 | rs9535753 | TT |
| LAMP3 | rs630527 | GG |
| FOXJ2 | rs7138264 | GG |
| OPCML | rs11606197 | TT |

| GENE | SNP | GENOTYPE |
|---|---|---|
| / | rs72956174 | TT |
| B3GALNT1 | rs4455332 | CC |
| C3ORF56 | rs11716691 | AA |
| IRX2 | rs72720951 | AA |
| ZNF799 | rs4804181 | AA |
| / | rs57169846 | GG |
| BDNF | rs6265 | CT |
| ALCAM | rs34476301 | AG |
| SIRT1 | rs3758391 | CT |
| TNF | rs1799724 | CT |
| SNRPB | rs2076650 | TC |
| A2M | rs11609582 | TA |
| APBB2 | rs13133980 | GC |
| BCHE | rs1803274 | CT |
| PRR16 | rs3991625 | CT |
| CEMIP2 | rs12237894 | GC |
| SALL1 | rs2075199 | CT |
| MRPS18C | rs10004897 | AG |
| SALL3 | rs7231688 | AG |
| CHD6 | rs6072411 | GA |
| HSD11B1 | rs60686175 | TC |
| / | rs10457441 | TT |
| TMEM106B | rs1990622 | AG |
| APOE | rs429358 | TT |
| TNS1 | rs13013766 | GG |
| / | rs62477365 | TT |
| BCL11A | rs6545794 | GG |
| IFNL3 | rs73050457 | CC |
| ABCA2 | rs908832 | GG |

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



# Heart & Blood Vessels

This section explores the genetic factors that influence your heart health, blood vessel function, and overall cardiovascular system performance. Understanding these genetic variations provides insights into your risk profile for heart disease, arrhythmias, and other cardiovascular conditions.

Your genetic profile affects fundamental aspects of cardiovascular health including coronary artery disease susceptibility, heart rhythm regulation, and lipid metabolism. This analysis examines your predisposition to various cardiovascular conditions and how your genes influence your heart's structure and function throughout your lifetime.

This comprehensive cardiovascular genetics assessment helps you understand your unique risk factors and empowers you to make informed decisions about heart-healthy lifestyle choices, preventive measures, and monitoring strategies tailored to your individual genetic predispositions.

**Topics include:**

- CAD
- Atrial fibrillation
- Lp(a)
- Nitic oxide (NOS3)

MORE LIKELY

## Coronary Artery Disease

More likely to have coronary artery disease

TYPICAL ACTIVITY

## NOS3 (Cardiovascular)

Likely typical NOS3 activity

TYPICAL LEVELS

## Lipoprotein(a)

Predisposed to typical Lipoprotein(a) levels

TYPICAL LIKELIHOOD

## Atrial Fibrillation

Typical likelihood of atrial fibrillation

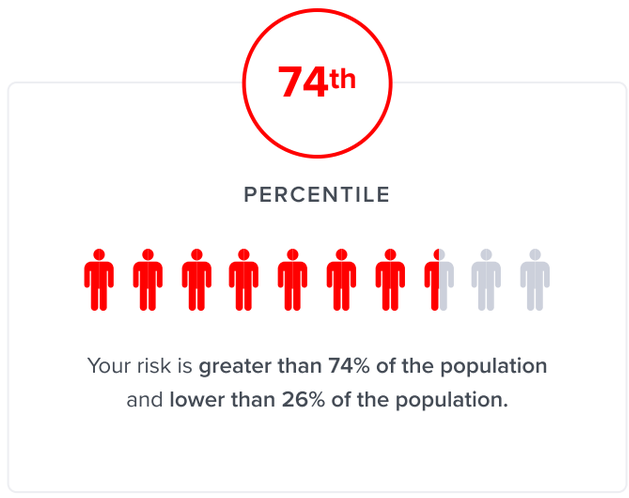
# Coronary Artery Disease

**Key Takeaways:**

- Over **18 million** people have heart disease in the U.S. A third of deaths from heart disease are preventable.
- Up to **40%** of differences in people's chances of getting coronary artery disease may be due to genetics.
- Other risk factors include excess weight, stress, sedentary lifestyle, smoking, and more.
- If you have a high genetic risk, take action on modifiable risk factors. Even with a low genetic risk, having other risk factors will still make you prone to heart disease.
- Click the **next steps** tab for relevant labs and lifestyle factors.

MORE LIKELY

**More likely to have coronary artery disease based on 1,049,366 genetic variants we looked at**




**In the US, 1 in 3 deaths from heart disease could be prevented.** That's about 92,000 deaths each year. **Imagine if we could save all those lives by striving to prevent heart disease** [R]!

*Coronary artery disease* is the most common type of heart disease. It affects the coronary arteries -- the large blood vessels that feed the heart. When these vessels become narrowed or blocked, they can't deliver as much oxygen to the heart. Because of this, heart muscle tissue can start to die off [R, R].

If a coronary artery is blocked suddenly, it can cause a heart attack. If the artery narrows slowly over a long period of time, it can cause chest pain and other problems [R].

Many factors can increase your risk of heart disease. These include [R, R]:

- Excess weight
- Unhealthy diet
- Stress
- Lack of exercise
- Smoking
- Air pollution
- Age
- High blood pressure
- High cholesterol
- Diabetes
- Genetics

According to the CDC, **over 18 million adults in the US have coronary artery disease**, and the rates keep increasing. However, death rates have been going down. This is likely due to improved diagnosis and treatment [R, R, R, R]!

Medications that doctors often prescribe for coronary artery disease include [R]:

- Low doses of aspirin, to help prevent blood clots
- Statins, to reduce cholesterol and slow down fat buildup in blood vessels
- Beta-blockers, to lower blood pressure and relax the heart

It's much easier to prevent heart disease than to treat it. To avoid heart disease, experts recommend a "heart-healthy" lifestyle, which includes [R]:

- Not smoking cigarettes
- Eating a healthy diet
- Staying physically fit
- Getting good-quality sleep

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| NOS3 | rs2070744 | CT |
| PEMT | rs12936587 | GA |
| COMT | rs4680 | GA |
| PCSK9 | rs11591147 | GG |
| ATG16L1 | rs10210302 | TT |
| NKX2-3 | rs10883365 | GG |
| FHL3 | rs190569784 | GG |
| SERPINA1 | rs112635299 | GG |
| ANGPTL4 | rs116843064 | GG |
| APOE | rs7412 | CC |
| IRGM | rs1000113 | CT |
| LDLR | rs6511720 | GG |
| IL23R | rs11805303 | CT |
| / | rs72711827 | GG |
| SORT1 | rs12740374 | GG |
| PHACTR1 | rs9349379 | GG |
| FBXL20 | rs72823390 | CC |
| PLPP3 | rs17114046 | AA |
| / | rs2457480 | AA |
| ADO | rs10761659 | AG |
| MCTP2 | rs28607113 | TT |

**Up to 40% of differences in people's chances of getting coronary artery disease may be attributed to genetics.** Genes that may contribute to coronary artery disease influence [R]:

- Fat metabolism (*APOE*, *APOB*, *LPL*, *LPA*, *PCSK9*)
- Inflammation (*IL5*, *IL6R*)
- Blood clotting (*SERPINA1*)
- Blood vessel function (*NOS3*, *TGFB1*, *VEGFA*, *ANGPTL4*)

Genetically higher levels of the following markers are causally associated with a higher risk of heart disease [R, R, R, R, R, R, R, R, R, R, R]:

- White blood cells
- Fasting insulin
- IGF-1
- ApoB
- Neutrophils
- L-carnitine

In contrast, genetically high total testosterone and EPA may be causally associated with a lower risk of coronary heart disease [R, R].

| GENE | SNP | GENOTYPE |
|---|---|---|
| PHOSPHO1 | rs191896574 | TC |
| FAM177B | rs17465982 | AA |
| NOS3 | rs3918226 | TC |
| MRPS6 | rs28451064 | AG |
| LPA | rs73596816 | AG |
| PEMT | rs7946 | CT |
| TWIST1 | rs2107595 | GA |
| EDNRA | rs17612693 | AT |
| TCF21 | rs1966248 | AT |
| DDI1 | rs2128739 | AC |
| FGD5 | rs148880716 | GG |
| LPA | rs140570886 | TT |
| LPA | rs147555597 | GG |
| PTGER4 | rs17234657 | TT |
| LPA | rs55730499 | CC |
| SEH1L | rs2542151 | TT |
| NOD2 | rs17221417 | CC |
| BSN | rs9858542 | GG |
| MAP3K4 | rs145099029 | AA |
| CDKN2B | rs145542470 | GG |
| NBEAL1 | rs72934535 | TT |
| SCAF11 | rs1291621 | GG |
| MTRNR2L7 | rs4934855 | AA |
| LPL | rs7011846 | GG |
| SOX11 | rs79576311 | GG |
| SMIM11A | rs149487184 | CC |
| BMP1 | rs73225842 | CC |
| BAG2 | rs223290 | CC |
| LRRC25 | rs11670056 | CC |

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

# NOS3 (Cardiovascular)

Among the different *NOS3* polymorphisms, rs1799983 has been most widely studied. The ‘T’ variant produces a protein that can’t reach its activation sites in cell membranes, ultimately decreasing NO production [R].

In line with the beneficial cardiovascular effects of NO, the ‘T’ variant has been associated with an increased risk of coronary heart disease and heart attack in several studies. It’s also more frequent in children with congenital heart disease and predicts a faster progression of heart damage in people with diabetes [R, R, R, R].

However, overproducing ‘GG’ genotype may also have negative effects on the heart. It’s associated with reduced heart function in people with kidney disease, increased risk of death in those with high blood pressure, and heart failure in African-Brazilians [R, R, R].

The ‘T’ allele of rs1549758 has also been associated with an increased risk of coronary heart disease and hypertension but is usually inherited with the ‘T’ allele of rs1799983, meaning you will most likely have both or neither of them [R].

Another SNP, rs2070744, is also linked to an increased risk of coronary heart disease. The ‘C’ allele can be bound by a protein that blocks *NOS3* production. However, the ‘T’ variant at this polymorphism is the one associated with myocardial infarction [R, R, R].

These variants may exert their harmful effects through their associations with:

- Higher blood pressure [R, R, R, R, R, R, R, R, R, R, R]
- Higher vessel stiffness and blood cholesterol [R, R, R, R]
- Increased risk of complications after heart surgery [R, R, R]
- Reduced effectiveness of conventional and alternative therapies [R, R]

The minor variants of rs179983 and rs2070744 have also been associated with:

- Worse athletic performance in power sports [R, R, R, R, R, R]
- Longer and more frequent migraines [R, R, R, R]

On the bright side, they are also linked to:

- Improved performance in aerobic sports and soccer [R, R, R]
- Greater decreases in triglycerides, cholesterol, and blood pressure in response to unsaturated fats such as omega-3 fatty acids and extra virgin olive oil [R, R, R, R, R]

Finally, the ‘T’ allele of rs3918226 also results in lower NOS3 levels and is associated with a higher risk and severity of heart and coronary events. Fortunately, this allele is extremely rare and most people (81-99%) have the ‘CC’ genotype [R, R, R].

TYPICAL ACTIVITY

**Likely typical NOS3 activity based on 2 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| NOS3 | rs2070744 | CT |
| NOS3 | rs1549758 | TC |
| NOS3 | rs3918226 | TC |

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

# Lipoprotein(A)

**Lipoprotein(a), or Lp(a), is a type of LDL**. It is made in the liver and carries fats such as cholesterol around the body. **Lp(a) may deposit on the artery walls**. This may lead to the formation of plaques that narrow the arteries. In line with this, higher Lp(a) levels have been associated with heart disease and stroke [R, R, R, R, R, R, R, R].

**Genetics strongly influence Lp(a) levels.** Up to **90%** of differences in people's Lp(a) levels may be due to genetics [R, R].

Genetically higher Lp(a) levels may be causally associated with:

- Heart health (cardiovascular diseases) [R, R, R, R, R]
- Stroke [R, R, R]
- Longevity (reduced) [R]
- Atrial fibrillation [R, R]
- Anemia [R]
- Prostate cancer [R]

The effect of diet on Lp(a) is still a matter of research [R].

TYPICAL LEVELS

**Predisposed to typical Lipoprotein(a) levels based on 831 genetic variants we looked at**

**71st**

PERCENTILE

Your risk is **greater than 71% of the population** and **lower than 29% of the population.**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| LPA | rs41267819 | GG |
| FADS2 | rs1535 | AA |
| LPA | rs76144756 | GG |
| LPA | rs143431368 | TT |
| SLC22A1 | rs182980975 | CC |
| LPA | rs41267809 | AA |
| LPA | rs73596816 | AG |
| PLG | rs145535174 | AA |
| LPA | rs41272114 | CC |
| LPA | rs4708871 | TT |
| CETP | rs5882 | GA |
| APOB | rs693 | AG |
| TCF7L2 | rs7903146 | TC |
| GCKR | rs780094 | CT |
| SLC22A3 | rs6919346 | CT |
| LPA | rs74617384 | AA |
| SLC22A3 | rs3918291 | TT |
| / | rs151135411 | GG |
| LPA | rs142720914 | GG |
| SLC22A3 | rs117446263 | GG |
| LPA | rs3798220 | TT |

| GENE | SNP | GENOTYPE |
|---|---|---|
| AGPAT4 | rs61735260 | GG |
| MRPL18 | rs146888147 | GG |
| SIDT2 | rs964184 | CC |
| PCSK7 | rs662799 | AA |
| APOA5 | rs3135506 | GG |
| LPA | rs10455872 | AA |
| SLC22A1 | rs146534110 | GG |
| SLC22A3 | rs118133674 | GG |
| PLG | rs4252152 | TT |
| / | rs200865946 | CC |
| LPA | rs41272112 | CC |
| LPA | rs200376184 | GG |
| SLC22A3 | rs8187722 | AA |
| PLG | rs41272078 | CC |
| LPA | rs41264848 | GG |
| SLC22A3 | rs3127573 | AA |
| PLG | rs4252128 | CC |
| SLC22A1 | rs2282143 | CC |
| LPA | rs140306630 | CC |
| IGF2R | rs12207188 | CC |
| MRPL18 | rs73020718 | AA |

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

# Atrial Fibrillation

**Key Takeaways:**

- Up to **60%** of differences in people's chances of having atrial fibrillation may be due to genetics.
- Risk factors include age, heart disease, high blood pressure, lung disease, sleep apnea, and thyroid disease.
- If you have a high genetic risk, you may lower your overall risk by taking action on risk factors that you can change.
- Symptoms include palpitations, chest pain, fatigue, dizziness, shortness of breath, and weakness.
- Click the **Recommendations** tab for potential dietary and lifestyle changes, and **next steps** for relevant labs.

Some of the risk factors for AFib include [source]:

- Older age
- Alcohol use
- Use of stimulants, including certain medications, caffeine, and tobacco
- Obesity
- Family history of AFib

The following conditions may contribute to AFib [source]:

- Heart disease (coronary artery disease, heart attack, congenital heart defects, heart valve problems)
- High blood pressure
- Lung diseases
- Thyroid disease
- Chronic kidney disease
- Diabetes and metabolic syndrome
- Sleep apnea

Up to **60%** of differences in people's chances of having atrial fibrillation may be due to genetics [source].

TYPICAL LIKELIHOOD

**Typical likelihood of atrial fibrillation based on 1,049,356 genetic variants we looked at**


**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| HP | rs2359171 | AA |
| PITX2 | rs2129977 | AG |
| PITX2 | rs112599895 | GA |
| PITX2 | rs143269342 | CC |
| TBX5 | rs883079 | TT |
| GJA5 | rs79187193 | GG |
| PITX2 | rs75021220 | TC |
| PITX2 | rs3853445 | TT |
| PITX2 | rs6847935 | TA |
| PITX2 | rs6843082 | GA |
| NEURL1 | rs11598047 | AG |
| PBXIP1 | rs11264280 | TC |
| PITX2 | rs17570669 | AA |
| SCN5A | rs7373065 | TC |
| PITX2 | rs13105878 | CA |
| MYOZ1 | rs6480708 | AC |
| MYOZ1 | rs60212594 | CG |
| CLIC6 | rs2834618 | GT |
| UBE4B | rs187585530 | GG |
| METTL11B | rs72700114 | GG |
| TXNDC12 | rs146518726 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| C11ORF45 | rs76097649 | GG |
| PITX2 | rs149829837 | TT |
| RPL3L | rs140185678 | GG |
| PITX2 | rs2595104 | GG |
| SH3PXD2A | rs35176054 | TT |
| SELL | rs12122060 | TT |
| FBXO32 | rs78332318 | CC |
| KCNN3 | rs34292822 | GG |
| FBXO32 | rs62521286 | AA |

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

# Miscellaneous

This section examines additional genetic factors that influence various aspects of your health and physiology beyond the primary categories. Understanding these genetic variations provides insights into your predisposition to specific conditions and metabolic processes that affect your overall well-being.

Your genetic profile affects diverse health areas including metabolic regulation, immune system function, and respiratory health. This analysis explores how your genes influence your susceptibility to conditions like insulin resistance, thyroid disorders, and asthma, providing a comprehensive view of your genetic health landscape.

This additional genetics assessment helps you understand important health considerations that significantly impact your daily life and long-term health outcomes, enabling you to make informed decisions about prevention and management strategies.

**Topics include:**

- Insulin Resistance
- Thyroid
- Asthma

MORE LIKELY

## Asthma

More likely to get asthma

TYPICAL

## Insulin Resistance

Predisposed to typical insulin resistance

TYPICAL LIKELIHOOD

## Hashimoto's Disease

Typical likelihood of Hashimoto's disease

LESS LIKELY

## Graves' Disease

Less likely to have Graves' disease

# Asthma

**Key Takeaways:**

- Up to **70%** of differences in people's chances of developing asthma may be due to genetics.
- About **300 million** people worldwide are believed to have asthma, and many will develop it at a young age.
- Asthma triggers include viral infections, tobacco smoke, cold air, pollen, some medications, chemical fumes, and stress.
- A high genetic risk may mean greater susceptibility to triggers, so take actions to reduce your risk.
- Click the **Recommendations** tab for potential dietary and lifestyle changes and **next steps** for relevant labs.

Asthma is a chronic condition of the airway and lungs. In response to a trigger, the airway becomes inflamed. This reaction narrows the tubes that carry air into the body [R].

The symptoms of an asthma attack include [R, R]:

- Difficulty breathing
- Coughing
- Wheezing
- Tightness in the chest

**About 300 million people are believed to have asthma worldwide.** Asthma is more common in children than in adults. It is also much more common in people living below the poverty line [R, R].

In people with asthma, attacks can be triggered by [R, R]:

- Viral infections
- Tobacco smoke
- Pollen
- Some medications
- Chemical fumes
- Stress
- Cold air

Asthma attacks can range from mild to severe. At their worst, they can close the airway and be fatal [R, R].

**Asthma has no known cure**. If you have asthma, your doctor may prescribe an inhaler to control attacks. Your doctor can also help you recognize triggers that can lead to an attack. Then you can take steps to avoid them [R, R, R].

The exact cause of asthma is unknown, but genetics is thought to play a major role [R].

In fact, **up to 70% of differences in people's chances of developing asthma may be attributed to genetics.** Genes involved in asthma may influence [R, R, R]:

- Inflammation (*IL33*, *IL1RL1*, *TSLP*, *ORMDL3*)
- Autoimmune reactions (*HLA-DQA1*, *HLA-DQB1*, *HLA-DQA2*)
- Lung cell death (*GSDML*)

Genetically high white blood cell count may be causally associated with asthma in people with African ancestry. In contrast, genetically higher IGF-1 levels may be causally associated with a lower risk of asthma [R, R].

MORE LIKELY

**More likely to get asthma based on 1,049,396 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 |
|---|---|---|
| STAT6 | rs3024971 | TT |
| PTGER4 | rs7720838 | TT |
| LPP | rs9865818 | GG |
| RUNX3 | rs760805 | TT |
| LRRC32 | rs2155219 | GT |
| TSLP | rs1438673 | TC |
| HLA-DQA1 | rs6906021 | TC |
| SH2B3 | rs10774625 | AG |
| GSDMB | rs9303280 | CT |
| NFATC2 | rs6021270 | TC |
| GATA3 | rs10795656 | GA |
| / | rs115468973 | TT |
| / | rs201184533 | CC |
| / | rs116189786 | AA |
| IL2RA | rs12722502 | CC |
| IL18R1 | rs78545931 | AA |
| IL18RAP | rs72823641 | TT |
| HLA-DRB5 | rs1064713 | GA |
| CCR7 | rs112401631 | TT |
| LINGO4 | rs12123821 | CC |
| KIAA1109 | rs17454584 | AA |

| GENE | SNP | GENOTYPE |
|---|---|---|
| IL33 | rs144829310 | GG |
| IL2RA | rs61839660 | CC |
| IL1RL1 | rs950880 | CC |
| IRF4 | rs11242709 | CC |
| IL13 | rs20541 | GG |
| SERPINB10 | rs12964116 | AA |
| OVOL1 | rs479844 | AA |
| NOD2 | rs2066844 | CC |
| TLR1 | rs17616434 | CC |
| OR2B6 | rs7767176 | GG |
| SMAD3 | rs17228058 | AA |
| FLG | rs61816761 | GG |
| KRT24 | rs8067124 | AA |
| LINGO4 | rs115045402 | GG |
| LRRC32 | rs55646091 | GG |

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

# Insulin Resistance

Insulin resistance is the reduction of the body's ability to control blood sugar levels. It happens when the muscles, liver, and fat cells no longer respond to insulin and have trouble taking sugar up [R].

In response, the pancreas is forced to produce more insulin than normal to keep blood sugar in balance. Hence, people with insulin resistance may have high insulin levels. Blood sugar levels may also rise eventually, paving the way for diabetes [R, R].

Homeostatic model assessment (HOMA-IR) helps measure insulin resistance. It is calculated using your fasting glucose and fasting insulin. The higher your HOMA-IR, the more insulin resistant you are [R, R].

Insulin resistance is commonly caused by two factors**: overeating and lack of physical activity**. These can cause a buildup of fat in the liver and muscles that lead to insulin resistance [R, R, R].

**Insulin resistance is associated with overweight and obesity**, especially due to the accumulation of belly fat. However, normal-weight people may also have insulin resistance. Other health conditions may also lead to insulin resistance, including [R]:

- Sleep apnea [R]
- Thyroid disorders [R, R, R]
- Polycystic ovary syndrome (PCOS ) [R, R]
- Pancreas disease [R, R]
- Acromegaly (too much growth hormone) [R]
- Cushing's syndrome (excess of cortisol) [R]
- Rare genetic diseases [R, R, R, R]

**Keep in mind that this report is not about the rare genetic disorders mentioned above.** They are very rare and usually diagnosed in infancy.

The risk of insulin resistance may also increase due to:

- Aging [R, R]
- Stress [R, R]
- Fasting [R, R, R]
- Western diet [R]
- Too little sleep [R, R, R, R]
- Pregnancy [R]
- Exposure to toxins (e.g., herbicides) [R, R, R]
- Some drugs (e.g., corticosteroids) [R, R]

**Genetics also influences insulin resistance.** Up to **65%** of differences in people's insulin resistance may be due to genetics [R, R].

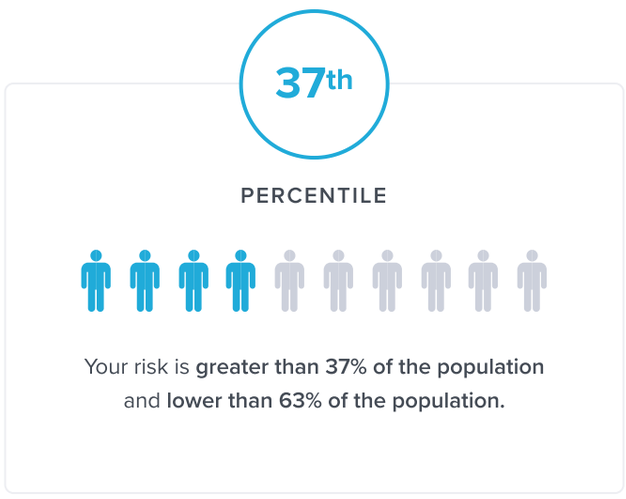
Insulin resistance may increase the risk of:

- Diabetes
- Liver disease
- Metabolic syndrome

Interestingly, insulin resistance may occur up to 15 years before diabetes develops. Read this post for a detailed list of tips to reduce insulin resistance [R].

TYPICAL

**Predisposed to typical insulin resistance based on 2,420 genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| GAS1 | rs9792548 | AA |
| PPARG | rs1801282 | CC |
| IRS1 | rs2943641 | TC |
| PPARG | rs3856806 | CC |
| FOXO3 | rs13217795 | TT |
| FOXO3 | rs2802288 | AA |
| IGF1 | rs35767 | GG |
| NAT2 | rs1208 | AA |
| TIMP4 | rs13081389 | AA |
| KLHL2 | rs17046216 | AA |
| LEPR | rs1137101 | AG |
| MRPS31 | rs4581585 | CC |
| ZC3H12C | rs475338 | AA |
| FBXO21 | rs2036313 | GG |
| HAPLN1 | rs1457105 | CC |
| / | rs12969333 | AA |
| DAAM2 | rs4345393 | GG |
| ME1 | rs11967452 | CC |
| KCNK17 | rs10456469 | GG |
| ORMDL3 | rs939345 | CC |
| ZIC2 | rs7338383 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| CSNK2A1 | rs6053042 | CC |
| RAB28 | rs1197712 | AA |
| ATP8B1 | rs10439020 | AA |
| MPC1 | rs2281056 | AA |
| MROH8 | rs11698899 | GG |
| RUNX3 | rs803323 | AA |
| TLR4 | rs13290714 | CC |
| SORCS1 | rs7088188 | CT |
| MDGA1 | rs17589516 | AA |
| CACNA1D | rs1401492 | CC |
| SLC10A2 | rs16962638 | AA |
| ATP10A | rs6576507 | TT |
| / | rs7043482 | AC |
| CSMD1 | rs2407314 | CC |
| FTO | rs9939609 | TT |
| TCERG1L | rs7077836 | GG |
| ADRB3 | rs4994 | AA |
| FABP2 | rs1799883 | CC |
| FTO | rs1421085 | TT |
| FTO | rs1121980 | GG |
| BRD1 | rs13057821 | CC |
| KL | rs9535766 | TT |
| UBR1 | rs17776090 | AA |
| BMP8A | rs710912 | CC |
| / | rs2873975 | GG |
| POLL | rs3730464 | AA |
| RUNX1 | rs17227476 | GG |
| NINL | rs11698267 | GG |
| FAM135B | rs10088248 | CC |

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

# Hashimoto's Disease

**Key Takeaways:**

- Up to **65%** of differences in people's chances of having Hashimoto's disease may be due to genetics.
- Risk factors include being female, middle age, pregnancy, other autoimmune diseases, and excessive iodine intake.
- It affects 1 to 2 percent of people in the U.S., occurring more often in women than men.
- Click the **Recommendations** tab for potential dietary and lifestyle changes, and **next steps** for relevant labs.

Risk factors for Hashimoto's disease include [R]:

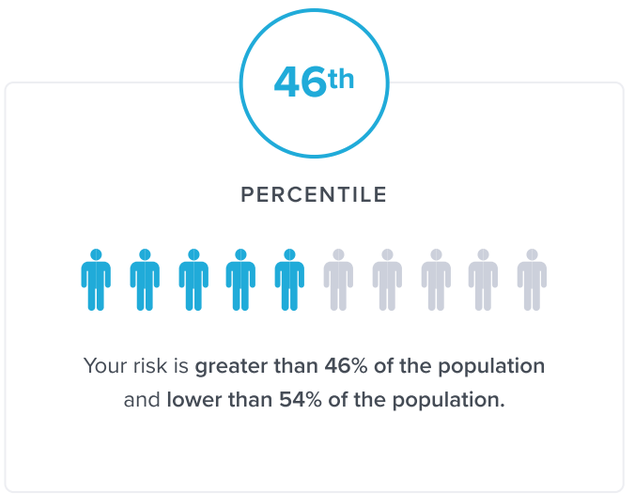
- Being female
- Middle age
- Pregnancy
- Excessive iodine intake
- Radiation exposure
- Having another autoimmune disease
- **Genetics**

Up to **65%** of differences in people's chances of having Hashimoto's disease may be due to genetics [R].

Hashimoto's disease is typically treated with medications to help normalize thyroid hormone levels. **It's important for people with Hashimoto's disease to work closely with their healthcare provider** to manage their condition and prevent complications.

TYPICAL LIKELIHOOD

**Typical likelihood of Hashimoto's disease based on 85 genetic variants we looked at**




**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CTLA4 | rs3087243 | GG |
| HLA-DPA1 | rs9277768 | TC |
| IL6 | rs1800795 | GG |
| CTLA4 | rs34636506 | AA |
| / | rs9271365 | TG |
| VAV3 | rs7537605 | GA |
| TRIB2 | rs1534422 | GG |
| PDE8B | rs1993945 | TA |
| SH2B3 | rs653178 | CT |
| STAT4 | rs11889341 | TC |
| TPO | rs11675434 | CT |
| CTLA4 | rs231775 | GA |
| CD69 | rs2110451 | AG |
| RPS26 | rs11611029 | CT |
| NIPSNAP1 | rs757024 | CG |
| SESN3 | rs4409785 | TC |
| ZNF668 | rs57348955 | AG |
| TNFRSF14 | rs2843403 | CT |
| PTPN22 | rs2476601 | GG |
| SLC25A27 | rs2270450 | CC |
| VAV3 | rs17020139 | GG |

| GENE | SNP | GENOTYPE |
|---|---|---|
| TRMO | rs7030280 | CC |
| PTPN22 | rs1230666 | GG |
| BACH2 | rs10944479 | GG |
| TNF | rs1799964 | TT |
| AP4B1 | rs12730735 | TT |
| TNF | rs1800629 | GG |
| CTLA4 | rs11571297 | TT |
| BACH2 | rs7754251 | GG |
| BACH2 | rs72928038 | GG |
| LPP | rs13093110 | CC |
| IL2RA | rs706779 | TC |
| GXYLT1 | rs4768412 | CC |

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

# Graves' Disease

**Key Takeaways:**

- Up to **80%** of differences in people's chances of getting Graves' disease may be due to genetics.
- Risk factors include young age, female sex, stress, smoking, and pregnancy.
- Symptoms include weight loss, rapid heartbeat, difficulty sleeping, eye bulging, and sexual dysfunction.
- If you have a high genetic risk, your overall risk is low due to its rarity. You can still improve this risk by taking action on those risk factors you can change.
- Click the **Recommendations** tab for potential dietary and lifestyle changes, and **next steps** for relevant labs.

Risk factors for Graves' disease include [R]:

- **Genetics**
- Being female
- Age under 40
- Other autoimmune disorders
- Emotional or physical stress
- Pregnancy
- Smoking

Up to **80%** of differences in people's chances of getting Graves' disease may be due to genetics [R].

LESS LIKELY

**Less likely to have Graves' disease based on 176 genetic variants we looked at**

**Your top variants that most likely impact your genetic predisposition:**

| GENE | SNP | GENOTYPE |
|---|---|---|
| CTLA4 | rs3087243 | GG |
| TSHR | rs179247 | AA |
| TSHR | rs28414437 | CA |
| SESN3 | rs4409785 | TC |
| CTLA4 | rs231779 | TC |
| TPO | rs11675434 | CT |
| IGLV3-21 | rs5751536 | GA |
| TSHR | rs2300519 | AT |
| CTLA4 | rs231775 | GA |
| CD40 | rs1569723 | CA |
| MAF | rs17689159 | CT |
| FCRL3 | rs1977710 | AG |
| UHRF1BP1 | rs9469899 | AG |
| STAT4 | rs12612769 | CA |
| TMPRSS3 | rs34544259 | GA |
| RNASET2 | rs13210649 | TG |
| TRIB2 | rs1534422 | GG |
| TSHR | rs4903964 | AG |
| SH2B3 | rs653178 | CT |
| ZNF668 | rs57348955 | AG |
| TNFRSF14 | rs2843403 | CT |
| IL2RA | rs706779 | TC |
| CD40 | rs1883832 | TC |
| HLA-DPA1 | rs9357156 | AA |
| SLAMF6 | rs12026490 | TT |
| ALDH2 | rs4646776 | GG |
| HLA-DQA1 | rs2187668 | CC |
| PTPN22 | rs2476601 | GG |
| MAGT1 | rs4826198 | A |

| GENE | SNP | GENOTYPE |
|---|---|---|
| TNF | rs1799964 | TT |
| MICB | rs361525 | GG |
| TNF | rs1800629 | GG |
| CTLA4 | rs11571297 | TT |
| BACH2 | rs7754251 | GG |
| BACH2 | rs72928038 | GG |
| FCRL3 | rs3761959 | CC |
| GXYLT1 | rs4768412 | CC |
| LPP | rs13093110 | CC |

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

# Recommendations Details

## 1 Aerobic Exercise (Cardio)

Engage in at least 150 minutes of moderate-intensity aerobic exercise or 75 minutes of vigorous-intensity activity each week. Distribute this time over at least 3 days per week, avoiding consecutive days of vigorous exercise to allow for recovery.

TYPICAL STARTING DOSE

**1 hour**

### Helps with these Symptoms & Conditions:

- Allergies
- Anxiety
- High Blood Pressure
- Migraines

### Helps with these Goals:

- Energy
- Immunity
- Mood

### Helps with these DNA Risks:

- Asthma
- Coronary Artery Disease
- Melanoma

### Helps with these Lifestyle Risks:

- Attention Deficit Hyperactivity Disorder (ADHD)
- Anxiety
- Asthma

## 2 Strength Training

Engage in strength training exercises, such as weight lifting or bodyweight exercises, for 60 minutes per session, 2 to 3 times per week. Ensure you work all major muscle groups and rest each muscle group for at least 48 hours before exercising it again.

TYPICAL STARTING DOSE

**1 hour**

### Helps with these Symptoms & Conditions:

- Anxiety
- High Blood Pressure

### Helps with these Goals:

Immunity

Mood

Muscle Growth

### Helps with these DNA Risks:

Coronary Artery Disease

Muscle Mass

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD)

Anxiety

## 3 Omega-3 (Fish Oil)

Take 1-2 g of omega-3 (fish oil) supplement daily, preferably with a meal to enhance absorption.

TYPICAL STARTING DOSE

**500 mg**

### Helps with these Symptoms & Conditions:

Anxiety

High Blood Pressure

Migraines

### Helps with these Goals:

Exercise Recovery

Immunity

Mood

### Helps with these DNA Risks:

Asthma

Coronary Artery Disease

Melanoma

GAD1 (Glutamate/GABA)

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD)

Anxiety

Asthma

## 4 Vitamin C

Take 500-2000 mg of vitamin C supplement daily. It can be taken at any time of the day, with or without food, according to personal preference or tolerance.

TYPICAL STARTING DOSE

**500 mg**

### Helps with these Symptoms & Conditions:

- Anxiety
- High Blood Pressure

### Helps with these Goals:

- Immunity

### Helps with these DNA Risks:

- Asthma
- Coronary Artery Disease

### Helps with these Lifestyle Risks:

- Anxiety
- Asthma

## 5 Music Therapy

Engage in music therapy sessions for at least 30 minutes a day, three times a week. These sessions can involve listening to music, playing an instrument, singing, or writing songs, facilitated by a certified music therapist if possible.

TYPICAL STARTING DOSE

**30 minutes**

### Helps with these Symptoms & Conditions:

- Anxiety
- High Blood Pressure
- Migraines

### Helps with these Goals:

- Exercise Recovery
- Mood

### Helps with these DNA Risks:

- Asthma
- Coronary Artery Disease

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD)

Anxiety

Asthma

## 6 Mediterranean Diet

Incorporate a variety of primarily plant-based foods, such as fruits, vegetables, whole grains, nuts, and legumes, into every meal. Choose healthy fats, like olive oil, over saturated fats and consume fish and poultry at least twice a week. Limit red meat to a few times a month and include a moderate amount of dairy products. Opt for water and red wine in moderation as your beverages.

### Helps with these Symptoms & Conditions:

Allergies

High Blood Pressure

### Helps with these Goals:

Energy

Mood

### Helps with these DNA Risks:

Asthma

Coronary Artery Disease

Melanoma

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD)

Asthma

## 7 Yoga

Practice yoga for at least 20 to 30 minutes a day, most days of the week. Choose a style that matches your fitness level and goals, and consider attending a class or using online resources to guide your practice.

TYPICAL STARTING DOSE

**30 minutes**

### Helps with these Symptoms & Conditions:

Anxiety

High Blood Pressure

Migraines

### Helps with these Goals:

Energy | Exercise Recovery | Immunity | Mood | Muscle Growth

### Helps with these DNA Risks:

Asthma | Coronary Artery Disease | Muscle Mass

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD) | Anxiety | Asthma

## 8 Ginkgo

Take 120 mg of Ginkgo supplement daily, preferably with meals to aid absorption. This dosage is typically split into two 60 mg doses taken in the morning and evening for best results.

TYPICAL STARTING DOSE

**120 mg**

### Helps with these Symptoms & Conditions:

Allergies | Anxiety | Migraines

### Helps with these DNA Risks:

Asthma | Coronary Artery Disease

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD) | Anxiety | Asthma

## 9 Relaxation Techniques

Incorporate relaxation techniques such as deep breathing exercises, meditation, or yoga into your daily routine. Spend at least 15-30 minutes each day practicing one of these techniques, preferably in a quiet, comfortable space without interruptions.

TYPICAL STARTING DOSE

**30 minutes**

### Helps with these Symptoms & Conditions:

Anxiety | High Blood Pressure | Migraines

### Helps with these Goals:

Energy | Immunity | Mood

### Helps with these DNA Risks:

⚠ Coronary Artery Disease

### Helps with these Lifestyle Risks:

⚠ Attention Deficit Hyperactivity Disorder (ADHD) | ⚠ Anxiety

## 10 Magnesium

Take up to 350 mg of magnesium daily as a supplement, preferably with a meal to enhance absorption.

TYPICAL STARTING DOSE

**250 mg**

### Helps with these Symptoms & Conditions:

Anxiety | High Blood Pressure | Migraines

### Helps with these Goals:

Energy | Exercise Recovery | Immunity | Mood

### Helps with these DNA Risks:

⚠ Asthma | ⚠ Coronary Artery Disease

### Helps with these Lifestyle Risks:

⚠ Attention Deficit Hyperactivity Disorder (ADHD) | ⚠ Anxiety | ◇ Asthma

## 11 Tai Chi

Practice Tai Chi for 30 to 60 minutes at least twice a week. Choose a quiet, spacious area and follow along with a qualified instructor, either in person at a class or through an online video tutorial, to ensure proper technique and maximum benefit.

TYPICAL STARTING DOSE

1 hour

### Helps with these Symptoms & Conditions:

- Anxiety
- High Blood Pressure

### Helps with these Goals:

- Energy
- Mood

### Helps with these DNA Risks:

- Coronary Artery Disease

### Helps with these Lifestyle Risks:

- Attention Deficit Hyperactivity Disorder (ADHD)
- Anxiety

## 12 Avoid Air Pollution

**Stay indoors** on days when air quality indexes (AQI) indicate high pollution levels, which are often reported by weather services or government environmental agencies. **Install air purifiers** in your home, especially in bedrooms, to reduce indoor pollutants. Limit outdoor exercise when air pollution warnings are issued, opting for indoor activities instead.

### Helps with these Symptoms & Conditions:

- Allergies
- Anxiety
- High Blood Pressure

### Helps with these Goals:

- Immunity
- Mood

### Helps with these DNA Risks:

Asthma

Coronary Artery Disease

### Helps with these Lifestyle Risks:

Anxiety

Asthma

## 13 Meditation

Set aside 10-20 minutes each day in a quiet space without distractions to practice meditation. Focus on your breath or perform guided meditation using an app or audio track.

TYPICAL STARTING DOSE

**30 minutes**

### Helps with these Symptoms & Conditions:

Anxiety

Migraines

### Helps with these Goals:

Energy

Immunity

Mood

### Helps with these DNA Risks:

Coronary Artery Disease

### Helps with these Lifestyle Risks:

Attention Deficit Hyperactivity Disorder (ADHD)

Anxiety

## 14 Methylfolate

Take an L-methyl folate supplement (400-800 micrograms daily), ideally with a meal, to improve absorption. This dosage is recommended for adults, including pregnant women, to support overall health, especially to reduce the risk of neural tube defects in developing fetuses. Continue daily use as part of your regular supplement routine.

TYPICAL STARTING DOSE

**400 mcg**

### Helps with these Symptoms & Conditions:

High Blood Pressure

### Helps with these Goals:

Immunity

Mood

### Helps with these DNA Risks:

Coronary Artery Disease

Melanoma

MTHFR

Folate (Vitamin B9)

15

## Walking

Incorporate at least 30 minutes of brisk walking into your daily routine, aiming for a minimum of five days a week. This can be done in one continuous session or broken into shorter periods, such as three 10-minute walks throughout the day.

TYPICAL STARTING DOSE

**30 minutes**

### Helps with these Symptoms & Conditions:

Anxiety

High Blood Pressure

### Helps with these Goals:

Energy

Mood

### Helps with these DNA Risks:

Coronary Artery Disease

### Helps with these Lifestyle Risks:

Anxiety

# Next Steps

Remember, your genes only tell one important part of your health story!

Now that you've seen your DNA-based results for this health topic, let's take a look at other contributing factors.

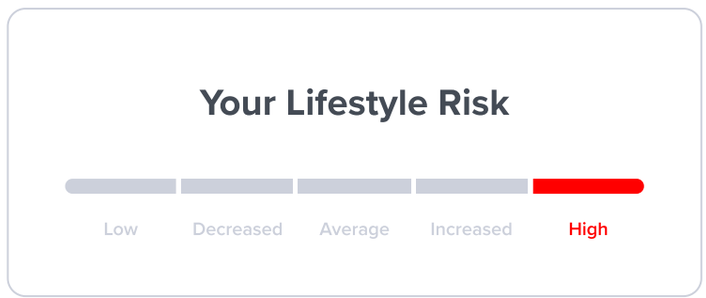
# Your Lifestyle Assessments

Ever heard of the term Nature vs. Nurture?

The thing is, both DNA and environment play a role in determining your health risks. The following assessments shows how much of an impact your lifestyle, environment and medical history are having on your health risks.

LIFESTYLE

**You have an increased risk of Attention Deficit Hyperactivity Disorder (ADHD) based on the answers you provided.**




## Factors impacting your risk:

Has your household ever received social welfare (e.g., Medicaid, housing assistance, AFDC etc.)?

**Yes**

Increasing Risk

How many years of formal education did your biological mother complete?

**13-14 years**

Increasing Risk

How much sleep do you get in a typical night?

**6 hours or less**

Increasing Risk

Do you have a parent or sibling who has ever been diagnosed with ADHD?

**Yes**

Increasing Risk

Did you grow up in a single-parent household for most of your early childhood?

**Yes**

Increasing Risk

What is your sex?

**Male**

Increasing Risk

Did your mother smoke while pregnant with you?

**No**

Decreasing Risk

Were you born early (before 37 weeks)?

**No**

Decreasing Risk

Has your biological mother ever suffered from depression?

**Not sure**

Decreasing Risk

LIFESTYLE

**You have a slightly increased risk of anxiety based on the answers you provided.**


## Factors impacting your risk:

Have either of your biological parents ever suffered from anxiety?

**Yes**

Increasing Risk

What is your current marital status?

**Single or not living with partner**

Increasing Risk

Do you consume at least 1000 mg caffeine per week (equivalent to 2 cups of coffee, 4 cups of tea, 6 cans of cola, or 1 energy drink per day)?

**Yes**

Increasing Risk

What is your sex?

**Male**

Increasing Risk

Do you regularly use drugs such as cannabis, cocaine, amphetamines, or opioids in a way that appreciably harms your health, social relationships, or occupational duties?

**Yes**

Increasing Risk

Have you ever struggled with substance misuse?

**Yes**

Increasing Risk

In a typical week, how many times do you participate in any physical activities or exercise for 30 minutes at a time? (such as walking, running, bike riding, weight training, yoga, etc.)

*Note: longer exercise equals more sessions (e.g., 1 hour = 2 sessions)

**8 or more**

Decreasing Risk

Do you smoke tobacco?

**No, never**

Decreasing Risk

Do you often experience periods of low mood?

**No**

Decreasing Risk

How much alcohol do you drink on a typical day?
Calculate your alcohol consumption in units here

**0 units**

Decreasing Risk

Did you ever suffer from physical abuse or physical bullying during your childhood?

**No**

Decreasing Risk

Did you ever suffer from sexual abuse during your childhood?

**No**

Decreasing Risk

Have you ever been diagnosed with rheumatoid arthritis (autoimmune joint inflammation)?

**No**

Decreasing Risk

What is your ethnicity?

**Other**

Decreasing Risk

Do you suffer from chronic pain?

**No**

Decreasing Risk

What is your current employment status?

**Self-employed**

Decreasing Risk

Did you ever suffer from emotional or physical neglect during your childhood?

**No**

Decreasing Risk

Have you ever been diagnosed with alcohol use disorder?

**No**

Decreasing Risk

LIFESTYLE

**You have an average risk of asthma based on the answers you provided.**


## Factors impacting your risk:

Your BMI:

**30.77**

Increasing Risk

---

Have you ever been diagnosed with atopic dermatitis (eczema)?

**Yes**

Increasing Risk

---

In a typical week, how many times do you participate in any physical activities or exercise for 30 minutes at a time? (such as walking, running, bike riding, weight training, yoga, etc.)

*Note: longer exercise equals more sessions (e.g., 1 hour = 2 sessions)

**8 or more**

Decreasing Risk

---

Did your mother smoke while pregnant with you?

**No**

Decreasing Risk

---

Have you ever been diagnosed with allergic rhinitis (hay fever)?

**No**

Decreasing Risk

---

Do you have a parent or sibling who has ever been diagnosed with asthma?

**No**

Decreasing Risk

---

How would you describe the environment you live in?

**Suburban**

Decreasing Risk

---

What is your height?

**178 cm**

No impact

---

What is your current weight?

**97.5 kg**

No impact

LIFESTYLE

**You have a slightly reduced risk of hashimoto's disease based on the answers you provided.**


## Factors impacting your risk:

Your BMI:
**30.77**
Increasing Risk

Have you ever been diagnosed with multiple sclerosis?
**No**
Decreasing Risk

Have you been diagnosed with psoriasis?
**No**
Decreasing Risk

Have you ever been diagnosed with rheumatoid arthritis (autoimmune joint inflammation)?
**No**
Decreasing Risk

Have you ever been diagnosed with lupus?
**No**
Decreasing Risk

Have you ever been diagnosed with type 1 diabetes?
**No**
Decreasing Risk

Do you have a parent or sibling who has been diagnosed with Hashimoto's disease (autoimmune underactive thyroid)?
**No**
Decreasing Risk

What is your sex?
**Male**
Decreasing Risk

What is your height?
**178 cm**
No impact

What is your current weight?
**97.5 kg**
No impact