

INSIG2 (Weight)

Gene Report

REPORT CATEGORY —



WEIGHT & BODY FAT

Sample Client

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omicsedge

Table of Contents

03 How this works

- 04 Impact
- 05 Evidence
- 06 Some things to keep in mind

07 Introduction

08 Your genetics

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.

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

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



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, a few 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 [INSIG2](#) gene encodes a protein also called INSIG2, which is short for ‘*Insulin-induced gene 2*’. INSIG2 regulates the production of cholesterol and fatty acids by blocking it when the levels of these molecules are high. As its name suggests, *INSIG2* expression increases when insulin secretion is abundant. This is the case in conditions such as diabetes and obesity [\[R\]](#), [\[R\]](#).

INSIG2 reduces the production of fatty molecules (via inhibiting SREBPs) [\[R\]](#), [\[R\]](#), [\[R\]](#).

Engineered mice lacking the *INSIG2* gene accumulated high levels of cholesterol and triglycerides in the liver due to their inability to inhibit SREBPs. Conversely, those producing high levels of this protein in the liver showed reduced fat production [\[R\]](#), [\[R\]](#).

INSIG2 Genetics

The minor ‘C’ variant of the [rs7566605](#) SNP has been associated with obesity and high BMI in multiple populations [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#).

Moreover, it was linked to increased fat and weight gain during pregnancy in American women and waist-to-hip ratio in Norwegian men [\[R\]](#), [\[R\]](#), [\[R\]](#).

Similarly, the ‘C’ variant was associated with childhood obesity in multiple studies [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#).

A meta-analysis investigating these discrepancies found the variant is overall unrelated to obesity, possibly due to different ethnicities between studies. However, it did find an association between the ‘C’ variant and extreme obesity (BMI> 37.5 kg/m²) [\[R\]](#).

The rs7566605 polymorphism is located near the *INSIG2* gene, in a region believed to affect its expression. Although its contribution to *INSIG2* expression and activity hasn’t been investigated, the variant might reduce INSIG2 based on its effects on body weight [\[R\]](#).

In a trial on American and Irish Caucasian men, carriers of the ‘C’ variant lost less body fat from resistance training [\[R\]](#).

Similarly, obese children and adolescents with the ‘C’ variant lost less weight from an intervention combining exercise and dietary education in two German studies [\[R\]](#), [\[R\]](#).

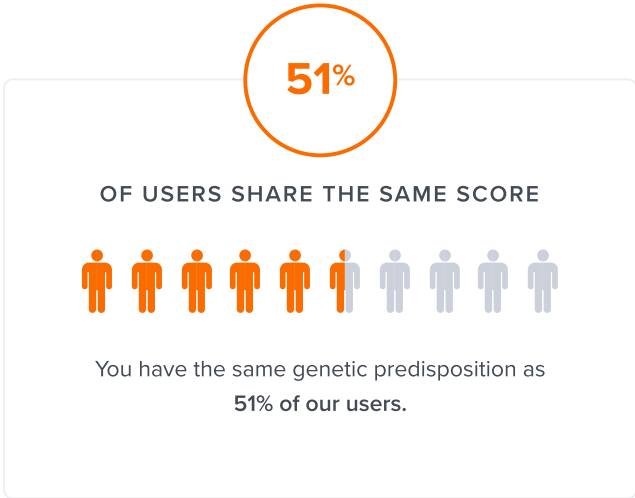
A Danish study failed to associate this variant with obesity but found that carriers gained more weight during periods of physical inactivity [\[R\]](#).

However, this variant increased the positive effects of a lifestyle intervention in a multi-ethnic American study, and carriers of the ‘G’ allele re-gained more intramuscular fat in the arm one year after stopping physical training [\[R\]](#), [\[R\]](#).



LOWER ACTIVITY

Predisposed to a lower INSIG2 activity based on the genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CCDC93	rs7566605	CG

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