SelfDecode™

SLC6A2 (Mental Health)

Gene Report

REPORT CATEGORY

MENTAL HEALTH

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

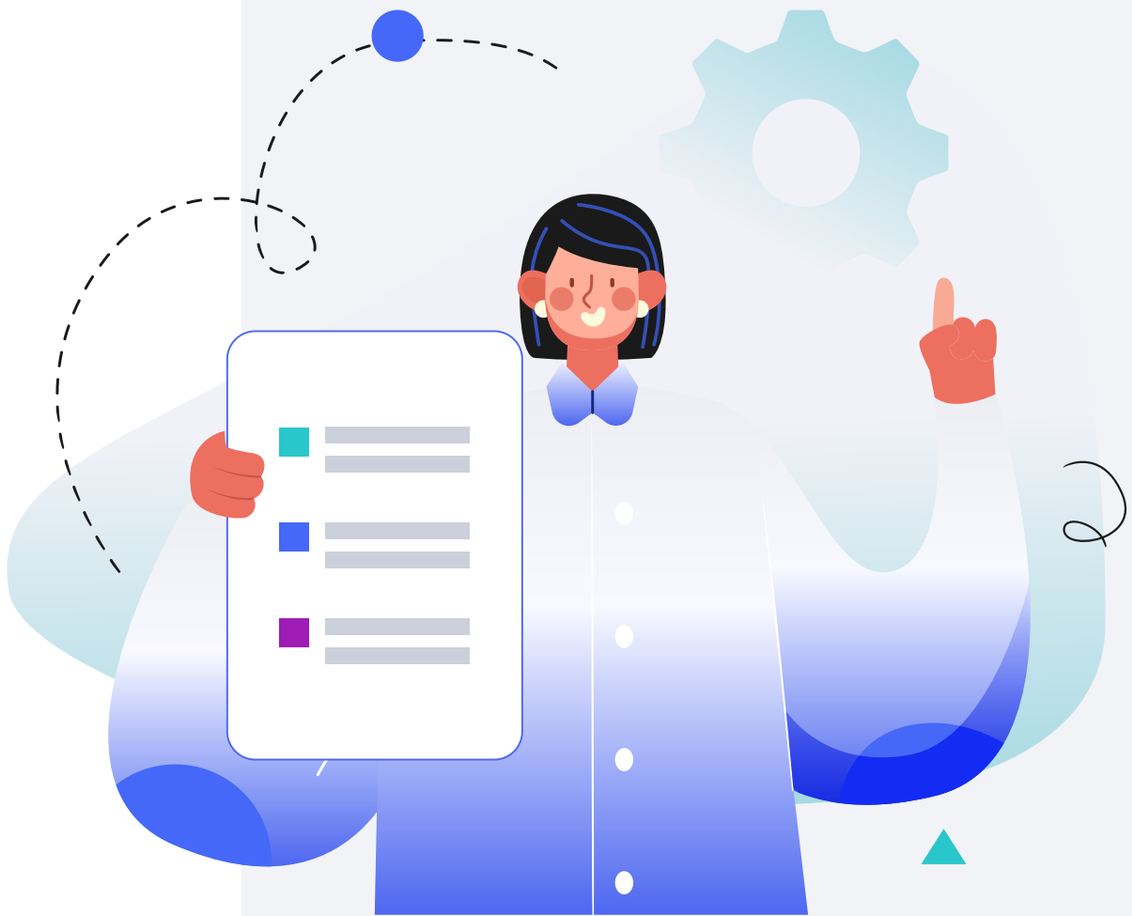
Male

HEIGHT

5ft 5" 165cm

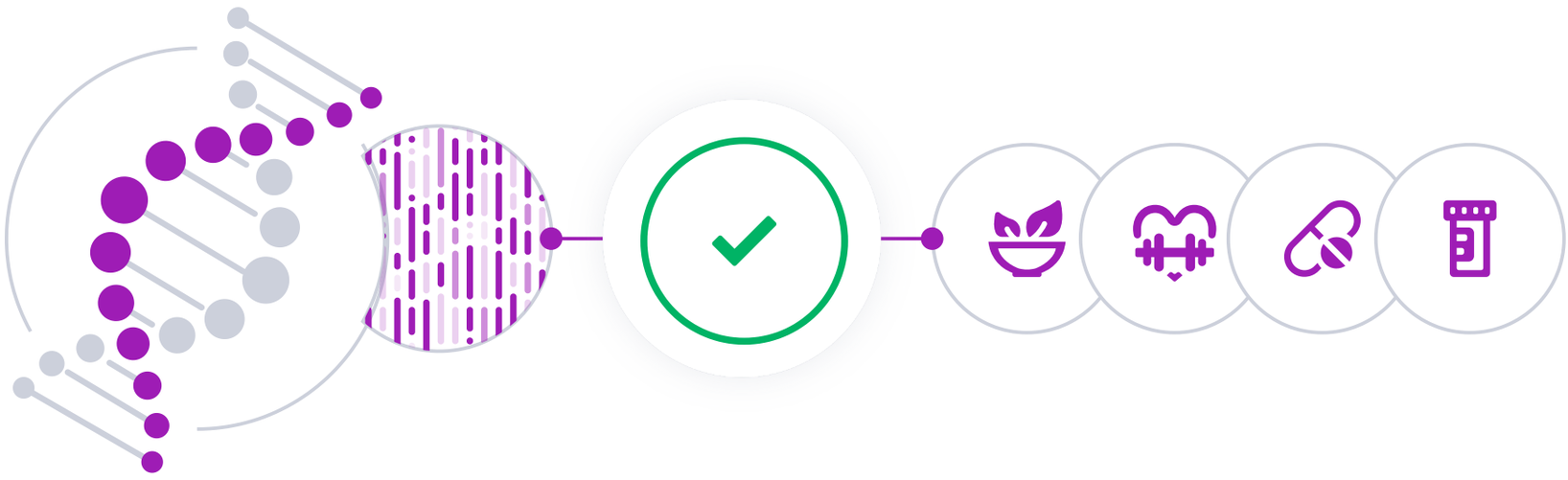
WEIGHT

137lb 62kg



How this works

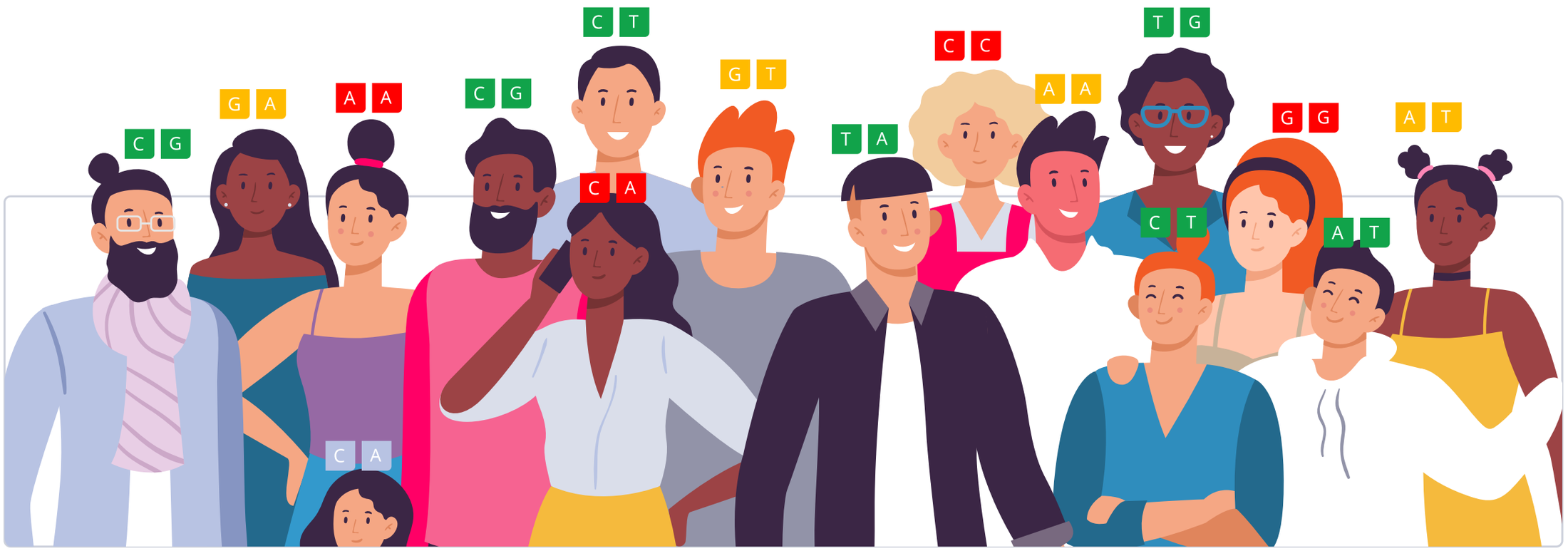
Our Wellness Reports analyze how your DNA influences your health.
We then use this analysis to give you personalized risk estimates and recommendations.



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.

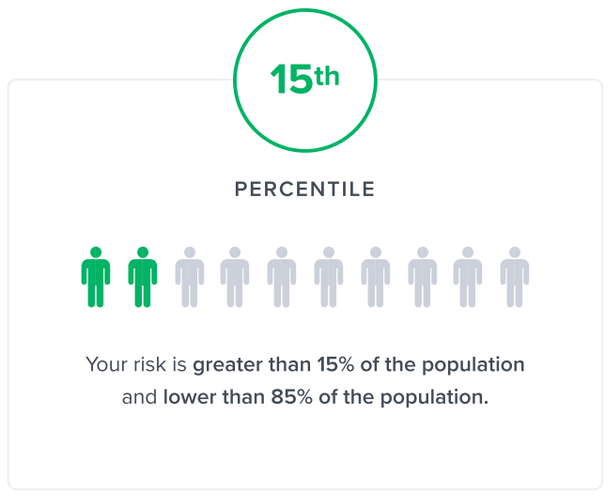
Genetic variants are parts of DNA that differ from person to person. Some can make you more vulnerable to certain health issues, while others may influence traits such as eye color.



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 *SLC6A2* gene encodes a member of the sodium:neurotransmitter symporter family called norepinephrine transporter (NET). As its name suggests, this protein plays a key role in norepinephrine transport and homeostasis [R].

Norepinpehrine is released from noradrenergic neurons during synaptic transmission. This neurotransmitter regulates mood, arousal, memory, learning, and pain perception, and supports the “fight or flight” stress response. NET functions to transport as much as 90% of this norepinephrine, together with sodium and chloride, back into the presynaptic neuron [R, R].

Mutations in this gene cause orthostatic intolerance, a syndrome characterized by lightheadedness, fatigue, altered mentation and syncope. Alternatively, certain gene variants have been associated with ADHD [R, R].

SLC6A2 Genetics

In line with the role of norepinephrine in several aspects of attention such as increased focus, memory recall, and alertness, dysfunction of the norepinephrine system has been linked to ADHD [R, R].

The following SLC6A2 variants have been associated with ADHD risk and worse inattention symptoms:

- 'T' at **rs3785143** (especially true for oppositional defiant disorder) [R, R, R, R, R, R]
- 'T' at **rs3785157** [R, R, R]
- 'C' at **rs11568324** [R, R]
- 'C' at **rs2242447** [R]
- 'T' at **rs28386840** [R, R, R]

These variants may increase *SLC6A2* expression and reduce norepinephrine levels in the brain, potentially contributing to ADHD symptoms.

Some of these variants have also been found to affect the effectiveness of ADHD treatment. For instance, multiple studies found that children with ADHD were more likely to respond to methylphenidate if they carried the risk allele at rs28386840 [R].

In contrast, carriers of the 'T' allele of rs3785143 may not respond to atomoxetine [R, R].

TYPICAL ACTIVITY

Likely typical SLC6A2 activity based on 5 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
SLC6A2	rs11568324	CC
SLC6A2	rs28386840	TA
CES1	rs2242447	CT
SLC6A2	rs3785143	CC
SLC6A2	rs3785157	CC

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