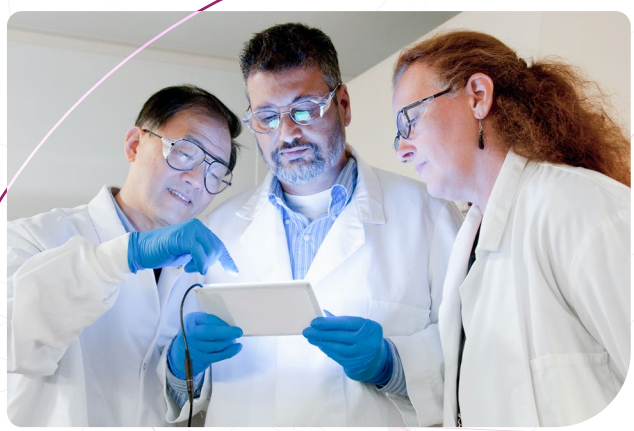
OMNOS™

regenerus labs

DNA guide

An introduction to genetic testing and Omnos' DNA test available via Regenerus

Contents



The Omnos DNA Test

£127

Prices quoted are RRP, please reach out to Customer Services or log in to the Regenerus practitioner portal for trade prices.

Buy now

How does Omnos conduct testing for DNA?

- Sample collection: buccal swab
- Testing lab: Eurofins
- Method of analysis is based on the Illumina Microarray (BeadArray Technology) using silica microbeads. Each array (BeadChip) allows for thousands of genotypes to be assayed at once with 99.1% accuracy. As DNA fragments pass over the BeadChip, each probe binds to a complementary sequence in the sample DNA. Allele specificity is conferred by a single base extension that incorporates one of four labelled nucleotides.

General information about Omnos DNA test

- Price: £127 RRP*
  - *Please see practitioner pricing in the Regenerus Portal
- All data is anonymised via ID numbers and no personal information is shared with the testing lab or 3rd party.
- Sample is destroyed after 90 days.
- How long is the process?
  - This is usually within 3 - 6 weeks of the lab receiving the sample.
- What is the process for ordering and sending results back?*
  - An order is made via the Regenerus practitioner portal, registration will be through the Regenerus External Registration page which will then link the kit to a specific order and user account. The patient will ship this back to Regenerus using the pre-paid Royal Mail envelope included in the test kit.
  - *All advice applicable to UK orders only.
- Our results are based on 190 different genes and over 250 related SNPs.
- The Omnos DNA test does not look at ancestry.

How can DNA affect our lives?

DNA (Deoxyribonucleic Acid) provides you with a unique blueprint, helping you understand what your greatest risks are and where your greatest potential lies. Think of these blueprints as an instruction manual for your body that are different for different cells and processes in the body; they determine the instructions of how you will grow and develop as an individual, but they are not your destiny. Diet, lifestyle, and environment will dictate how these instructions are read and used.

Why do an at-home DNA test?

A DNA test allows you to learn about your genetic makeup and provides personalised information about your health, risk factors, and other traits. By understanding these elements, you can be more proactive about your health by implementing lifestyle changes such as food choices, exercise, stress reduction and others that would counteract your genes. Some tests look at heritage or medical risk, however, this test is neither for the purpose of ancestry nor designed to diagnose a medical condition and should not be used as a substitute for visiting a doctor.

Watch this video on how to take an at-home DNA test

The difference between methylation testing and genotyping

In the Omnos DNA test, we look at how multiple genes interact with each other to impact risk factors. While a single gene may be well researched and can have large impacts on risk, in personal cases, it is very important to assess whether these are directly through gene-to-gene interaction or indirectly through gene-product interaction.

Methylation vs Genotyping:

Genotyping and methylation testing are two different types of genetic testing that are used to study different aspects of an individual's DNA.

- At Omnos we use genotyping, which is a process where specific variations in an individual's DNA sequence are identified. This type of testing can be used to identify genetic variations that may be associated with certain diseases or conditions. Genotyping can also be used to determine an individual's ancestry or to study genetic variations in populations.
- Methylation testing, on the other hand, is a process where the addition of a methyl group to a specific part of a DNA molecule is studied. Methylation is an epigenetic modification that can alter the expression of genes without changing the underlying DNA sequence. This type of testing can be used to study the role of epigenetics in various diseases and conditions, including cancer.

Note: The Omnos test is able to test for genes that are involved in methylation, which would give an idea about an individual's ability to methylate, however, if you are interested in testing methylation metabolites through the plasma to assess methylation status you can do so here: **Methylation Plasma Profile**.

In summary, genotyping is used to identify genetic variations in an individual's DNA sequence, while methylation testing is used to study epigenetic modifications that can alter gene expression. Both types of testing have important applications in various fields of research and medicine.

The Omnos Report

- Omnos' ethos to testing
  - At Omnos we believe your genes are not your fate. They provide your blueprint and help connect the dots towards better health through data integration with other functional tests and help you make better informed decisions that are much more personalised.

Download a sample report here

Which areas do we look into?

1. Nutrient deficiency
2. Endocrine risk
3. Neurocognitive risk
4. Cardiometabolic risk
5. Gastroenterology & immunity risk
6. Exercise & recovery potential

*Methylation and Detoxification are included as sub-sectors

Full glossary and gene list here.

- Multi Gene vs Single Gene outcomes:
  - Each subsection is informed by a combination of SNPs that can affect their overall risk for a specific outcome. This is why you can see the same SNP linked to different results. Single SNP results apply to some conditions, however, more often than not it may be important to consider multiple SNP interactions to understand the overall risks associated with a certain condition.
- What recommendations can be made from genes alone?
  - Even though your Gene test provides insights into the blueprint of how optimally your body can function, they are not the only factors to consider when deciding on recommendations.
  - If you would like to see how genes interact with other test results such as blood biomarkers and/or get advice and lifestyle recommendations, you can buy and run this test through the Omnos platform.

What is Gene testing?

A quick look at the history

The history of DNA began with the discovery of its structure by James Watson and Francis Crick in 1953. Subsequently, advancements in technology led to the development of polymerase chain reaction (PCR) in the 1980s, facilitating DNA testing. The field of DNA testing expanded rapidly with applications in forensic science, paternity testing, and disease diagnosis.

In parallel, the fields of Nutrigenomics and Nutrigenetics emerged in the late 20th century, focusing on how genes interact with diet to impact health. With the completion of the Human Genome Project in 2003, the link between genetics and nutrition became clearer. This paved the way for personalised nutrition based on individual genetic profiles.

Today, DNA testing has become widely accessible, allowing individuals to uncover their genetic heritage and potential health risks, while Nutrigenomics and Nutrigenetics continue to advance personalised dietary recommendations based on genetic data, offering new insights into optimal nutrition and wellness.

- What is a Genome?

"The complete set of genes or genetic material present in a cell or organism"

Our bodies are made up of 100 trillion cells, each with their own complete set of genetic instructions. This complete set of genetic material, also called **DNA**, is known as the genome and is packed into the **nucleus** of the cell in structures called **chromosomes**.

Most human cells have 46 chromosomes arranged in 23 pairs, containing in total about 20,000 to 25,000 genes. Some genomes are incredibly small, such as those found in viruses and bacteria, whereas other genomes, like the human genome, can be made of 3.2 billion bases of DNA. So, if it were possible to unravel the DNA from a single cell and stretch it out, it would measure about 2 metres (6 feet) in length.

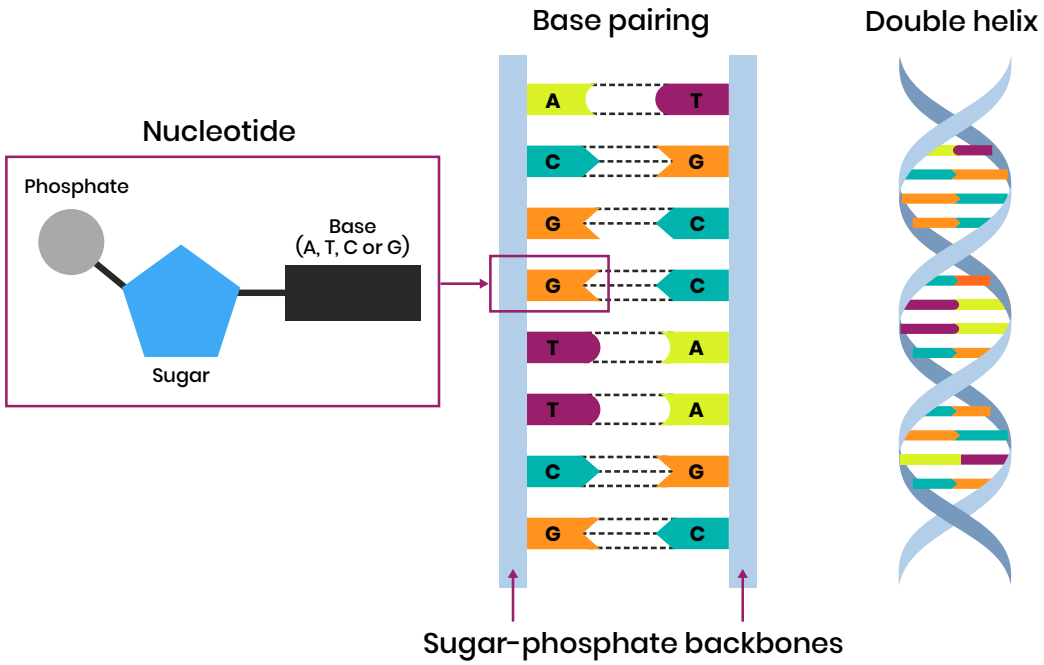
DNA (Deoxyribonucleic Acid)

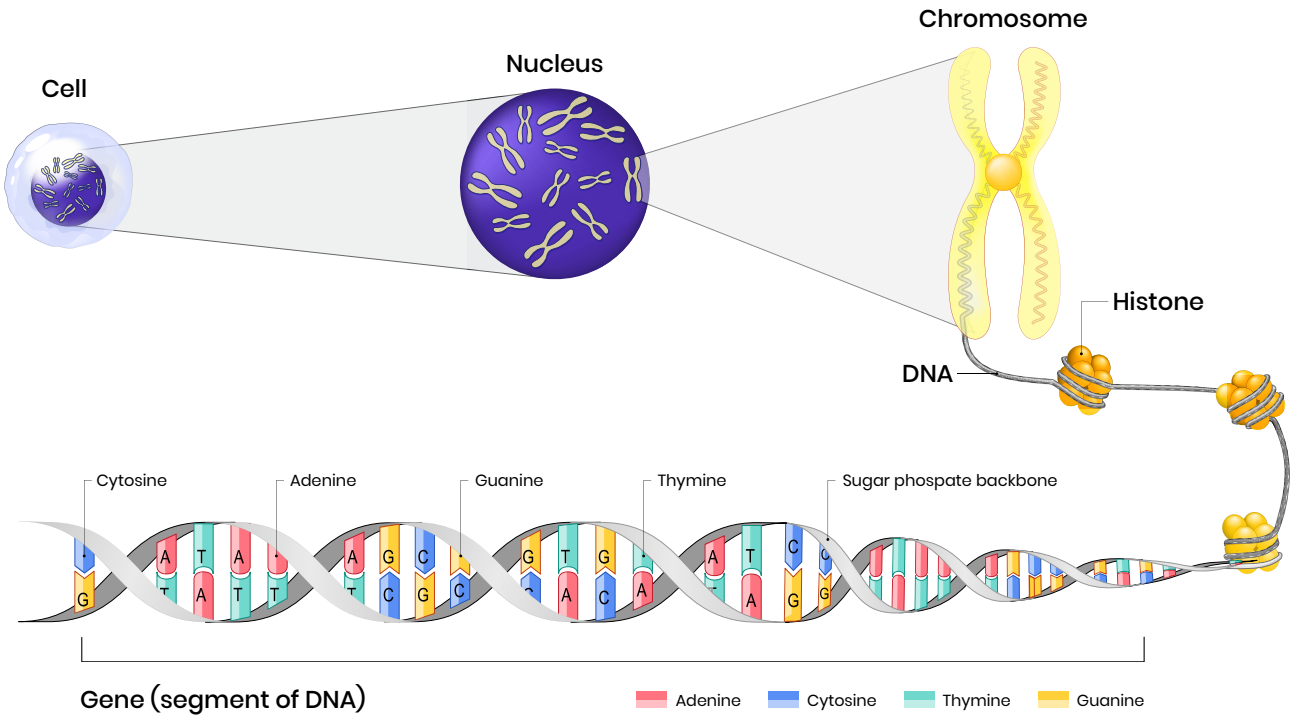
DNA is made of two linked strands that wind around each other to resemble a twisted ladder — a shape known as the double helix. The double-stranded helix is made up of repeating units called nucleotides, known as the basic building blocks of DNA.

Each nucleotide consists of a sugar molecule (deoxyribose), a phosphate group, and a nitrogenous base; there are four types of nitrogenous bases in DNA that can be grouped into two categories:

- Purines: Adenine (A) and Guanine (G)
- Pyrimidine: Cytosine (C) and Thymine (T)

Base pairs, on the other hand, are formed when two complementary nitrogenous bases come together and bind in the DNA molecule. Adenine (A) always pairs with thymine (T), and cytosine (C) always pairs with guanine (G), and these pairings are held together by hydrogen bonds.





In the DNA double helix, two strands of nucleotides wind around each other in a twisted ladder-like structure. The sugar-phosphate backbone forms the sides of the ladder, and the nitrogenous bases form the rungs. The specific pairing of the above nucleotides, A:T and C:G ensure that the two strands are complementary to each other. This complementary base pairing is crucial during DNA replication and cell division, as it allows for more reliable and accurate copying during mitosis and transmission of genetic information from one generation of cells to the next. This simple four-letter code can then be combined in 256 unique variations that help make up the up to 25 000 genes in your genome.

Gene

A **gene** is a sequence of DNA that provides the production of proteins, which are the building blocks of the body and perform many essential functions, such as fighting infections, digesting food and others. They are inherited from our parents and determine many of our traits, such as eye colour, hair colour, height etc. They can also influence our risk of developing certain diseases or conditions.

All genes are split into protein-coding genes and non-coding genes. Non-coding genes were thought to be 'junk' as they do not provide information to build proteins; but we now understand that they are involved in the regulation of gene expression depending on the cell type and environmental conditions.

We all, as humans, have the same genes, but carry **different versions** of those genes.

SNPs

Single Nucleotide Polymorphism (SNP)

Human DNA consists of about 3 billion nucleotide pairs, 99.9% of which is the same for all people. A Single Nucleotide Polymorphism (SNP) is defined by a single nucleotide substitution at a specific position in the DNA sequence, where one nucleotide base (A, T, C, or G) is replaced by another. Changes of individual nucleotide bases within a gene can occur due to random mutation or stress induced mutation which can then be passed down and create a variation in the genetic landscape of the human population describing the 0.1% difference.

Allele

The word allele is used to reference the different versions of genes and is a shortened form of the word allelomorph (other form).

Here are the 3 classifications of allele pairs:

- Homozygous Wild type - Matches wider population
- Heterozygous - One Allele variation
- Homozygous - Two Allele variations

These classifications depend on whether you are inheriting variations from neither, one, or both parents.

What is a Phenotype?

The above is not to be confused with "phenotype," as this refers to the observable physical, biochemical, and behavioural traits or characteristics of an individual, resulting from both genetic factors (genotype) and environmental influences. In other words, a phenotype is the expression of the genotype in the observable traits of an individual (i.e. eye colour, hair colour, glucose response, food & drug metabolism etc.)

	Gene	**Allele**
Definition	A section of DNA that encodes for a certain trait	A variant form of a gene

An individual inherits two alleles for each gene, one from each parent and therefore, each pair of alleles will represent the genotype of a specific gene. Genotypes are described as homozygous if there are two identical alleles at a particular location and as heterozygous if the two alleles differ.

Allele variations can include an individual or multiple nucleotide changes within a section of DNA. However, a SNP is defined as a single base change in a DNA sequence that occurs in a significant proportion (more than 1%) of a large population. SNPs occur on average once in every 300 nucleotides and are the basis on which DNA testing is interpreted.

To summarise, a Genome consists of DNA; DNA includes several Genes; Genes include multiple Alleles, and one or more SNPs can occur within an Allele.

What is the difference between epigenetics and genetics?

- What you are born with vs. how your environment shapes your life
  - Epigenetics is the study of how an organism grows and develops and how chemical reactions switch parts on or off in strategic locations and at strategic times within the genome. Epigenetics 'tags' genes and reacts to the outside world, lifestyle, diet and environment, without changing the underlying DNA sequence. The DNA code is fixed for life, but epigenetics are flexible.
  - When babies are conceived, they inherit genetic material from both their biological mother and father, which includes genes and epigenetic patterns. They will inherit half of their genes from their biological mother and the other half from their biological father, which will contain the instructions for building and maintaining the body, influencing traits such as eye colour, height, and susceptibility to certain diseases.
  - Additionally, babies are born with relatively "tag-free" DNA, meaning that they do not inherit extensive epigenetic modifications from their parents. During the process of sperm and egg cell formation, the epigenetic marks are largely (but not all) erased, and the DNA is reset to a mostly pristine state. This erasure ensures that the offspring will develop with a clean epigenetic slate, ready to establish its own epigenetic patterns during development. However, it is essential to note that some epigenetic marks may escape the erasure process and be passed from one generation to the next. These are known as "imprinted" genes, where specific genes can retain epigenetic tags from the mother or father, and play critical roles in development and growth, and their proper regulation is essential for normal development.
- Expression vs. silencing
  - Expression references a gene being "switched on" or an increase in its productivity. Whereas silencing is referring to a gene being "switched off" or decrease in its productivity.

Case study examples based on gene results

Sports performance:

Recovery - Increased Potential

- COMT - rs4680
- IL-1B - rs1143634
- CRP - rs1205
- MYRF - rs174537
- IL1A - rs1800587
- APOC1 - rs1065853
- AMPD1 - rs17602729
- TNFA - rs1800629
- IL-6 - rs1800795
- NRF2 - rs35652124

Muscle building - Medium Risk

- ACVR1B - rs2854464
- FAM9B - rs5934505
- ACTN3 - rs1815739
- FSHB - rs11031006
- SHBG - rs1799941

Endurance - High Risk

- ADRB2 - rs1042713
- VDR - rs1544410
- NOS3 - rs2070744
- PPARA - rs4253778
- AGT - rs699
- PPARGC1A - rs8192678
- ADRB3 - rs4994
- BDKRB2 - rs1799722
- ACTN3 - rs1815739
- NFIA-AS2 - rs1572312
- IL6 - rs1800795
- PPARG - rs1801282
- ADRB2 - rs1042714

Summary of DNA results:

- Variants in AGT, NOS3, and ADRB2 may provide additional capacity to perform well in endurance exercise.
- The IL-6 gene releases a protein that can increase cytokine response, which can lead to inflammation. Different genotypes have been shown to have higher or lower levels of IL-6, both at rest and post exercise, thus potentially affecting recovery rate post-exercise.
- NRF2 triggers an antioxidant-release in response to the oxidative stress the body goes through after exercising. Having a variation in this gene may cause a reduced capacity to deal with the oxidative stress, which may need support through food.
- Testosterone, in particular, is known to play a crucial role in muscle development. FSHB and SHBG genes are involved in testosterone production and its availability in tissues. We can see that variations in these genes will impact testosterone productivity & availability, ultimately affecting the ability to build muscles at a quicker pace.
- When considering this we have to be careful not to push the person towards endurance exercise without mitigating the potential issue that endurance exercise can cause.

Actionable recommendations are:

- Increase food rich in:
  - Adequate protein intake to prevent muscle breakdown
  - Increase cruciferous vegetable intake to help SHBG reduction
  - Increase antioxidants & anti-inflammatory foods to modulate cortisol and reduce oxidative stress
- Warm up/ Stretching/ Rest days

Body Composition:

Obesity - High Risk

- ADRB2 - 1042713
- PEMT - 7946
- IRS1 - 2943641
- FAAH - 324420
- CETP - 3764261
- CETP - 5882
- CETP - 708272
- CNR1 - 806368
- APOA2 - 5082
- FTO - 9939609
- ADIPOQ - 17300539
- MC4R - 17782313
- PPARG - 1801282

Weight loss resistance - High Risk

- APOC3 - 5128
- ADRB2 - 1042713
- ADRB2 - 1042714
- CLOCK - 1801260
- APOA5 - 662799
- PLIN1 - 894160
- APOA2 - 5082
- FTO - 9939609
- ADRB3 - 4994
- TCF7L2 - 7903146

Summary of DNA results:

- Poor sleep hygiene due to CLOCK could lead to increased poor eating habits & snacking. APOA2, ADIPOQ, PPAR and TCFL2 will affect diets higher in saturated fat and sugar will lead to impaired lipid and carbohydrate metabolism.
- Stress/emotional eating can lead to increased snacking due to MC4R, specifically of fatty foods, in addition to decreased insulin and impaired fat metabolism.
- FTO variants may lead to lower insulin release, and a higher fat storage.

Actionable recommendations are:

- Better sleep hygiene.
- Limit saturated fats and simple carbohydrates and increase protein intake.
- Include MUFAs & complex carbohydrates, specifically, wholegrains.

Detoxification - Low Risk

Phase 1:

- CYP2C19 - rs12248560
- CYP1A1 - rs1048943
- CYP2C9 - rs1799853
- CYP3A4 - rs1041988
- CYP1B1 - rs1056836
- CYP1B1 - rs1800440
- CYP3A4 - rs2740574
- CYP2C19 - rs4244285
- CYP1B1 - rs1056827
- CYP2R1 - rs10741657
- CYP1A2 - rs762551
- CYP2A6 - rs1801272
- GSTM1 - rs366631
- GSTP1 - rs1695

Phase 2:

- NAT1 - rs4986782
- NAT2 - rs1801279
- NAT2 - rs1041983
- NAT2 - rs1495741
- NAT2 - rs1799930
- NAT2 - rs1799931
- SULT1A1 - rs1042157
- GPX1 - rs1050450
- NAT2 - rs1208
- MTHFR - rs1801133
- NAT2 - rs1801280

Summary of DNA results:

- The CYP1B1 and SULT1A1 genes work together in the detoxification of oestrogen, with CYP1B1 being responsible for the initial metabolism of the hormone (phase 1), and SULT1A1 playing a role in the subsequent detoxification (phase 2 or conjugation) of reactive intermediate metabolites. A variation in each of these genes may cause an impaired oestrogen elimination, causing it to stay longer in the system, and as a consequence to be reabsorbed into the system resulting in excessive levels of circulating oestrogen.
- GSTM1 and GSTP1 are associated with the removal of free radicals created during the detoxification process. Variations in the GSTP1 and GSTM1 genes can influence the efficiency of detoxification by decreasing the proteins' activities, which may result in reduced conjugation of electrophiles with glutathione (a strong antioxidant in the body) and a higher risk of oxidative damage.
- GPX1 is also involved in the detoxification/ removal of reactive oxygen species (ROS) and other harmful compounds, but requires the trace element selenium to function properly. The variation we see in the GPX1 gene can reduce the body's ability to detoxify those harmful compounds through changes in enzyme activity and selenium availability.
- Overall, the impaired oestrogen metabolism can result in a range of symptoms, such as irregular menstrual cycles (in women), mood swings, weight gain, decreased libido, increased risk of cardiovascular disease, osteoporosis, cognitive decline and more. Also, in order to counteract the formation of free radicals during oestrogen metabolism, the body has a number of antioxidant defence mechanisms, such as glutathione, whose metabolism seems to also be impaired here.

Actionable recommendations are:

- Increase cruciferous vegetable intake to help with glutathione levels
- Provide adequate protein intake
- Adequate Selenium levels

Methylation:

- MTHFR – rs1801131, rs1801133
- MTRR – rs1801394, rs162036
- MTR – rs1805087
- BHMT – rs567754, , rs3733890
- PEMT – rs7946
- SHMT – rs1979277
- CBS – rs234706
- CTH – rs1021737
- MTHFD1 – rs2236225
- FUT2 – rs601338, rs1047781
- SUOX – rs705702

Summary of DNA results:

- Multiple genes are involved in the methylation process.
- Due to the genetic variations in the MTHFR and MTR gene, low vitamin B9 (folate) levels coupled with low Vitamin B12 levels may increase homocysteine levels.
- BHMT is involved in converting homocysteine to methionine. Having a variation in the BHMT gene will impair this conversion, leading to lower conversion rates, potentially causing a buildup of homocysteine.
- However, we can see that the CBS gene is of wild type, so there is some ability to pull out homocysteine and utilise it in the production of glutathione.

Actionable recommendations are:

- Additional Blood tests required
- Increase foods rich in:
  - Vitamin B2, B6, B9, B12
  - Choline, Betaine, and Zinc

Results states according to DNA sub sections

Nutrient deficiency risk	Endocrine risk	Neurocognitive risk	Cardiometabolic risk	Gastroenterology & Immunity risk	Exercise & Recovery potential
Calcium need	Estrogen dysregulation	Brain function	Circadian Rhythm dysregulation	Gluten sensitivity	Injury potential
Iodine need	Thyroid dysregulation	Memory loss during inflammation	Obesity	Food Sensitivity	Endurance performance
Magnesium need	Poor Reproductive health	Probability of Aggressive behaviour	Weight loss resistance	Dairy intolerance	Muscle building
Omega 3 need	Hair Loss Potential	Probability of Impulsive behaviour	Type 2 Diabetes	Caffeine sensitivity	Power performance
Potassium need	Iodine need	Probability for Anxiety	Caffeine sensitivity	Detoxification	Recovery
Iron overload		Potential for expressing Empathy	Cardiovascular risk	Infection	Weight Loss resistance from exercise
Iodine need		Potential for expressing Extraversion	Blood Pressure dysregulation	Immune system dysregulation	Restless leg syndrome
Vitamin A need		Potential for expressing Anger	Melatonin need	Circadian Rhythm dysregulation	
Vitamin B12 need		Probability of Agreeableness	Omega 3 need	Obesity	
Vitamin C need		Potential for Depression	Potassium need	Weight Loss resistance	

Nutrient deficiency risk	Endocrine risk	Neurocognitive risk	Cardiometabolic risk	Gastroenterology & Immunity risk	Exercise & Recovery potential
Vitamin D need		Insomnia	Methylation	Type 2 diabetes	
Vitamin E need		Susceptibility to stress		Poor Respiratory disease infection outcome	
Iodine need		Potential for Nicotine dependency		Antioxidants need	
Vitamin K need		Alcohol sensitivity		Methylation	
Zinc need		Alcoholism			
Vision		Addictive behaviour			
Antioxidants need		Melatonin need			
Bone density loss		Circadian Rhythm			
Skin ageing		Poor Eating behaviour			
Restless leg syndrome		Restless leg syndrome			
Migraines		Migraines			
Skin sensitivity		Potential for reduced longevity/ ageing			
Skin health		Methylation			
Methylation					

Gene Glossary

Name	Description	Function	Why test for it
AANAT	AANAT (arylalkylamine N-acetyltransferase) is an enzyme that plays a critical role in the production of melatonin, a hormone that regulates the sleep-wake cycle.	AANAT assists in the conversion of serotonin into melatonin, a substance important for regulating the circadian rhythm, sleep-wake cycles, and other physiological processes.	Testing for variations in the AANAT gene can provide insights into an individuals' sleep patterns, circadian rhythm disorders, and potential personalised healthcare interventions.
ACE	The ACE (Angiotensin-Converting Enzyme) gene encodes an enzyme that plays a crucial role in the renin-angiotensin-aldosterone system (RAAS) pathway, which regulates blood pressure and fluid balance.	The ACE protein converts angiotensin I to angiotensin II, a potent vasoconstrictor that narrows blood vessels and increases blood pressure. Aside from increasing blood pressure, this process stimulates the release of aldosterone, which promotes the retention of sodium and water in the kidneys. Additionally, ACE is involved in the degradation of bradykinin, a vasodilator that can also lower blood pressure.	Variations in the ACE gene have been associated with differences in ACE activity, potentially influencing blood pressure regulation and cardiovascular health.
ACE2	The ACE2 (angiotensin-converting enzyme 2) gene encodes a protein that plays a critical role in regulating the renin-angiotensin-aldosterone system (RAAS), which controls blood pressure and fluid balance. It is expressed in various tissues throughout the body, including the lungs, heart, and kidneys.	ACE2 acts as a counterbalance to the effects of ACE. It acts as a negative regulator by converting angiotensin II to angiotensin 1-7, which has vasodilatory and anti-inflammatory effects.	Testing can provide insights into blood pressure dysregulation as well as viral infections risk assessment and guide preventive measures and/or management strategies.
ACTN3	The ACTN3 (alpha-actinin-3) gene encodes a protein that is primarily expressed in fast-twitch muscle fibres, which are important for high-intensity activities such as sprinting and powerlifting.	The ACTN3 protein is involved in muscle contraction and in the assembly and maintenance of sarcomeres, the basic contractile units of muscle cells. In other words, it plays a role in muscle force production and adaptation to exercise. Genetic variations in the ACTN3 gene have been associated with differences in athletic performance, with some studies suggesting that individuals with certain variants may have an advantage in power and speed-based activities. However, the relationship between ACTN3 and athletic performance is complex and influenced by various environmental factors.	Testing for the ACTN3 gene helps identify genetic variations, which influences muscle fiber type composition, and therefore, provide insights into athletic performance potential, muscle strength, and power characteristics. It may help tailor training programs and optimise sports performance.
ACVR1B	The ACVR1B (activin A receptor type 1B) gene encodes a protein that belongs to the transforming growth factor-beta (TGF-β) superfamily of receptors. ACVR1B is primarily expressed in skeletal muscle and is involved in muscle growth and regeneration.	The ACVR1B protein binds to ligands such as activin, myostatin, and GDF11, which regulate various biological processes, including muscle growth, bone formation, and neurogenesis.	Understanding ACVR1B genetic variations can provide insights into bone density health, body composition, and susceptibility to certain diseases.

Name	Description	Function	Why test for it
ADA	The ADA (adenosine deaminase) gene encodes an enzyme that plays a critical role in purine metabolism, which is important for the synthesis of DNA and RNA.	ADA plays a role in the breakdown of adenosine and deoxyadenosine, into inosine and deoxyinosine, respectively. It also plays a role in immune function.	Testing for variants in the ADA gene can reveal potential deficiencies in the ADA protein activity and aid in being proactive and managing personalised management strategies for individuals with ADA-related conditions.
ADD1	The ADD1 (α-adducin) gene encodes a protein that is involved in the regulation of the cytoskeleton in cells. It is primarily expressed in the renal tubules and vascular smooth muscle cells.	The ADD1 protein interacts with other major component proteins of the cytoskeleton to provide structural support to cells. It also plays a role in regulating sodium and potassium transport in the kidneys and contributes to the maintenance of blood pressure.	Testing for the ADD1 genetic variations help in the assessement of susceptibility to hypertension and cardiovascular diseases risk, and aid in the implementation of personalised strategies for better management of blood pressure.
ADH1B	The ADH1B (alcohol dehydrogenase 1B) gene encodes an enzyme that is involved in the metabolism of alcohol, and is primarily expressed in the liver and stomach.	The ADH1B protein plays a key role in the metabolism of ethanol by converting it to acetaldehyde, which is further metabolised to acetate by aldehyde dehydrogenase. Genetic variations in the ADH1B gene can influence an individual's alcohol metabolism and tolerance.	Testing can provide insights into alcohol-related health risks, such as susceptibility to alcohol-related liver outcomes, and inform personalised interventions for alcohol consumption and related health management.
ADH1C	The ADH1C (alcohol dehydrogenase 1C) gene encodes an enzyme that is primarily expressed in the liver and is involved in the metabolism of ethanol. It is responsible for a smaller proportion of alcohol metabolism compared to ADH1B.	The ADH1C protein catalyses the oxidation of ethanol to acetaldehyde, which is further metabolised to acetate by aldehyde dehydrogenase. Genetic variations in the ADH1C gene can affect the rate of alcohol metabolism and have been associated with differences in alcohol sensitivity.	Testing can provide insights into the risk of alcohol-related health issues, including alcohol dependence, liver diseases etc. It can also inform on personalised interventions and risk assessment related to alcohol consumption and associated health outcomes.
ADIPOQ	The ADIPOQ (adiponectin) gene encodes a protein hormone that is primarily produced and secreted by adipose tissue (fat cells), and plays an important role in regulating glucose and lipid metabolism, insulin sensitivity, inflammation, and cardiovascular function.	The ADIPOQ protein enhances insulin sensitivity and promotes the oxidation of fatty acids, thereby reducing the risk of insulin resistance, type 2 diabetes, and cardiovascular disease. Altered levels (low levels) of adiponectin have been associated with insulin resistance, metabolic syndrome, and increased risk of cardiovascular disease.	Testing can provide insights into risk assessment and guide interventions for better metabolic health management.
ADORA2A	The ADORA2A (adenosine A2a receptor) gene encodes a protein that belongs to the G protein-coupled receptor family and is primarily expressed in the brain.	The ADORA2A protein gets activated by binding to the neurotransmitter adenosine, and is involved in various physiological processes, including neurotransmission, regulating oxidative stress, inflammation, and immune responses.	These variations can impact individual responses to caffeine and influence sleep quality. Testing can provide insights into personalised caffeine sensitivity, sleep patterns, and guide lifestyle choices for better sleep and overall well-being.

Name	Description	Function	Why test for it
ADRB2	The ADRB2 (beta-2 adrenergic receptor) gene encodes a protein that belongs to the G protein-coupled receptor family. It is primarily expressed in the lungs, heart, and blood vessels.	Activation of the ADRB2 receptor (by binding to norepinephrine) can stimulate the sympathetic nervous system and promote fight or flight responses. It is involved in regulating various physiological processes, including glycogenolysis, and regulating bronchodilation, cardiac contractility, and vasodilation.	Testing can aid in personalised treatment selection and optimise the management of conditions such as asthma and cardiovascular diseases.
ADRB3	The ADRB3 (beta-3 adrenergic receptor) gene encodes a protein that belongs to the G protein-coupled receptor family and is primarily expressed in adipose tissue.	The ADRB3 receptor-protein plays a role in regulating lipolysis (the breakdown of fat), thermogenesis (heat production), and glucose metabolism.	Testing can provide insights into personalised approaches for weight management and metabolic health.
AFG3L1P	AFG3L1P (AFG3-like AAA ATPase 1 pseudogene) is a non-functional pseudogene that is thought to have originated from the AFG3L1 (AFG3-like AAA ATPase 1) gene. The AFG3L1 gene encodes a mitochondrial inner membrane protein that is involved in the regulation of mitochondrial dynamics, protein quality control, and cellular energy metabolism.	The AFG3L1P protein belongs to a family of proteins that play a role in the degradation of misfolded and damaged proteins.	Testing can provide insights into risk assessment for skin-related conditions.
AGER	The AGER (advanced glycosylation end-product specific receptor) gene encodes a protein called the receptor for advanced glycation end products (RAGE), which is a member of the immunoglobulin superfamily. It is expressed in a wide variety of cells and tissues including the lung, kidney, and immune cells.	The receptor for advanced glycation end products (RAGE) is involved in multiple physiological and pathological processes including inflammation, oxidative stress, and tissue damage. The activation of RAGE can trigger the release of proinflammatory cytokines and promote the development of chronic diseases, such as diabetes and other.	Testing can provide insights into personalised disease risk assessment and potential preventive measures.
AGT	The AGT (angiotensinogen) gene encodes a protein called angiotensinogen, which is the precursor of the vasoconstrictor peptide hormone angiotensin II. It is involved in the regulation of various physiological processes, such as blood pressure, electrolyte balance, and fluid homeostasis through vasoconstrictor.	Angiotensinogen is mainly produced in the liver and is released into the bloodstream, where it is converted to angiotensin II through several processes, and regulates blood pressure by constricting blood vessels and stimulating the release of aldosterone, a hormone that promotes sodium retention and potassium excretion.	Testing can provide insights into interventions for better management of conditions such as blood pressure regulation, and the risk of developing hypertension and cardiovascular diseases.
AHR	The AHR (aryl hydrocarbon receptor) gene encodes a protein that belongs to a family of transcription factors.	The AHR protein is involved in the regulation of gene expression in response to ligand binding, such as environmental pollutants and endogenous metabolites. AHR is primarily expressed in the liver, lung, and immune cells, where it plays a role in the metabolism and detoxification of xenobiotics and the regulation of immune responses.	Testing can provide insights into personalised susceptibility to certain diseases and guide lifestyle choices to minimise exposure to harmful environmental factors.

Name	Description	Function	Why test for it
AKT1	The AKT1 (protein kinase B alpha) gene encodes a serine/threonine protein kinase.	This serine/threonine kinase is involved in the regulation of various cellular processes, such as cell proliferation, differentiation, and survival. AKT1 is primarily involved in the PI3K/AKT/mTOR signalling pathway associated with diabetes, and neurodegeneration.	Testing can provide insights into mental health outcomes risk assessment.
ALDH2	The ALDH2 (aldehyde dehydrogenase 2) gene encodes an enzyme that is mainly expressed in the liver, but it is also found in other tissues, such as the brain, heart, and lungs.	The ALDH2 protein plays a crucial role in the detoxification of aldehydes, which are toxic byproducts of ethanol, by oxidizing them to their corresponding carboxylic acids.	Testing can provide insights into personalised risk assessment for alcohol-related conditions, such as alcohol flushing syndrome and alcohol dependence, and inform lifestyle choices related to alcohol consumption.
AMPD1	The AMPD1 (adenosine monophosphate deaminase 1) gene encodes an enzyme that plays a key role in the regulation of adenosine triphosphate (ATP) synthesis in skeletal muscle.	AMPD1 catalyses the deamination of AMP to inosine monophosphate (IMP), which provides an alternative pathway for the generation of ATP during periods of high energy demand, such as exercise. Individuals with genetic variants that result in reduced AMPD1 activity have been shown to have a reduced capacity for ATP synthesis during exercise and may be at increased risk for muscle fatigue and muscle damage, resulting in differences in performance and muscle fatigue.	Testing can provide insights into an individual's athletic potential and guide personalised training strategies for optimised sports performance.
ANK3	The ANK3 (ankyrin 3) gene encodes a protein that is involved in the formation and maintenance of neuronal axons and dendrites.	The ANK3 protein interacts with several ion channels and transporters, including voltage-gated sodium and calcium channels, and regulates their localisation and activity and neurotransmission; therefore, affecting neural function and communication.	Testing can provide insights into the assessment and guide interventions for certain mental health conditions such as depression.
ANKK1	The ANKK1 (ankyrin repeat and kinase domain-containing 1) gene encodes a protein hat is primarily expressed in the brain.	The ANKK1 protein is involved in the regulation of dopamine neurotransmission, which is implicated in reward procesing, motivation, and addiction. Variations in the ANKK1 gene have been associated with altered dopamine signaling.	Testing can provide insights into personalised susceptibility to addiction and guide interventions for prevention strategies.
AOC1	The AOC1 (amine oxidase, copper containing 1) gene encodes an enzyme called diamine oxidase (DAO), which is responsible for the degradation of histamine and other biogenic amines.	The DAO enzyme is primarily expressed in the intestine, where it helps to regulate the levels of histamine and other biogenic amines that are produced by gut bacteria and ingested from food. Variation in this gene could result in a dysregulation of AOC1 and DAO activity that could be implicated in food allergies, migraines, and inflammatory bowel disease.	Testing can aid in identifying individuals with reduced DAO activity and guide dietary and lifestyle adjustments to manage histamine-related symptoms.

Name	Description	Function	Why test for it
APOA2	The APOA2 (apolipoprotein A-II) gene encodes a protein that is a component of high-density lipoprotein (HDL) particles.	APOA2, mainly produced by the liver, is involved in the transport and metabolism of lipids in the body including cholesterol and triglycerides. Genetic variations in APOA2 have been associated with altered lipid profile. Additionally, APOA2 has been implicated in the regulation of appetite and food intake.	Testing can provide insights into risk assessment for obesity and guide dietary recommendations for weight management.
APOA5	The APOA5 (apolipoprotein A-V) gene encodes a protein that is primarily synthesised in the liver and circulates in the plasma regulating the metabolism of triglycerides, as well as in insulin secretion and glucose metabolism.	APOA5 enhances the activity of enzymes that break down triglycerides, helping to regulate their levels in the body. Genetic variations in APOA5 have been associated with altered lipid metabolism, specifically higher triglyceride levels, and ultimately a higher risk of cardiovascular diseases.	Testing can provide insights into risk assessment for triglyceride levels, and ultimtely cardiovascular health, and guide interventions such as dietary modifications.
APOC1	The APOC1 (apolipoprotein C-I) gene encodes a protein that is a component of very low-density lipoprotein (VLDL) and high-density lipoprotein (HDL) particles, and is primarily synthesised in the liver.	The APOC1 protein is involved in the regulation of lipid metabolism, mainly by inhibiting the breakdown of triglycerides. Genetic variations in APOC1 have been associated with alterations in lipid levels, specifically, cholesterol and triglycerides, which may influence the risk of cardiovascular diseases.	Testing can aid in risk assessment and guide interventions for altered levels of plasma lipids, and ultimately, cardiovascular health.
APOC3	The APOC3 (apolipoprotein C-III) gene encodes a protein that is primarily synthesised in the liver and is present in very low-density lipoprotein (VLDL) and high-density lipoprotein (HDL) particles. The APOC3 gene has also been implicated in insulin resistance.	The APOC3 protein plays a key role in the regulation of triglyceride metabolism by inhibing their breakdown. Genetic variations in the APOC3 gene may result in elevated levels of triglycerides and reduced HDL levels.	Testing can provide insights into risk assessment for heart health and guide interventions such as dietary modifications to manage triglyceride levels.
APOE	The APOE (apolipoprotein E) gene codes for a protein primarly synthesised in the liver, brain, and other organs, that plays a key role in lipid metabolism and transport.	The APOE protein is involved in the transport and clearance of cholesterol from the bloodstream and the brain.	Testing can provide insights into risk assessment and guide preventive measures for altered cholesterol metabolism, and ultimately cardiovascular health.
AR	The AR (androgen receptor) gene encodes a protein that belongs to the steroid receptor superfamily. It plays a critical role in the development and maintenance of male sexual characteristics and is expressed in various tissues, including the prostate gland, seminal vesicles, testes, and other androgen-responsive tissues.	The AR protein plays a critical role in the development and maintenance of male sexual characteristics such as, facial hair, deepening of the voice, etc. It is responsible for binding and responding to male sex hormones such as testosterone, and mediates their effects on target tissues. Variations in the AR gene can potentially lead to androgen insensitivity characterised by varying degrees of feminisation in individuals with XY chromosomes, potential hair loss in both male and females, and other.	Testing can provide insights into risk assessment, potential treatment selection, and management strategies for these conditions.

Name	Description	Function	Why test for it
ASIP	The ASIP (agouti signaling protein) gene encodes a protein that regulates the pigmentation of skin and hair.	ASIP binds to melanocortin 1 receptors (MC1R) and inhibits the production of eumelanin, a pigment that produces black and brown colors in hair and skin. Variations in the ASIP gene can lead to differences in skin and hair colour, due to the difference in melanin production.	Testing can provide insights into personalised characteristics and genetic ancestry related to pigmentation.
BCMO1	The BCMO1 (Beta-carotene 15'-monooxygenase 1) gene codes for an enzyme called beta-carotene oxygenase 1, mainly expressed in the small intestine and liver, which is involved in the metabolism of beta-carotene.	The BCMO1 enzyme converts dietary beta-carotene to retinal, which can be further converted to retinol (active vitamin A) that is essential for vision, immune function and other physiological processes, or it can be stored in the liver. Variations in the BCMO1 gene can affect the efficiency of beta-carotene metabolism, which may impact the body's vitamin A status.	Testing can provide insights into personalised nutritional needs for vitamin A and guide dietary recommendations for optimal health.
BDKRB2	The BDKRB2 (Bradykinin B2 receptor) gene encodes the bradykinin B2 receptor-protein, which is involved in the regulation of vascular tone, regulation of blood pressure, inflammation, and pain perception.	The B2 receptor is activated by bradykinin, a vasodilator, and as a result, stimulates the release of nitric oxide, another potent vasodilator, along with prostaglandins, which play a role in pain perception. Additionally, Bradykinin increases vascular permeability, promoting the recruitment of inflammatory cells to damaged tissues. It also plays a role in the renin-angiotensin system, a critical regulator of blood pressure and fluid balance in the body.	Testing can provide insights into risk assessment and guide prevention and/or management strategies for hypertension, cardiovascular diseases, and inflammatory disorders.
BDNF	The BDNF (brain-derived neurotrophic factor) gene is involved in the production of a protein called BDNF, which plays a key role in the development and survival of neurons in the brain.	The BDNF protein plays a critical role in neuroplasticity, as well as the formation and maintenance of synapses known as connections between neurons that allow them to communicate with each other. Variations in the BDNF gene can impact neuroplasticity, cognitive function, and mood regulation.	Testing can provide insights into susceptibility to neurological disorders and guide prevention approaches for mental health conditions.
BHMT	The BHMT gene encodes the enzyme Betaine-Homocysteine Methyltransferase, which plays a critical role in one of the pathways that regulates the levels of homocysteine, an amino acid that is linked to several health problems, including cardiovascular disease.	The BHMT protein catalyses the transfer of a methyl group from betaine to homocysteine, thereby producing methionine and dimethylglycine; this process is important for regulating the levels of homocysteine. The BHMT enzyme also contributes to DNA methylation. Variations in the BHMT gene can affect nutrient utilisation, methylation, and impact homocysteine levels, potentially influencing cardiovascular health and other conditions	Testing can provide insights into personalised risk assessment for conditions like cardiovascular diseases, neural tube defects, and methylation disorders, guiding appropriate interventions and nutritional strategies.

Name	Description	Function	Why test for it
BTBD9	BTBD9 (BTB Domain Containing 9) is a gene that encodes a protein involved in regulating the function of the nervous system. Research has suggested an association with increased risk of developing restless legs syndrome (RLS), a neurological disorder characterised by an irresistible urge to move the legs.	The exact role of BTBD9 in the development of Restless Leg Syndrom is still not fully understood, but studies have suggested that it may be involved in regulating the activity of neurons in the brain that control movement.	Testing can aid in risk assessment and guide prevention and/or management strategies for individuals with this sleep-related movement disorder, such as restless leg syndrom.
CACNA1	The CACNA1 gene encodes for the Alpha-1 Subunit of a Voltage-Gated Calcium Channel, and is expressed in various tissues, including the heart, brain, and muscle.	This protein is responsible for regulating the influx of calcium ions into cells affecting various cellular processes, including muscle contraction, hormone and neurotransmitter release, and gene expression. Certain variants can impact channel function and influence heart health and neurological disorders, such as epilepsy and migraine.	Testing can provide insights into neurological and cardaic health risk assessment.
CAT	The CAT (Catalase) gene encodes for the enzyme catalase, which plays a crucial role in protecting cells from oxidative stress.	The catalase enzyme plays a crucial role in protecting cells from damage caused by hydrogen peroxide, a reactive oxygen species (ROS) that can cause oxidative damage to cellular components such as DNA, proteins, and lipids, by catalysing its breakdown into water and oxygen. The acitivity of this enzyme is particularly important in cells that are exposed to high levels of oxidative stress, such as liver cells, and in cells that produce high levels of ROS, such as immune cells.	Testing can provide insights into risk assessment for oxidative stress-related conditions and guide preventive measures to promote better health.
CBS	The CBS (cystathionine beta-synthase) gene encodes an enzyme called cystathionine beta-synthase that plays a critical role in the biosynthesis of cysteine, an amino acid involved in many important biological processes.	CBS catalyses the first step in the transsulfuration pathway, converting homocysteine and serine into cystathionine, a reaction critical for the production of cysteine. This reaction is involved in the metabolism of methionine and the regulation of homocysteine levels.	Testing can provide insights into personalised risk assessment on homocysteine levels which can influence the risk of cardiovascular outcomes and other health conditions, and guide interventions for these conditions.
CCL2	The CCL2 (C-C motif chemokine ligand 2) gene encodes a protein known as monocyte chemoattractant protein-1 (MCP-1), a small cytokine protein that is involved in immune and inflammatory responses. It is secreted by various cells such as monocytes, macrophages, and endothelial cells in response to inflammatory stimuli.	MCP-1 plays a crucial role in the immune system by attracting and recruiting monocytes, a type of white blood cell, to sites of inflammation or injury. This chemokine facilitates the migration of monocytes from the bloodstream into tissues, where they can contribute to the immune response and tissue repair. Variations in the CCL2 gene may lead to a dysregulation in CCL2 expression, which could be associated with various inflammatory conditions and immune response.	Testing can provide insights into risk assessment for inflammatory disorders, such as rheumatoid arthritis, cardiovascular diseases, improper immune function, and other, and guide prevention and/or management strategies.

Name	Description	Function	Why test for it
CDKN2B	The CDKN2B-AS1 (cyclin-dependent kinase inhibitor 2B antisense RNA 1) gene, also known as ANRIL, is a long non-coding RNA which has been implicated in various biological processes, including cell proliferation and apoptosis, and has been shown to regulate the expression of several other genes.	This protein is involved in the control of the cell cycle by interacting with chromatin-modifying proteins and other regulatory molecules to modulate gene expression and cellular processes critical for normal development and homeostasis. Certain variants of the CDKN2B-AS1 gene have been linked to an increased risk of conditions like age-related macular degeneration, cardiovascular diseases, type 2 diabetes, and other.	Testing can provide insights into risk assessment and guide preventive measures for age-related macular degeneration outcomes, cardiovascular diseases, type 2 diabetes, and other.
CETP	The CETP gene encodes the cholesteryl ester transfer protein (CETP), which plays a crucial role in lipoprotein metabolism.	CETP is involved in the transfer of cholesterol esters from high-density lipoprotein (HDL) particles to very low-density lipoproteins (VLDL) and low-density lipoproteins (LDL). This results in a reduction in HDL cholesterol levels and an increase in VLDL and LDL cholesterol levels. Variations in the CETP gene can impact lipid metabolism and high-density lipoprotein (HDL) cholesterol levels.	Testing can provide insights into cardiovascular risk assessment and guide interventions for managing cholesterol levels and preventing heart disease.
CETP	The CETP gene encodes the cholesteryl ester transfer protein (CETP), which plays a crucial role in lipoprotein metabolism.	CETP is involved in the transfer of cholesterol esters from high-density lipoprotein (HDL) particles to very low-density lipoproteins (VLDL) and low-density lipoproteins (LDL). This results in a reduction in HDL cholesterol levels and an increase in VLDL and LDL cholesterol levels. Variations in the CETP gene can impact lipid metabolism and high-density lipoprotein (HDL) cholesterol levels.	Testing can provide insights into cardiovascular risk assessment and guide interventions for managing cholesterol levels and preventing heart disease.
CHRNA3	The CHRNA3 (cholinergic receptor nicotinic alpha 3 subunit) gene encodes a subunit of the nicotinic acetylcholine receptor and is expressed in the brain and other tissues such as the lungs.	This protein is involved in neurotransmission in the central and peripheral nervous systems involved in reward and addiction pathways. Certain variants of the CHRNA3 gene have been linked to an increased risk of nicotine addiction and smoking-related outcomes.	Testing can provide insights into personalised susceptibility to smoking behaviours and guide smoking cessation strategies for better health outcomes.
CHRNA5	The CHRNA5 (cholinergic receptor nicotinic alpha 5 subunit) gene encodes a subunit of the nicotinic acetylcholine receptor, and a member of a superfamily of ligand-gated ion channels.	This protein is involved in neurotransmission in the central and peripheral nervous systems, specifically, it mediates fast signal transmission at synapses, and influences reward and addiction pathways. Certain variants of the CHRNA5 gene have been linked to an increased risk of nicotine addiction and smoking-related outcomes.	Testing can provide insights into personalised susceptibility to smoking behaviours and guide smoking cessation strategies for better health outcomes.

Name	Description	Function	Why test for it
CLOCK	The CLOCK (Circadian Locomotor Output Cycles Kaput) gene encodes a protein involved in regulating circadian rhythms, which are the body's internal biological clocks that control various physiological processes.	This protein is involved in regulating the body's circadian rhythm, which is the internal biological clock that helps regulate sleep-wake cycles, hormone release, metabolism, and other physiological processes, over a 24-hour cycle. Certain variants of the CLOCK gene can influence individual sleep-wake cycles and susceptibility to circadian rhythm disorders.	Testing can provide insights into sleep management and lifestyle adjustments for better circadian health and related conditions such as, hormone imbalance, stress, pituitary function, and other.
CNR1	The CNR1 (cannabinoid receptor type 1) gene encodes the CB1 receptor, which is a G protein-coupled receptor primarily found in the brain and nervous system.	The CB1 receptor plays a key role in the endocannabinoid system, which is involved in various physiological processes, including pain modulation, appetite regulation, mood control, and immune function. It is activated by endocannabinoids, which are naturally occurring compounds in the body, as well as by phytocannabinoids, which are compounds found in the cannabis plant. This activation can affect neurotransmitter release and signaling pathways, influencing cognitive function, behavior, and other physiological responses. Variations in the CNR1 gene can impact individual responses to cannabinoids and may be associated with conditions like substance abuse, psychiatric outcomes, and metabolic disorders.	Testing can provide insights into risk assessment and guide preventative and/or management strategies for conditions such as, addictive behaviour, impulsive behaviour, metabolic disorders, and other.
COL1A1	The COL1A1 gene encodes the Alpha-1 Chain of Type I Collagen, a major component of the extracellular matrix in connective tissues in the body.	The COL1A1 gene is involved in the synthesis of Type I Collagen, which is essential for maintaining the function and structural support for various connective tissues such as skin, bones, and tendons.	Testing can provide insights into risk assessment and guide preventive measures and management strategies for conditions associated with certain variants of the COL1A1 gene such as bone density, fracture risk, and certain connective tissue outcomes.
COL5A1	The COL5A1 gene encodes the Alpha-1 Chain of Type V Collagen, which is a component of the extracellular matrix in connective tissues.	Type V Collagen contributes to the structural integrity and elasticity of tissues such as skin, tendons, and blood vessels.	Testing can provide insights into risk assessment and guide preventive measures and management strategies for conditions that can impact connective tissue integrity and increase the risk of outcomes such as tendon injuries and skin elasticity.
COMT	The COMT (catechol-O-methyltransferase) gene encodes an enzyme called catechol-O-methyltransferase that plays a role in the breakdown and inactivation of neurotransmitters such as dopamine, epinephrine, and norepinephrine in the brain and other tissues.	The activity of the COMT enzyme affects the levels and availability of dopamine, epinephrine, and norepinephrine in the brain, which can impact various functions including mood, cognition, and pain perception.	Testing can provide insights into susceptibility to conditions related to mood regulation, cognitive performance, pain sensitivity, and guide preventative approaches for better management.

Name	Description	Function	Why test for it
CRP	The CRP (C-reactive protein) gene encodes a protein called C-reactive protein, which is an important biomarker of inflammation.	CRP is produced in the liver and released into the bloodstream in response to inflammation in the body, particularly acute infection or tissue injury. It helps to activate the immune system and aids in the clearance of pathogens and damaged cells. Certain variants of the CRP gene can impact CRP levels, a marker of inflammation and cardiovascular risk.	Testing can provide insights into risk assessment for cardiovascular and inflammatory outcomes and guide preventive measures and management strategies.
CTH	The CTH (cystathionine gamma-lyase) gene encodes an enzyme called cystathionine gamma-lyase, which plays a critical role in sulfur amino acid metabolism.	The CTH protein catalyses the breakdown of cystathionine into cysteine, which is an essential amino acid for protein synthesis and antioxidant defense. Additionally, CTH is involved in the production of hydrogen sulfide (H2S), a gasotransmitter that has various physiological functions, including regulating blood vessel dilation, neurotransmission, oxidative-stress, and cellular energy metabolism. The CTH protein also contributes to DNA methylation. Variants in this gene can affect homocysteine levels and impact the risk of cardiovascular diseases and other conditions.	Testing can provide insights into risk assessment and guide interventions for cardiac health health conditions and methylation.
CTLA4	CTLA4 (cytotoxic T-lymphocyte-associated protein 4) is a protein expressed on the surface of immune cells called T-cells, which play a key role in regulating the immune response.	CTLA4 acts as a negative regulator of T-cell activation, meaning it helps to control and reduce the activity of T-cells and helps prevent excessive immune responses and autoimmunity.	Testing can provide insights into risk assessment and guide preventive and/or management strategies for autoimmune conditions such as type 1 diabetes and thyroid disorders.
CYP1A1	The CYP1A1 gene encodes an enzyme involved in the metabolism of various drugs and environmental toxins.	The enzyme produced by this gene belongs to the Cytochrome P450 family, and is responsible for converting substances like polycyclic aromatic hydrocarbons (PAHs) found in tobacco smoke, pollutants, and certain dietary compounds into forms that can be excreted from the body, reducing their harmful effects. Variations in the CYP1A1 gene can influence the efficiency of toxin metabolism, potentially affecting an individual's susceptibility health conditions related to exposure to environmental toxins.	Testing can provide insights into risk assessment for conditions related to detoxification pathways, potentially affecting susceptibility to environmental exposures and guide preventive measures.
CYP1A2	The CYP1A2 gene encodes an enzyme called Cytochrome P450 1A2, which is involved in the metabolism of various substances in the body, including drugs, toxins, and environmental chemicals, in the liver.	CYP1A2 primarily metabolises caffeine and certain medications, such as some antidepressants and antipsychotics. Genetic variations in the CYP1A2 gene can influence the rate at which the protein metabolises caffeine and some pharmaceuticals.	Testing can provide insights into whether an individual is a fast or slow caffeine metaboliser, and personalised caffeine consumption guidelines and health management.

Name	Description	Function	Why test for it
CYP1B1	The CYP1B1 gene encodes an enzyme part of the cytochrome P450 family called cytochrome P450 1B1, and is primarily involved in the metabolism of various and xenobiotics and endogenous compounds such as hormones.	This enzyme plays a role in the activation and detoxification of environmental toxins, drugs, and some hormones. Additionally, the CYP1B1 gene is implicated in the metabolism of estrogens and the synthesis of prostaglandins, both of which have important roles in reproductive and inflammatory processes. Certain variants of the CYP1B1 gene can influence drug metabolism rates and may impact drug efficacy and adverse effects.	Testing can provide insights into drug responses and guide medication selection and dosing through the GP for optimised therapeutic outcomes.
CYP2A6	The CYP2A6 gene encodes an enzyme called cytochrome P450 2A6, which is expressed in the liver and primarily responsible for the metabolism of nicotine, the major component of tobacco smoke.	This enzyme plays a crucial role in the breakdown and clearance of nicotine from the body. Genetic variations in the CYP2A6 gene can affect the activity of the enzyme, leading to differences in nicotine metabolism and, consequently, variations in smoking behaviors and nicotine dependence.	Testing can provide insights into personalised susceptibility to smoking behaviours and guide smoking cessation strategies for better health outcomes.
CYP2C9	The CYP2C9 gene encodes an enzyme called cytochrome P450 2C9, which is primarily found in the liver and is involved in the metabolism of various drugs, including nonsteroidal anti-inflammatory drugs (NSAIDs), anticoagulants (like warfarin), and anticonvulsants.	This enzyme plays a significant role in the breakdown and elimination of medications like nonsteroidal anti-inflammatory drugs (NSAIDs), anticoagulants (like warfarin), and anticonvulsants from the body. Variations in the CYP2C9 gene can affect the activity of the enzyme, which may impact an individual's response to certain medications and their risk of adverse drug reactions.	Testing can provide insights into drug responses and guide medication selection and dosing for optimised therapeutic outcomes.
CYP2C19	The CYP2C19 gene encodes an enzyme called cytochrome P450 2C19, which is involved in the metabolism of various drugs, including certain antiplatelet agents (e.g., clopidogrel), antidepressants (e.g., citalopram), and proton pump inhibitors (e.g., omeprazole).	This gene affects how quickly or slowly a person's body processes these drugs, which can affect their effectiveness and potential side effects. Variations in the CYP2C19 gene can lead to differences in the activity of the enzyme, with some variants causing the enzyme to be less effective or not functional at all. This can result in variations in drug metabolism.	Testing can provide insights into drug responses and guide medication selection and dosing through the GP for optimised therapeutic outcomes.
CYP2D6	The CYP2D6 gene encodes an enzyme called cytochrome P450 2D6, which is responsible for metabolising a significant number of medications, including antidepressants, antipsychotics, pain medications, and beta-blockers.	The enzyme helps convert medications like antidepressants, antipsychotics, pain medications, and beta-blockers into their active or inactive forms, influencing their effectiveness and potential side effects. Genetic variations in the CYP2D6 gene can lead to differences in enzyme activity, resulting in variations in drug metabolism among individuals. This can affect drug efficacy, toxicity, and the required dosage.	Testing can provide insights into drug responses and guide medication selection and dosing through the GP for optimised therapeutic outcomes.

Name	Description	Function	Why test for it
CYP2R1	The CYP2R1 gene encodes an enzyme called cytochrome P450 2R1, which is involved in the metabolism of vitamin D.	The enzyme helps convert medications like antidepressants, antipsychotics, pain medications, and beta-blockers into their active or inactive forms, influencing their effectiveness and potential side effects. Genetic variations in the CYP2D6 gene can lead to differences in enzyme activity, resulting in variations in drug metabolism among individuals. This can affect drug efficacy, toxicity, and the required dosage.	Testing can provide insights into drug responses and guide medication selection and dosing through the GP for optimised therapeutic outcomes.
CYP3A4	CYP3A4 is a gene that encodes for the Cytochrome P450 3A4 enzyme primarily found in the liver and is involved in the metabolism of drugs, toxins, and other compounds.	In the liver, this enzyme is responsible for converting vitamin D into an active form that can be used by the body, and can also be used as a biomarker for vitamin D status. Variations in the CYP2R1 gene can affect the efficiency of this conversion process and thus impact an individual's vitamin D status.	Testing can provide insights into risk assessment for vitamin D-related conditions, vitamin D requirements, and guide appropriate supplementation strategies for optimal health.
CYP4F2	The CYP4F2 gene encodes an enzyme called cytochrome P450 4F2 that plays a role in the metabolism of vitamin K, fatty acids, eicosanoids, and other lipids.	This enzyme is involved in the synthesis of epoxyeicosatrienoic acids (EETs), which have various roles in the cardiovascular and renal systems. It also metabolises vitamin K and arachidonic acid, which are important in blood clotting and inflammation, respectively. Variations in the CYP4F2 gene may contribute to altered levels of EETs and vitamin K, therefore, potentially influencing cardiovascular health and coagulation processes.	Testing can provide insights into risk assessment for cardiovascular diseases and guide nutritional interventions.
CYP17A	The CYP17A1 gene encodes an enzyme called cytochrome P450 17A1, which plays a key role in steroid hormone biosynthesis.	The CYP17A enzyme plays a key role in two important pathways: the production of cortisol, and the synthesis of sex hormones, including both androgens (such as testosterone) and estrogens. Specifically, it converts cholesterol to pregnenolone, which is then converted to either progesterone or DHEA, a precursor of androgens and estrogens. Variations in the CYP17A1 gene can impact the enzyme's activity and subsequently influence hormone levels. It has therefore been associated with conditions such as polycystic ovary syndrome (PCOS) and hormone-related outcomes.	Testing can provide insights into risk assessment and guide interventions for conditions affecting hormone levels.

Name	Description	Function	Why test for it
DAO	The DAO (D-amino acid Oxidase) gene is responsible for the production of the DAO enzyme which breaks down histamine, an important chemical messenger in the body involved in various physiological processes, including allergic and inflammatory responses.	The DAO enzyme is primarily found in the intestines, where it helps to break down histamine from food, and in the kidneys and liver, where it breaks down histamine produced by the body. Variations in the DAO gene can affect the activity of the enzyme, potentially leading to impaired histamine metabolism and contributing to conditions such as histamine intolerance or allergic reaction. Particularly, a deficiency in DAO activity can lead to increased levels of histamine, causing symptoms such as headaches, flushing, and gastrointestinal distress.	Testing can provide insights into personalised risk assessment and guide dietary and lifestyle adjustments to manage histamine-related conditions.
DBH	The DBH gene encodes the enzyme dopamine beta-hydroxylase (DBH), which is involved in the production of the neurotransmitter norepinephrine within the nervous system.	DBH plays a role in converting dopamine to norepinephrine, which in turn helps regulate many functions in the body, including heart rate, blood pressure, and mood. Variations in the DBH gene have been associated with differences in enzyme activity and levels of norepinephrine in the body. The changes in norepinephrine levels could be linked to several health conditions, including depression, anxiety, and cardiovascular disease.	Testing can provide insights into risk assessment strategies for conditions like ADHD, depression, and cardiovascular disorders.
DIO1	The DIO1 gene encodes an enzyme called Type 1 Iodothyronine Deiodinase (DIO1), which is involved in the regulation of thyroid hormone levels in the body.	DIO1 primarily converts the less active thyroid hormone, thyroxine (T4), into the more active form, triiodothyronine (T3), in various tissues, including the liver and kidneys. This conversion is crucial for the regulation of metabolism, growth, and development. Variations in the DIO1 gene can influence the activity of the enzyme, potentially impacting thyroid hormone levels and metabolic function.	Testing can provide insights into personalised risk assessment for thyroid-related disorders and guide appropriate nutritional interventions.
DIO2	The DIO2 gene encodes an enzyme called type 2 iodothyronine deiodinase (D2), which is responsible for converting the thyroid hormone thyroxine (T4) into its active form, triiodothyronine (T3), in various tissues throughout the body including the brain, liver, and skeletal muscles.	DIO2 activity helps regulate the levels of T3, which is essential for maintaining metabolism, body temperature, and normal growth and development. Research has found that the D2 enzyme also plays a role in the regulation of thermogenesis in brown adipose tissue. Genetic variations in the DIO2 gene can influence the efficiency of this conversion process and impact thyroid hormone levels, potentially affecting metabolism and other physiological functions.	Testing can provide insights into personalised risk assessment for thyroid-related disorders and guide appropriate nutritional interventions.
DOT1L	The DOT1L gene encodes an enzyme called Disruptor of Telomeric Silencing 1-Like (DOT1L). DOT1L is responsible for a specific type of histone modification known as methylation.	DOT1L plays a crucial role in regulating gene expression by adding methyl groups to histone proteins, which helps regulate gene transcription, DNA damage response, and DNA replication.	Testing can provide insights into risk assessment for outcomes impacted by gene expression and guide preventive measures for better health outcomes.

Name	Description	Function	Why test for it
DRD1	The DRD1 (Dopamine receptor D1) gene encodes a receptor protein that is a member of the dopamine receptor family, and is primarily found in the brain.	On the surface of certain brain cells, the DRD1 receptor binds to dopamine, which triggers a signalling pathway mediating the effects of dopamine such as reward, motivation, and motor control. Activation of the DRD1 receptor can also initiate signaling pathways that regulate neuronal activity and influence behaviors and cognitive processes. Variations in the DRD1 gene have been associated with a potential of several neurological disorders.	Testing can provide insights into risk assessment and guide management approaches for neurological disorders such as ADHD.
DRD2	The DRD2 (Dopamine receptor D2) gene encodes the dopamine D2 receptor, which is a G protein-coupled receptor that is primarily expressed in the brain.	Activation of the DRD2 receptor inhibits the production of cyclic AMP, a signaling molecule involved in various cellular processes. Also, the DRD2 receptor plays a key role in modulating dopamine signaling such as the regulation of reward, pleasure, and motivation, and is a target for many drugs used in the treatment of psychiatric disorders. Variations in the DRD2 gene have been associated with various psychiatric conditions and behavioral traits, including addiction, aggression, and impulsivity.	Testing can provide insights into risk assessment and guide management approaches for neurological disorders.
DRD3	The DRD3 (Dopamine receptor D3) gene encodes a receptor protein that belongs to the dopamine receptor family, and is primarily found in the brain.	The DRD3 receptor lays a role in modulating dopamine neurotransmission. It is involved in regulating reward, motivation, and certain cognitive functions. Variations in the DRD3 gene have been associated with various psychiatric disorders and addictive behaviors.	Testing can provide insights into risk assessment and guide management approaches for neurological disorders, and addictive behaviours.
DRD4	The DRD4 (Dopamine receptor D4) gene encodes a receptor protein that is a member of the dopamine receptor family, and is primarily found in the brain.	DRD4 is involved in modulating dopamine neurotransmission. It plays a role in various brain functions, including reward, motivation, and cognition. Variations in the DRD4 gene have been associated with a potential for various behavioral traits and psychiatric disorders.	Testing can provide insights into risk assessment and guide management approaches for neurological disorders such as ADHD.
EDA2R	The EDA2R (Ectodysplasin A2 receptor) gene encodes a receptor protein that is involved in the signaling pathway of ectodysplasin A2 (EDA-A2), which is a member of the tumor necrosis factor receptor family.	The binding of EDA-A2 to the EDA2R plays a key role in the development and maintenance of hair, teeth, and sweat glands, and is involved in the formation of the skin, hair follicles, and other ectodermal structures.	Testing can provide insights into risk assessment, potential treatment selection, and management strategies for conditions such as hair loss, and other.
EGF	The EGF (Epidermal Growth Factor) gene encodes a protein called epidermal growth factor, which plays a crucial role in cell growth, division, and differentiation.	EGF binds to the epidermal growth factor receptor (EGFR) and activates downstream signaling pathways involved in cell proliferation, development, and tissue repair, specifically skin development and wound healing. Certain variants of the EGF gene can influence EGF levels and signaling, affecting cell growth, wound healing, and tissue repair.	Testing can provide insights into susceptibility to certain diseases and guide management strategies for improved health outcomes.

Name	Description	Function	Why test for it
EPHX1	The EPHX1 (Epoxide Hydrolase 1) gene encodes an enzyme called microsomal epoxide hydrolase responsible for the metabolism of certain drugs, and of epoxides, which are toxic compounds.	EPHX1 catalyses the conversion of reactive epoxides into more water-soluble and less toxic diols, facilitating their elimination from the body. It is also involved in the detoxification of certain environmental toxins, such as polycyclic aromatic hydrocarbons found in cigarette smoke and air pollution, as well as the metabolism of endogenous compounds, such as arachidonic acid. Variations in the EPHX1 gene have been associated with variations in enzyme activity and susceptibility to certain diseases, including cardiovascular diseases, as well as responses to environmental toxins.	Testing can provide insights into risk assessment for toxin-related diseases, cardiovascular outcomes, and guide preventive measures.
ESR1	The ESR1 (Estrogen Receptor 1) gene encodes the estrogen receptor alpha (ERα), which is a nuclear receptor protein involved in mediating the effects of estrogen in various tissues throughout the body including the breast, uterus, and bone, and is involved in a wide range of biological processes, such as development, reproduction, and metabolism.	ERα binds to estrogen and regulates the expression of target genes involved in cell growth, differentiation, and reproductive functions. It also plays a crucial role in female reproductive development, bone health, cardiovascular health, and breast tissue development.	Testing can provide insights into risk assessment and guide preventive measures for conditions hormone-related outcomes, and other conditions such as osteoporosis.
FAAH	The FAAH (Fatty Acid Amide Hydrolase) gene encodes an enzyme called fatty acid amide hydrolase. This enzyme is responsible for the breakdown of endocannabinoids, which are lipid-based signaling molecules that bind to cannabinoid receptors in the body.	By metabolising endocannabinoids, FAAH regulates their levels and duration of action, thus modulating various physiological processes such as pain sensation, inflammation, mood, and appetite. Variations in the FAAH gene have been associated with altered endocannabinoid signaling and have been implicated in conditions such as pain disorders, anxiety, and addiction.	Testing can provide insights into susceptibility to pain disorders, anxiety, and other related conditions, guiding appropriate interventions and management.
FABP2	The FABP2 (fatty acid-binding protein 2) gene codes for a protein involved in the absorption and metabolism of dietary fats in the small intestine.	ABP2 is responsible for the transport of fatty acids from the intestinal lumen to the enterocyte where they are metabolised or incorporated into lipoprotein particles for transport to other tissues. This process is essential for the uptake of dietary fats and their subsequent utilisation by the body for energy production, storage, and other physiological functions. Variants in the FABP2 gene have been associated with differences in fat absorption and metabolism, and may contribute to the risk of obesity, type 2 diabetes, and other metabolic disorders.	Testing can provide insights into risk assessment and guide dietary and lifestyle interventions for better metabolic health.
FACTOR V	The FACTOR V gene, also known as F5, provides instructions for producing a protein called coagulation factor V. This protein is an essential component of the blood clotting cascade, which helps stop bleeding after an injury.	Factor V plays a crucial role in the formation of a stable blood clot by assisting in the conversion of prothrombin to thrombin, a key enzyme involved in clot formation. Variations in the F5 gene can contribute to an increase in the risk of developing abnormal blood clots.	Testing can provide insights into risk assessment for clotting and guide preventive measures.

Name	Description	Function	Why test for it
FADS1	The FADS1 (Fatty Acid Desaturase 1) gene encodes an enzyme that is involved in the metabolism of fatty acids.	The FADS1 enzyme catalyses the conversion of dietary essential fatty acids, such as linoleic acid and alpha-linolenic acid, into long-chain polyunsaturated fatty acids (PUFAs) ike arachidonic acid and docosahexaenoic acid (DHA), which play critical roles in various biological processes, including cell membrane structure and function, inflammation, and brain development. Variations in the FADS1 gene have been associated with alterations in PUFA metabolism. Specifically, they can impact the conversion of omega-3 and omega-6 fatty acids, affecting cardiovascular health and inflammatory responses and have been implicated in conditions such as cardiovascular disease, inflammatory disorders, and cognitive function.	Testing can provide insights into dietary recommendations (PUFA, omega 3 and other) and guide interventions for optimal health.
FADS2	The FADS2 (Fatty Acid Desaturase 2) gene encodes an enzyme that is involved in the metabolism of fatty acids.	The FADS2 enzyme catalyses the conversion of certain dietary fatty acids, such as linoleic acid and alpha-linolenic acid, into longer-chain polyunsaturated fatty acids (PUFAs) like arachidonic acid and docosahexaenoic acid (DHA). These PUFAs are essential components of cell membranes and play important roles in various biological processes, including inflammation, immune function, and brain development. Variations in the FADS2 gene have been associated with alterations in PUFA metabolism and have been linked to conditions such as cardiovascular disease, metabolic disorders, and cognitive function.	Testing can provide insights into dietary recommendations (PUFA, omega 3 and other) and guide interventions for optimal health.
FAM9B	Research suggests that the FAM9B (Family With Sequence Similarity 9, Member B) gene may be involved in neuronal development and function, as well as in the regulation of immune responses.	It is located on chromosome X and variants in this gene have been associated with various conditions, including androgen deficiencies, schizophrenia, bipolar disorder, and intellectual disability, but the exact mechanism behind these associations is still being studied. Further research is needed to determine the specific role of FAM9B in the body and its potential implications for human health.	Testing can provide insights into potential androgen deficiency.
FCGR2A	The FCGR2A (Fc fragment of IgG receptor IIa) gene encodes a receptor protein called Fc gamma receptor IIA (FcγRIIA) that is found on the surface of various immune cells, including macrophages, monocytes, and neutrophils.	FcγRIIA plays a role in the immune response by binding to antibodies that have attached to foreign invaders such as bacteria or viruses, and as a result, triggering the immune cell to engulf and destroy the invader. Variations in the FCGR2A gene may affect the strength of this immune response, potentially increasing or decreasing susceptibility to certain infections or autoimmune diseases.	Testing can provide insights into risk assessment and guide treatment strategies for autoimmune and infectious outcomes.

Name	Description	Function	Why test for it
FKBP5	The FKBP5 (FK506-binding protein 5) gene encodes a protein that plays a crucial role in regulating the body's response to stress. FKBP5 has been implicated in various physiological and pathological processes, including stress-related disorders such as anxiety and depression.	The FKBP5 protein interacts with certain receptors in the brain, such as glucocorticoid receptors, which are involved in the stress response and the regulation of inflammation. Variations in the FKBP5 gene have been associated with altered stress response, increased susceptibility to psychiatric disorders like depression and post-traumatic stress disorder (PTSD), and potential effects on the regulation of the body's immune and inflammatory processes.	Testing can provide insights into risk assessment and guide interventions and management for stress-related disorders like depression, anxiety, and post-traumatic stress disorder.
FSHB	The FSHB (follicle-stimulating hormone beta subunit) gene is responsible for encoding the beta subunit of follicle-stimulating hormone (FSH), a hormone expressed in the pituitary gland and essential for reproductive function.	FSH plays a key role in the regulation of the menstrual cycle and sperm production. It stimulates the growth and development of ovarian follicles in females and the production of sperm in males. Variations in the FSHB gene can influence FSH production, potentially affecting fertility and reproductive health in both men and women.	Testing can provide insights into risk assessment for fertility-related conditionand guide appropriate interventions.
FTO	The FTO (fat mass and obesity-associated) gene is involved in the regulation of body weight, fat mass, and metabolism, and is primarily expressed in the brain and adipose tissue.	Variations in the FTO gene have been associated with an increased risk of obesity and related metabolic disorders, such as type 2 diabetes. The exact function of the FTO gene is not yet fully understood, but it appears to be involved in the regulation of energy balance, appetite regulation, and the preference for high-calorie foods. The FTO gene may affect energy metabolism by altering the activity of certain brain regions involved in appetite control and energy expenditure. Variations of the FTO gene have been associated with increased appetite, food cravings, and a higher risk of obesity. Further research is being conducted to fully understand the specific mechanisms by which the FTO gene affects body weight and metabolism.	Testing can provide personalised recommendations for diet, exercise, and other lifestyle factors to help manage weight and prevent obesity-related health conditions.
FUT2	The FUT2 (fucosyltransferase 2) gene is responsible for encoding the alpha-1,2-fucosyltransferase enzyme that adds fucose molecules to the surface of cells and secretions in the body and is primarily expressed in the digestive and respiratory tracts.	These fucose molecules play a role in the development and functioning of the immune system and the maintenance of the gut microbiota. Additionally, it is responsible for the synthesis of H antigen in the body, which is the precursor of ABO blood group antigens. Variations in the FUT2 gene are associated with differences in blood group phenotypes and secretor status and can impact an individual's ability to secrete fucose into their body fluids, affecting the composition of their gut microbiome and influencing susceptibility to certain infections. Additionally, FUT2 variants have been associated with levels of vitamin B12, impacting nutrient metabolism.	Testing can provide insights into risk assessment for conditions like infections, IBS, autoimmune diseases, and nutrient absorption, and guide preventive measures.

Name	Description	Function	Why test for it
GABRA2	The GABRA2 (gamma-aminobutyric acid receptor subunit alpha-2) gene encodes a subunit of the gamma-aminobutyric acid A receptor (GABA-A receptor), which is the primary inhibitory neurotransmitter in the central nervous system.	This receptor plays a crucial role in regulating neuronal excitability and has been linked to anxiety, addiction, stress-response and other behavioral disorders. Specifically, it plays a role in regulating the effects of alcohol on the brain's reward system, influencing an individual's vulnerability to developing addictive behaviors. Further research is ongoing to fully understand the precise mechanisms and implications of GABRA2 in addiction and related disorders. Variations in the GABRA2 gene have been associated with increased susceptibility to alcoholism and other substance use disorders, as well as anxiety and mood disorders.	Testing can provide insights into gentic risk to alcohol dependence and other substance use disorders, mood, and guide management strategies for these conditions.
GABRA4	The GABRA4 gene encodes the alpha-4 subunit of the gamma-aminobutyric acid (GABA) A receptor, which is a member of the ligand-gated ion channel family that is involved in the regulation of inhibitory neurotransmission in the central nervous system.	The GABA A receptor helps regulate neuronal excitability; the alpha-4 subunit combines with other subunits to form a functional GABA-A receptor, which, when activated by the neurotransmitter GABA, opens a chloride ion channel and hyperpolarises the neuron, inhibiting its firing. Variations in the GABRA4 gene have been associated with various neurological and psychiatric conditions, including epilepsy, anxiety, and schizophrenia.	Testing can provide insights into the genetic factors contributing to neurological conditions, as well as autism spectrum disorder (ASD) and may help in their management and support.
GAD1	The GAD1 gene, also known as glutamate decarboxylase 1, is responsible for producing an enzyme called GAD67. This enzyme plays a critical role in the synthesis of gamma-aminobutyric acid (GABA), the primary inhibitory neurotransmitter in the central nervous system.	GAD1 is responsible for catalysing the decarboxylation of glutamate to GABA, and therefore plays a critical role in the regulation of GABAergic neurotransmission. GABA helps regulate neuronal excitability and plays a key role in maintaining the balance between excitation and inhibition in the brain. Variations in the GAD1 gene have been associated with an increased risk of neuropsychiatric conditions such as schizophrenia, bipolar disorder, and autism spectrum disorder, as well as with changes in GABA concentrations in the brain, suggesting its importance in brain function and mental health.	Testing can provide insights into susceptibility to neuropsychiatric disorders and guide management strategies for these conditions.
GC	The GC gene encodes the protein called vitamin D-binding protein (VDBP), which is responsible for transporting vitamin D and its metabolites in the bloodstream.	VDBP binds to vitamin D and helps transport it to target tissues and organs where it plays a crucial role in calcium metabolism, bone health, and immune function. Variations in the GC gene have been associated with variations in circulating vitamin D levels and susceptibility to certain diseases, including osteoporosis and autoimmune disorders.	Testing can provide insights into vitamin D status, guide supplementation, and optimise bone and overall health. Further testing is required.

Name	Description	Function	Why test for it
GDF5	The GDF5 gene encodes the growth differentiation factor 5 protein, which is a member of the transforming growth factor-beta (TGF-beta) superfamily.	GDF5 plays a crucial role in the development and maintenance of bones, joints, and other skeletal tissues. It is involved in regulating cell differentiation, proliferation, and maturation of chondrocytes, which are essential for proper skeletal development and joint function. It is also involved in the formation of cartilage, which is a flexible connective tissue found in many areas of the body, including the joints. Variations in the GDF5 gene have been associated with a risk of skeletal disorders, including osteoarthritis, skeletal dysplasias, and congenital joint malformations.	Testing can provide insights into conditions that can impact bone and cartilage formation, and guide management strategies for them.
GNB3	The GNB3 gene encodes a protein called Guanine Nucleotide-Binding Protein Subunit Beta-3, which plays a role in intracellular signaling pathways that are activated by G protein-coupled receptors.	This protein helps transmit signals from cell surface receptors to the inside of cells, regulating various cellular processes including neurotransmitter release, hormone secretion, and cell proliferation. GNB3 gene has been associated with several conditions, including hypertension, obesity, and mood disorders. Variations in the GNB3 gene can affect the activity of G protein signaling pathways, potentially influencing cellular responses to various signals and contributing to the development of these conditions.	Testing can provide insights into risk assessment of conditions such as obesity and guide management and/or prevention strategies for these outcomes.
GPX1	The GPX1 gene encodes an enzyme called glutathione peroxidase 1 (GPx-1), which plays a crucial role in protecting cells from oxidative damage.	GPX1 is responsible for converting hydrogen peroxide and other reactive oxygen species (ROS) into harmless substances, thereby preventing cellular damage to proteins, lipids, and DNA and maintaining oxidative balance. This gene is involved in antioxidant defense mechanisms and is important for maintaining the health and integrity of various tissues and organs. Variations in the GPX1 gene may influence individual susceptibility to oxidative stress-related diseases, such as cardiovascular and neurodegenrative disorders.	Testing can provide insights into risk assessment for oxidative stress-related disorders and guide preventive measures for better detoxification and improved overall health.
GSK3B	The GSK3B (Glycogen synthase kinase 3 beta) gene encodes a protein that is involved in multiple cellular processes, including cell proliferation, differentiation, and apoptosis.	GSK3B plays a key role in the regulation of glycogen synthesis and insulin signaling. It is also involved in the function of neurotransmitters and the regulation of gene expression, transcription, and translation. Variations in the GSK3B gene are associated with dysregulation of the GSK3B pathway, which has been implicated in various diseases, including diabetes and neurological disorders.	Testing can provide insights into risk assessment for various outcomes including neurological disorders such as depression.

Name	Description	Function	Why test for it
GSTM1	The GSTM1 gene codes for an enzyme called Glutathione S-Transferase Mu 1, which is involved in the detoxification of harmful substances in the body.	GSTM1 is involved in the metabolism and elimination of various toxins and reactive intermediates, including environmental pollutants, carcinogens, drugs, and oxidative stress-inducing molecules. It catalyses the conjugation of glutathione, a powerful antioxidant, to various toxic compounds, making them more water-soluble and easier to eliminate from the body. Genetic variations in the GSTM1 gene can affect individual susceptibility to certain diseases, environmental exposures, and drug responses.	Testing can provide insights into risk assessment for optimal detoxification and guide preventive and/or management measures to optimise overall health.
GSTP1	The GSTP1 gene codes for the enzyme glutathione S-transferase pi 1 (GSTP1), which is involved in the detoxification of harmful substances in the body.	The GSTP1 enzyme catalyses the conjugation of glutathione with a wide range of electrophilic compounds, including carcinogens, drugs, and environmental toxins, making them more water-soluble and easier to eliminate from the body. Variations in the GSTP1 gene can affect the activity of the enzyme and may influence an individual's susceptibility to diseases related to exposure to toxic substances.	Testing can provide insights into risk assessment for optimal detoxification and guide preventive and/or management measures to optimise overall health.
GSTT1	The GSTT1 (Glutathione S-transferase theta 1) gene encodes the glutathione S-transferase theta 1 enzyme expressed in the liver, which is involved in the detoxification of toxic compounds in the body.	The GSTT1 enzyme catalyses the conjugation of glutathione with electrophilic compounds, including several environmental toxins, drugs, and carcinogens.	Testing can provide insights into risk assessment for optimal detoxification and guide preventive and/or management measures to optimise overall health.
HFE	The HFE (hemochromatosis protein) gene encodes a protein involved in the regulation of iron metabolism in the body.	The HFE protein plays a crucial role in the absorption, transport, and storage of iron in the body. Variations in the HFE gene can disrupt iron homeostasis, leading to an excessive accumulation of iron in tissues such as the liver, heart, and pancreas. This can result in conditions such as hemochromatosis, characterised by the accumulation of iron in various organs and tissues, which can cause organ damage if left untreated.	Testing can provide insights into risk assessment for iron-related conditions and guide appropriate interventions for better health outcomes.
HLA	The HLA-DQB1 (human leukocyte antigen (HLA) complex) gene encodes a protein called major histocompatibility complex class II (MHC-II) beta chain. MHC-II proteins are critical for the immune system's ability to recognise and present antigens to immune cells	HLA-DQB1 is involved in the formation of MHC-II complexes and antigen binding. These complexes play a crucial role in immune surveillance, allowing immune cells to identify and respond to foreign substances, such as pathogens or abnormal cells. Variations in the HLA-DQB1 gene can influence antigen presentation and immune responses.	Testing can provide insights into personalised risk assessment for gluten sensitivity and celiac disease and guide management strategies for these conditions.

Name	Description	Function	Why test for it
HMNT	The HNMT gene encodes for the histamine N-methyltransferase enzyme, which is responsible for the degradation of histamine in the body, and is involved in many physiological processes, including inflammation, immune response, and neurotransmission. However, excessive histamine levels can lead to allergic reactions and other health problems.	HNMT helps regulate histamine levels in various tissues and organs by converting histamine into its inactive form. Variations in the HNMT gene can influence the enzyme's activity, potentially impacting histamine levels and contributing to conditions such as allergies, asthma, and other histamine-related disorders.	Testing can provide insights into personalised risk assessment, and guide dietary and lifestyle adjustments for better histamine management.
HTR1A	The HTR1A (5-hydroxytryptamine receptor 1A) gene encodes the serotonin 1A receptor, a subtype of serotonin receptors found in the brain and other tissues.	Serotonin is a key hormone that stabilises mood, feelings of well-being, and happiness, and helps with sleep, eating, and digestion. When serotonin binds to this receptor, it modulates various physiological and behavioural processes, including mood, anxiety, and cognition. Variations in the HTR1A gene have been linked to imbalances in serotonin levels, and as a consequence, may contribute to mood and anxiety disorders.	Testing provides insights into risk assessment for neural outcomes resulting from impaired serotonin levels such as, depression, anxiety and other.
IL-1B	The IL-1B gene encodes the protein interleukin-1 beta (IL-1β), which is a pro-inflammatory cytokine involved in the body's immune response and inflammation.	IL-1β plays a crucial role in coordinating immune cell activation and inflammation by stimulating the production of other inflammatory molecules. It is involved in various physiological processes, including the regulation of immune responses, fever induction, and tissue repair. Variations in the IL-1β gene can contribute to chronic inflammation and the development of inflammatory diseases.	Testing can provide insights into risk assessment for inflammatory conditions, such as autoimmune diseases and chronic inflammatory disorders, and guide preventive and/or management strategies for them.
IL	The IL-1B gene encodes the protein interleukin-1 beta (IL-1β), which is a pro-inflammatory cytokine involved in the body's immune response and inflammation.	IL-1β plays a crucial role in coordinating immune cell activation and inflammation by stimulating the production of other inflammatory molecules. It is involved in various physiological processes, including the regulation of immune responses, fever induction, and tissue repair. Variations in the IL-1β gene can contribute to chronic inflammation and the development of inflammatory diseases.	Testing can provide insights into risk assessment for inflammatory conditions, such as autoimmune diseases and chronic inflammatory disorders, and guide preventive and/or management strategies for them.
IL-1A	The IL-1A gene encodes the protein interleukin-1 alpha (IL-1α), which is a pro-inflammatory cytokine involved in the body's various physiological processes, including the initiation of immune responses and inflammation, cell proliferation, and wound healing.	IL-1A functions similarly to IL-1β and plays a critical role in regulating immune cell activation, inflammation, and tissue repair. It is released by immune cells and can stimulate the production of other inflammatory molecules. Variations in the IL-1a gene can contribute to inflammatory disorders and autoimmune diseases.	Testing can provide insights into risk assessment for inflammatory conditions, such as autoimmune diseases and chronic inflammatory disorders, and guide preventive and/or management strategies for them.

Name	Description	Function	Why test for it
IL-2	The IL-2 gene codes for the interleukin-2 protein, which is a cytokine that plays a role in the immune system's response to infections .	IL-2 is primarily produced by activated T cells and stimulates the growth and proliferation of various immune cells, including T cells, B cells, and natural killer (NK) cells. It is involved in immune tolerance, and in the regulation of immune responses, promoting the activation and expansion of immune cells to enhance the body's defense against pathogens.	Testing can provide insights into risk assessment for infection and autoimmune conditions, and guide preventive and/or management strategies for them.
IL-4	The IL4 gene encodes the protein interleukin-4 (IL-4), which is a cytokine involved in immune regulation and allergic responses.	Il-4 plays a key role in regulating the differentiation of T helper cells, promoting the production of antibodies by B cells, and suppressing the activity of some immune cells. It is important in the body's response to infections and in the development of allergic reactions, and has been implicated in the development of certain autoimmune diseases.	Testing can provide insights into risk assessment for allergic and autoimmune conditions, and guide preventive and/or management strategies for them.
IL-6	The IL-6 (Interleukin-6) gene codes for the interleukin-6 protein, which is a cytokine involved in various immune and inflammatory responses and is produced by various cell types, including immune cells.	IL-6 plays a role in regulating the immune system, promoting inflammation, and modulating the acute phase response. It also has diverse functions outside of the immune system, including roles in tissue regeneration, metabolism, and the central nervous system. According to research, IL-6 is implicated in various diseases, including autoimmune disorders and chronic inflammation.	Testing can provide insights into risk assessment for allergic and autoimmune conditions, and guide preventive and/or management strategies for them.
IL-8	The IL-8 (Interleukin 8) gene codes for the interleukin-8 protein, which is a chemokine involved in immune responses and inflammation. IL-8 is produced by various cells, primarily by immune cells in response to infection, tissue damage, or inflammation, as well as in endothelial and epithelial cells.	IL-8 attracts white blood cells, specifically neutrophils, to the site of infection or injury. This helps to contain the infection and promote healing. In addition to its role in the immune system, IL-8 has also been implicated in various disease processes, including some autoimmune disorders.	Testing can provide insights into risk assessment for allergic and autoimmune conditions, and guide preventive and/or management strategies for them.
IL-10	The IL-10 gene codes for the interleukin-10 (IL-10) protein, which is an important anti-inflammatory cytokine, and plays a crucial role in regulating the immune system.	IL-10 acts as a regulator of the immune system by suppressing excessive immune responses and promoting an anti-inflammatory environment. It inhibits the production of pro-inflammatory cytokines and modulates the activity of immune cells, such as macrophages, T cells, and B cells. Overall, IL-10 helps maintain immune homeostasis, prevents tissue damage caused by inflammation, and plays a crucial role in resolving inflammation after an immune response.	Testing can provide insights into risk assessment for allergic and autoimmune conditions, and guide preventive and/or management strategies for them.

Name	Description	Function	Why test for it
IL-13	The IL-13 (Interleukin 13) gene is responsible for the production of the IL-13 protein, which is an important cytokine involved in immune response regulation, particularly in allergic and inflammatory processes.	IL-13 plays a role in asthma, allergic diseases, and immune responses against parasites. It acts by binding to specific receptors on immune cells, such as mast cells, eosinophils, and macrophages, triggering the production of pro-inflammatory molecules like immunoglobulin E (IgE) and other antibodies, and influencing the immune cell function. It also contributes to tissue remodeling and repair processes in certain diseases. IL-13 is associated with an increased risk of developing allergic diseases, such as asthma and atopic eczema.	Testing can provide insights into risk assessment for allergic and autoimmune conditions, and guide preventive and/or management strategies for them.
IL-17a	The IL-17A gene encodes for a cytokine called interleukin-17A (IL-17A), which plays an important role in the immune response.	IL-17A is mainly produced by a type of T helper cell called Th17 cells and plays a crucial role in the defense against bacterial and fungal infections. It promotes inflammation by stimulating the production of other inflammatory molecules and recruiting immune cells to the site of infection or tissue damage. Variations in the IL-17A are associated with a risk of various autoimmune and inflammatory diseases, including rheumatoid arthritis, psoriasis, and inflammatory bowel disease.	Testing can provide insights into risk assessment for autoimmune and inflammatory conditions, and guide preventive and/or management strategies for them.
IL-18	The IL-18 (Interleukin 18) gene codes for the production of the IL-18 protein, which is a pro-inflammatory cytokine involved in the immune response.	IL-18 plays a role in regulating immune responses against infections and tumors by stimulating the production of other cytokines, such as interferon-gamma (IFN-γ), and activates natural killer (NK) cells and T cells. Additionally, IL-18 is implicated in inflammatory diseases and can contribute to the development of conditions like rheumatoid arthritis, asthma, and inflammatory bowel disease. Some research has also shown IL-18 to have a role in metabolism regulation and glucose homeostasis.	Testing can provide insights into risk assessment for autoimmune and inflammatory conditions, and guide preventive and/or management strategies for them.
IRF4	The IRF4 gene encodes a protein called interferon regulatory factor 4 (IRF4), which is a transcription factor involved in regulating gene expression in immune cells.	IRF4 plays a crucial role in the development, differentiation, and function of various immune cells, including B cells, T cells, and dendritic cells. It helps regulate immune responses, such as antibody production, T cell activation, and cytokine production. Additionally, IRF4 is involved in the control of cell growth, survival, and apoptosis in immune cells. Certain variants of the IRF4 gene can impact immune responses and skin pigmentation.	Testing can provide insights into immune function and skin-related conditions risk assessment.

Name	Description	Function	Why test for it
IRS1	The IRS1 (insulin receptor substrate 1) gene provides instructions for making a protein that is involved in regulating the way the body uses insulin to control blood sugar levels.	The IRS1 protein acts as a key mediator in the insulin signaling pathway, transmitting signals from the insulin receptor to downstream signaling molecules, which allows cells to take up glucose from the blood for energy or storage. Variations in the IRS1 gene have been associated with insulin resistance, leading to high blood sugar levels and an increased risk of type 2 diabetes, and other metabolic disorders.	Testing can help assess a genetic risk for developing metabolic disorders, and guide targeted prevention and/or management lifestyle strategies.
LCT	The LCT (lactase) gene encodes the enzyme lactase, which is responsible for the breakdown of lactose, the main sugar found in milk and dairy products, into glucose and galactose allowing for their absorption in the intestine.	The LCT gene plays a crucial role in lactose tolerance, determining an individual's ability to digest lactose throughout their lifespan. Lactase is primarily produced in the small intestine during infancy and early childhood to facilitate digestion of milk, but its production typically decreases in adulthood. Variations in the LCT gene can result in lactose intolerance, where individuals have reduced or absent lactase activity, leading to digestive symptoms such as bloating, gas, and diarrhea upon consuming lactose-containing foods.	Testing can help identify identify a predisposition to lactose intolerance, allowing for personalised dietary recommendations and management strategies.
LEPR	The LEPR (Leptin Receptor) gene is responsible for encoding the leptin receptor, a protein that plays a key role in regulating appetite, energy balance, and body weight.	The leptin receptor, located in various tissues including the hypothalamus, allows leptin, a hormone produced by fat cells, to bind and signal the brain to reduce appetite and increase energy expenditure. Variations in the LEPR gene can affect the function of the leptin receptor and lead to leptin resistance, where the body does not properly respond to leptin, resulting in increased appetite and reduced energy expenditure, which can contribute to obesity and metabolic disorders.	Testing can provide insights into a genetic predisposition to metabolic disorders, and help guide weight management strategies for better health outcomes.
LPA	The LPA (Lipoprotein(a)) gene encodes a protein called lipoprotein(a), structurally similar to low-density lipoprotein (LDL), but it also contains an additional protein called apolipoprotein(a), and is involved in transporting fats and cholesterol throughout the body.	The specific function of lipoprotein(a) in the body is not completely understood, but it is thought that elevated levels of lipoprotein(a) have been associated with an increased risk of cardiovascular diseases. Variations in the LPA gene can influence the levels of lipoprotein(a) in the bloodstream and impact an individual's cardiovascular health.	Testing can help assess a genetic risk for developing cardiovascular disease, and guide targeted prevention and management strategies, such as lifestyle modifications.

Name	Description	Function	Why test for it
LPL	The LPL (Lipoprotein Lipase) gene encodes an enzyme called lipoprotein lipase, found primarily in the muscles and adipose tissue, that plays a critical role in lipid metabolism, specifically in the breakdown of triglycerides.	Lipoprotein lipase helps hydrolyse triglycerides present in lipoprotein particles (from circulating chylomicrons and very low-density lipoproteins (VLDLs)), allowing the release of fatty acids for energy utilisation by various tissues. Variations in the LPL gene can lead to deficiencies in lipoprotein lipase activity, which can result in lipid metabolism disorders such as high triglyceride levels.	Testing can help assess a genetic risk for developing dyslipidemia, and guide preventive measures for better heart health, such as dietary interventions.
LRP1	The LRP1 (Low-Density Lipoprotein Receptor-Related Protein 1) gene encodes a cell surface receptor called LRP1. This receptor is involved in multiple cellular processes, including lipid metabolism, cellular signaling, and endocytosis.	LRP1 plays a critical role in the clearance of various molecules, including cholesterol-rich lipoproteins, from the bloodstream, and beta amyloid from the brain. Variants in LRP1 are associated with decreased clearance of amyloid beta, which can trigger neuroinflammation and pain pathways leading to migraine headaches. These variants are also associated with an increased risk of cardiovascular disoders, and neurodegenaritve diseases.	Testing can help identify individuals at risk for developing migraines and guide targeted prevention and management strategies, such as lifestyle changes.
MAOA	The MAOA (Monoamine Oxidase A) gene encodes an enzyme called monoamine oxidase A. This enzyme plays a crucial role in the metabolism and breakdown of various neurotransmitters in the brain, including serotonin, dopamine, and norepinephrine.	Serotonin, dopamine, and norepinephrine play critical roles in mood regulation, cognition, and behavior. By breaking down these neurotransmitters, MAOA helps regulate their levels in the brain and maintain proper neurotransmission. Variations in the MAOA gene have been linked to altered levels of neurotransmitters, which can influence mood, behavior, and mental health conditions such as aggression and impulsivity. Additionally, the activity of MAOA can also be influenced by environmental factors, such as stress and childhood experiences.	Testing can provide insights into risk assessment and guide treatment strategies for conditions like behavioral traits, aggression, and mood disorders.
MAOB	The MAOB (Monoamine Oxidase B) gene encodes an enzyme called monoamine oxidase B that is involved in the metabolism and breakdown of various neurotransmitters, such as dopamine, phenethylamine, and trace amines.	Specifically, MAO-B breaks down excess dopamine in the brain, preventing it from accumulating to toxic levels. Overall, regulating the levels of the various neurotransmitters, MAOB helps maintain proper neurotransmission and overall brain function. Variations in the MAOB gene have been associated with various neurological conditions.	Testing can provide insights into risk assessment and guide management strategies for neurological conditions as well as conditions like behavioral traits, aggression, and mood disorders.
MAP3K1	The MAP3K1 (Mitogen-Activated Protein Kinase Kinase Kinase 1) gene encodes a protein kinase that is part of the mitogen-activated protein kinase (MAPK) signaling pathway. This pathway is involved in transmitting signals from the cell surface to the nucleus, regulating various cellular processes such as cell growth, differentiation, and survival.	The MAP3K1 functions as a serine/threonine kinase and has complex roles in the immune system, cardiac tissue, testis, and wound healing. Variations in the MAP3K1 gene have been associated with developmental disorders.	Testing can provide insights into risk assessment for regulation of cell death, survival, migration and differentiation, and guide management strategies through lifestyle.

Name	Description	Function	Why test for it
MBL2	The MBL2 (mannose-binding lectin 2) gene encodes a protein called mannose-binding lectin (MBL), which is part of the innate immune system.	MBL plays a role in recognising and binding to certain sugar molecules present on the surface of pathogens, such as bacteria, viruses, and fungi. By binding to these pathogens, MBL activates the immune response, leading to their elimination. Variations in the MBL2 gene can affect the production or function of MBL, potentially impacting the individual's susceptibility to infections and autoimmune diseases.	Testing can provide insights into risk assessment for infections and autoimmune conditions, and guide preventive measures for better immune health through lifestyle and diet.
MC1R	The MC1R gene encodes the melanocortin-1 receptor, a protein primarily expressed in melanocytes, the cells responsible for producing melanin, the pigment that gives color to the skin, hair, and eyes.	Activation of the MC1R receptor triggers a signaling pathway that stimulates the production of eumelanin, a form of melanin that provides a darker pigmentation. Variations in the MC1R gene can lead to reduced MC1R activity, resulting in decreased eumelanin production and an increased likelihood of red hair, fair skin, and increased sensitivity to ultraviolet (UV) radiation / sunburn.	Testing can provide insights into risk assessment for skin and hair pigmentation and guide sun protection strategies for better skin health.
MC4R	The MC4R (Melanocortin-4 receptor) gene codes for the melanocortin 4 receptor protein, which is expressed in various regions of the brain, specifically the hypothalamus, and plays a key role in regulating appetite and energy balance.	The MC4R protein acts as a receptor for melanocortin hormones and responds to those signals to regulate food intake, energy expenditure, and body weight. Variations in the MC4R gene have been associated with an increased risk of obesity.	Testing can provide insights into risk assessment for snacking, obesity and metabolic disorders, and guide weight management strategies for better health outcomes.
MCM6	The MCM6 (minichromosome maintenance complex component 6) gene codes for an enzyme called lactase which is responsible for breaking down lactose, a sugar found in milk and other dairy products. Additionally, MCM6 is a component of the MCM complex, which acts as a helicase enzyme to unwind DNA and initiate replication during cell division.	The activity of the MCM6 gene is essential for individuals to digest lactose throughout their lives. The MCM6 gene regulates the expression of the lactase gene (LCT), and variations in the MCM6 gene are associated with lactose intolerance, where individuals have reduced or absent lactase activity, leading to symptoms such as bloating, gas, and diarrhea when consuming lactose-containing foods.	Testing can help identify identify a predisposition to lactose intolerance, allowing for personalised dietary recommendations and management strategies.
MEIS1	MEIS1 (myeloid ecotropic viral integration site 1) gene codes for a transcription factor protein that plays a crucial role in the regulation of gene expression and the development of multiple organs and tissues during embryonic development.	The MEIS1 protein is particularly important in the development of the nervous system, limb formation, and the formation of blood cells. In adults, the gene is expressed in various tissues, including the brain, and is involved in the regulation of neuronal development and function. Variations in the MEIS1 gene have been associated with an increased risk for several conditions, including hematological disorders (blood-related disorders) and neurological disorders such as restless legs syndrome.	Testing can aid in risk assessment and guide prevention and/or management strategies for individuals with this sleep-related movement disorder, such as restless leg syndrom.

Name	Description	Function	Why test for it
MnSOD/SOD2	The MnSOD (manganese superoxide dismutase) or SOD2 (superoxide dismutase 2) gene encodes an enzyme called manganese superoxide dismutase. This enzyme is crucial for the body's defense against oxidative stress, which is caused by an imbalance between the production of harmful reactive oxygen species (ROS) and the body's ability to neutralise them.	MnSOD/SOD2 helps convert superoxide radicals into less harmful molecules, protecting cells from oxidative damage. By reducing the levels of superoxide radicals, MnSOD/SOD2 prevents the formation of other reactive oxygen species that can damage cellular macromolecules such as DNA, proteins, and lipids. Variations in the MnSOD/SOD2 gene can contribute to various diseases associated with oxidative stress, including neurodegenerative disorders.	Testing can provide insights into risk assessment for oxidative stress-related outcomes and guide preventive measures for better health.
MTHFD1	The MTHFD1 gene provides instructions to make an enzyme called methylenetetrahydrofolate dehydrogenase 1 (MTHFD1), which plays a role in folate metabolism.	The MTHFD1 enzyme plays a role in processing the conversion of homocysteine to methionine, an amino acid required for various cellular processes, including protein synthesis and DNA methylation. Additionally, MTHFD1 is involved in the production of nucleotides, which are the building blocks of DNA and RNA. Variations in the MTHFD1 gene are associated with a reduced enzyme stability, meaning it is degraded more rapidly. Therefore, this can impact folate metabolism and may be associated with increased risk of certain health condition such as neural tube defects.	Testing can provide insights into the vatiants' impact on the folate cycle, and as a risk assessment on neural tube defects and guide proper food and lifestyle management for better health outcomes.
MTHFR	The MTHFR gene encodes an enzyme called methylenetetrahydrofolate reductase, which is involved in the folate metabolism pathway.	This enzyme helps convert the amino acid homocysteine to methionine, an essential step in the synthesis of DNA, RNA, and proteins. Additionally, MTHFR is important for the production of methyl groups required for DNA methylation, a process that regulates gene expression. Variations in the MTHFR gene can lead to reduced enzyme activity, potentially affecting folate metabolism and increasing the risk of certain health conditions, including cardiovascular disease and neural tube defects.	Testing can provide insights into the vatiants' impact on the folate cycle, and as a risk assessment on neural tube defects and guide proper food and lifestyle management for better health outcomes.
MTR	The MTR (5-methyltetrahydrofolate-homocysteine methyltransferase) gene encodes the enzyme methionine synthase (MS), which plays a critical role in the methionine cycle and the metabolism of folate and homocysteine.	MS converts homocysteine to methionine, an essential amino acid required for protein synthesis and various biochemical reactions. This enzyme also relies on vitamin B12 (cobalamin) as a cofactor. Variations in the MTR gene can impair MS activity, leading to elevated levels of homocysteine and potential disruption of folate metabolism, which may contribute to certain health conditions, such as cardiovascular disease and neurological disorders.	Testing can provide insights into the vatiants' impact on the folate and the methionine cycle, and a risk assessment on cardiovascular outcomes and neurological disorders, as well as, guide proper food and lifestyle management for better health outcomes.

Name	Description	Function	Why test for it
MTRR	The MTRR (Methionine synthase reductase) gene encodes the enzyme methionine synthase reductase, which plays a crucial role in maintaining the activity of methionine synthase (MS), an enzyme involved in the metabolism of folate and homocysteine.	Methionine synthase reductase helps maintain the active form of methionine synthase by reducing/regenrating the active form of its cofactor known as vitamin B12 (cobalamin). Variations in the MTRR gene can lead to reduced methionine synthase activity, elevated homocysteine levels, and impaired folate metabolism, which may contribute to various health conditions, including cardiovascular disease and neural tube defects.	Testing can provide insights into the vatiants' impact on the folate and the methionine cycle, and a risk assessment on cardiovascular outcomes and neurological disorders, as well as, guide proper food and lifestyle management for better health outcomes.
MX1	The MX1 gene encodes the MX1 protein (Myxovirus resistance protein 1), an interferon-inducible protein, which plays a critical role in the innate immune response against viral infections.	The MX1 protein inhibits viral replication by targeting and disrupting the life cycle of many RNA viruses, including influenza virus, vesicular stomatitis virus, and HIV-1. It acts by interfering with viral RNA synthesis and preventing the release of newly formed viral particles from infected cells.	Testing can provide insights into risk assessment for viral infections and guide preventive measures to enhance immune defense.
MYD88	The MYD88 gene encodes a protein called Myeloid Differentiation Primary Response 88 (MYD88), which plays a crucial role in the innate immune response to microbial infections.	The MYD88 protein is an adaptor molecule that mediates signaling from Toll-like receptors (TLRs) and interleukin-1 receptors (IL-1Rs) to activate nuclear factor-kappa B (NF-κB) and mitogen-activated protein kinase (MAPK) pathways, leading to the production of proinflammatory cytokines and chemokines. It is also involved in various cellular processes, including cell growth, differentiation, and apoptosis. Variations in the MYD88 gene have been linked to various immunodeficiencies, including susceptibility to bacterial infections, while aberrant MyD88 signaling has been associated with autoimmune and inflammatory disorders.	Testing can provide insights into risk assessment altered immune function and increased susceptibility to infections and autoimmune diseases. and guide preventive and/or management strategies for these conditions.
MYRF	The MYRF (Myelin regulatory factor) gene encodes a transcription factor that plays a critical role in the development, function, and maintenance of the central nervous system.	The MYRF protein is primarily involved in the formation and maintenance of myelin, a protective sheath that surrounds and insulates nerve fibers that is essential for proper nerve impulse conduction. MYRF regulates the expression of genes involved in myelin synthesis and promotes the differentiation of oligodendrocytes, the cells responsible for producing myelin in the central nervous system. Variations in the MYRF gene have been associated with abnormal myelination leading to an increased risk of developing neurological dysfunctions, including multiple sclerosis and schizophrenia.	Testing can provide insights into risk assessment for myelin-related outcomes and guide appropriate interventions for better neural and overall health.

Name	Description	Function	Why test for it
NAT1	The NAT1 (N-Acetyltransferase 1) gene encodes an enzyme that is responsible for the metabolism of a variety of drugs (particularly xenobiotics and drugs) and environmental chemicals (including aromatic and heterocyclic amines), and is primarily expressed in the liver, but it is also present in other tissues, including the bladder and breast.	The NAT1 enzyme catalyses the transfer of an acetyl group from acetyl-CoA to the substrate molecule. This process helps in the detoxification and elimination of these compounds from the body. This process helps in the detoxification and elimination of these compounds from the body. Variations in the NAT1 gene have been associated with differences in enzyme activity and may contribute to individual variations in drug response, as well as susceptibility to certain environmental factors and diseases, which may have implications for drug efficacy and toxicity.	Testing can provide insights into drug responses and detoxification phase I processes, and guide proper preventive and/or management strategies.
NAT2	The NAT2 (N-Acetyltransferase 2) gene encodes an enzyme that is primarily expressed in the liver, but also found in other tissues, and is involved in the metabolism of various drugs, environmental chemicals, and toxins.	NAT2 catalyses the transfer of an acetyl group from acetyl-CoA to the substrate molecules, which can affect the efficacy and toxicity of these compounds. Variations in the NAT2 gene can influence an individual's ability to metabolise certain medications, leading to variations in drug response and potential toxicity.	Testing can provide insights into drug responses and detoxification phase II processes, and guide proper preventive and/or management strategies.
NFE2L2	The NFE2L2 (Nuclear factor erythroid 2-related factor 2) encodes a transcription factor called NRF2, which regulates the expression of genes involved in antioxidant response and detoxification pathways.	The NRF2 transcription factor plays a critical role in cellular defense against oxidative stress. When activated, NRF2 promotes the production of antioxidant enzymes and phase II detoxification enzymes, which help protect cells from oxidative damage and maintain cellular homeostasis. NRF2 activation is important in reducing inflammation, combating oxidative stress, and promoting cellular survival in the face of various stressors and toxic insults. Variations in the NRF2 gene have been associated with the risk of various diseases, including neurodegenerative disorders, cardiovascular diseases, and antioxidants response.	Testing can provide insights into risk assessment oxidative stress-related outcomes, and guide preventive measures for better health outcomes.
NFIA	The NFIA-AS2 gene, also known as Natural Antisense Transcript for Nuclear Factor I A, is a long non-coding RNA gene that is transcribed into a non-coding RNA molecule, and is complementary to the NFIA gene.	NFIA is a transcription factor involved in the development and function of the nervous system, specifically the differentiation of various cell types, including neurons and glial cells. Studies have shown that NFIA-AS2 is highly expressed in the brain and is involved in the regulation of neurogenesis and synaptic plasticity. It has also been linked to several neurological disorders, including schizophrenia and autism spectrum disorder. While more research is needed to fully understand the role of NFIA-AS2, it is believed to regulate the expression of NFIA by interacting with it at the RNA level.	Testing can provide insights into risk assessment of neural outcomes.

Name	Description	Function	Why test for it
NOS3	The NOS3 (Nitric Oxide Synthase 3) gene encodes for the endothelial nitric oxide synthase (eNOS) enzyme, which is responsible for the production of nitric oxide (NO) in the endothelial cells lining blood vessels. NO plays a crucial role in regulating blood vessel tone, promoting vasodilation, and maintaining healthy cardiovascular function. It also has anti-inflammatory and anti-thrombotic effects.	NOS3 plays a crucial role in regulating vascular tone, promoting vasodilation, and maintaining proper blood flow. It is also involved in the regulation of inflammation, immune responses, and cardiovascular homeostasis. Some researchers suggest that it may improve athletic performance through its effect on heart rate and energy balance. Variations in the NOS3 gene have been linked to various cardiovascular diseases such as hypertension, atherosclerosis, and coronary artery disease.	Testing can provide insights into risk assessment for heart-related conditions and blood pressure dysregulation, as well as a potential assessment for an improved sports performance. This information can be utilised to guide proper preventive measures for better cardiovascular health, and optimise energy production and use.
NPSR1	The NPSR1 (Neuropeptide S receptor 1) gene encodes a receptor protein that interacts with neuropeptide S (NPS). NPSR1 is primarily expressed in the brain, particularly in regions involved in regulating stress responses, anxiety, and fear.	Activation of the NPSR1 receptor by NPS has been implicated in modulating various physiological and behavioral processes, including arousal, sleep-wake cycle, anxiety, fear, pain perception, memory, and respiratory function. Genetic variations in the NPSR1 gene have been associated with susceptibility to anxiety disorders and other psychiatric conditions.	Testing can provide insights into risk assessment for mental disorders such as anxiety and susceptibility to asthma and allergies.
NQ01	The NQO1 gene encodes the enzyme NAD(P)H quinone dehydrogenase 1, also known as NQO1. This enzyme plays a role in protecting cells from oxidative stress, which is caused by an imbalance between the production of reactive oxygen species (ROS) and the ability of the body to detoxify them.	NQO1 helps to prevent oxidative damage by reducing quinones to hydroquinones and by converting superoxide anions to hydrogen peroxide, more stable and less toxic compounds. Additionally, NQO1 is involved in the metabolism of certain medication. Variations in the NQO1 gene can influence an individual's susceptibility to various diseases, including cardiovascular disorders and neurodegenerative conditions.	Testing can provide insights into risk assessment for detoxification processes and guide preventive and/or management strategies for condition resulting from oxidative stress.
NRF2	The NFE2L2 (Nuclear factor erythroid 2-related factor 2) encodes a transcription factor called NRF2, which regulates the expression of genes involved in antioxidant response and detoxification pathways.	The NRF2 transcription factor plays a critical role in cellular defense against oxidative stress. When activated, NRF2 promotes the production of antioxidant enzymes and phase II detoxification enzymes, which help protect cells from oxidative damage and maintain cellular homeostasis. NRF2 activation is important in reducing inflammation, combating oxidative stress, and promoting cellular survival in the face of various stressors and toxic insults. Variations in the NRF2 gene have been associated with the risk of various diseases, including neurodegenerative disorders, cardiovascular diseases, and antioxidants response.	Testing can provide insights into risk assessment oxidative stress-related outcomes, and guide preventive measures for better health outcomes.

Name	Description	Function	Why test for it
OAS	The OAS1 gene encodes an enzyme called 2'-5'-oligoadenylate synthetase 1 (OAS1). This enzyme is part of the innate immune response and plays a crucial role in defending the body against viral infections.	Upon viral infection, OAS1 is activated and synthesises 2'-5'-oligoadenylate (2-5A) molecules. These 2-5A molecules then activate a downstream protein called RNase L, which degrades viral RNA and inhibits viral replication. OAS1 is therefore an important component of the antiviral defense system in the body. OAS-1 also induces an inflammatory response to help fight off the infection. Variations in the OAS-1 gene have been associated with susceptibility to certain viral infections.	Testing can provide insights into risk assessment for viral diseases and guide preventive measures for better immune health.
OAS	The OAS1 gene encodes an enzyme called 2'-5'-oligoadenylate synthetase 1 (OAS1). This enzyme is part of the innate immune response and plays a crucial role in defending the body against viral infections.	Upon viral infection, OAS1 is activated and synthesises 2'-5'-oligoadenylate (2-5A) molecules. These 2-5A molecules then activate a downstream protein called RNase L, which degrades viral RNA and inhibits viral replication. OAS1 is therefore an important component of the antiviral defense system in the body. OAS-1 also induces an inflammatory response to help fight off the infection. Variations in the OAS-1 gene have been associated with susceptibility to certain viral infections.	Testing can provide insights into risk assessment for viral diseases and guide preventive measures for better immune health.
OPRM1	The OPRM1 gene encodes the Mu-Opioid Receptor, which is primarily expressed in the central nervous system and plays a key role in the body's response to opioids; endogenous opioids such as endorphins and exogenous opioids such as morphine.	Activation of the mu-opioid receptor by opioid drugs, such as morphine, leads to pain relief, euphoria, a reduction in anxiety, and feelings of reward and pleasure, but it can also lead to dependence and addiction. Variations in the OPRM1 gene can influence an individual's response to opioids and may contribute to differences in pain sensitivity and susceptibility to opioid addiction.	Testing can provide insights into pain management strategies and potentially guide opioid use by doctors to minimise potential risks and improve patient outcomes.
OR10A2	The OR10A2 gene encodes a specific olfactory receptor protein called Olfactory Receptor Family 10 Subfamily A Member 2, which is involved in the sense of smell.	These receptor proteins detect and bind to odor molecules, initiating a signaling cascade that sends information to the brain, allowing us to perceive and distinguish different smells. OR10A2 specifically recognises and responds to certain odorants, contributing to the sense of smell and the ability to distinguish various aromas in the environment.	Testing can provide insights into sensitivity to aldehydes in some food, leading to a soapy aftertaste, and therefore, its potential impact on food choices.
OXTR	The OXTR gene encodes the Oxytocin Receptor, a protein found on the surface of cells in various tissues throughout the body, inlcuding the brain, heart, uterus, and other tissues.	Oxytocin is involved in various physiological and behavioral processes, including social bonding, trust, empathy, and maternal-infant bonding. The oxytocin receptor protein enables the binding and signaling of oxytocin, allowing it to exert its effects on target tissues and modulate social behaviors and emotional responses. Variations in the OXTR gene have been associated with an altered oxytocin receptor function, leading to potential individual differences in social behavior, emotional processing, and stress response.	Testing can provide insights into traits related to social bonding such as empathy, and emotional responses.

Name	Description	Function	Why test for it
PDE8B	The PDE8B gene encodes an enzyme called phosphodiesterase 8B, which is involved in regulating levels of cyclic AMP (cAMP) and cyclic guanosine monophosphate (cGMP) within cells.	PDE8B specifically breaks down cAMP, an important molecule that is involved in many cellular processes, including signal transduction, gene expression, and energy metabolism. By controlling cAMP levels, PDE8B plays a role in a variety of physiological processes, such as immune response, inflammation, and metabolism. It may also play a role in regulating TSH (thyroid-stimulating hormone) levels. Certain genetic variants in the PDE8B gene have been associated with altered TSH levels, which could influence thyroid function. However, the exact mechanisms and clinical significance of these associations require further investigation to fully understand the gene's impact on thyroid health.	Testing can provide insights into risk assessment for thyroid-related conditions and guide preventive measures for better thyroid and overall health.
PDYN	The PDYN gene encodes a protein called prodynorphin, which is a precursor for the production of endogenous opioids, including dynorphins; endogenous opioids are neuropeptides that bind to opioid receptors in the brain and spinal cord, modulating pain perception and regulating mood and reward pathways.	The PDYN gene is involved in regulating the synthesis and release of dynorphins, which can have effects on pain perception, stress response, and addictive behaviors. Variations in the PDYN gene have been implicated in various conditions, including chronic pain, mood disorders, and addiction.	Testing can provide insights into into risk assessment for pain perception, mood disorders, and addiction susceptibility.
PEMT	Phosphatidylethanolamine N-Methyltransferase (PEMT) is an enzyme encoded for by the gene PEMT, which is responsible for the conversion of phosphatidylethanolamine (PE) into phosphatidylcholine (PC) in the liver.	As part of its activity PEMT produces homocysteine, which plays an important role in the methylation cycle. PEMT's activity is especially important in the liver and brain which require large amounts of PC, and choline which is derived from PC breakdown, to maintain normal function. Variations in the PEMT gene can lead to alterations in phosphatidylcholine levels and may contribute to conditions such as liver disease and metabolic disorders.	Testing can provide insights into risk assessment for liver-related conditions, cardiovascular health, and ability to methylate, and guide dietary recommendations for better health outcomes.
PER2	The PER2 gene encodes a protein that plays a critical role in regulating the body's circadian rhythm, which is the internal 24-hour biological clock that governs various physiological processes, such as sleep-wake cycles, hormone secretion, and metabolism.	The PER2 protein interacts with other clock genes to form a feedback loop that controls the timing of various physiological processes throughout the day, and helps to keep the circadian clock ticking in sync. Variations in the PER2 gene can result in a range of circadian-related disorders, such as sleep disorders, mood disorders, and metabolic disorders.	Testing can provide insights into risk assessment for circadian-related outcomes and guide sleep-related interventions for better sleep and overall health.

Name	Description	Function	Why test for it
PGR	The PGR gene encodes the progesterone receptor, a protein that binds to and is activated by the hormone progesterone, and is expressed in several tissues, including the uterus, mammary gland, ovary, and brain.	The progesterone receptor plays a critical role in reproductive biology by regulating the development and function of the female reproductive system. Specifically, it regulates the menstrual cycle, prepares the uterus for pregnancy, and maintains the pregnancy. Additionally, the progesterone receptor is expressed in other tissues, where it may have a role in regulating inflammation, metabolism. Certain variants may impact progesterone receptor activity and hormonal responses.	Testing can provide insights into risk assessment for hormone-related conditions and guide management strategies, particularly in reproductive health and hormone replacement therapies.
PI3	The Peptidase inhibitor 3 (PI3) gene encodes a protein known as elafin that functions as a protease inhibitor.	Elafin is involved in regulating the activity of enzymes that break down proteins, such as proteases, and helps protect tissues from damage caused by excessive protease activity. It is expressed in a variety of tissues, including the skin, lung, and digestive tract, where it plays a role in modulating immune responses, inflammation, and tissue repair. Variations in the PI3 gene have been associated with various inflammatory and autoimmune disorders.	Testing can provide insights into risk assessment for certain inflammatory and autoimmune outcomes, and guide preventive and/or management strategies.
PLIN1	The PLIN1 gene encodes a protein called perilipin-1, which plays a crucial role in regulating lipid metabolism and storage within adipocytes (fat cells).	Perilipin-1 coats the surface of lipid droplets in adipocytes and acts as a protective barrier, preventing the breakdown and release of stored triglycerides. It helps in controlling the balance between lipid storage and lipolysis (the breakdown of stored fats). Variations in the PLIN1 gene have been associated with disorders related to abnormal lipid metabolism.	Testing can provide insights into risk assessment for impaired lipid metabolism, obesity and lipid-related disorders, and guide preventive measures and/or management strategies for better metabolic health.
PON1	The PON1 gene encodes the enzyme paraoxonase 1 (PON1), which is involved in the detoxification of certain environmental chemicals and the protection against oxidative stress.	PON1 has the ability to hydrolyse and detoxify a range of toxic substances, including organophosphate pesticides and lipid peroxidation products. It also plays a role in preventing the oxidation of low-density lipoprotein (LDL) cholesterol, which is important for reducing the risk of cardiovascular diseases. Genetic variations in the PON1 gene can influence individual susceptibility to environmental toxins, oxidative stress, cardiovascular disease, and innate immune responses	Testing can provide insights into risk assessment for oxidative stress and cardiovascular outcomes, and guide preventive measures and/or management strategies for better health outcomes.
PPARA	The PPARA gene encodes the transcription factor peroxisome proliferator-activated receptor alpha (PPARα), which is a nuclear receptor involved in regulating various metabolic processes, and is primarily expressed in tissues that are metabolically active, such as the liver, heart, and muscle.	PPARα plays a crucial role in lipid metabolism, particularly in the breakdown of fatty acids and their subsequent utilisation for energy production. It regulates the expression of genes involved in fatty acid oxidation, ketogenesis, and lipid transport. PPARα also has anti-inflammatory and antioxidant properties. Genetic variations in the PPARA gene can impact lipid metabolism, energy homeostasis, and the risk of metabolic disorders such as dyslipidemia and insulin resistance.	Testing can provide insights into risk assessment for altered lipid metabolism and cardiovascular health, and guide preventive measures and/or management strategies for better cardiovascular and metabolic health.

Name	Description	Function	Why test for it
PPARG	The PPARG gene encodes for a transcription factor called Peroxisome Proliferator-Activated Receptor Gamma (PPAR-⊠), which plays a crucial role in regulating adipocyte differentiation, glucose homeostasis, and lipid metabolism.	PPARG is primarily expressed in adipose tissue, where it controls the differentiation and function of adipocytes. It promotes adipogenesis, the storage of excess energy as triglycerides, and regulates the expression of genes involved in promoting insulin sensitivity and lipid metabolism. Activation of PPARG can improve insulin sensitivity, enhance glucose uptake, improve lipid metabolism, and modulate inflammation, making it an important target for managing metabolic disorders such as obesity and type 2 diabetes.	Testing can provide insights into risk assessment for diabetes and obesity and guide preventive measures for better metabolic outcomes.
PPARGC1A	The PPARGC1A gene encodes for a transcriptional coactivator called Peroxisome proliferator-activated receptor gamma coactivator 1-alpha, which plays a crucial role in regulating energy metabolism and mitochondrial function. It is particularly abundant in tissues with high energy demands, such as skeletal muscle, liver, and brown adipose tissue.	PPARGC1A is involved in coordinating cellular responses to various environmental and physiological stimuli, such as exercise, cold exposure, and nutrient availability. It acts as a transcriptional coactivator, meaning it enhances the activity of other genes involved in energy production and utilisation such as genes involved in mitochondrial biogenesis, oxidative metabolism, and antioxidant defense. Variations in the PPARGC1A gene have been associated with metabolic disorders and impaired mitochondrial function.	Testing can provide insights into risk assessment for metabolic disorders, as well as its affect on exercise response, and guide lifestyle interventions for better metabolic health.
PTPRD	The PTPRD (Protein Tyrosine Phosphatase Receptor Type D) gene encodes a protein that belongs to a family of enzymes called protein tyrosine phosphatases, primarily expressed in the brain and involved in regulating neuronal growth and differentiation.	Specifically, the PTPRD protein plays a role in the development and maintenance of synaptic connections between neurons, which are essential for proper brain function. Variations in the PTPRD gene have been associated with various neurological disorders, including autism spectrum disorder, schizophrenia, and epilepsy.	Testing can provide insights into risk assessment for neurological disorders, cognitive function, and for restless leg syndrom.
SCL6A3	The SCL6A3 (Solute carrier family 6 member 3) gene encodes the dopamine transporter protein (DAT), that plays a critical role in regulating dopamine signaling in the brain. More specifically, it responsible for re-uptake of dopamine from the synaptic cleft into presynaptic neurons, a neurotransmitter involved in the regulation of reward, movement, and attention.	By removing dopamine, the DAT helps regulate the duration and intensity of dopamine signaling, thereby influencing neurotransmission and behavior. Variations in the SCL6A3 gene have been associated with variations in dopamine transporter function, which can affect dopamine levels and neurotransmission in the brain, and thus be implicated in several psychiatric and neurological disorders, including attention deficit hyperactivity disorder (ADHD), and addiction.	Testing can provide insights into risk assessment neuropsychiatric outcomes related to impared dopamine re-uptake, and addiction susceptibility.

Name	Description	Function	Why test for it
SHBG	The SHBG (sex hormone-binding globulin) gene provides instructions for making a protein that binds to sex hormones (primarily testosterone and estrogen) in the bloodstream.	The SHBG protein regulates the levels of free or unbound hormones that are available to be used by the body's cells. Variations in the SHBG gene can affect the amount of SHBG protein produced and, therefore, the levels of free sex hormones. Dysregulation of SHBG has been linked to several health conditions, including polycystic ovary syndrome (PCOS), and metabolic syndrome. Levels of SHBG in the blood can be influenced by various factors other than genetics, including age, and lifestyle factors such as diet and exercise.	Testing can provide insights into risk for impaired hormone profiles and guide interventions for hormone-related conditions, including fertility and metabolic health.
SHMT	The SHMT gene encodes the enzyme serine hydroxymethyltransferase (SHMT), which plays a crucial role in one-carbon metabolism.	SHMT is an enzyme of the methylation cycle that converts dietary folate and/or folic acid into a variety of other cellular products, some of which are critical methyl donor for numerous methylation reactions in the body, including the methylation of DNA, RNA, proteins, and lipids. Thus, the SHMT gene, and its relevant enzyme are essential for the regulation of one-carbon metabolism and the maintenance of proper methylation patterns in the body. Variations in the SHMT gene are associated with an alteration in SHMT enzyme within the cell, which in turn reduces the availability of the substrate required by the MTHFR enzyme.	Testing can provide insights into risks associated with folate metabolism and disease susceptibility, and guide preventive measures and/or management strategies for better health outcomes.
SLC2A2	The SLC2A2 gene encodes the glucose transporter protein 2 (GLUT2), which plays an important role in glucose homeostasis in the body.	GLUT2 is primarily expressed in the liver, pancreas, and intestine and is responsible for transporting glucose in and out of these tissues. In the liver, GLUT2 facilitates the release of glucose into the bloodstream during periods of high glucose availability, while in the pancreas, it plays a role in sensing glucose levels and regulating insulin secretion. Variations in the SLC2A2 gene have been linked to several metabolic disorders, including diabetes mellitus.	Testing can provide insights into risk assessment for an impaired glucose metabolism and diabetes, and guide preventive measures and/or management strategies for better metabolic health.
SLC6A4	The SLC6A4 (Solute Carrier Family 6 Member 4) gene encodes the serotonin transporter (SERT) protein, which is responsible for the re-uptake of serotonin from the synapse back into the presynaptic neuron.	The SLC6A4 gene plays a crucial role in determining the amount, availability, and duration of serotonin signaling in the brain, an important neurotransmitter involved in mood regulation, cognition, and various physiological processes. Genetic variations in SLC6A4 have been linked to differences in the expression and function of the serotonin transporter, and as a result associated with several psychiatric disorders, including depression, anxiety, and obsessive-compulsive disorder.	Testing can provide insights into risk assessment for mood disorders impacted by an altered serotonin re-uptake.

Name	Description	Function	Why test for it
SLC6A15	The SLC6A15 (Solute Carrier Family 6 Member 15) gene encodes a protein called the neutral amino acid transporter B(0)AT2. This transporter is responsible for the uptake of certain amino acids, such as tryptophan, phenylalanine, and tyrosine, from the bloodstream into neurons and across cell membranes.	These amino acids are important for various physiological processes, including protein synthesis, neurotransmitter production, and regulation of mood and behavior. The SLC6A15 gene and its encoded transporter play a role in the regulation of amino acid levels in the body, influencing neurotransmitter availability and potentially impacting mental health and neurological functions. Variations in the SLC6A15 gene may contribute to changes in neurotransmitter levels, leading to disturbances in brain function and mental health.	Testing can provide insights into risk assessment for neural conditions affected by an impaired neurotransmitter re-uptake.
SLC22A4	MUSHROOM SENSITIVITY NOT BEING USED The SLC22A4 gene encodes a protein called solute carrier family 22 member 4 (SLC22A4), also known as organic cation transporter 1 (OCT1), which is mainly expressed in the liver and is responsible for the uptake and elimination of many drugs and endogenous compounds.	MUSHROOM SENSITIVITY NOT BEING USED OCT1 mediates the transport of a diverse range of organic cations, including certain drugs and toxins from the bloodstream. Variations in the SLC22A4 gene have been associated with altered drug response and increased risk of various diseases, including autoimmune disorders, inflammatory bowel disease.	MUSHROOM SENSITIVITY NOT BEING USED Testing can provide insights into risk assessment for inflammatory and autoimmune outcomes such as inflammatory bowel disease (IBD), and guide management strategies for these conditions.
SLC23A2	The SLC23A2 (Solute Carrier Family 23 Member 2) gene encodes a protein called sodium-dependent vitamin C transporter 2 (SVCT2), which is responsible for the transport of vitamin C (ascorbic acid) into cells, an essential nutrient with antioxidant properties that is involved in numerous biological processes, including collagen synthesis, immune function, and iron absorption.	The SLC23A2 gene plays a critical role in maintaining adequate vitamin C levels in the body by facilitating its uptake from the bloodstream into various tissues and cells, ensuring proper cellular function and overall health. Variations in the SLC23A2 gene have been associated with vitamin C deficiency and other disorders related to vitamin C metabolism.	Testing can provide insights into risk assessment for vitamin C requirements and guide nutritional interventions for better health outcomes.
SLC30A8	The SLC30A8 (Solute Carrier Family 30 Member 8) gene encodes a protein called zinc transporter 8 (ZnT8), which is primarily expressed in pancreatic beta cells.	ZnT8 plays a crucial role in the regulation of insulin secretion by transporting zinc ions into the insulin-containing vesicles of beta cells. This process is necessary for the proper folding and maturation of insulin, and its subsequent release into the bloodstream in response to high glucose levels. Variations in the SLC30A8 gene have been associated with an increased risk of type 2 diabetes.	Testing can provide insights into diabetes risk assessment through insulin release, and guide preventive measures and/or management strategies for better metabolic health.
SOD1	The SOD1 gene codes for the enzyme copper-zinc Superoxide Dismutase 1, which plays an essential role in the body's defense against oxidative stress.	The SOD1 enzyme converts harmful superoxide radicals to less damaging hydrogen peroxide and molecular oxygen, and is particularly abundant in cells that are exposed to high levels of oxidative stress, such as neurons and muscle cells. Variations in the SOD1 gene have been associated with oxidative stress related outcomes, and the development of progressive neurodegenerative disorders.	Testing can provide insights into oxidative stress risk assessment and guide preventive measures for better health outcomes.

Name	Description	Function	Why test for it
SOD2	The SOD2 gene encodes an enzyme called manganese superoxide dismutase (SOD2), located in the mitochondria and is responsible for removing superoxide radicals, a harmful byproduct of cellular respiration.	SOD2 helps protect cells from oxidative damage by converting superoxide radicals into oxygen and hydrogen peroxide, thus, maintaining cellular health and preventing oxidative stress-related diseases. Variations in the SOD2 gene have been associated with various oxidative-stress related conditions, including neurodegenerative disorders.	Testing can provide insights into risk assessment for conditions linked to oxidative damage and guide preventive measures and/or management strategies for better health outcomes.
SULT1A1	The SULT1A1 gene encodes for the enzyme Sulfotransferase 1A1, which is involved in the process of sulfonation, a phase II detoxification pathway in the body that helps in the metabolism and elimination of various drugs, hormones, and xenobiotics.	The SULT1A1 protein specifically catalyses the transfer of a sulfate group from a specific coenzyme to various substrates, resulting in their conjugation and increased water solubility for easier excretion. The SULT1A1 enzyme plays a crucial role in drug metabolism and the regulation of endogenous compounds, such as, estrogen and thyroid hormones, as well as xenobiotics such as drugs, dietary compounds, and environmental toxins, contributing to overall detoxification processes in the body. Variations in the SULT1A1 gene have been associated with altered drug metabolism.	Testing can provide insights into detoxification ability and certain drug responses, and guide preventive measures and/or management strategies for certain health conditions and improved overall health.
SUOX	The SUOX gene encodes an enzyme called Sulfite Oxidase that plays a critical role in the body's sulfur metabolism.	The SUOX enzyme is involved in converting sulfite, a toxic compound produced during the breakdown of sulfur-containing amino acids, into sulfate, which is a harmless form that can be excreted in the urine. Variations in the SUOX gene can lead to a deficiency in the enzyme sulfite oxidase, leading to the a buildup of toxic levels of sulfite in the body, which is characterised by neurological abnormalities, seizures, and other systemic symptoms.	Testing can provide insights into risk assessment for sulfite oxidase deficiency, a rare metabolic disorder, and guide appropriate management strategies.
TAS2R38 (145)	The TAS2R38 (Taste receptor type 2 member 38) gene codes for a bitter taste receptor known as TAS2R38, which is primarily expressed on the taste buds of the tongue.	This receptor is involved in the perception of bitter tastes, particularly those associated with certain chemical compounds found in foods and beverages. Variations in the TAS2R38 gene can influence an individual's ability to taste and perceive certain bitter compounds, such as those present in cruciferous vegetables like broccoli, Brussels sprouts, coffee, and beer. These genetic variations can affect individual preferences for certain foods and may impact dietary choices.	Testing can provide insights into taste perception and guide dietary choices for better health outcomes.

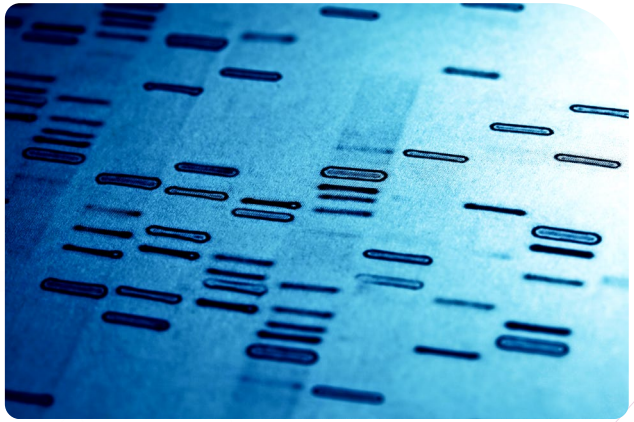
Name	Description	Function	Why test for it
TAS2R38 (785)	The TAS2R38 (Taste receptor type 2 member 38) gene codes for a bitter taste receptor known as TAS2R38, which is primarily expressed on the taste buds of the tongue.	This receptor is involved in the perception of bitter tastes, particularly those associated with certain chemical compounds found in foods and beverages. Variations in the TAS2R38 gene can influence an individual's ability to taste and perceive certain bitter compounds, such as those present in cruciferous vegetables like broccoli, Brussels sprouts, coffee, and beer. These genetic variations can affect individual preferences for certain foods and may impact dietary choices.	Testing can provide insights into taste perception and guide dietary choices for better health outcomes.
TAS2R38 (886)	The TAS2R38 (Taste receptor type 2 member 38) gene codes for a bitter taste receptor known as TAS2R38, which is primarily expressed on the taste buds of the tongue.	This receptor is involved in the perception of bitter tastes, particularly those associated with certain chemical compounds found in foods and beverages. Variations in the TAS2R38 gene can influence an individual's ability to taste and perceive certain bitter compounds, such as those present in cruciferous vegetables like broccoli, Brussels sprouts, coffee, and beer. These genetic variations can affect individual preferences for certain foods and may impact dietary choices.	Testing can provide insights into taste perception and guide dietary choices for better health outcomes.
TCF7L2	The TCF7L2 (Transcription factor 7-like 2) gene encodes for a transcription factor that plays a crucial role in the regulation of blood glucose levels by controlling insulin secretion in response to changes in blood glucose levels.	The gene is involved in the Wnt signaling pathway, which is important for cell proliferation, differentiation, and survival. Variations in this gene have been associated with an increased risk of type 2 diabetes, possibly through its effects on insulin secretion and glucose metabolism. It may also play a role in the development of certain neurodegenerative diseases.	Testing can provide insights into diabetes risk assessment and guide preventive measures and/or management strategies for better metabolic health.
TERT	The TERT (Telomerase reverse transcriptase) gene encodes the Telomerase Reverse Transcriptase enzyme, which is involved in maintaining the length and stability of telomeres that are protective caps at the ends of chromosomes that shorten with each cell division.	The Telomerase enzyme plays a vital role in cell longevity and cell division, particularly in stem cells and germ cells, by adding repetitive DNA sequences to the telomeres, preventing them from eroding too quickly. Variations in the TERT gene can lead to telomere dysfunction and may contribute to ageing and related outcomes.	Testing can provide insights into aging-related risks.

Name	Description	Function	Why test for it
TF	The TF (Transferrin) gene encodes the protein called transferrin, which plays a crucial role in iron transport and homeostasis in the body.	Transferrin binds to iron and transports it throughout the bloodstream, delivering it to cells and tissues where it is needed. It helps regulate iron levels by binding to excess iron and preventing its toxic effects. Additionally, transferrin is involved in immune responses, as it can limit the availability of iron to pathogens, thereby inhibiting their growth and replication. Variations in the TF gene may lead to a altered levels of TF; a reduced availability in TF that can lead to anemia and impaired growth and development, while excess levels of TF have been associated with various diseases.	Testing can provide insights into risk assessment and guide preventive measures for iron-related health conditions.
TFR2	The TFR2 (Transferrin Receptor 2) gene encodes a protein called transferrin receptor 2 that is primarily expressed in the liver and is involved in the regulation of iron homeostasis and erythropoiesis.	In the liver, TFR2 regulates hepcidin synthesis, a hormone that controls iron absorption and recycling in the body. Variations in the TFR2 gene have been linked to iron overload, which can lead to organ damage and dysfunction.	Testing can provide insights into risk assessment and guide preventive measures for better iron metabolism.
TLR4	The TLR4 gene encodes the Toll-like receptor 4, a protein that plays an essential role in the immune system's recognition of bacterial pathogens and the activation of the innate immune response.	It is expressed on the surface of various immune cells and recognises lipopolysaccharides (LPS) present in the outer membrane of gram-negative bacteria. Upon binding to LPS, TLR4 triggers a signaling cascade that activates transcription factors, leading to the production of pro-inflammatory cytokines, chemokines, and antimicrobial peptides. TLR4-mediated signaling is critical for initiating an immune response against bacterial infections and maintaining immune homeostasis. Variations in the TLR4 gene could be implicated in different immune responses to various infectious and inflammatory diseases.	Testing can provide insights into immune system profiling and guide preventive measures and/or management strategies for infections and inflammatory conditions.
TMPRSS2	The TMPRSS2 gene encodes the transmembrane protease serine 2 enzyme, which plays a critical role in various physiological processes.	One the prominent roles of the TMPRSS2 enzyme is facilitating viral entry, particularly for the coronavirus known as SARS-CoV-2, which causes COVID-19. TMPRSS2 is involved in the priming and activation of the spike protein of the virus, allowing it to enter host cells more efficiently. The gene is also expressed in various tissues and has functions beyond viral entry, including tissue remodeling, development, and hormone regulation. Certain variants can impact viral susceptibility and disease severity.	Testing can provide insights into viral susceptibility and disease severity risk assessment, and guide preventive measures for better health outcomes.

Name	Description	Function	Why test for it
TNF	"The terms TNF and TNF-alpha are often used interchangeably to refer to the same gene and its protein product. The TNF (Tumor Necrosis Factor) gene is responsible for encoding the TNF protein, which plays a crucial role in various physiological and pathological processes, including immune response modulation, tissue development and repair, and the pathogenesis of autoimmune diseases and chronic inflammation."	"TNF is a pro-inflammatory cytokine produced by various immune cells in response to infection, injury, or other immune signals. It acts as a signaling molecule, activating immune responses, promoting inflammation, and regulating cell survival and death. Variations in the TNF gene can lead to an overproduction of TNF, contributing to chronic inflammation and tissue damage, and thus, can affect an individual's susceptibility to certain diseases and their response to inflammation (i.e. chronic inflammatory conditions, such as rheumatoid arthritis and psoriasis)"	Testing can provide insights into inflammatory risk assessment and guide preventive and/or management strategies for immune-related conditions.
TNFA	Tumour Necrosis Factor-Alpha (TNFA) is a multifunctional pro-inflammatory cytokine protein that belongs to the tumour necrosis factor superfamily.	TNFA is involved in many biological processes and are associated with inflammations, viral infections and disease outcome particularly in respiratory tract infections.	Testing can provide insights into inflammatory risk assessment and guide preventive and/or management strategies for immune-related conditions.
TPH2	The TPH2 gene encodes the enzyme tryptophan hydroxylase 2, which is responsible for the synthesis of serotonin in the brain, a neurotransmitter that is involved in various physiological and behavioral processes, including mood, emotions, sleep, appetite, and cognition.	Variations in the TPH2 gene can influence the activity or expression of tryptophan hydroxylase 2, affecting serotonin levels in the brain. Altered serotonin levels have been associated with neurological outcomes, such as depression, anxiety, as well as other behavioural and mood-related traits.	Testing can provide insights into serotonin synthesis, which can result in neurological outcomes and guide prevention approaches for mental health conditions.
UCP1	The UCP1 gene codes for Uncoupling Protein 1, which is primarily expressed in brown adipose tissue. This protein plays a crucial role in thermogenesis, which is the process of heat production in the body, and is primarily activated by cold exposure and sympathetic nervous system signaling.	UCP1 helps to generate heat by uncoupling the electron transport chain from ATP synthesis, which results in the release of energy in the form of heat. This process is important for maintaining body temperature and has also been implicated in the regulation of energy balance and metabolic disorders.	Testing can provide insights on regulation of energy expenditure and metabolic balance, and guide preventive and/or management strategies for these outcomes.
UCP2	The UCP2 gene encodes for a protein called Uncoupling Protein 2, which is found in the inner mitochondrial membrane of cells, and plays a role in regulating the production of ATP, the main energy currency of the cell.	"UCP2 can transport protons out of the mitochondrial matrix, thereby reducing the proton gradient used to drive ATP synthesis and increasing the rate of respiration. It is also involved in regulating reactive oxygen species (ROS) production, which is important in preventing cellular damage from oxidative stress. Variations in the UCP2 gene have been linked to various diseases, including obesity and diabetes."	Testing can provide insights on regulation of energy expenditure and metabolic balance, and guide preventive and/or management strategies for these outcomes.
UCP3	The UCP3 gene codes for Uncoupling Protein 3, which is primarily expressed in skeletal muscle tissue.	The UCP3 protein plays a role in regulating energy metabolism and thermogenesis by uncoupling oxidative phosphorylation in mitochondria, leading to the dissipation of energy as heat; this process is involved in the control of fatty acid oxidation, glucose metabolism, and protection against oxidative stress. UCP3 has also been associated with energy homeostasis, obesity, and exercise-induced adaptation in skeletal muscle, contributing to the overall regulation of energy expenditure and metabolic balance in the body.	Testing can provide insights on regulation of energy expenditure and metabolic balance, and guide preventive and/or management strategies for these outcomes.

Name	Description	Function	Why test for it
UGT1A6	The UGT1A6 gene codes for the enzyme UDP-glucuronosyltransferase 1A6, which is involved in the process of glucuronidation, a phase II metabolic reaction that helps in the detoxification and elimination of various endogenous compounds and exogenous substances, such as drugs and environmental toxins.	UGT1A6 specifically catalyses the glucuronidation of a wide range of compounds, including bilirubin, steroid hormones, drugs, and carcinogens. By adding a glucuronic acid moiety to these substances, UGT1A6 facilitates their excretion from the body, promoting overall metabolic and chemical homeostasis. Variations in the UGT1A6 gene have been associated with altered drug metabolism and susceptibility to drug-induced toxicity.	Testing can provide insights into drug efficacy.
VDR	The VDR gene encodes the Vitamin D Receptor, a nuclear receptor protein that binds to and mediates the actions of vitamin D in the body and present in many tissues and cells, including the intestine, bone, immune cells, and others.	When activated by vitamin D, the receptor binds to specific regions of DNA, regulating the expression of various genes involved in calcium and phosphate metabolism (essetial for the formation and maintenance of healthy bones), immune function, cell growth, and differentiation. Variations in the VDR can influence vitamin D signaling and may contribute to certain diseases or conditions related to vitamin D deficiency or dysregulation, such as osteoporosis, and autoimmune disorders.	Testing can provide insights into vitamin D requirements and guide preventive measures for better health outcomes.
VEGF	The VEGF (Vascular Endothelial Growth Factor) gene plays a crucial role in angiogenesis, the process of forming new blood vessels.	The VEGF protein stimulates the growth and proliferation of endothelial cells, which line the inner walls of blood vessels. It promotes the formation of new blood vessels during development, wound healing, and tissue repair. Variations in the VEGF gene can affect its expression and activity, impacting angiogenesis and potentially contributing to various diseases, including cardiovascular disorders.	Testing can provide insights into risk assessment for cardiovascular-related conditions and guide preventive measures for better health outcomes.
VKORK1	The VKORC1 (Vitamin K Epoxide Reductase Complex Subunit 1) gene is responsible for encoding a protein that plays a vital role in the process of blood clotting.	VKORC1 is involved in the reduction of vitamin K epoxide to its active form, which is essential for the production of several blood clotting factors. Variations in the VKORC1 gene can affect the amount of vitamin K available for clotting factor synthesis, leading to an increased risk of bleeding disorders or blood clots.	Testing can provide insights into whether an individual may be more sensitive or less sensitive, or even resistant to the anticoagulant effect of warfarin.
WWC1	The WWC1 gene encodes the WW and C2 domain-containing protein 1 that plays a role in various biological processes, particularly in neuronal development and memory formation.	The WWC1 protein is involved in regulating the growth and branching of dendrites, the specialised extensions of nerve cells that receive and transmit signals in the brain. Additionally, WWC1 is implicated in synaptic plasticity, which is crucial for learning and memory. Variations in the WWC1 gene have been associated with altered protein function and expression levels, which can lead to changes in cellular processes and potentially contribute to disease development in cognitive functions and memory performance.	Testing provide insight into cognitive and memory impairement risk.

Name	Description	Function	Why test for it
XRCC1	The XRCC1 gene codes for the X-ray repair cross-complementing protein 1, which plays a crucial role in the repair of damaged DNA.	Specifically, XRCC1 is involved in the base excision repair pathway, which repairs damage to individual nucleotides within DNA strands. It interacts with other proteins involved in this pathway, such as DNA ligase III, DNA polymerase beta, and PARP1, to repair DNA damage caused by environmental factors such as radiation and chemical exposure. Variations in the XRCC1 gene have been associated with an increased risk of conditions related to DNA damage.	Testing can provide insights into risk assessment for DNA damage-related conditions and guide preventive measures for better health outcomes.
ZPR1	The Zinc finger protein 1 (ZPR1 or ZNF1) gene encodes a transcription factor that contains zinc finger motifs, which are involved in DNA binding and gene regulation.	This protein binds to specific DNA sequences and can activate or repress the expression of target genes. It is found in many tissues throughout the body, including the brain, liver, and immune system, and is involved in diverse biological processes, including cell differentiation, development, and growth. Research has shown that variations in this gene may be associated with various conditions, including cardiovascular disease and neurological outcomes.	Testing provide insights into risk assessment for cardiac outcomes, impaired lipid profile, and cellular membrane health.



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*All information is true as of September 2023