SelfDecode™

CYP2C9 (Detox)

Gene Report

REPORT CATEGORY

DETOX

Sample Client

Report date: 15 January 2026

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DISCLAIMER

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

Personal information

NAME

Sample Client

SEX AT BIRTH

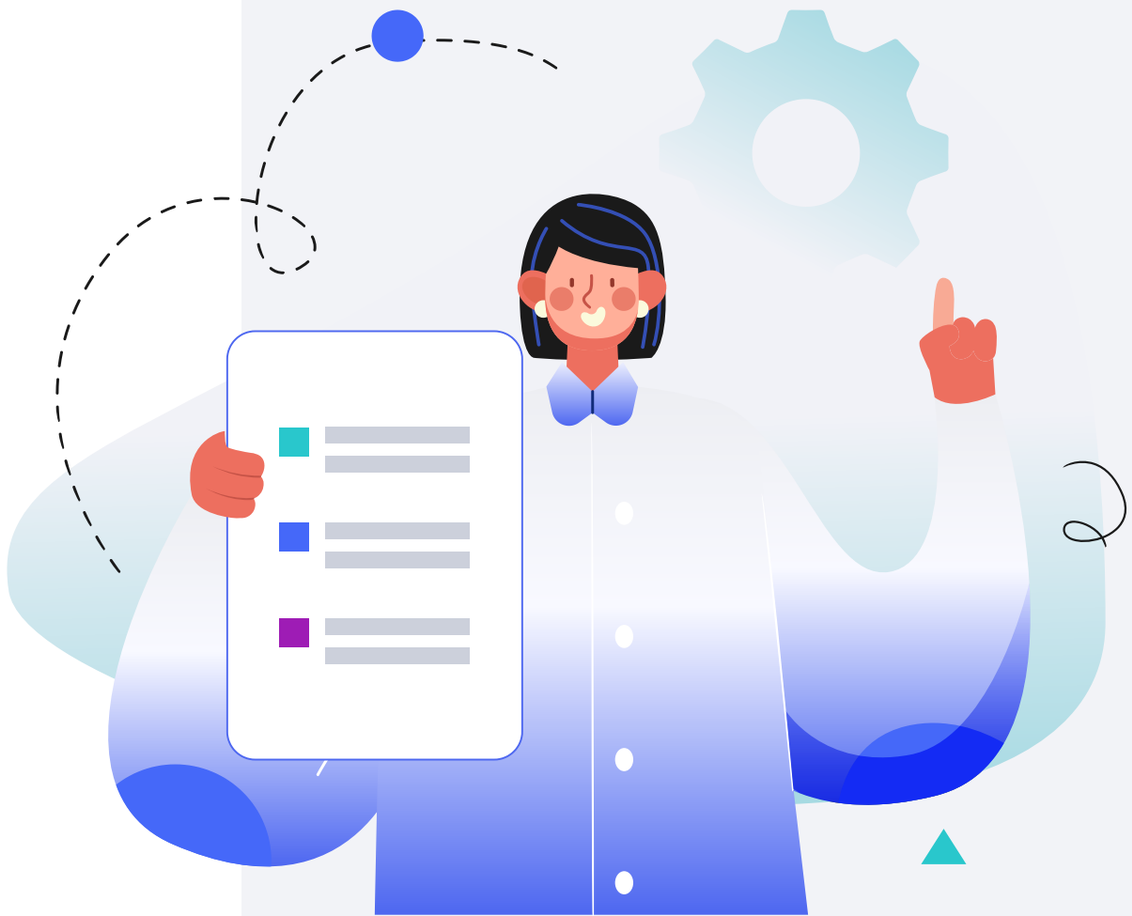
Male

HEIGHT

5ft 5" 165cm

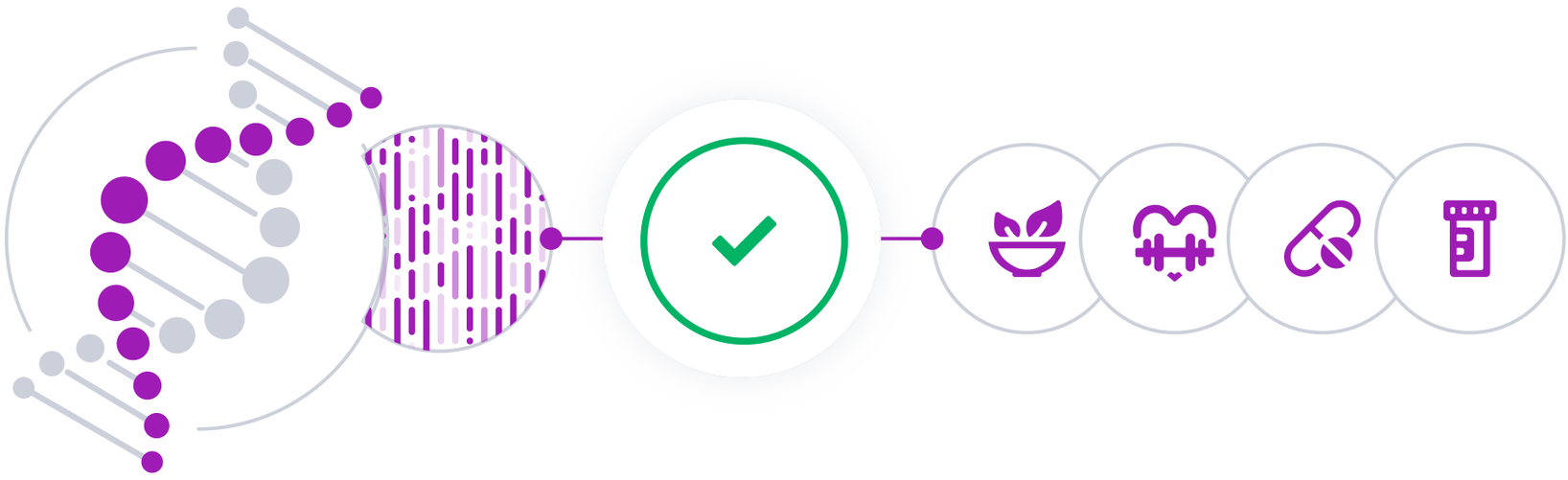
WEIGHT

137lb 62kg



How this works

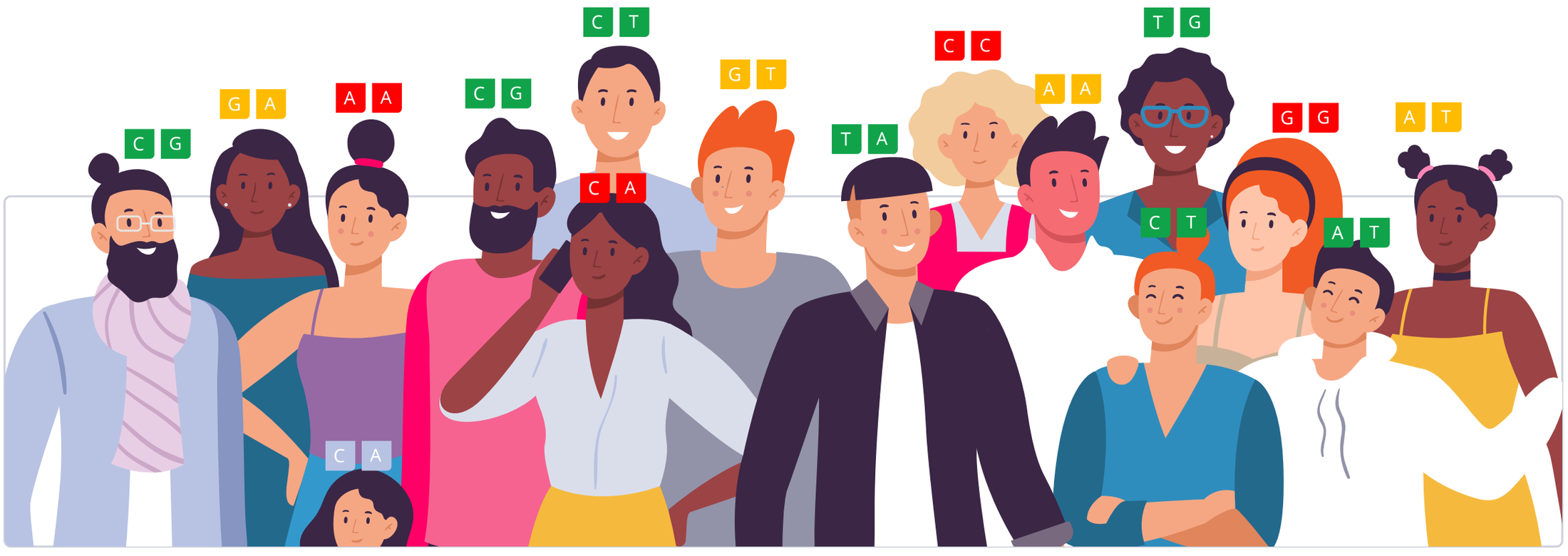
Our Wellness Reports analyze how your DNA influences your health.
We then use this analysis to give you personalized risk estimates and recommendations.



Similarly, our Trait Reports look at how your DNA influences your traits.

Your DNA is like an instruction manual — it contains a lot of information.
You can think of it as a blueprint for your body.

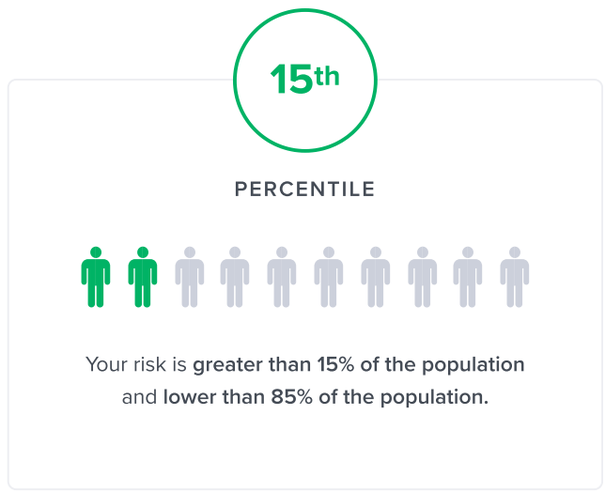
Genetic variants are parts of DNA that differ from person to person. Some can make you more vulnerable to certain health issues, while others may influence traits such as eye color.



We use artificial intelligence and machine learning to analyze all this information. We then summarize your results as a risk score or display it on a gauge.

When we give a risk score, the risk icon tells you if you are at a higher or lower risk compared to other people:

In total, we analyze up to 83 million genetic variants.



Genotype color info: AA You don't have any risk alleles | AA You have 1 risk allele | AA You have 2 risk alleles

Your risk is also displayed as a percentile. This will tell you how your risks compare to our sample population. The lower your percentile number, the lower your risk. The "50th percentile" would be an average risk.

Similarly, the gauge tells you your relative risk score compared to our sample population, or it indicates a specific trait or haplotype you are more likely to have based on your genetic variants.

When applicable, we also list top evidence-based recommendations that may help lower your risk. The focus is on recommendations that may be of benefit to you, based on your genetics.

Our recommendations come in four categories: lifestyle, diet, supplements and drugs.
The following icons tell you which category a recommendation falls into:

Our team of scientists also ranks each recommendation.
We rank based on impact and the strength of evidence in the medical literature.

Impact shows how strongly a recommendation will affect your health in a certain area.
Evidence is how much scientific support there is for the recommendation. Rankings are from 1 to 5 (low to high):

Impact

Impact scores range from 1-5. These scores reflect how much of an effect each recommendation can have. An impact score of 5 predicts the biggest effect.

When a recommendation affects something we can measure, we use those measurements to assign the impact score. For example, a recommendation that decreases cholesterol by 20% will have a higher impact score than one that decreases it by 5%.

Some recommendations affect things that we cannot directly measure, like stress or mood. For these, the impact score is based on how well they work relative to other recommendations and standard treatments. The best ones get the highest scores.

If there is a lot of research that shows a recommendation works especially well for your genotype, the impact score gets increased.

Recommendation Evidence

5 / 5

Recommendations that are considered effective and generally recommended by experts and medical bodies.

4 / 5

Recommendations that are considered likely effective and that have multiple independent meta-analyses and a great many studies supporting them.

3 / 5

Recommendations that are considered possibly effective and have many studies supporting them

2 / 5

Recommendations that have insufficient evidence, with two or several clinical trials supporting them, or many studies but with ambiguous results.

1 / 5

Recommendations that have insufficient evidence, with a single clinical trial, or with many studies most of which didn't find support for the recommendation.

0 / 5

No evidence in humans.

Genotype-specific Evidence

High-quality

Direct evidence that a recommendation helps more in people with your gene variant (many clinical trials, afew large clinical trials, or a meta-analysis).

Medium-quality

Direct evidence that a recommendation helps more in people with your gene variant (a few clinical trials or one large clinical trial).

Low-quality

Direct evidence that a recommendation helps more in people with your gene variant (a single clinical trial or more trials with inconsistent results).

Indirect

A recommendation may help more in people with your gene variant because it targets a specific gene or protein affected by your variant (e.g., MTHFR, dopamine).

In theory

A recommendation may help more in people with your gene variant because it targets a specific mechanism affected by your variant (e.g., inflammation, oxidative stress).

Some things to keep in mind:

- Genetics doesn’t play a considerable role in a condition or a trait.
- There is not enough research available to estimate a genetic predisposition.
- There are technical limitations to estimating or presenting a genetic predisposition.
- The topic is sensitive, and a genetic predisposition should only be estimated and presented by a healthcare professional.

Introduction

CYP2C9 is one of the cytochrome P450 monooxygenases (CYP enzymes). These are **enzymes that eliminate most of the drugs and toxins** from the human body [R].

CYP2C9 is the third most important cytochrome P450 in terms of the number of drugs metabolized. Specifically, it's responsible for the metabolic clearance of up to 15-20% of all drugs undergoing Phase I detox. CYP2C9 metabolizes multiple antidiabetic, antiepileptic, antihypertensive, anti-inflammatory, anticoagulant, and cholesterol-lowering drugs [R, R, R, R, R, R, R, R].

CYP2C9 also metabolizes many hormones and other compounds naturally found in the body, such as progesterone, testosterone and arachidonic acid [R].

Importantly, CYP2C9 metabolizes the psychoactive component THC from cannabis. Specifically, its the main enzyme responsible for the hydroxylation of THC to 11-OH-THC (a metabolite that still has psychoactive properties but is less potent than THC) [R, R, R, R].

Alternatively, THC and its metabolites can inhibit this enzyme and reduce its effectiveness at metabolizing drugs [R, R, R, R, R].

The enzyme is primarily found in the liver, heart, and blood vessels. In the liver, it accounts for about 20% of total CYP content [R, R].

The following chemicals may increase CYP2C9 activity [R, R]:

- Limonene
- Melatonin
- Quercetin
- Bisphenol A
- Rifampicin

In contrast, CYP2C9 activity may be decreased by [R, R, R, R, R, R, R, R, R, R, R]:

- Garlic
- Pomegranate
- Hops
- Apigenin
- Starfruit juice
- Cranberry
- Chamomile
- Goji berries
- Saint John's wort
- Baicalein
- Licorice
- Caffeic acid
- Quercetin
- African lettuce
- Goldenseal
- Berberine
- THC
- CBD
- Amiodarone

- Fluconazole
- Sulphapenazole

Genetics of CYP2C9 and THC Metabolism

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.