SelfDecode™

SIRT3 (Longevity)

Gene Report

REPORT CATEGORY

LONGEVITY

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

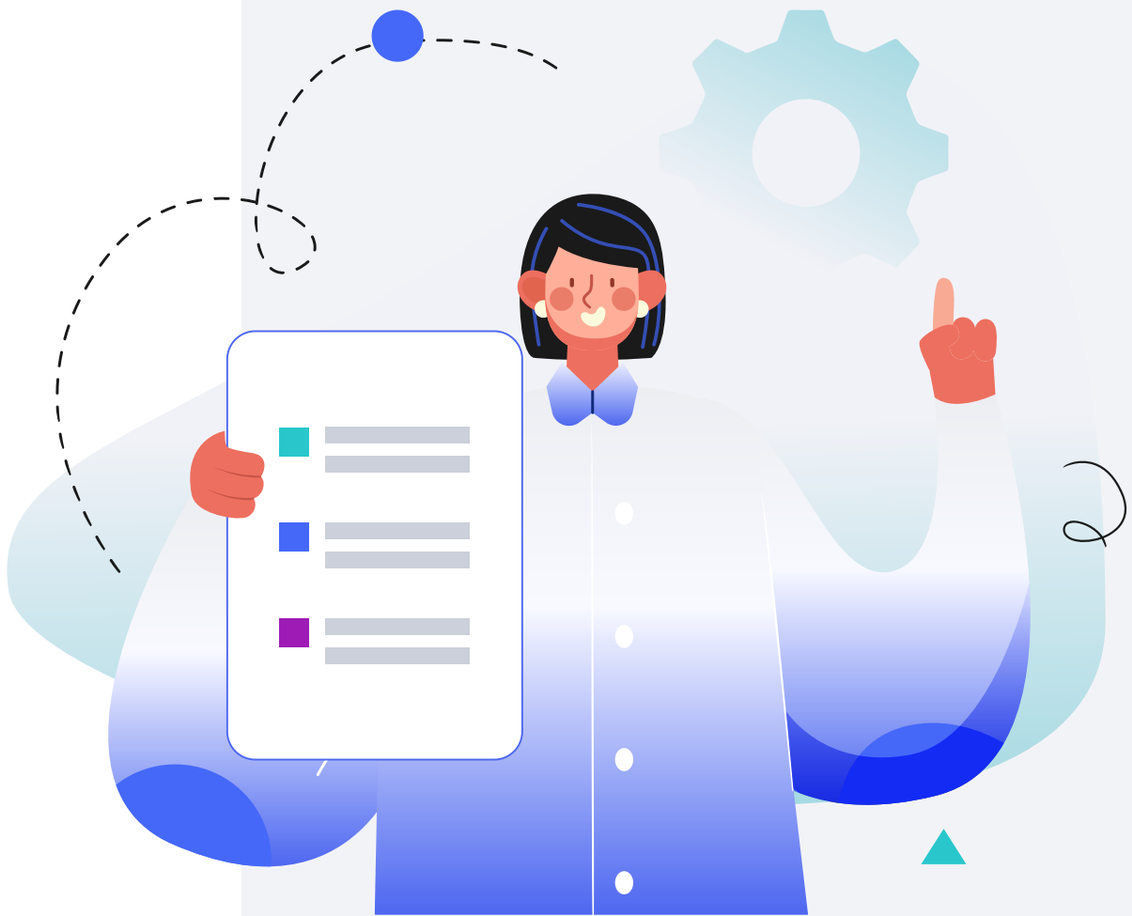
Male

HEIGHT

5ft 5" 165cm

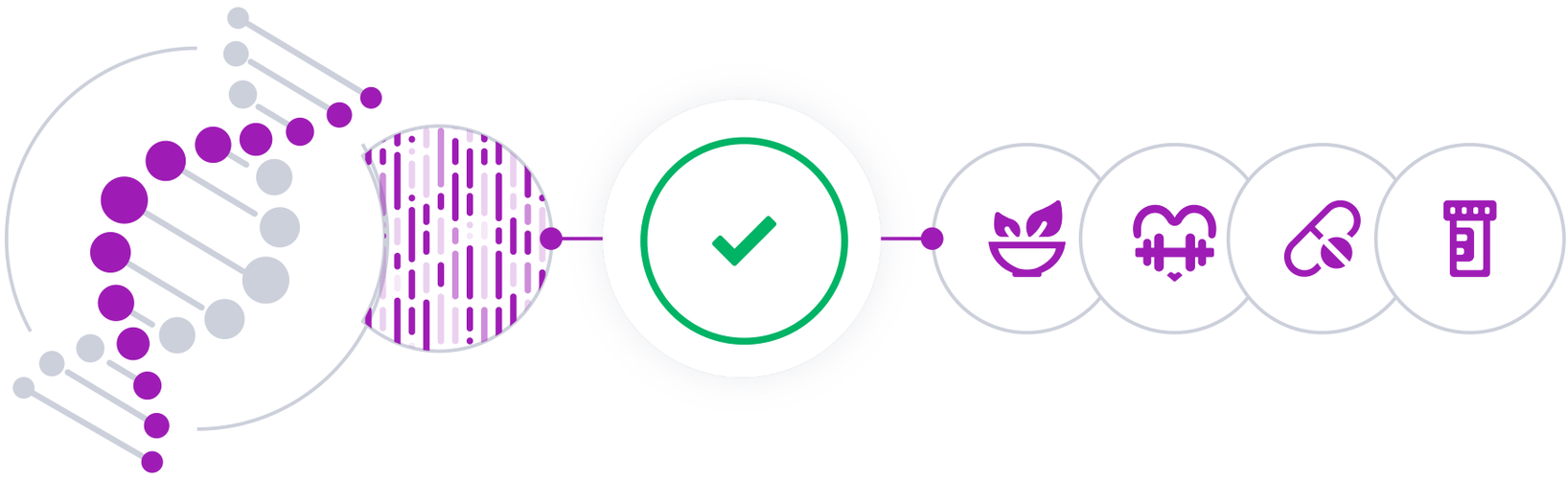
WEIGHT

137lb 62kg



How this works

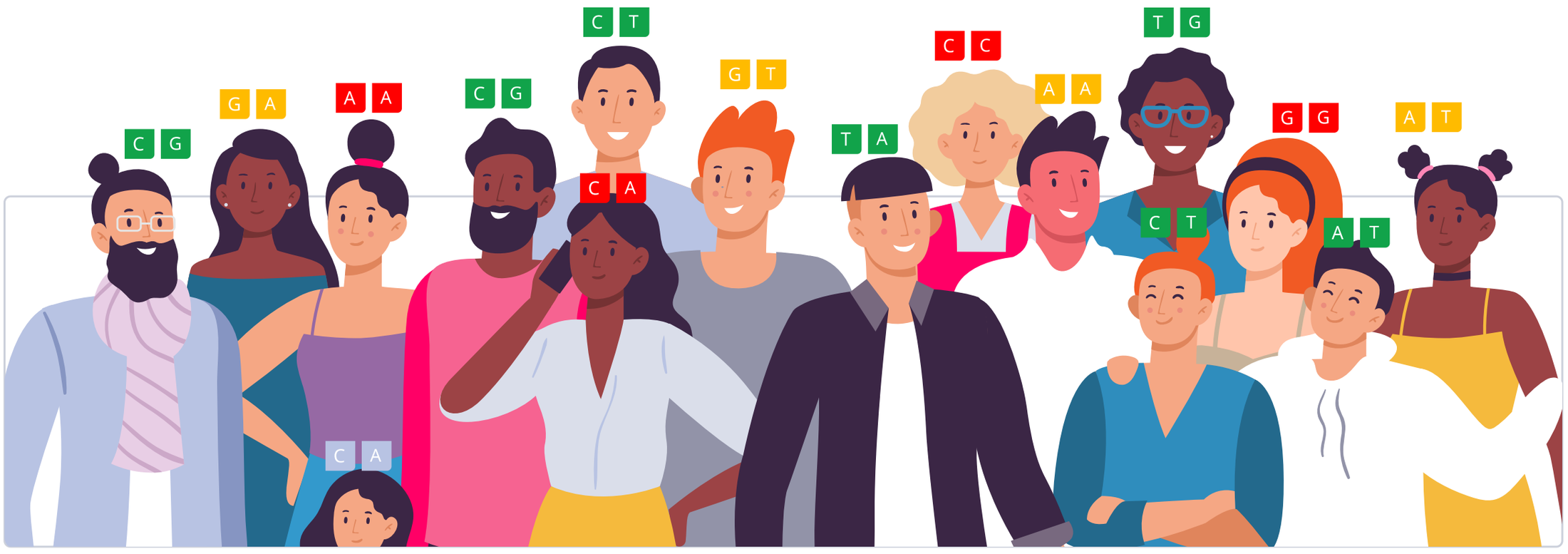
Our Wellness Reports analyze how your DNA influences your health.
We then use this analysis to give you personalized risk estimates and recommendations.



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 *SIRT3* gene encodes a sirtuin protein. Sirtuins are a group of mitochondrial enzymes heavily implicated in aging, cell death, inflammation, mental and physical stress resistance, and energy metabolism. They regulate and "turn off" other genes, especially those involved in the process of aging [R, R, R].

When your cells experience stress, acetyl groups are added to proteins as a response to changes induced by inflammation and oxidation. Sirtuins (like SIRT3) remove these acetyl groups to keep the protein in service longer than usual [R, R].

Many age-related and degenerative diseases are characterized by low sirtuin activity, including [R, R]:

- Cancer
- Alzheimer's disease
- Parkinson's disease
- Huntington's disease
- Amyotrophic lateral sclerosis (ALS)
- Kennedy's disease

Sirtuin activity is also unusually low in chronic inflammation. Some researchers believe that activating the sirtuins may help manage obesity, atherosclerosis, diabetes, and other inflammatory diseases [R].

Given all of this, it's not surprising that *SIRT3* has been touted as a longevity gene. Some of the mechanisms by which SIRT3 may affect aging include:

- Reducing oxidative stress by promoting ROS scavenging [R]
- Supporting mitochondrial function [R]
- Improving fat and sugar metabolism [R, R]
- Reducing the risk of cancer [R]
- Helping fight off infections [R, R]
- Activating other longevity proteins such as FOXO3 [R]

SIRT3 Genetics

A handful of studies have shown that people with certain *SIRT3* variants are more likely to live very long lives. One of the variations with the strongest effect so far is **rs11555236** (G477T). People homozygous for the minor 'A' allele may live longer lives. This variant has been found to increase SIRT3 levels [R, R, R].

Another SNP with a potential impact on lifespan is **rs4980329**: the 'T' allele is more common among long-lived individuals. This variant has also been associated with a decreased risk of ALS and ischemic stroke from the rupture of unstable carotid plaques [R, R, R].

In contrast, the 'T' allele of **rs11246020** may decrease SIRT3 activity and has been associated with an increased risk of metabolic syndrome and stomach cancer, and higher HbA1c levels. However, this allele has been linked to lower increments in triglyceride levels after meals [R, R, R, R].

The 'A' allele of **rs28365927**, believed to reduce SIRT3 activity, has been associated with an increased risk of NAFLD and higher ALT levels in people with his condition. However, it has also been associated with a decreased risk of coronary artery disease [R, R].

A variant encoding a form of the protein with reduced activity, 'G' at **rs185277566**, has been associated with an increased risk of myocardial infarction and infertility in women exposed to war toxins [R, R].

Finally, the 'T' allele of **rs3782118**, believed to increase SIRT3 activity, has been associated with a decreased risk of tuberculosis [R].

TYPICAL ACTIVITY

Predisposed to typical SIRT3 activity based on 5 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SIRT3	rs11555236	CC
SIRT3	rs4980329	CC
SIRT3	rs3782118	CT
IFITM2	rs28365927	GG
RIC8A	rs185277566	CC
SIRT3	rs11246020	CC

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