

CYP3A5 (Detox/Blood Pressure)

Gene Report

REPORT CATEGORIES —



HEART & BLOOD
VESSELS



DETOX



CANCER

Sample Client

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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.

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 [CYP3A5](#) gene encodes cytochrome P450 3A4, a member of the cytochrome P450 monooxygenase superfamily of enzymes. These proteins eliminate most drugs from the body [\[R\]](#), [\[R\]](#).

This enzyme is very similar in structure and function to [CYP3A4](#). However, unlike CYP3A4, its activity varies greatly between people, and many don’t have a functional version of this enzyme. CYP3A5 is functional in most Africans but only in a few Whites. In people who do have this enzyme, it can represent over 50% of the total liver CYP3A activity [\[R\]](#), [\[R\]](#).

CYP3A4 in particular is responsible for processing approximately 45–60% of prescribed drugs, including:

- Immunosuppressants such as cyclosporine A, tacrolimus, and sirolimus [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#)
- Antihypertensive drugs such as felodipine and nifedipine [\[R\]](#), [\[R\]](#)
- Anticancer drugs such as lapatinib, imatinib, and vincristine [\[R\]](#), [\[R\]](#), [\[R\]](#)
- Antiemetics such as granisetron [\[R\]](#)
- Antiseizure medications such as carbamazepine [\[R\]](#)
- Sedatives such as midazolam and alprazolam (Xanax) [\[R\]](#)
- Cholesterol-lowering drugs such as simvastatin and atorvastatin [\[R\]](#)
- Antibiotics such as erythromycin [\[R\]](#)
- Antiretroviral drugs such as saquinavir [\[R\]](#)
- TNF inhibitors such as etanercept [\[R\]](#)

This enzyme is mainly found in the liver, kidneys, and lungs. Importantly, its activity in the kidneys is involved in blood pressure regulation and certain variants have been associated with hypertension [\[R\]](#), [\[R\]](#).

CYP3A5

Genetics

There are over 25 variants of this enzyme, but many of them are non-functional. The fully functional variant is known as the *CYP3A5*1*. Only individuals with at least one *CYP3A5*1* have large amounts of the enzyme. They metabolize some CYP3A substrates more rapidly than do people without this enzyme [R].

The frequency of the functional variant is substantially different across ethnic groups. The functional enzyme is found in 45–94% of subjects of African descent, 8–15% of Whites, and 23–40% of Asians [R, R].

The main non-functional variant is the ‘C’ allele of [rs776746](#), commonly designated as *CYP3A5*3*. Its frequency ranges from 14% among sub-Saharan Africans to over 95% in European populations [R, R].

This variant has been mainly studied regarding its ability to metabolize immunosuppressive drugs such as tacrolimus and sirolimus. Compared to the expresser *CYP3A5*1* allele, this variant has been associated with lower dose requirements and a decreased risk of kidney graft rejection (in Asian patients) [R, R, R, R, R, R, R, R, R, R].

Similarly, the ‘C’ allele has been associated with a better response to and lower required dose of:

- Anticoagulants [R]
- Antiseizure medications [R]
- Anticancer drugs [R]

The *CYP3A5*3* allele has also been associated with higher blood pressure in Whites, but not in Africans. However, this variant may protect against salt-sensitive hypertension. This may be because it reduces sodium reabsorption in the kidneys [R, R, R, R].

However, this variant has also been associated with an increased risk of the following cancer types:

- Leukemia [R, R]
- Prostate cancer [R]
- Colorectal cancer [R]



TYPICAL ACTIVITY

Predisposed to a typical CYP3A5 activity based on 2 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CYP3A5	rs10264272	CC
CYP3A5	rs41303343	TT
CYP3A5	rs776746	CC

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

The ‘T’ allele of [rs10264272](#) encodes another non-functional variant, commonly referred to as *CYP3A5**6. It is frequent in Africans (7-17%), but rare or absent in Europeans and Asians [[R](#), [R](#)].

This variant has been associated with higher levels of immunosuppressive drugs such as tacrolimus and cyclosporine due to slower clearance [[R](#), [R](#), [R](#)].

Finally, the ‘TA’ allele of [rs41303343](#) encodes another non-functional variant (*CYP3A5**7) that has also been associated with higher levels of immunosuppressive drugs. This variant is most common in Africans (12%) and usually absent in other ethnicities such as Europeans and Asians [[R](#), [R](#), [R](#)].