SelfDecode™

HLA (Inflammation)

Gene Report

REPORT CATEGORY

INFLAMMATION & AUTOIMMUNITY

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

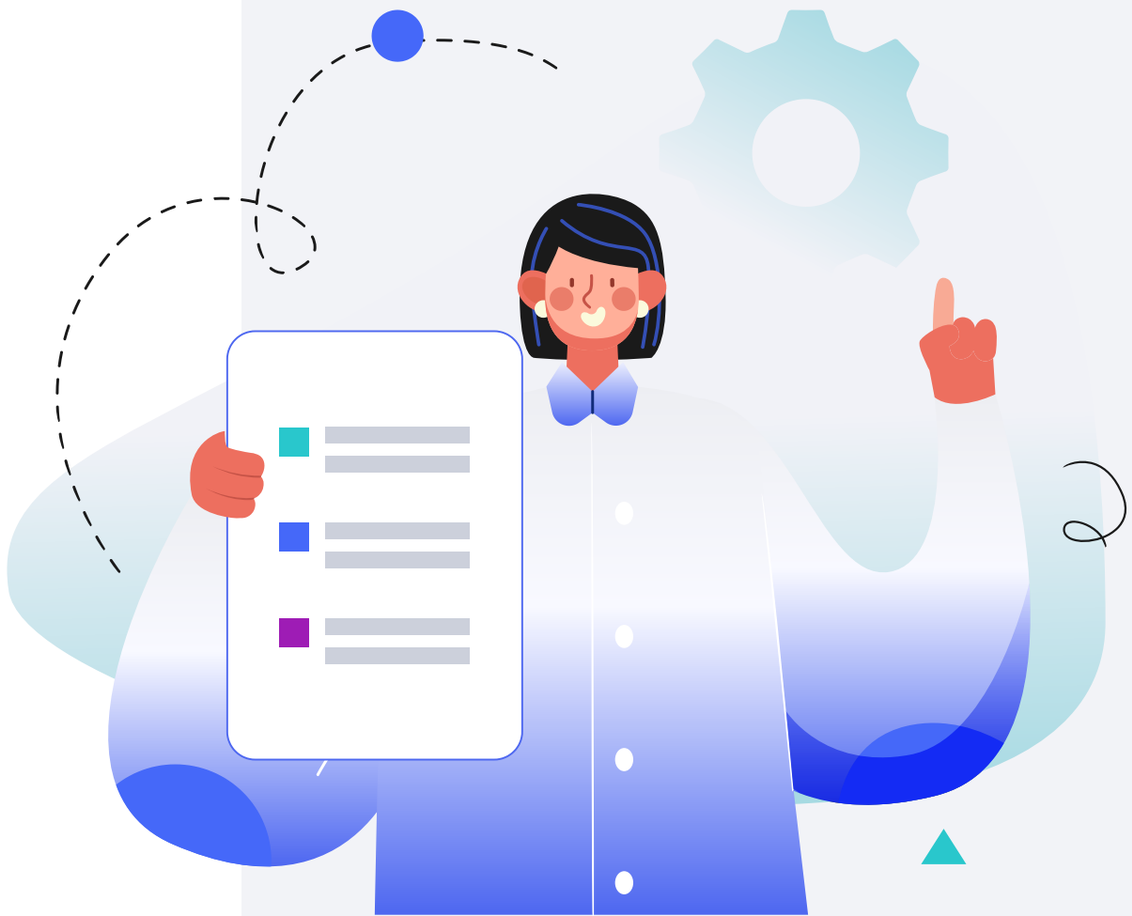
Male

HEIGHT

5ft 5" 165cm

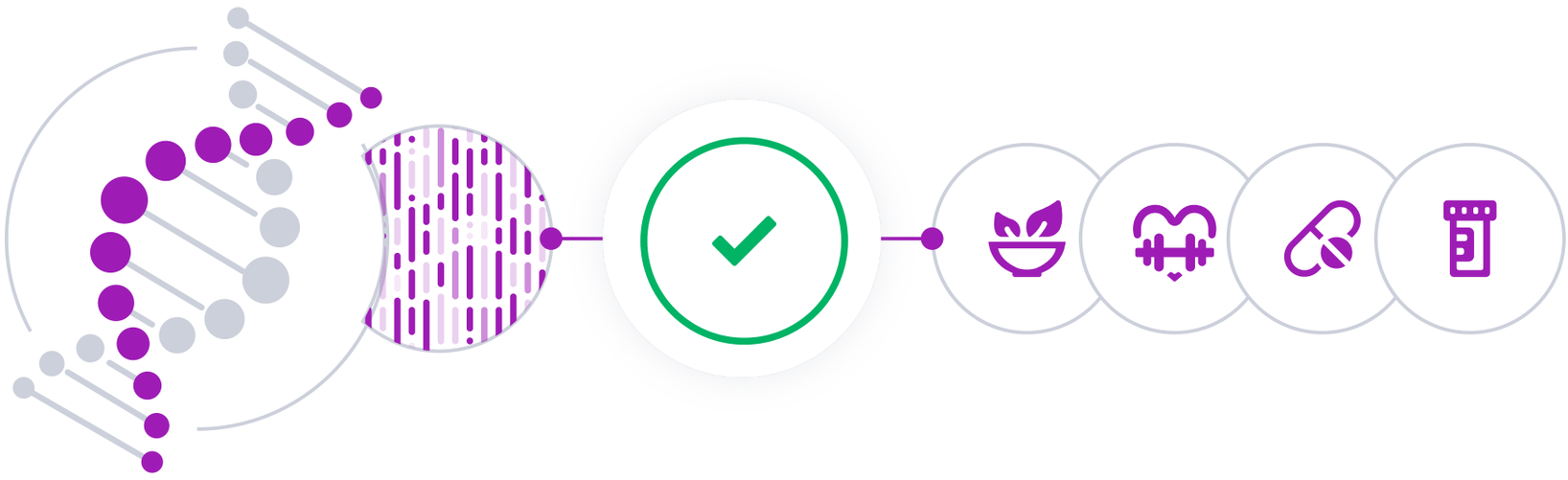
WEIGHT

137lb 62kg



How this works

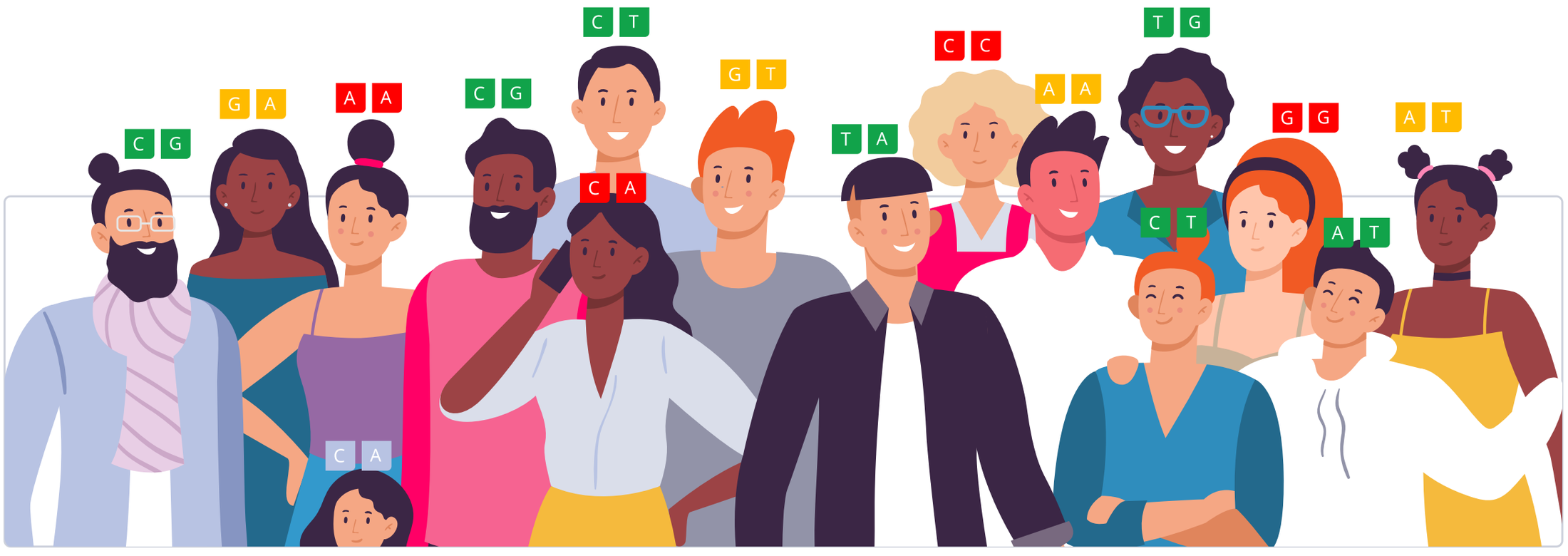
Our Wellness Reports analyze how your DNA influences your health.
We then use this analysis to give you personalized risk estimates and recommendations.



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.

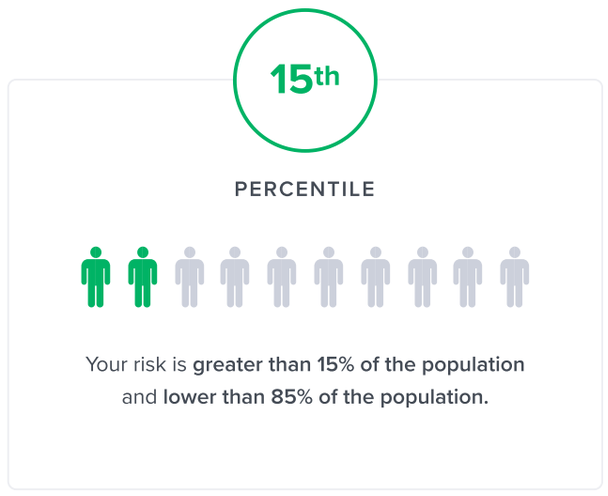
Genetic variants are parts of DNA that differ from person to person. Some can make you more vulnerable to certain health issues, while others may influence traits such as eye color.



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.



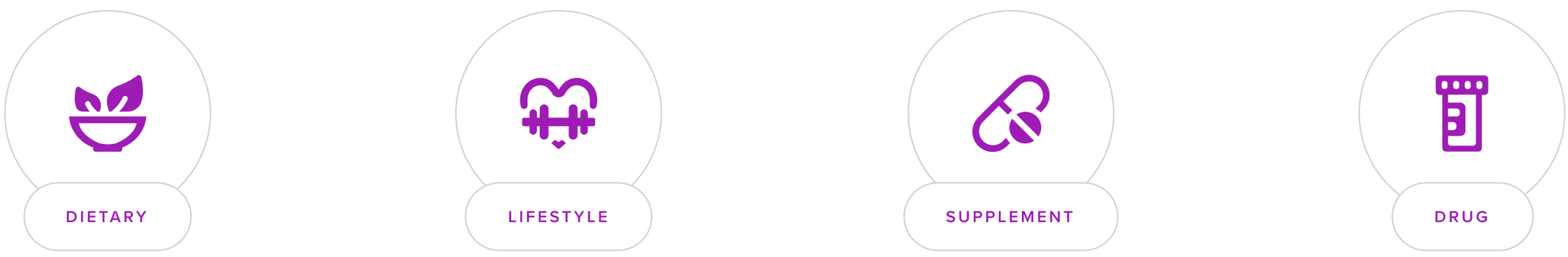
Genotype color info: AA You don't have any risk alleles | AA You have 1 risk allele | AA You have 2 risk alleles

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 *human leukocyte antigen (HLA)* system is a group of human genes encoding the major histocompatibility complex (MHC) proteins. HLAs are proteins or antigens on the surface of white blood cells. They help flag and remove external agents that may harm the body or cause infections [R].

This system has three groups or classes. *HLA-A*, *HLA-B*, *HLA-C*, *HLA-E*, *HLA-F*, and *HLA-G*, genes belong to class I. These proteins consist of a heavy and a light chain, and are found in all cell types except red blood cells. They regulate innate immune responses by presenting proteins from inside the cell to natural killer cells so the infected cell can be destroyed [R, R, R].

Class II proteins consist of an alpha and a beta chain that are combined to form a heterodimer. Genes belonging to this class include *HLA-DQA1*, *HLA-DQA2*, *HLA-DRA*, *HLA-DRB1*, *HLA-DRB5*, *HLA-DOA*, *HLA-DOB*, *HLA-DMA*, and *HLA-DMB*, among others. They present antigens from outside the cell to T-helper cells, which can cause these cells to become activated. Upon activation, T-helper cells stimulate B cells to make antibodies that target specific antigens. These antibodies can then attack and neutralize said antigens [R, R].

HLAs corresponding to class III encode components of the complement system [R].

HLA genes come in many different forms, and there are millions of their possible combinations. Their diversity ensures that humans are protected against a huge array of disease agents, but it can be a double-edged sword: some types of HLAs are associated with allergies and autoimmune disorders. Conditions linked to *HLA* variants include [R, R, R]:

- Celiac disease
- Allergies, including to peanuts
- Alopecia
- Rheumatoid arthritis
- Type 1 and type 2 diabetes
- IBD
- Autoimmune thyroid disease
- Spondyloarthritis
- Lupus

HLA Genetics

HLA-B27 is a form of HLA-B that reatly increases the risk of certain autoimmune diseases that fall under the umbrella of spondyloarthritis. It is inherited in a dominant fashion; that is, you have the same risk of autoimmune diseases if you have one or two copies of the risk allele. The following rare alleles have been associated with HLA-B27 [R, R, R, R, R]:

- 'A' at rs4349859
- 'G' at rs13202464
- 'T' at rs116488202

Two alleles — DQA1*0501 and DQB1*0201 — form the DQ2.5 haplotype, which codes for the DQ2.5 receptor on white blood cells. The 'T' variant of rs2187668 serves as a genetic marker — it tags the DQ2.5 haplotype with high precision. This variant has been associated with:

- Celiac disease [R, R]
- Allergies to latex and fruits [R]
- Grave's disease [R, R, R, R]

The 'C' variant of rs9275596, located between *HLA-DQB1*, *HLA-DQA2*, and *HLA-DQB2*, causes structural changes in this DNA region that may affect its interaction with regulatory proteins. This variant has been linked to an increased risk of [R]:

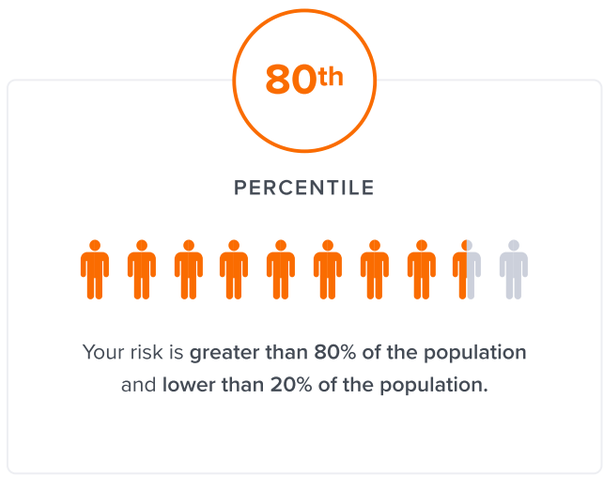
- Peanut allergy [R, R]
- Shrimp allergy [R]
- Multiple sclerosis [R]
- Primary sclerosing cholangitis [R]

The 'G' allele at rs2395185 marks the allele HLA-**DRB1*1101** and is linked to a higher expression of the *HLA-DRB1* and *DQA1* genes. This variant has been associated with higher rates of ulcerative colitis in several studies, as well as with type 1 diabetes. On the bright side, it also predicts a better response to anti-TNF treatment [R, R, R, R, R, R, R].

Another polymorphism, rs9271366, marks HLA-**DRB1*1502** and may have a role in IBD by changing the HLA-DR structure. Its 'G' allele has been associated with higher rates of ulcerative colitis in different populations [R, R, R, R, R, R, R].

HIGHER ACTIVITY

Likely higher HLA activity based on 15 genetic variants we looked at



Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
HLA-DQA2	rs9275596	CT
/	rs9271366	AG
HLA-DRB1	rs2516049	CT
HLA-DQA2	rs2395185	TG
HLA-DQA2	rs9275572	AG
HLA-DQA1	rs6906021	CT
HLA-DQA2	rs9271588	CT
HLA-DQA2	rs9275524	CT
HLA-DOB	rs10484565	GA
HLA-DQA1	rs9784858	GC
MICA	rs4349859	GG
HLA-DRB5	rs3763313	AA
HLA-DQA1	rs2187668	CC
HLA-C	rs13202464	AA
MICA	rs116488202	CC
TAP2	rs2071479	CC

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

The ‘C’ allele of rs3763313 has also been associated with higher rates of Crohn’s disease and ulcerative colitis. This variant has also been associated with an increased risk of tuberculosis but may be protective against dilated cardiomyopathy [R, R, R, R].

Two variants believed to increase or altere HLA activity that are always inherited together, ‘G’ at rs9275572 and ‘C’ at rs9275524, have been associated with increased odds of *alopecia areata* (patchy hair loss) [R, R].

Another variant, ‘C’ at rs6906021, is believed to increase *HLA-DQA1* activity and has been linked to increased allergic sensitization and hypothyroidism [R, R].

The ‘C’ variant of rs9271588 is also believed to increase *HLA-DQA1* activity and has been associated with:

- Allergy to wheat protein [R]
- Natural killer T-cell lymphoma [R]

People with the “C” allele at rs2516049 have 15% higher rates of hypothyroidism. The same SNP is also associated with [R, R, R, R]:

- Epstein-Barr virus infection
- Asthma
- Ulcerative colitis

Both the ‘A’ allele of rs10484565 and the ‘C’ allele of rs9784858 have been associated with an increased risk of rheumatoid arthritis, especially in smokers [R, R, R].

Finally, the ‘T’ allele of rs2071479 has been associated with higher blood sugar levels due to type 1 and type 2 diabetes. The ‘C’ allele of this variant may cause the production of proteins with decreased activity [R, R].