SelfDecode™

CDKN2B-AS (Cardiovascular)

Gene Report

REPORT CATEGORY

HEART & BLOOD VESSELS

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

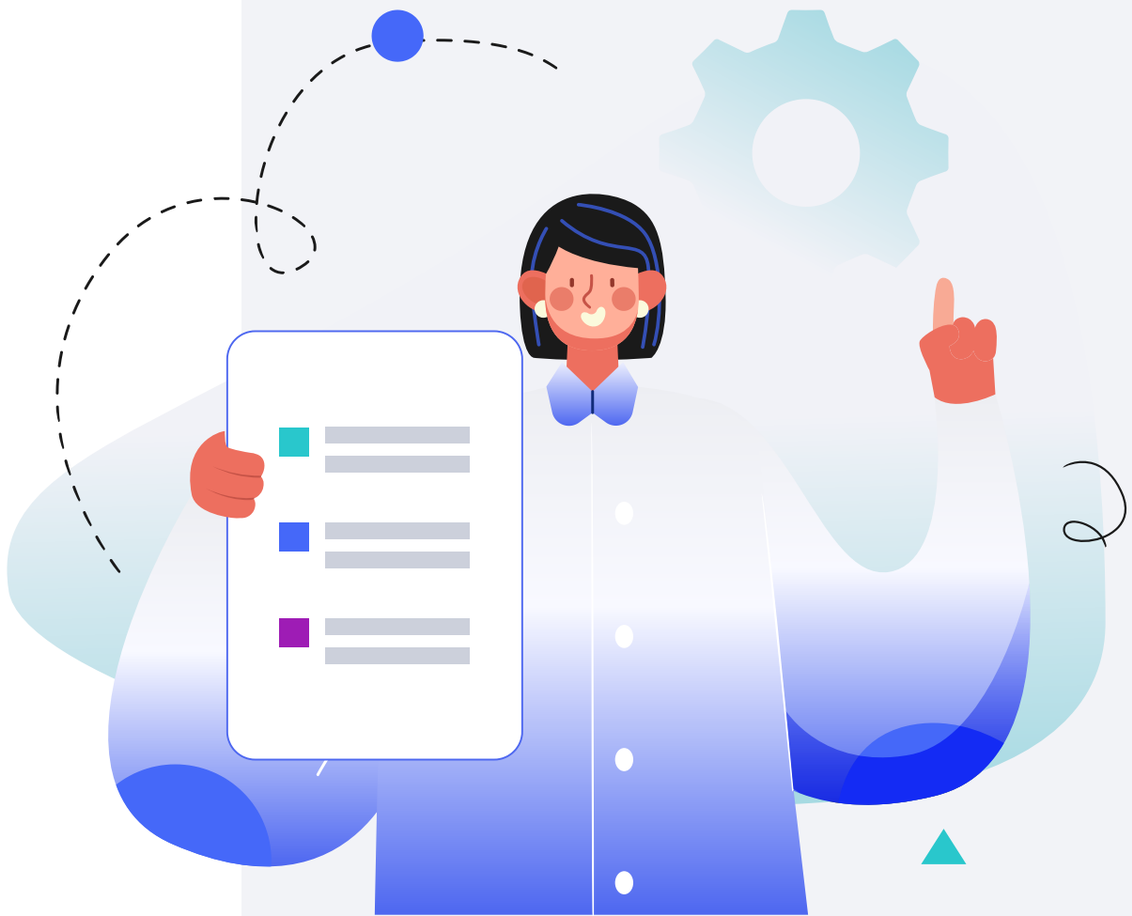
Male

HEIGHT

5ft 5" 165cm

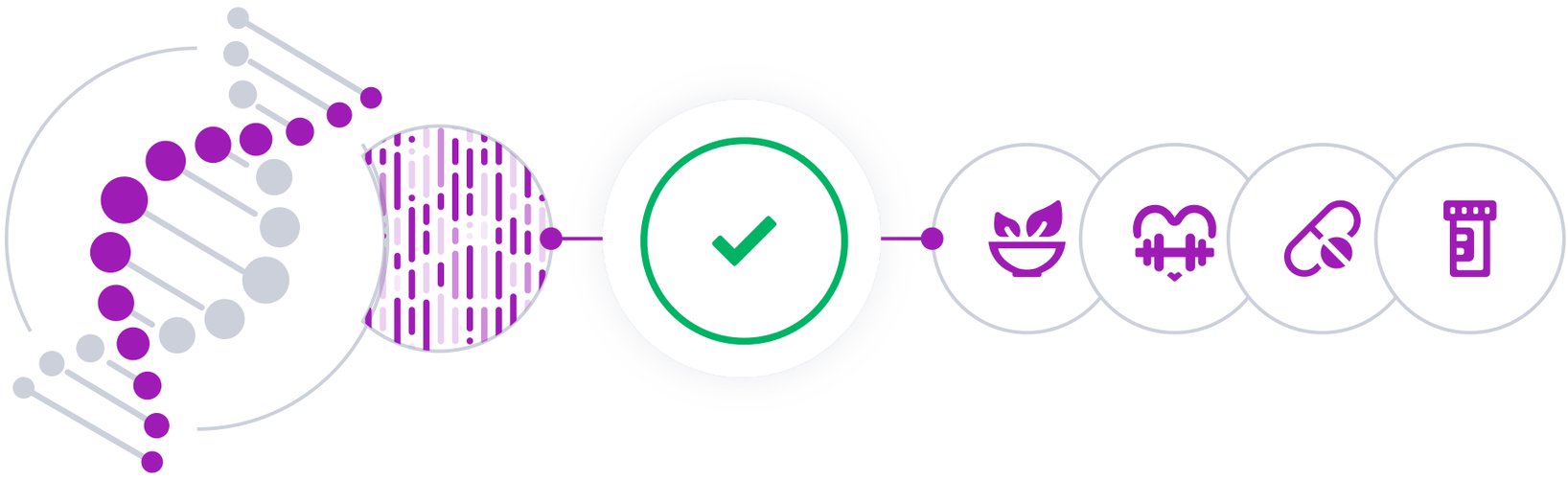
WEIGHT

137lb 62kg



How this works

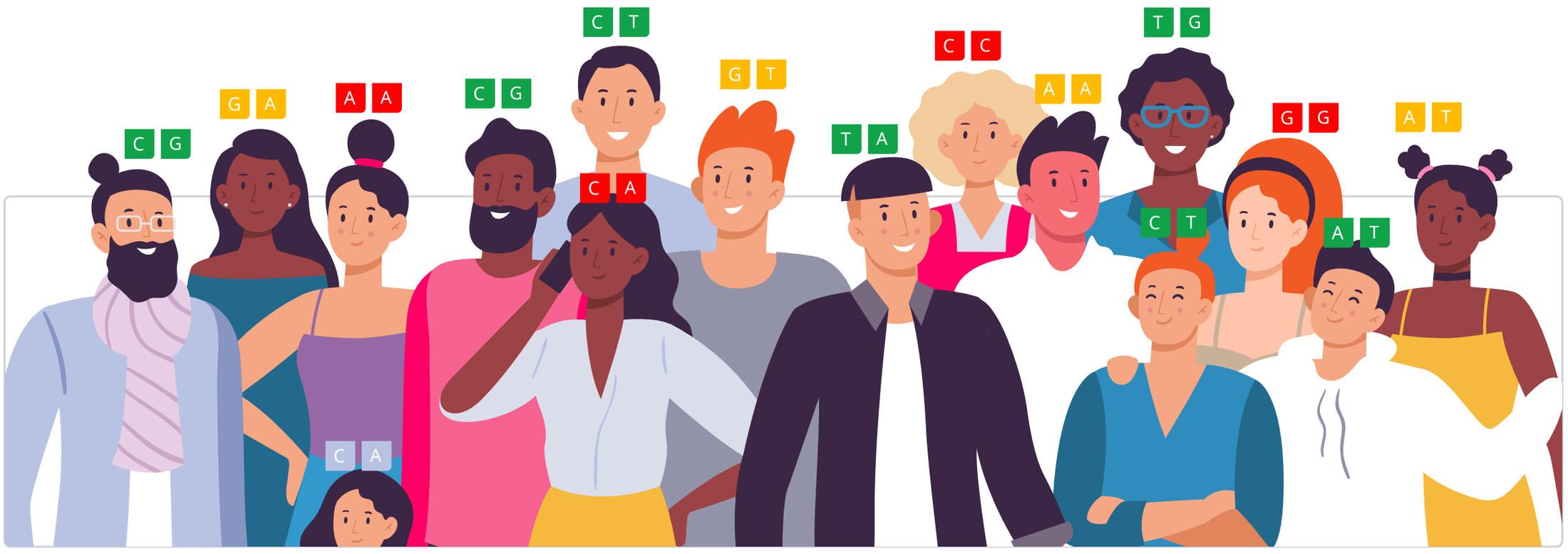
Our Wellness Reports analyze how your DNA influences your health.
We then use this analysis to give you personalized risk estimates and recommendations.



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.

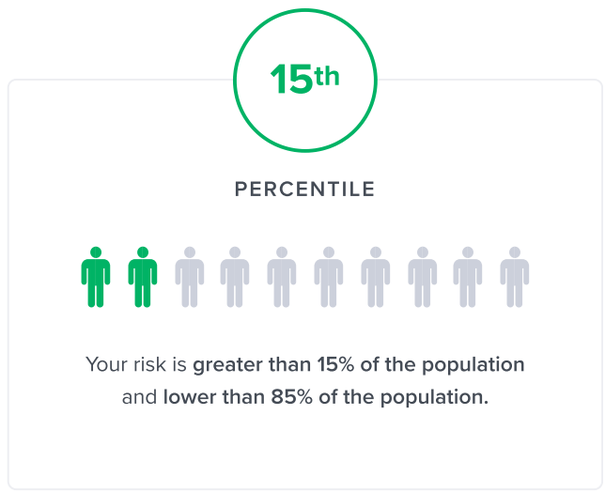
Genetic variants are parts of DNA that differ from person to person. Some can make you more vulnerable to certain health issues, while others may influence traits such as eye color.



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

The *CDKN2B-AS* (‘*CDKN2B and CDKN2A antisense cis and trans regulatory RNA 1*’) gene, also known as *ANRIL* (‘*antisense non-coding RNA in the INK4 locus*’), encodes a regulatory RNA molecule. It is located between the *CDKN2A* and *CDKN2B* genes and can inhibit their expression [R].

The *CDKN2A* gene encodes several proteins, including p16(INK4a) and p14(ARF). Both function as tumor suppressors, which means they keep cells from growing and dividing too rapidly or in an uncontrolled way. These proteins help regulate the cell cycle [R].

The *CDKN2B* gene encodes cyclin-dependent kinase 4 inhibitor B, also known as multiple tumor suppressor 2 (MTS-2). *CDKN2B* gene expression is dramatically increased by TGF-beta (transforming growth factor beta), which has a wide variety of functions including blocking the growth and development of some types of cells [R, R, R].

Variants in the *CDKN2B-AS* gene have been associated with an increased susceptibility to cardiovascular disease, as well as other conditions such as cancers, diabetes, or Alzheimer’s disease [R].

CDKN2B-AS Genetics

The most widely investigated *CDKN2B-AS* variant is **rs10757278**. Its minor 'G' allele has been associated with an increased risk of:

- Coronary artery disease [R, R, R, R, R]
- Ischemic stroke [R, R, R, R]
- Myocardial infarction [R]
- Intracranial aneurysm [R, R]
- Cancer (especially, breast and prostate) [R]

Another well-researched variant, the 'G' allele of **rs10757274**, has been associated with an increased risk of:

- Coronary artery disease [R, R, R, R, R, R, R]
- Ischemic stroke [R, R, R, R]
- Sudden cardiac death [R]
- Angina pectoris [R]

The 'G' allele of **rs2383206** also increases *CDKN2B-AS* expression. This variant has been associated with an increased risk of:

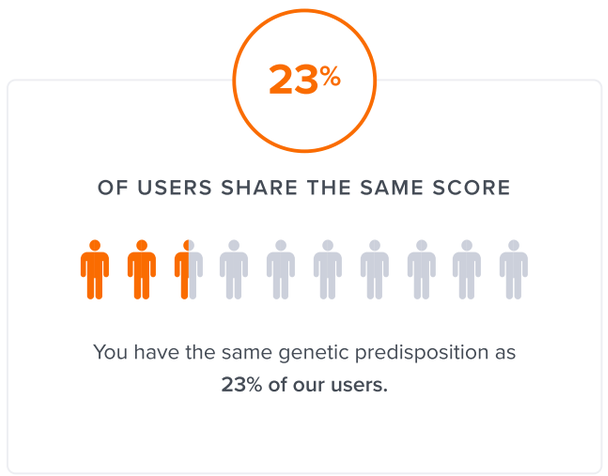
- Coronary artery disease [R, R, R, R, R]
- Ischemic stroke [R, R, R]

Finally, the 'G' allele of **rs2383207** has been associated with an increased risk of coronary artery disease [R, R, R].

These variants are associated with lower expression of a region in this gene and are usually inherited together, meaning you will most likely have all or none of them [R].

LOWER ACTIVITY

Predisposed to a lower CDKN2B-AS activity based on the genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CDKN2B	rs10757278	GG
CDKN2A	rs10757274	GG
CDKN2B	rs2383206	GG
CDKN2B	rs2383207	GG

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