FUNCTIONAL GENOMIC ANALYSIS™
Supporting Health through Science & Nutrition
Formerly MethylGenetic Nutrition Analysis™

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Your Genomic Resource Genetic Variant Nutritional Assessment

Welcome to the new and exciting world of MethylGenetic Nutrition. This report was created by a health professional for you, and is based upon your own unique DNA that you inherited from your parents. It is called a nutritional genetic variant report. This is not a medical test, nor does it test for any disease. This report does not include genes that are associated with disease.

In addition, the nutritional suggestions are not treatment for disease. This report is designed to help you, based upon your unique genetic make-up, to discover where your body may be lacking in the production of antioxidants and other nutrients and molecules needed for health. Working with a qualified health practitioner, trained in genetic nutrition, allows you a unique ability to customize a nutritional program based upon these individualized results. This is the most scientific method to determine your nutritional needs.

Your body is made up of DNA, and this DNA is essentially instructions that make enzymes. These enzymes are what make antioxidants and many other molecules that restore and rebuild the body. Most of the time, the DNA properly makes the enzymes; however, quite often we have what are called variants, which we inherit from our parents, where the DNA may not function 100% effectively. When this happens, the desired action may not be performed as efficiently as possible. Lack of antioxidants or lack of the nutrients that rebuild us may cause us to age faster and increase our susceptibility to breaking down.

This DNA report focuses only on the DNA that makes antioxidants, which neutralize the harmful free radicals, and other important nutrients like folate, B12, SAMe, choline, and the enzymes that help the body rebuild and restore itself and enzymes that help you handle gluten and break down histamine. It also reports on genes that help create and break down neurotransmitters that may impact mood.

You will note below that there is a Gene Name, and in the column called Variants, you will notice it is either blank, has a 1, or has a 2. If it is blank, this means the enzymes are likely working at near 100% efficiency. If there is a 1, this means one parent gave you a less than perfect DNA copy to make the enzyme, and if there is a 2, then both parents gave you a less than optimal gene copy to make the enzyme. A single variant is called heterozygous, and two variants are considered homozygous. Homozygous variants will result in even less production of the enzymes than heterozygous variants.

Quite simply, when we are able to identify where your DNA may not be working at 100% efficiency, we are able to determine what supplementation, dietary changes or lifestyle changes may be necessary to support you.

Also, it's important to know, just because you have genetic variants, that does not mean they are being, what is called, expressed or having an impact on you. When you have variants, it's important to use testing to determine if the variants are being expressed, and the appropriate support is needed. For example, many people have found they have the MTHFR variant and took methyl folate and had rather negative results.

Genetic Variants That May Impact Digestive Health

For those with health challenges, inflammation or irritation in the digestive system, dysbiosis (an imbalance of good bacteria and bad bacteria) and digestive disturbances are often common. If there are issues here, this may be the first step you and your health care provider may want to address. Proper function of the intestinal tract is critical for the absorption of nutrients. Unfortunately, there are many genetic variants that may impact digestive function.

Inflammation from free radicals called Peroxynitrite and Zonulin may irritate or damage the delicate intestinal lining. Genetic issues that reduce the levels of important antioxidants like Glutathione and Super Oxide Dismutase (SOD) can also contribute to digestive issues. When there are low methyl groups as a result of MTHFR genetic variants, along with genetic variants in the enzymes that help break down histamine, the high histamine will create higher levels of zonulin, which may irritate the intestinal tract and disrupt digestion.

Variants in the HLA genes may contribute to gluten sensitivity, and further the potential for gut inflammation. And finally, variants in the FUT2 gene may impact the production of prebiotics, to support probiotics. Variants here may cause disruption in the good bacteria of the gut and has the potential to impair B12 assimilation. Impaired B12, among other things, may reduce the production of methyl groups, thus resulting in less than optimal histamine clearing.

All of these factors should be considered when assessing gut health. Supporting gut health, if an issue, is likely the first step needed in nutritional support this would include, but are not limited to, reducing histamine, eliminating gluten if an issue, reducing peroxynitrite by supporting the genetic issues contributing to it.

However, all of this information is a potential predisposition, not a diagnosis that there is a problem.

Gene Name	Variants	Metrics	
HLA			
HLA-DQA2 (rs2858331)		AA 34.6%	Gluten is a molecule found in wheat, barley and rye. For some individuals gluten can cause a myriad of problems, including stomach/intestinal discomfort, muscle and joint pain, depression and stress. Variants in the HLA gene increase the potential of difficulty with gluten. If you have these variants, speak to your health care professional about if eliminating gluten from your diet may be advisable.
HLA-DQ2.5 (rs2187668)		CC 78.7%	
HLA-DQ8 (rs7454108)	2	CC 1.3%	
HLA-DQ2.2 (rs7775228)		TT 73.9%	
HLA-DQ2.2 (rs2395182)		TT 63.1%	
KIAA1109			
IL2-21 (KIAA1109) (rs6822844)		GG 73.2%	The KIAA1109 gene is associated with furture potential gluten susceptibillity.
IL2-21 (KIAA1109) (rs13119723)		AA 73.2%	
MCM6			
MCM6 (rs182549)		CC 24.3%	Lactose is a sugar found in milk and dairy products. The MCM6 gene influences the LCT gene which is the gene that provides instructions for making an enzyme called lactase. Lactase breaks down lactose found in milk and dairy products into smaller sugars called glucose and galactose for absorption. The body then absorbs these simpler sugars into the bloodstream. Lactose intolerance in adulthood is caused by gradually decreasing activity of the LCT gene after infancy.
MCM6 (rs4988235)		GG 24.4%	
Peanut Allergy			
HLA-DQA2 (rs9275596)		TT 44.5%	Studies have shown that peanut allergies are one of the most common food allergies. Variations in this gene may cause the potential for peanut sensitivity.
HLA-DRA (rs7192)		GG 39.9%	
Caffeine Metabolization			
CYP1A2 (rs762551)	1	AC 41.1%	Studies have shown that individuals with the A allele in this gene are faster metabolizer of caffeine.
BCMO1			
BCMO1 A379V (rs7501331)		CC 60.4%	BCMO1 or Beta-Carotene Oxygenase 1 is a protein coding gene. The protein encoded by this gene is a crucial enzyme in beta-carotene metabolism to vitamin A. It catalyzes the oxidative cleavage of beta-carotene into two retinal molecules. Vitamin A metabolism is important for vital processes such as vision, embryonic development, and skin protection. Polymorphisms in this gene can affect serum retinol concentration. The most significant SNPs are BCMO1 A379V rs7501331, BCMO1 R267S rs12934922, and BCMO1 rs4889294 Research has found that double mutations in both BCMO1 A379V rs7501331 and BCMO1 R267S rs12934922 can cause a substantial reduction in the conversion of beta-carotene into retinol l in Females.
BCMO1 R267S (rs12934922)	1	AT 48.9%	
BCMO1 (rs8046134)	2	AA 5%	
BCMO1 (rs74029092)		AA 91.8%	
BCMO1 (rs78857556)		AA 96.3%	
BCMO1 (rs9924126)	2	GG 17.1%	
BCMO1 (rs117546625)		AA 93.2%	
BCMO1 (rs7194812)	2	GG 6.7%	
BCMO1 (rs62044256)		CC 94.5%	
BCMO1 (rs118072436)		CC 91.1%	
BCMO1 (rs149697391)		CC 99.7%	
BCMO1 (rs199858016)		GG 100%	
BCMO1 (rs143238312)		GG 98.3%	
BCMO1 (rs74324342)		GG 95.6%	
BCMO1 (rs146685123)		GG 99.4%	
BCMO1 (rs6564860)	1	TC 44.6%	
BCMO1 (rs76459433)		GG 95.4%	
BCMO1 (rs7188650)	1	TC 35.8%	
BCMO1 (rs75397794)		TT 96.6%	

FUT2		
FUT2 (rs492602)	1	AG 48.9%
FUT2 (rs601338)	1	GA 48.7%
FUT2 (rs602662)	1	GA 48.9%
FUT2 (rs16982241)		GG 73.7%
FUT2 (rs281377)	1	CT 48.3%
FUT2 (rs1800022)		CC 97.9%
FUT2 (rs1047781)		AA 98.4%
FUT2 (rs485186)	1	AG 48.9%
FUT2 (rs603985)	1	TC 48.8%
FUT2 (rs504963)	1	GA 49%
FUT2 (rs503279)	1	TC 48.5%
FUT2 (rs1800030)		GG 99.9%
FUT2 (rs516246)	1	CT 48.1%
FUT2 (rs143120145)		GG 99.9%
FUT2 (rs746012824)		CC 100%
FUT2 (rs200626231)		CC 99.7%
FUT2 (rs632111)	1	AG 43.1%

Your intestinal tract contains a vast microbial ecosystem with beneficial bacteria that contribute to immune health, good digestion, neurotransmitter production, generation of important nutrients such as vitamin B12, among other things. Maintaining a healthy intestinal flora is essential for overall body health. This bacterial community depends on prebiotics as a food source to maintain good health and proper balance of the gut flora population. The FUT2 gene is responsible for making these prebiotics.

Variants in the FUT2 enzyme may create a potential for disruptions in the composition of the intestinal flora. The use of antibiotics can be particularly stressful to the gut health of someone with this variant. There is potential for a variety of adverse effects if the intestinal flora becomes disturbed or imbalanced. Your health care practitioner may want to monitor gut health with this variant, and recommend appropriate support such as supplementation with prebiotics and/or probiotics.

Genetic Variants That May Influence Histamine Levels

Histamine is produced by the body in response to inflammatory triggers such as allergy, infection and insect bites. The resulting redness and swelling can be a beneficial reaction by bringing blood flow and white blood cells to the site, but it can also be a problem if excessive, uncontrolled, or inappropriate. Anti-histamine drugs are commonly used to temporarily block this uncomfortable response.

To modulate the histamine response, the HNMT genes direct the production of enzymes that break down the histamine. If there are a lot of variants in these genes, an individual may express allergic symptoms such as hives, rashes, insomnia, and sensitivity to some foods and airborne allergens.

Over time, elevated histamine levels may contribute to the creation of zonulin, an inflammatory molecule that can stimulate the intestinal wall and contribute to leaky gut syndrome, with attendant digestive disturbances. With a lot of histamine issues it will be beneficial to eliminate foods that stimulate histamine release or that contain high histamine such as alcohol and fermented foods, and use appropriate supplementation to support histamine removal.

Speak to your health care professional for an individualized program if this is a concern for you.

Gene Name	Variants	Metrics
ABP1 (Histamine Breakdown)		
ABP1 (rs35070995)		AA 99.9%
ABP1 (rs201353384)		GG 100%
ABP1 (rs150589026)		GG 99.9%
AOC1 (ABP1) (rs2071514)		GG 64%
ABP1 (rs184475301)		CC 100%

The enzyme DAO helps break down Histamine. If there are many genetic variants in this gene, you may have low levels of DAO, and it may be possible that Histamine is high. If this is a concern, speak to your health care professional about reducing histamine through supplementation and dietary modifications.

Among all polymorphisms found in DAO sequence, it has been proved that only one of the 7 polymorphisms, (with reference rs1049793) has relation with low DAO activity.

However, for informational and research purposes the other three that are genotyped are included.

HNMT (Histamine Transferase)			
HNMT (rs1050891)	1	AG 33.3%	The HNMT gene combines a histamine molecule with a methyl group (CH3) to reduce the histamine to a harmless substance. If you have inherited a lot of genetic variants in the HNMT gene, you may have difficulty breaking down histamine. High histamine can cause allergies, skin rashes, frequent hives, feeling stressed, difficulty sleeping, and intestinal inflammation from Zonulin. If this is an issue for you, speak to your health professional about supplementing with natural substances that reduce histamine, and dietary changes.
HNMT (rs1455158)	1	CT 33.8%	
HNMT (rs1580111)	1	CT 47.7%	
HNMT (rs2737385)	1	TG 33.3%	
HNMT (rs3828168)	1	CT 33.1%	
HNMT (rs185021833)		AA 99.9%	
HNMT (rs17583889)		CC 68.2%	
HNMT (rs62168714)	1	GA 26.3%	
HNMT (rs2187)		GG 95.2%	
HNMT (rs200213699)		TT 99.9%	
HNMT (rs113138471)		TT 99.8%	
GRHPR			
GRHPR (rs2768659)	1	AG 44%	Variations in this gene may cause a reduction in the conversion of glyoxylate to glycolate. Glyoxylate builds up and is converted to a compound called oxalate. The oxalate is then filtered through the kidneys and is either excreted in the urine as a waste product or combines with calcium to form calcium oxalate.
GRHPR (rs41278295)		AA 92.2%	
GRHPR (rs78920863)		CC 99.9%	
GRHPR (rs57303764)		CC 99.9%	
GRHPR (rs200106110)		GG 99.8%	
GRHPR (rs12552734)		GG 97.9%	
GRHPR (rs199560759)		GG 99.9%	
GRHPR (rs143596402)		TT 99.8%	
Oxalate Genes			
SPP1 (rs6840362)		CC 51.7%	The protein encoded by SPP1 is involved in the attachment of osteoclasts to the mineralized bone matrix. The encoded protein is secreted and binds hydroxyapatite with high affinity. The osteoclast vitronectin receptor is found in the cell membrane and may be involved in the binding to this protein. This protein is also a cytokine that upregulates expression of interferon-gamma and interleukin-12. Studies have shown that the GG genotype for rs2853744 increases the likelihood for calcium oxalate urolithiasis.
SPP1 (rs4754)	1	TC 39.9%	
SPP1 (rs78051010)		AA 100%	
SPP1 (rs188523569)		CC 100%	
SPP1 (rs138638879)		GG 99.9%	
KIT			The KIT gene provides instructions for making the KIT protein. The KIT protein can be found in the cell membrane of certain cells where stem cell factors bind to it. This binding activates the KIT protein, which will then activate other proteins inside the cell by adding a cluster of oxygen and phosphorus atoms at specific positions. This process is called phosphorylation and leads to the activation of a series of proteins in multiple signaling pathways. The signaling pathways stimulated by the KIT protein control many important cellular processes such as cell growth, proliferation, survival, and migration. KIT protein signaling is important for the development of certain cell types, including reproductive cells, hematopoietic stem cells, mast cells, interstitial cells of Cajal (ICCs), and melanocytes.
HRH1			
HRH1 T-17C (rs901865)		CC 68.3%	Histamine is a ubiquitous messenger molecule released from mast cells, enterochromaffin-like cells, and neurons. Its various actions are mediated by histamine receptors. The protein encoded by the HRH1 gene mediates the contraction of smooth muscles, the increase in capillary permeability due to contraction of terminal venules, the release of catecholamine from adrenal medulla, and neurotransmission in the central nervous system. HRH1 has been associated with multiple processes, including memory, learning, circadian rhythm, and thermoregulation. HRH1 has also been known to contribute to the pathophysiology of allergic diseases such as atopic dermatitis, asthma, anaphylaxis and allergic rhinitis.
HRH2			
HRH2 (rs2067474)		GG 92.1%	Histamine receptor H2 belongs to the family 1 of G protein-coupled receptors. HRH2 is an integral membrane protein and stimulates gastric acid secretion. HRH2 also regulates gastrointestinal motility and intestinal secretion and is thought to be involved in regulating cell growth and differentiation.

HRH4		
HRH4 A617G (rs11662595)		AA 82%
HRH4 C413T (rs11665084)		CC 82.8%

The HRH4 gene encodes a histamine receptor that is predominantly expressed in haematopoietic cells. This protein is thought to play a role in inflammation, and allergy responses.

FCER1A		
FCER1A (rs2427827)		#N/A
FCER1A (rs2251746)		TT 55.9%
FCER1A (rs2298805)		GG 99.6%

The immunoglobulin epsilon receptor (IgE receptor) is the initiator of the allergic response. When two or more high-affinity IgE receptors are brought together by allergen-bound IgE molecules, mediators such as histamine that are responsible for allergy symptoms are released. The protein encoded by the FCER1A gene represents the alpha subunit.

DARC		
DARC (rs12075)	1	AG 47.9%
DARC (rs3027009)	1	AG 13.3%

The protein encoded by the DARC gene is a glycosylated membrane protein and a non-specific receptor for several chemokines. The encoded protein is the receptor for the human malarial parasites Plasmodium vivax and Plasmodium knowlesi.

IL13		
IL13 (rs1295686)		CC 60.6%
IL13 (rs1800925)	2	TT 4.3%
IL13 (rs20541)		GG 63%

The IL13 gene encodes an immunoregulatory cytokine produced primarily by activated Th2 cells. This cytokine is involved in several stages of B-cell maturation and differentiation. It up-regulates CD23 and MHC class II expression, and promotes IgE isotype switching of B cells. This cytokine down-regulates macrophage activity, thereby inhibits the production of pro-inflammatory cytokines and chemokines. This cytokine is found to be critical to the pathogenesis of allergen-induced asthma but operates through mechanisms independent of IgE and eosinophils.

RAD50		
RAD50 (rs2244012)	1	AG 33.5%
RAD50 (rs17772565)		CC 88.8%
RAD50 (rs6596086)	1	TC 33.6%
RAD50 (rs587782078)		GG 100%
RAD50 (rs764122619)		TT 99.9%
RAD50 (rs2040704)	2	GG 5%
RAD50 (rs778555849)		CC 100%
RAD50 (rs587782090)		GG 100%
RAD50 (rs587780150)		CC 99.9%
RAD50 (rs750586158)		CC 98.9%
RAD50 (rs587781576)		CC 99.9%
RAD50 (rs397507177)		CC 99.8%
RAD50 (rs786203485)		CC 99.9%

The protein encoded by the RAD50 gene is similar to Saccharomyces cerevisiae Rad50 (a protein involved in DNA double-strand break repair). This protein forms a complex with MRE11 and NBS1. The protein complex binds to DNA and has numerous enzymatic activities that are required for nonhomologous joining of DNA ends. This protein, cooperating with its partners, is important for DNA double-strand break repair, cell cycle checkpoint activation, telomere maintenance, and meiotic recombination.

Genetic Variants That May Impact Cell Health & Energy Production

Your body is made up of 60-100 trillion cells, and you will be as healthy as your cells. The genetic and nutritional components that keep your cells healthy and strong are complex, and this portion of your report shows some of the factors. In the future, this report will continue to expand.

Inside your cells, there is something called the mitochondria, that takes the fats, carbs and proteins from your diet, and through the citric acid cycle, creates a molecule called ATP. ATP is your energy, and if you are low in ATP, you will be tired. ATP also plays an important role in many functions. Genetic variants in these genes may impact your ATP levels, and create inflammation rather than energy.

Gene Name	Variants	Metrics
Carnitine Transportation		
SLC22A5 (rs2631367)	2	GG 27.6%
SLC22A5 (rs2073643)	1	TC 49.4%
SLC22A5 (rs274551)	2	CC 70.3%
SLC22A5 (rs274567)	2	TT 15.5%
SLC22A5 (rs188698686)		AA 100%
SLC22A5 (rs72552726)		GG 99.8%
SLC22A5 (rs139203363)		GG 99.9%
SLC22A5 (rs144020613)		TT 99.9%
SLC22A5 (rs185551386)		GG 100%
SLC22A5 (rs200125400)		GG 100%
SLC22A5 (rs28383481)		GG 99%
SLC22A5 (rs72552734)		GG 99.9%
SLC22A5 (rs756260416)		GG 100%
SLC22A5 (rs796052035)		GG 100%
SLC22A5 (rs142447950)		TT 100%
SLC22A5 (rs377724489)		AA 99.9%
SLC22A5 (rs11568520)		CC 100%
SLC22A5 (rs72552725)		AA 100%
SLC22A5 (rs114269482)		CC 100%
SLC22A5 (rs144547521)		CC 99.9%
SLC22A5 (rs150278881)		CC 99.9%
SLC22A5 (rs151231558)		GG 99.8%
SLC22A5 (rs201082652)		GG 99.7%
SLC22A5 (rs202088921)		CC 99.9%
SLC22A5 (rs28383480)		GG 99.9%
SLC22A5 (rs386134199)		CC 100%
SLC22A5 (rs386134222)		CC 99.9%
SLC22A5 (rs72552732)		CC 100%

Fats from our diet play an important role in the body. They are both a source of energy inside your cells and also support the membranes of many tissues.

Carnitine is an amino acid derivative that is synthesized in the human body. Carnitine is required for mitochondrial β-oxidation of long-chain fatty acids for energy production.

The SLC22A5 gene provides instructions for making a protein called OCTN2. This protein is positioned within the cell membrane, where it transports carnitine into the cell.

If there are many variants here, and other tests indicate difficulties with delivering fats, speak to your health professional about the right supplements that may include a special mixture of Carnitine, Pantethine and Choline, blended in the right way to support healthy fatty acid usage.

PANK		
PANK1 (rs2038921)		AA 19.8%
PANK1 (rs10881606)	1	TC 43.8%
PANK1 (rs6586201)	1	CT 39.7%
PANK1 (rs11185792)		CC 70.7%
PANK1 (rs11185824)		AA 96.8%
PANK1 (rs11592870)		CC 94.6%
PANK1 (rs1359623)	2	CC 24.3%
PANK1 (rs1359624)		TT 53.1%
PANK1 (rs138335787)		TT 99.8%
PANK1 (rs35595938)		AA 93.7%
PANK1 (rs56410209)		GG 96.8%
PANK1 (rs61853459)		CC 93.4%
PANK1 (rs79813860)		GG 93.8%
PANK1 (rs943126)	1	CT 21.4%
PANK2 (rs4815628)	1	TC 49.7%
PANK2 (rs137852959)		GG 99.8%
PANK2 (rs137852961)		CC 99.9%
PANK2 (rs137852962)		CC 100%
PANK2 (rs138402319)		TT 100%
PANK2 (rs188211202)		AA 100%
PANK2 (rs41279404)		GG 95.1%
PANK2 (rs41279408)		CC 100%
PANK2 (rs71647844)		CC 98%
PANK2 (rs863223343)		TT 100%
PANK3 (rs13185224)		TT 67.1%
PANK3 (rs1542469)		TT 97%
PANK4 (rs1980789)		AA 91.1%
PANK4 (rs116387284)		GG 94.7%
PANK4 (rs117214274)		CC 99.8%
PANK4 (rs118152794)		GG 99.9%
PANK4 (rs2494625)		CC 53.6%
PANK4 (rs75875515)		GG 94.3%
PANK4 (rs76591030)		CC 96.8%

This gene encodes members of the pantothenate kinase family. Pantothenate kinase catalyzes the ATP-dependent phosphorylation of pantothenate (vitamin B5) to give 4′-phosphopantothenate. This reaction is the first and rate limiting step in the synthesis of coenzyme A (CoA).

Coenzyme A (CoA) is a pantothenic acid derived metabolite that is essential for many crucial cellular processes including energy, lipid and amino acid metabolism. About 4% of all known enzymes utilize CoA as a cofactor and CoA thioesters are essential for over 100 different reactions of the intermediary metabolism, such as the Krebs Cycle. In humans, CoA synthesis requires cysteine, pantothenate, and ATP.

FADS		
FADS1 (rs174546)		CC 45%
FADS1 (rs174547)		TT 45.1%
FADS1 (rs174548)		CC 48.9%
FADS1 (rs174549)		GG 50.3%
FADS1 (rs174550)		TT 45.1%
FADS1 (rs174556)		CC 50.5%
FADS1 (rs174545)		CC 45%
FADS1 (rs174555)		TT 50.4%
FADS2 (rs174570)		CC 73.1%
FADS2 (rs1535)		AA 44.6%
FADS2 (rs174575)		CC 56%
FADS2 (rs174576)		CC 43.5%
FADS2 (rs2072114)		AA 76.6%
FADS2 (rs174579)		CC 63.6%
FADS2 (rs174602)		TT 60.8%
FADS2 (rs174593)		TT 55%
FADS2 (rs117983270)		TT 93.7%
FADS2 (rs12284876)		AA 90%
FADS2 (rs12577276)		AA 91.4%
FADS2 (rs150710203)		CC 100%
FADS2 (rs174572)		CC 57.3%
FADS2 (rs174574)		CC 43%
FADS2 (rs174577)		CC 43.5%
FADS2 (rs174578)		TT 43.1%
FADS2 (rs174582)		AA 63.1%
FADS2 (rs174583)		CC 43.4%
FADS2 (rs174600)		TT 47.9%
FADS2 (rs174601)		CC 39.6%
FADS2 (rs174605)	1	GT 36.5%
FADS2 (rs174610)	1	AG 50.5%
FADS2 (rs174616)	1	GA 50.4%
FADS2 (rs174618)	1	TC 48.4%
FADS2 (rs174619)	1	AG 49.4%
FADS2 (rs199630600)		CC 99.9%
FADS2 (rs2277284)		GG 98.6%
FADS2 (rs2524299)		AA 75.5%
FADS2 (rs2727270)		CC 76.8%
FADS2 (rs2727271)		AA 76.7%
FADS2 (rs2845573)		AA 83.5%
FADS2 (rs498793)	1	TC 43.6%
FADS2 (rs639394)		AA 81.2%
FADS2 (rs99780)		CC 43.3%
FADS2 (rs75992720)		TT 91%
FADS3 (rs174450)	1	GT 49.4%
FADS3 (rs1000778)	1	AG 38.9%
FADS3 (rs174455)	1	GA 46.7%
FADS3 (rs7115739)		GG 89.8%
FADS3 (rs7942717)	1	AG 16.4%

The proteins encoded by the FADS1, FAD2, and FADS3 genes are members of the fatty acid desaturase (FADS) gene family. Desaturase enzymes regulate the unsaturation of fatty acids through the introduction of a double bond between the carbons of the fatty acyl chain.

A fatty acid is a carboxylic acid with a long aliphatic chain. This aliphatic chain can either be saturated or unsaturated. Fatty acids that have carbon-carbon double bonds are known as unsaturated. Fatty acids without double bonds are known as saturated.

Fatty acids are usually derived from triglycerides or phospholipids. Fatty acids are important sources of fuel because, when they are metabolized, they yield large quantities of ATP. Fatty acid composition in membranes plays an important role in cellular processes. Many cell types can use either glucose or fatty acids for this purpose.

Variations in these genes may affect long-chain polyunsaturated fatty acids metabolism.

ACAT		
ACAT-2 (rs25683)		AA 19.9%
ACAT1 (rs117187961)		CC 94.6%
ACAT2 (rs71565752)		CC 94.6%
ACAT1 (rs115763401)		GG 99.9%
ACAT1 (rs117486562)		GG 96.4%
ACAT1 (rs120074141)		GG 100%
ACAT1 (rs7931681)		AA 56.2%
ACAT1 (rs762991875)		GG 100%
ACAT1 (rs151080188)		TT 99.9%
ACAT1 (rs199524907)		AA 99.8%
ACAT1 (rs10749914)		AA 36.6%
ACAT1 (rs148639841)		AA 99.7%
ACAT1 (rs120074144)		CC 99.8%
ACAT1 (rs118025250)		GG 98%
ACAT2 (rs75757546)		GG 94.3%
ACAT2 (rs192445956)		GG 99.9%
ACAT2 (rs41258114)		TT 90.9%
ACAT2 (rs202015012)		CC 100%
ACAT2 (rs146437481)		CC 99.9%

The ACAT gene is very important, as it takes both fats and proteins, and turns them into a molecule which is the first step of energy production inside the cell. From a nutritional standpoint, ACAT genetic variants may be the most significant. When the ACAT gene is not doing its job, there may be fatigue from not enough energy production, and inflammation in the body from fats being oxidized.

The ACAT2 protein is limited to only two cell types, enterocytes in the small intestine and hepatocytes.

The product of the ACAT2 gene is an enzyme involved in lipid metabolism, and it encodes cytosolic acetoacetyl-CoA thiolase. Acetoacetyl-CoA thiolase condenses two molecules of acetyl-CoA to give acetoacetyl-CoA.

If you have variants in the very first one listed, ACAT1-02, this one is the most clinically significant. However, many variants in the others may contribute to lowered energy production. With these variants, your health professional may want to do other testing, to see how this variant is impacting your ability to create energy inside the cells.

SLC16A1		
SLC16A1 (rs76612089)		CC 96.7%
SLC16A1 (rs11585690)		AA 95%
SLC16A1 (rs3849174)		TT 61%
SLC16A1 (rs113206463)		CC 92.1%
SLC16A1 (rs4839272)		GG 62.5%
SLC16A1 (rs77373295)		GG 100%
SLC16A1 (rs79074237)		GG 93%
SLC16A1 (rs9429505)		AA 60.4%
SLC16A1 (rs2149035)		GG 92.2%

Carbohydrates in our diet, through a process called Glycolysis, turns these foods into energy. Genetic variants in these genes, may lessen your ability for this pathway to work effectively. These genes support the transport of what is called Pyruvate and Lactate, which is part of the process of creating energy from carbohydrates.

Your health professional will discuss options with you if you need support in this area, based upon the genetic variants, and possibly other testing to see if carbohydrate metabolism is an issue.

ACSL1		
ACSL1 (rs4862417)	1	AG 37.6%
ACSL1 (rs41278587)		GG 94.8%
ACSL1 (rs6552828)	2	GG 35.2%
ACSL1 (rs34107464)		GG 94.9%
ACSL1 (rs11132255)		GG 67.1%
ACSL1 (rs56818253)		GG 99.8%
ACSL1 (rs34202162)	1	GA 49.1%
ACSL1 (rs80004090)		AA 96.9%
ACSL1 (rs35357283)		TT 96.8%
ACSL1 (rs56076431)		AA 91.5%
ACSL1 (rs7681334)	1	AG 46%
ACSL1 (rs2292899)	1	AG 36.5%
ACSL1 (rs10022018)		AA 28.5%
ACSL1 (rs3749233)		CC 58.4%
ACSL1 (rs116577687)		CC 95.7%
ACSL1 (rs111738099)		CC 94.1%
ACSL1 (rs59902981)		CC 96.4%
ACSL1 (rs72695633)		CC 96.8%

The ACSL1 gene supports the creation of energy from fats. Variants here could impact energy levels.

TALDO1			
TALDO1 (rs142801207)		TT 100%	TALDO1 is a key enzyme in the synthesis of NADPH for lipid biosynthesis. This enzyme also helps to maintain glutathione in a reduced state to prevent cellular damage from oxygen radicals.
TALDO1 (rs147119975)		TT 99.9%	
TALDO1 (rs10902219)	1	AG 39.3%	
TALDO1 (rs11302)		AA 98.7%	
TALDO1 (rs145938996)		AA 99.9%	
TALDO1 (rs200597243)		AA 99.9%	
TALDO1 (rs201836196)		CC 100%	

Glutathione

Glutathione is the master antioxidant that clears dangerous toxins from the body and supports the immune system and the liver. Glutathione takes the hydrogen peroxide made from SOD and turns it into O2, which is oxygen.

Gene Name	Variants	Metrics	
CTH			
CTH (rs72680736)		CC 94.6%	The CTH enzyme supports the making of cysteine, another amino acid in glutathione.
CTH (rs75972648)		CC 99.9%	
CTH (rs116767084)		TT 97.6%	
CTH (rs76106863)		TT 95.6%	
CTH (rs180923713)		TT 94.4%	
CTH (rs41313347)		CC 98%	
CTH (rs142475948)		GG 98.3%	
CTH (rs149505686)		GG 100%	
CTH (rs17131305)		GG 86%	
SHMT			
SHMT2 (rs34095989)		GG 37.5%	The SHMT enzymes support the making of glycine, one of the three amino acids in glutathione.
SHMT2 (rs11557166)		CC 98.4%	

GCL			
GCLC (rs4715407)		GG 82.6%	The major determinants of GSH synthesis are the availability of cysteine, the sulfur amino acid precursor, and the activity of the rate-limiting enzyme, glutamate cysteine ligase (GCL).
GCLC (rs9474588)	1	AG 22.7%	
GCLC (rs77516417)		AA 96.1%	
GCLC (rs680403)	2	CC 24.1%	
GCLC (rs648595)	1	GT 49.3%	
GCLC (rs547222)		TT 84%	
GCLC (rs41271289)		CC 95.8%	
GCLC (rs41271285)		TT 98%	
GCLC (rs3799700)		CC 57.9%	
GCLC (rs3799694)		TT 83.9%	
GCLC (rs2397147)		TT 40.1%	
GCLC (rs200246491)		CC 100%	
GCLC (rs17884118)		TT 96.1%	
GCLC (rs17884046)		CC 72.4%	
GCLC (rs17883718)		GG 99.9%	
GCLC (rs17193216)		AA 95.3%	
GCLC (rs143809584)		GG 100%	
GCLC (rs12525474)	1	CT 22.9%	
GCLC (rs12524652)	1	CT 3%	
GCLC (rs12524550)	1	CT 5.1%	
GCLC (rs114704032)		TT 95.8%	
GCLM (rs3789453)	1	TC 40.2%	
GCLM (rs17881908)	1	CT 4.5%	
GCLM (rs17376966)		TT 97.1%	
GSS			
GSS (rs28938472)		TT 100%	The protein encoded by GSS catalyzes the second step of glutathione biosynthesis.
GSS (rs193267972)		CC 100%	
GSS (rs34239729)		CC 99.9%	
GSS (rs138659144)		TT 100%	
GSS (rs199658514)		CC 100%	
GSS (rs28936396)		GG 100%	
GSS (rs35416056)		GG 91.1%	
GLRX			
GLRX (rs1047420)	2	AA 14.3%	GLRX catalyzes the reversible reduction of GSH to GSSG.
GLRX (rs9314160)	2	AA 19.2%	

GSR			
GSR (rs8190996)	1	GA 49.2%	GSR is a central enzyme in cellular antioxidant defense.
GSR (rs2978663)		TT 37.9%	
GSR (rs2978662)		AA 64.8%	
GSR (rs141805635)		CC 99.8%	
GSR (rs2551698)		AA 85.9%	
GSR A43851G (rs2551715)		CC 37.5%	
GSR (rs8190886)		CC 99.7%	
GSR (rs201269023)		AA 99.8%	
GSR (rs117706888)		TT 98.6%	
GSR (rs201272704)		GG 100%	
GSR (rs10088455)		CC 97.7%	
GSR (rs145851500)		GG 98.5%	
GSR (rs8190942)		GG 98.1%	
GSR (rs8190954)		GG 91.1%	
GSR (rs8190955)		GG 98.7%	
GSTs			
GSTP1 (rs1138272)		CC 85.1%	The GSTM1 and GSTP1 genes are responsible for making glutathione.
GSTP1 (rs1695)	1	AG 44.1%	
GGT			
GGT1 (rs5751902)	1	CT 46%	The GGT family of genes encodes a gamma-glutamyltransferase enzyme that catalyzes the transfer of gamma-glutamyl functional groups from glutathione. The gamma-glutamyl is then transferred to amino acids, peptides, and also water. The transfer to water will then create glutamate. GGT is present in the cell membranes of many tissues, such as the kidneys, bile duct, pancreas, gallbladder, spleen, heart, brain, and seminal vesicles.
GGT1 T17549C (rs5751901)		TT 39.5%	
GGT1 (rs186765281)		AA 96.4%	
GGT1 (rs2330809)		CC 92.4%	
GGT1 (rs4820599)		AA 49.6%	
GGT5 (rs7288201)		TT 95.8%	
GGT5 (rs2267073)		CC 27%	
GGT5 (rs140980900)		GG 98%	
GGT5 (rs116976546)		GG 92.2%	
GGT5 (rs2275984)	2	CC 9%	
GGT5 (rs149456868)		CC 99.8%	
GGT5 (rs117249571)		GG 95.2%	
GGT6 (rs11657054)	1	AG 37%	
GGT7 (rs112171725)		GG 91.1%	
GGT7 (rs17122844)		CC 60.1%	
GGT7 (rs6119534)	1	CT 47.1%	

Detoxification - SOD, Glutathione, CYP & PON1

We now know that the aging process is a result of what are called free radicals. Your cells use oxygen to make energy, and it is believed that, during this process, 5-10% of the oxygen can become a free radical called superoxide. Superoxide combines with a valuable molecule called nitric oxide and forms the very dangerous molecule, peroxynitrite. Peroxynitrite is an oxidizing agent that breaks us down and is implicated in many health conditions.

Fortunately, our body makes three important molecules that protect us from these oxidizing agents. These molecules are superoxide dismutase (SOD), glutathione and catalase. Through these molecules, called antioxidants, we have the ability to neutralize this superoxide molecule. If we have the right DNA and the right ingredients, our body makes superoxide dismutase. Superoxide dismutase turns superoxide into hydrogen peroxide, and then molecules called glutathione and catalase turn them into oxygen and water. We have genes that make superoxide dismutase, glutathione and catalase. Unfortunately, it is also possible to have genetic variants on these genes, where we do not make these antioxidants as efficiently as we should. If this is our inherited condition, it is very valuable to know this, as supplementation that provides or supports the production of these molecules may be very helpful.

In our liver, we also have an enzyme called CYP, cytochrome P450 that helps the body removal many chemicals, including drugs and caffeine. Variants in any of these genes may impact our ability to remove toxic substances. And finally, we make an enzyme called PON1 (Peroxynase), that helps with both clearing pesticides, but also making the good

cholesterol, HDL.

Gene Name	Variants	Metrics	
Detox Ability - SOD			
SOD2 A16V (rs4880)		AA 26%	The SOD enzyme makes the very powerful antioxidant superoxide dismutase (SOD). SOD neutralizes the free radical superoxide. Variants on this gene may increase the amount of superoxide radicals, and subsequently may also increase the formation of the nasty oxidative agent, peroxynitrite, another free radical.
SOD3 (rs2855262)	1	TC 45.7%	
SOD1 (rs4816407)		AA 85.3%	
SOD1 (rs1041740)	1	CT 41.6%	
SOD2 (rs143582231)		GG 100%	
SOD3 (rs8192290)		TT 92.7%	
SOD3 (rs2536512)	1	GA 41.3%	
Catalase			
CAT (rs17881734)		GG 97.4%	The CAT gene provides instructions for making an enzyme called catalase. Catalase is a key antioxidant enzyme in the body's defense against oxidative stress. Oxidative stress is when there is an imbalance between the production of free radicals and the body's defense against the free radicals harmful effects. Catalase will convert the reactive oxygen species hydrogen peroxide to water and oxygen. This alleviates the toxic effects of hydrogen peroxide. Variants in this gene have been associated with decreases in catalase activity.
CAT (rs17881288)		AA 97.4%	
CAT (rs769217)		CC 58.1%	
CAT (rs17881586)		GG 96.6%	
CAT (rs79974132)		GG 97%	
CAT (rs78209054)		CC 99.8%	
CAT (rs524154)		AA 48.4%	
CAT (rs181531383)		GG 99.8%	
CAT (rs17268652)		TT 88.8%	
CAT (rs148868158)		GG 99.9%	
CAT (rs148712764)		AA 99.7%	
CAT (rs148174786)		CC 99.8%	
CAT (rs144648293)		GG 99.6%	
CAT (rs12270780)		GG 53.9%	
CAT (rs10836235)		CC 80.6%	
SULT			
SULT1A1 (rs147218626)		CC 99.9%	Sulfotransferases (SULTs) are a family of enzymes involved in catalyzing the sulfate conjugation of many hormones, neurotransmitters, drugs, bile acids, peptides, lipids, and xenobiotic compounds. The sulfate molecule is significant in detoxification. People with variated SULT SNPs may have slowed detoxification and may be sensitive to toxins, hormones, xenobiotics, and heavy metals.
SULT1A1 (rs117720319)	1	GA 5.3%	
SULT1C3 (rs112050262)		GG 97.2%	
SULT1C3 G535A (rs2219078)	1	GA 33.1%	
SULT1C3 M194T (rs6722745)	1	TC 40.7%	
SULT1C3 (rs10209928)	1	CT 34.3%	
SULT1C3 (rs17819861)		TT 86.2%	
SULT1C3 (rs200821230)		CC 100%	
SULT1C3 (rs114486672)		CC 97.5%	
SULT1C3 (rs111455491)		TT 95.8%	
SULT2A1 G9598T (rs2547231)		AA 70.8%	
SULT2A1 (rs11083904)		GG 92.1%	
SULT2A1 (rs2910393)		CC 54.1%	
SULT2A1 (rs34468125)		GG 53.3%	

Detox Ability - CYP		
CYP1A1*4 C2453A (rs1799814)		GG 91.2%
CYP1A2 (rs762551)	1	AC 41.1%
CYP1B1 L432V (rs1056836)		GG 32.8%
CYP1B1 R48G (rs10012)		GG 45.7%
CYP2C19 (rs12248560)		CC 62.8%
CYP2C9*3 A1075C (rs1057910)	1	AC 12%
CYP2C9*2 A C430T (rs1799853)		CC 77.1%
CYP2E1*1B G9896C (rs2070676)		CC 75.7%
CYP2E1*4 A4768G (rs6413419)		GG 94.5%
CYP3A4*1B (rs2740574)		TT 91.7%
CYP3A4*3 M445T (rs4986910)		AA 98.8%
ABP1		

CYP, which stands for Cytochrome P450, are enzymes that help the liver clear toxic substances that can harm us. This is called Phase 1 liver detox.

If there are many variants in CYP enzymes, dangerous substances may not be cleared as effectively as they should.

If there are many variants in CYP, along with variants in PON1, SOD and Glutathione, it may be possible that you have more difficulty than others, in removing toxic substances. Speak to your health care professional how you may support detoxification if this is a concern for you.

PON1 - Paraoxonase		
PON1 Q192R (rs662)		TT 48.6%
PON1 (rs854555)	2	CC 40.8%
PON1 (rs3917550)		GG 76.7%
PON1 (rs854565)	1	GA 42.5%
PON1 (rs2299260)	1	TC 29.7%
PON1 (rs854562)	1	CT 42%
PON1 (rs3917594)		CC 100%
PON1 (rs3917503)		CC 42.6%
PON1 (rs854568)	1	AG 36.9%
PON1 (rs3917477)		AA 91.7%
PON1 (rs854552)		TT 55%
PON1 (rs13306698)		TT 99.6%
PON1 (rs854570)	1	CA 46.9%
PON1 (rs2057681)	2	AA 48.8%
PON1 (rs199851417)		GG 99.8%

Pesticide use has been increasing over the years, and has become quite controversial.

Our body needs the ability to detox from them and the PON1 (Paraoxonase) gene, along with Glutathione, plays an important role in helping the body clear them.

PON1 (Paraoxonase) plays a large role in removing pesticides. It is also involved with supporting HDL function, crucial for healthy circulation.

The most important gene so far is the first one listed, the PON1 Q192R, however, the rest may play an important role as well.

If you have variants in PON1 Q192R, talk to your health care professional about how a custom designed supplement may support the function of PON1. You may want to eat organic foods as much as possible, and limit exposure to strong chemicals.

Nrf2

Nrf2 supports the production, recycling, and the expression of glutathione, SOD, and catalase. It is like a sprinkler system in a building, as it expresses the antioxidants when there is oxidative stress.

Gene Name	Variants	Metrics
NFE2L2		
NFE2L2 (rs2001350)		TT 80.9%
NFE2L2 (rs13001694)		AA 42.5%
NFE2L2 (rs10930781)		GG 79.5%
NFE2L2 (rs11686945)		TT 88.3%
NFE2L2 (rs181294188)		CC 99.9%
NFE2L2 (rs199673454)		TT 100%
NFE2L2 (rs34468415)		AA 43.5%

The NFE2L2 gene has major involvement in the defense against oxidative stress. The NFE2L2 gene encodes Nrf2. Nrf2 regulates and activates the intracellular antioxidant response element signaling pathway (ARE). The antioxidant response element signaling pathway controls the expression of genes whose protein products are involved in detoxication, inflammation, injury, elimination of reactive oxygen species, electrophilic agents, and enhanced cellular antioxidant capacity.

In addition to this critical function, Nrf2 also regulates iron sequestration, NADPH production, the enzymes that reduce Hydrogen Peroxide, and has influence of the critical process of Autophagy (the cleaning of cellular debris).

KEAP1			
KEAP1 (rs9676881)	2	AA 14.7%	Under normal conditions, Nrf2 is repressed by a negative regulator KEAP1. When cells are exposed to oxidative stress, or electrophiles, Nrf2 escapes KEAP1 and activates the ARE to maintain cellular redox homeostasis.
KEAP1 (rs35074907)		GG 95.8%	
KEAP1 (rs36009424)		TT 95.8%	
KEAP1 (rs45524632)		CC 96.4%	
G6PD			
G6PD (rs1050828)		CC 99.7%	The G6PD gene provides instructions for making an enzyme called glucose-6-phosphate dehydrogenase. This enzyme is active in all types of cells, and is involved in the processing of carbohydrates. This enzyme also plays a critical role in red blood cells, and helps protect red blood cells from damage.
G6PD (rs1050829)		TT 99%	
G6PD (rs5030870)		CC 100%	
G6PD (rs5030868)		GG 99.8%	
G6PD R493H (rs72554664)		CC 99.8%	
G6PD (rs2230037)		GG 79.9%	
G6PD (rs76645461)		AA 100%	
G6PD (rs398123552)		AA 99.4%	
G6PD (rs370918918)		CC 100%	
G6PD (rs782487723)		CC 99.9%	
G6PD (rs782003279)		CC 99.9%	
G6PD (rs371489738)		CC 95%	
G6PD (rs189237568)		CC 99.8%	
G6PD (rs782757170)		GG 99.9%	
PGD			
PGD (rs4846219)	1	AC 49.9%	PGD encodes an enzyme that catalyzes a oxidative decarboxylation that results in a reduction of NADP to NADPH.
PGD (rs41274480)		GG 94.8%	
PGD (rs11547610)		GG 100%	
PGD (rs145784341)		GG 100%	
PGD (rs115789191)		TT 96.3%	
ME1			
ME1 (rs2179847)	1	TC 10.7%	ME1 encodes a cytosolic, NADP-dependent enzyme that generates NADPH for fatty acid biosynthesis.
ME1 (rs1954537)	1	GA 16.4%	
ME1 (rs77805030)		AA 95%	
ME1 (rs77781534)		AA 98.3%	
ME1 (rs75378445)		AA 93.1%	
ME1 (rs75479542)		CC 94.4%	
ME1 (rs192599924)		AA 99.3%	
ME1 (rs149760142)		AA 99.9%	
ME1 (rs3778203)		CC 96.5%	
ME1 (rs2038242)	1	CT 6.5%	
ME1 (rs117917150)		CC 93.8%	
ME1 (rs117364746)		CC 95.7%	
ME1 (rs116892712)		CC 98%	
ME1 (rs1144184)	1	CT 47.8%	
ME1 (rs111500971)	1	CT 5%	
ME1 (rs117556624)		GG 94.2%	
ME1 (rs117380707)		GG 95.5%	
ME1 (rs75188642)		TT 95.6%	
ME1 (rs117250534)		TT 96.9%	
ME1 (rs75758427)		TT 99.9%	

IDH1		
IDH1 (rs34218846)		CC 89.1%
IDH1 (rs76993564)		GG 98.8%
IDH1 (rs72989215)		GG 96.7%
IDH1 (rs59684347)		CC 88.7%
IDH1 (rs34599179)		TT 98%
IDH1 (rs200591678)		AA 100%
IDH1 (rs192514135)		CC 99.9%
IDH1 (rs185564694)		AA 100%
IDH1 (rs148542200)		TT 100%
IDH1 (rs1437410)	1	AG 48.5%
IDH1 (rs142923780)		AA 99.8%
IDH1 (rs142883642)		TT 99.4%
IDH1 (rs116460523)		CC 97.1%

IDH1 catalyzes the reversible oxidative decarboxylation of isocitrate to yield α-ketoglutarate as part of the Krebs Cycle.

IDH1 is also the primary producer of NADPH in most tissues.

MTHFR - Making the Folate & Folinic Acid You Need to Rebuild Your Cells

Folate is critical for many cellular functions. The body makes several enzymes, called MTHFR, that create the folate we need for these critical functions. Unfortunately, we can inherit genetic variants that may limit our production, utilization, and absorption of this critical nutrient.

The C677T MTHFR gene makes the enzyme that makes the methylfolate needed for the conversion of methionine into homocysteine. With this variant, homocysteine may be higher.

Gene Name	Variants	Metrics
Folate Receptor Sites		
FOLR2 (fetal) (rs651933)	1	GA 49.1%
FOLR3 (gamma) (rs7925545)		AA 90.9%
SLC19A1 (rs1051266)		TT 19.2%
DHFR		
DHFR (rs1650697)		GG 56.5%
DHFR (rs75989359)		CC 99.6%
DHFR (rs72765554)		CC 93.2%
DHFR (rs387906619)		GG 100%
DHFR (rs1643657)	2	CC 6.9%
DHFR (rs1643650)	2	CC 6.9%
DHFR (rs11951910)	1	TC 17.3%
DHFR (rs115707956)		GG 97.5%
DHFR (rs10072026)		TT 80.7%
MTHFR		
MTHFD1 C105T (rs1076991)	2	CC 21.3%
MTHFR A1298C (rs1801131)		TT 47.6%
MTHFR C677T (rs1801133)		GG 41.9%
MTHFS (rs6495446)		CC 54.5%

If there are FOLR variants, this may mean the folate cannot be transported into the cells and may indicate the need for more folate.

The DHFR enzyme plays two roles. It helps support the transformation of folic acid into methyl folate, and also supports the conversion of BH2 into BH4. When BH2 is not converted back into BH4, this may impact neurotransmitters and then create free radicals.

The more variants in the FOLR, MTHFR and DHFR genes, the more their potential need for supplementing with folate and eating folate rich foods.

Methylation - What Makes Everything Work

The methylation process is a critical one in the body. Methylation turns genes on and off and regulates just about every body function including the rebuilding and repairing of the body. Therefore, it is crucial that you methylate properly.

To methylate properly, we need something called SAMe. The body has a complex mechanism to make it. When SAMe performs its appropriate task, it turns into homocysteine, a substance that needs to be recycled back into SAMe and turned into the master antioxidant, glutathione.

Folate, methyl B12, choline, and the proper function of many enzymes are needed for this process to work properly. Below are listed the enzymes and the possible variants that can make this process work less optimally. When there are deficiencies, supplementation may be helpful.

MTR/MTRR - Using B12 and Methylfolate to Convert Homocysteine into Methionine

Gene Name	Variants	Metrics	
MTR(upregulation)			
MTR A2756G (rs1805087)		AA 65.5%	The MTR enzyme combines methylfolate, methyl B12, and homocysteine to make methionine, which is then converted back into SAMe. If this does not happen, homocysteine cmay become high. Variants in this enzyme may increase the speed of this process, thus using up the ingredients needed to make it work properly. When the MTR and MTRR variants are present together, it may be more difficult to convert the homocysteine into methionine.
MTRR(B12)			
MTRR A66G (rs1801394)		AA 23%	The MTRR enzymes attach a methyl molecule (CH3) to B12 to make it methyl B12, the type of B12 needed to convert homocysteine into methionine. Variants in this gene may increase the amount of methyl B12 needed.
All B12 Factors			
MTR A2756G (rs1805087)		AA 65.5%	B12 plays many roles in the body, such as energy creation and iron absorption. Variants in the GIF enzyme may reduce the body's ability to absorb B12, and the TCN1 and TCN2 may impact the transportation of B12. FUT2 variants, as they impact digestion, may impact B12 assimilation. The more variants in this section, the potential higher the need for B12.If there a lot of variants, your health care professional may want to do more testing for B12 status.
MTRR A66G (rs1801394)		AA 23%	
FUT2 (rs492602)	1	AG 48.9%	
FUT2 (rs601338)	1	GA 48.7%	
FUT2 (rs602662)	1	GA 48.9%	
TCN1 (rs526934)		AA 53%	

PEMT & BHMT - Using Trimethylglycine (TMG) to Convert Homocysteine into Methionine

The body uses the amino acid methionine to make the very important SAMe. After SAMe does its job in donating methyl groups, it turns into Homocysteine. The PEMT enzymes make choline which is used by the BHMT enzyme to recycle Homocysteine back into Methionine.

If there are variants in the PEMT and BHMT enzymes, this conversion may be hampered, and may lead to high Homocysteine. Too high of a Homocysteine level may have a negative health impact. Your health care professional can help you convert Homocysteine into Methionine if this is an issue for you.

Gene Name	Variants	Metrics	
Choline			
PEMT (rs4244593)		TT 17.4%	Choline is made by the PEMT enzyme, variants of which may reduce the amount of choline produced. TMG (a metabolite of choline) is needed for the liver, the brain, and for supporting the BHMT enzyme's conversion of homocysteine into methionine.
PEMT (rs7946)	2	TT 48.9%	
PEMT (rs9893413)		GG 98%	
PEMT (rs750546)		CC 23%	
PEMT (rs74454529)		GG 85.7%	
PEMT (rs70963102)		CC 94.2%	
PEMT (rs4646409)		GG 72.9%	
PEMT (rs4646404)		GG 46.8%	
PEMT (rs4646400)		CC 86.3%	
PEMT (rs4646364)		CC 97.3%	
PEMT (rs4646355)		CC 99.1%	
PEMT (rs4646341)	1	GA 48.3%	
PEMT (rs3785499)		TT 26%	
PEMT (rs3760188)		CC 31.9%	
PEMT (rs187793131)		AA 99.3%	
PEMT (rs187428036)		CC 98.9%	
PEMT (rs149963778)		CC 99.6%	
PEMT (rs149238701)		GG 99.9%	
PEMT (rs147868279)		CC 99.9%	
PEMT (rs116958978)		GG 96.8%	
PEMT (rs116934548)	1	CT 3.9%	
BHMT			
BHMT R239Q (rs3733890)		GG 48.7%	The BHMT enzyme supports the conversion of homocysteine back into methionine so it can be made into SAMe. Variants in this enzyme may increase homocysteine levels and the associated risks.
BHMT-02 (rs567754)	1	CT 44.8%	
BHMT (rs72764959)		TT 91.7%	
BHMT (rs59866108)		GG 98.5%	
BHMT (rs56709544)		CC 99.9%	
BHMT (rs506500)	1	CT 41.5%	
BHMT (rs3797546)	1	TC 10.6%	

GAMT, AHCY & MAT

Gene Name	Variants	Metrics	
AHCY			
AHCY (rs819146)		TT 74.7%	The AHCY enzyme converts S-Adenosyl-L-homocysteine (SAH) into homocysteine. Variants in this enzyme are unpredictable as to how they impact methylation. Blood tests that measure methionine, SAMe, SAH, homocysteine and cysteine may be helpful when this variant exists.
AHCY (rs150066229)		GG 100%	
AHCY (rs144169873)		TT 99.8%	
AHCY (rs13043752)		GG 96.8%	
AHCY (rs117592090)		GG 94.8%	

GAMT (Creatine)		
GAMT (rs80338735)		CC 97%
GAMT (rs77168423)		CC 61.1%
GAMT (rs760101382)		CC 99.9%
GAMT (rs753198836)		CC 99.1%
GAMT (rs370421531)		CC 100%
GAMT (rs200444143)		CC 100%

The body uses the GAMT enzyme to covert SAMe into Creatine. Creatine is needed to build muscle strength. If you do not make enough creatine, muscle mass loss may occur as you age.

MAT		
MAT1 (rs11595587)		GG 93.5%
MAT1 (rs12242871)		AA 30.1%
MAT1 (rs1985908)		AA 45.6%
MAT1 (rs7081756)	1	GT 45.2%
MAT1A (rs78196299)		CC 99.9%
MAT1A (rs1832683)	2	TT 3.5%
MAT1A (rs118204001)		AA 100%
MAT1A (rs117880525)		CC 97.8%
MAT1A (rs117407472)		AA 96.9%
MAT1A (rs116659053)		GG 100%

The MAT gene takes the amino acid methionine and converts into the very important molecule SAMe. SAMe has about 165 functions in the body. If there are many variant in the MAT gene, or not enough ATP, the methionine does not get converted into SAMe and there can be high levels of methionine. Variants in AHCY can contribute to this issue as well.

If there are a lot of MAT variants, your health care professional may suggest blood work to check methionine levels. If taking B12 or choline makes you feel significantly worse, and there are a lot of MAT variants, this may be an issue you need to address.

Reducing high methionine foods may be helpful if this condition exists. High methionine may cause neurological issues and urine that smells like boiled cabbage.

Transsulfuration

The Transsulfuration process takes homocysteine and turns it into the master antioxidant, glutathione. The CBS enzyme, particularly the C699T, is a brake that holds the homocysteine back so that it flows at the appropriate rate. However, when there are variants in the CBS genes, the homocysteine can rush down too. It may have the potential to cause the creation of excess ammonia.

Gene Name	Variants	Metrics
SUOX		
SUOX (rs141735896)		CC 99.2%
SUOX (rs76537761)		GG 99.1%
SUOX (rs144817821)		GG 100%
SUOX (rs150528313)		GG 100%
SUOX (rs143300414)		TT 100%
SUOX (rs773125)		#N/A
SUOX (rs121908007)		GG 99.9%
SUOX (rs189671778)		GG 100%

The SUOX gene provides instructions for making an enzyme called sulfite oxidase. Sulfite oxidase helps break down amino acids that contain sulfur when they are no longer needed.

Transsulfuration			
CBS A13637G (rs2851391)	2	TT 19.9%	Variants in the CBS enzymes, may cause excess ammonia. It may also create excess sulfites and sulfates.
CBS C19150T (rs4920037)	1	GA 33.3%	
CBS C699T (rs234706)	1	GA 43.3%	
CBS (rs863223432)		CC 99.9%	
CBS (rs863223434)		GG 99.5%	
CBS (rs786204609)		CC 99.7%	
CBS (rs774926464)		CC 100%	
CBS (rs77267155)		CC 99.8%	
CBS (rs772450760)		AA 99.9%	
CBS (rs76668025)		CC 97%	
CBS (rs760124)	1	TC 13%	
CBS (rs73220906)		CC 98.2%	
CBS (rs6586282)		CC 70.1%	
CBS (rs62217672)		CC 98.2%	
CBS (rs28934891)		CC 99.9%	
CBS (rs234714)	1	CT 34.1%	
CBS (rs234709)	1	CT 46.7%	
CBS (rs2124459)		TT 35.4%	
CBS (rs2124458)		TT 41.1%	
CBS (rs199948079)		CC 100%	
CBS (rs1789953)		CC 72%	
CBS (rs138211175)		CC 99.7%	
CBS (rs121964965)		CC 96.3%	
CBS (rs121964962)		CC 99.9%	
CBS (rs11701048)		CC 83.5%	
CBS (rs112219271)		CC 94.4%	
CBS (rs1005585)		TT 91.1%	
Ammonia & Glutamate Production Estimates			
CBS C699T (rs234706)	1	GA 43.3%	

Neurotransmitters - The Key to Your Mood, Energy & Much More

Many genes control the production and breakdown of the neurotransmitters that control our mood. The neurotransmitters, serotonin and GABA, may be relaxing and help you feel good, while dopamine, epinephrine and norepinephrine give you drive but may cause anxiousness when too high.

Mood is also impacted by the creation of BH4 which can be reduced by many genetic variants. Check the BH4 report to see if this may be contributing to mood concerns.

Gene Name	Variants	Metrics	
MAOA			
MAOA (rs5906938)		GG 56%	The MAO gene supports the breaking down of Serotonin, Dopamine, and Norepinephrine. If Serotonin is low, this may be helpful. Under some conditions high Serotonin may create stress.
MAOA (rs3810709)	1	CT 40.5%	
Dopamine			
COMT (MIR4761) (rs6269)	2	GG 15.8%	The COMT enzyme breaks down dopamine. Variants in this enzyme actually preserve dopamine, increasing its bioavailability. But if dopamine is already too high, it may cause agitation, or difficulty thinking clearly. COMT also plays a role in breaking down some hormones.
COMT H62H (MIR4761) (rs4633)		CC 24.9%	
COMT V158M (rs4680)		GG 25%	
COMT-61 P199P (mood swings) (rs769224)		GG 95.3%	

Glutamate Production Factors		
CBS C699T (rs234706)	1	GA 43.3%

GABA (Glutamate to GABA)		
GAD1 (rs2241165)	1	TC 38.4%
GAD1 (rs701492)		CC 52.4%
GAD1 (rs77492508)		CC 97.4%
GAD1 (rs76344572)		CC 96.3%
GAD1 (rs4668328)		GG 95.8%
GAD1 (rs4667661)		CC 95.8%
GAD1 (rs45576034)		CC 95.7%
GAD1 (rs3791875)		AA 93.9%
GAD1 (rs3791852)		CC 99.9%
GAD1 (rs2241164)		TT 45.7%
GAD1 (rs186477656)		TT 99.1%
GAD1 (rs1420385)	1	AG 50.1%
GAD1 (rs12612498)		GG 96.2%
GAD2 (rs8190612)		CC 77.2%
GAD2 (rs8190646)		AA 83%
GAD2 (rs2368160)	1	GA 41.3%
GAD2 (rs8190608)		TT 93.2%
GAD2 (rs992990)	1	CA 40%
GAD2 (rs7902107)	1	TC 41.2%
GAD2 (rs8190656)		GG 96%
GAD2 (rs77034511)		TT 99.9%
GAD2 (rs61735922)		GG 99.4%
GAD2 (rs2839672)		CC 98.9%
GAD2 (rs185111133)		GG 100%
GAD2 (rs182756899)		GG 99.9%
GAD2 (rs181850411)		GG 99.9%
GAD2 (rs117225132)		GG 95.6%
GAD2 (rs7908975)		AA 82%
GAD2 (rs201989484)	2	CC 60.9%
GAD2 (rs150583361)		TT 100%
GAD2 (rs143186590)		TT 99.9%
GAD2 (rs76059287)		TT 94%
GAD2 (rs201538283)		AA 100%
GAD2 (rs184941465)		TT 100%
GAD2 (rs201691653)		GG 70.9%
GAD2 (rs150392847)		AA 100%
GAD2 (rs143745134)		CC 100%
GAD2 (rs117901773)		CC 97.1%
GAD2 (rs117577922)		GG 95.9%
GAD2 (rs117407742)		GG 96.5%
GAD2 (rs11015018)	1	GT 41.2%

The GAD enzyme converts glutamate (which may make you anxious) into GABA (which may be calming).

Variants in the GAD enzyme may increase the glutamate and keep the GABA low.

DAO			
DAOA (rs2391191)		GG 38.5%	Variants in the DAO genes impact neurotransmitters in ways that are not yet fully known, but may increase anxiety or over activity of the brain function.
DAO (rs11114086)		CC 69.1%	
DAO (rs113576450)		CC 100%	
DAO (rs200127576)		CC 99.6%	
DAO G109284478T (rs6539460)		GG 55.3%	
DAO (rs75607844)		AA 97%	
DAO (rs76412212)		GG 98.4%	
DAO (rs79034390)		GG 98%	
Oxytocin Receptor			
OXTR (rs2268492)		CC 51.3%	OXTR or Oxytocin Receptor encodes a protein that belongs to the G-protein coupled receptor family and acts as a receptor for oxytocin. Oxytocin receptors regulate a variety of different behaviors such as stress, anxiety, social recognition, bonding, and maternal behavior.
OXTR (rs53576)	2	GG 45.9%	
OXTR (rs2268491)	1	CT 21.7%	
OXTR (rs2254298)	1	GA 22.1%	
OXTR (rs115396476)		GG 95.7%	
OXTR (rs140488139)		GG 100%	
OXTR (rs151257822)		CC 99.9%	
OXTR (rs200966415)		GG 100%	
OXTR (rs2268495)		GG 59.9%	
OXTR (rs2324728)		CC 59.9%	
OXTR (rs237885)	1	TG 48.7%	
OXTR (rs237891)		TT 32.2%	
OXTR (rs237899)	2	AA 14.4%	
OXTR (rs237913)	2	AA 8.3%	
OXTR (rs34880121)		CC 37.3%	
OXTR (rs34992398)		GG 81.2%	
OXTR (rs61183828)		TT 90.1%	
OXTR (rs77943865)		GG 91.5%	
OXTR (rs78062775)		CC 88.2%	
OXTR (rs918316)	1	TC 16.5%	
OXTR Empathy			
OXTR (rs53576)	2	GG 45.9%	Studies have shown that individuals with the GG genotypes are more empathetic, can become more attached, feel less lonely, have a decreased level of sociality, employ more sensitive parenting techniques, and have lower rates of autism.

Nitric Oxide & Other Circulation Genes

Nitric oxide was once named the molecule of the year, and a Nobel Prize was awarded for its discovery. It plays a role in circulation, preventing blood clots, mood, and regulating blood sugar. It is also needed for male erectile function.

Gene Name	Variants	Metrics
Nitric Oxide & NOS		
NOS2 (rs2297518)	1	GA 31.5%
NOS2 (rs4795067)	1	AG 45.3%
NOS2 (rs9797244)	1	TC 31%
NOS2 (rs944722)		TT 28.1%
NOS2 (rs3794766)	1	CT 36.2%
NOS2 (rs3794764)	1	GA 35%
NOS2 (rs3794756)		CC 97%
NOS2 (rs3730014)		GG 96.8%
NOS2 (rs28999409)		GG 96.1%
NOS2 (rs28998828)		CC 52.3%
NOS2 (rs28998810)		GG 95.7%
NOS2 (rs11080344)	1	CT 48.7%
NOS2 (rs2314812)	1	CT 28.3%
NOS2 (rs2297516)	1	AC 48%
NOS2 (rs150704221)		CC 75.8%
NOS2 (rs142205241)		TT 99.9%
NOS3 (rs1800779)	1	AG 46.2%
NOS3 (rs891512)		GG 62.8%
NOS3 (rs3918174)		AA 72.4%
NOS3 (rs891511)	2	GG 39.4%
NOS3 (rs7830)	1	GT 43.5%
NOS3 (rs3918201)		GG 99.4%
NOS3 (rs3918184)	1	CT 45.7%
NOS3 (rs2853792)	1	AG 45.1%
NOS3 (rs2070744)	1	TC 45%
NOS3 (rs200507709)		CC 100%
NOS3 (rs1808593)		TT 57.1%
NOS3 (rs149539813)		GG 99.7%
NOS3 (rs141089940)		GG 99.7%
NOS3 (rs1007311)	1	AG 48.2%

The NOS enzyme is responsible for converting L-Arginine into nitric oxide. Variants in this enzyme, along with low BH4, may result in the creation of a dangerous free radical called super oxide instead of nitric oxide. The last enzyme listed in the list to the left, is the most significant gene for making nitric oxide. Variants on this one have the greatest impact on nitric oxide production, but the others play a role as well.

This is called NOS uncoupling, which can lead to the creation of peroxynitrite,a free radical.

If this is a concern, speak to your health care professional how targeted nutrition can support the NOS enzyme. Adequate levels of BH4 are also needed to convert arginine into nitric oxide.

BH4 - Critical for Mood & Reducing Inflammation

BH4 or tetrahydrobiopterin is a very important molecule. It is needed to make Serotonin, Dopamine, (both for mood), Melatonin (for sleep) and Nitric Oxide for circulation, After BH4 make the neurotransmitters Serotonin and Dopamine, it converts into BH2, then needs to be turned back into BH4. The DHFR and QDPR enzymes are needed for this conversion, while SAMe, NADH and folinic acid are co-factors.

Variants that lower SAMe and the MTHFR A1298C variants may lower what the body needs to make BH4, while variants in DHFR and QDPR may lower the conversion of BH2 to BH4.

The more variants listed here, the more potential for low BH4 and high BH2, which results in the production of the free radical peroxynitrite, which is bad for the body. If this occurs with genetic variants in SOD and glutathione which neutralizes the peroxynitrite, there is more potential for free radicals.

If inflammation is a concern for you, speak to your health care professional about the approach that is right for you.

Gene Name	Variants	Metrics
BH4 Factors		
CBS C699T (rs234706)	1	GA 43.3%
SHMT2 (rs34095989)		GG 37.5%
MTHFR A1298C (rs1801131)		TT 47.6%
BH2 to BH4 Conversion		
QDPR (rs1031326)		TT 14.3%
QDPR (rs74546454)		TT 93.4%
QDPR (rs744731)		TT 53.5%
QDPR (rs2597774)		TT 49.7%
QDPR (rs2244804)		AA 42.7%
QDPR (rs12512471)		TT 93.3%
QDPR (rs10939729)		CC 92.8%
Peroxynitrite Factors		
MTHFR A1298C (rs1801131)		TT 47.6%
SHMT2 (rs34095989)		GG 37.5%
QDPR (rs1031326)		TT 14.3%
CBS C699T (rs234706)	1	GA 43.3%
GSTP1 (rs1695)	1	AG 44.1%
GSTP1 (rs1138272)		CC 85.1%
SOD2 A16V (rs4880)		AA 26%
SOD3 (rs2855262)	1	TC 45.7%
NOS2 (rs2297518)	1	GA 31.5%
NOS3 (rs1800779)	1	AG 46.2%

MTHFR A1298C may reduce the materials needed for BH4, while CBS699 and BHMT 08 may reduce it with excess ammonia, while variants in DHFR and QDPR may reduce the conversion of BH2 to BH4.

If this is a concern for you, speak to your health care professional how you can boost BH4.

Reviewing this list may give you clues as to there may be a potential for peroxynitrite production is.

Another component to consider, is to view the Urea Cycle function as well, as lowered urea function will cause more BH4 to be used for ammonia reduction.

Vitamin D

Adequate vitamin D levels are very important. Not only is vitamin D needed to help absorb calcium for bone health, it also plays a role in the immune system.

Gene Name	Variants	Metrics
Vitamin D Receptor		
VDR BsmI (rs1544410)	1	CT 47.5%
VDR TaqI (rs731236)	1	AG 47.3%
Cell Membrane Protection		
G6PD (rs1050828)		CC 99.7%
G6PD (rs1050829)		TT 99%

The VDR Taq variant may reduce Vitamin D in the body. Speak to your health care provider about measuring Vitamin D levels, and the appropriate supplementation if needed.

The VDR FOK variant may be related to blood sugar issues. Speak to your health care provider about regularly monitoring your blood sugar levels.

If there are variants in the BSM, this may impact bone density. Speak to your health care provider about checking your bone health as you age.

SHBG		
SHBG (rs1799941)		GG 58.4%
SHBG (rs13894)		GG 86.4%
SHBG (rs6258)		CC 98.8%
SHBG (rs145273466)		CC 100%
SHBG (rs143269613)		GG 100%
SHBG (rs146779355)		GG 100%
SHBG (rs147372392)		AA 100%
SHBG (rs150060755)		GG 99.8%
SHBG (rs186960957)		GG 100%
SHBG (rs368589266)		CC 99.9%
SHBG (rs372114420)		GG 100%
SHBG (rs373254168)		CC 100%
SHBG (rs373769356)		CC 100%
SHBG (rs559734425)		CC 100%
SHBG (rs6259)		GG 79.4%
SHBG (rs748472215)		GG 99.8%
SHBG (rs757764436)		GG 99.7%
SHBG (rs758705398)		CC 99.9%
SHBG (rs758850354)		GG 100%
SHBG (rs765509320)		CC 100%
SHBG (rs775922128)		AA 99.9%

The SHBG (Sex Hormone Binding Globulin) binds to Testosterone and Progesterone. If the variants cause less binding globulin, there is the potential for higher Testosterone and Estrogen, and lower Progesterone. If this is a concern, speak to your health care provider about testing hormones.

For men, variants here may lead to lower testosterone as you age. Speak to your health professional about measuring hormones and the appropriate plan for you.

Cardiovascular Genes		
ACE Del 16 (rs4343)		GG 27.4%
ADD1 G460W (rs4961)		GG 65.3%
AGT C4072T (rs699)	1	GA 48.4%
MTHFR C677T (rs1801133)		GG 41.9%

Iron oxidation Potential		
CBS C699T (rs234706)	1	GA 43.3%
GSTP1 (rs1138272)		CC 85.1%
GSTP1 (rs1695)	1	AG 44.1%
HFE C282Y (rs1800562)		GG 89.4%
HFE H63D (rs1799945)		CC 74.2%
HFE S65C (rs1800730)		#N/A
HFE (rs62625346)		GG 100%
HFE (rs140080192)		GG 99.8%
HFE (rs9366637)		CC 84.5%
HFE (rs2071302)		TT 97.6%
SOD2 A16V (rs4880)		AA 26%
SOD3 (rs2855262)	1	TC 45.7%
SLC40A1 (rs7596205)		GG 83.7%
SLC40A1 (rs35623329)		TT 55.8%
SLC40A1 (rs34206448)		TT 56.4%
SLC40A1 (rs1123110)	1	AG 46.1%
SLC40A1 (rs7586757)	1	CT 43.2%
SLC40A1 (rs387907377)		CC 99.6%
SLC40A1 (rs199683014)		CC 100%
SLC40A1 (rs10188785)	1	GT 47.3%

HFE SNPs, in combination with these others, may increase the potential for oxidized iron.

APOE		
APOE (rs429358)	1	TC 23%
APOE (rs7412)		CC 86.5%

The protein encoded by APOE is a major apoprotein of the chylomicron. This protein binds to a specific liver and peripheral cell receptor, and is essential for the normal catabolism of triglyceride-rich lipoprotein constituents.

There are three common isoforms of the APOE gene. These isoforms include E2, E3 and E4 and they are determined by rs429358 and rs7412. Everyone inherits two APOE genes, one from each parent. Because of this it is possible for someone to have one of the following six combinations or “genotypes”, E2/E2 , E2/E3, E2/E4, E3/E3, E3/E4, or E4/E4.

The following table can be used to determine the combination of someone’s isoform.

rs429358	rs7412	APOE Status
TT	TT	E2/E2
TT	CT	E2/E3
TC	CT	E2/E4
TT	CC	E3/E3
TC	CC	E3/E4
CC	CC	E4/E4

Studies have shown that of all six genotypes, E4/E4 is associated with the greatest risk for high cholesterol.The APO E3/E3 genotype is considered normal. E2 is associated with lower levels of cholesterol. E4 is associated with higher levels of cholesterol.

mTOR

The mammalian target of rapamycin (mTOR) signaling pathway senses and integrates a variety of different environmental cues to regulate organismal growth and homeostasis.

The mTOR pathway regulates homeostasis by directly influencing protein synthesis, transcription, autophagy, metabolism, and organelle biogenesis and maintenance.

Gene Name	Variants	Metrics
mTOR		
MTOR (rs12139042)		GG 94.5%
MTOR (rs17036350)		CC 93.1%
MTOR (rs41274520)		GG 95.7%
MTOR (rs115259480)		CC 96.1%
MTOR (rs117348385)		CC 99.5%
MTOR (rs12122483)		CC 97.1%
MTOR (rs140269225)		CC 100%
MTOR (rs79619380)		CC 98.8%
MTOR (rs2076655)		AA 48.5%
MTOR (rs72647298)		AA 94.1%
MTOR (rs116203135)		TT 96.7%
MTOR (rs12142905)		TT 93.9%
MTOR (rs142063530)		TT 99.7%
MTOR (rs28730693)		TT 99.7%
MTOR (rs34889369)		TT 94.4%
MTOR (rs74225573)		TT 92.9%
MTOR (rs7525957)		TT 52.5%
MTOR (rs138733485)		GG 99.9%
MTOR (rs77086655)	1	GA 7.6%
MTOR (rs111320347)		CC 97.1%
MTOR (rs140288227)		CC 99.9%

The protein encoded by MTOR facilitates cellular responses to stresses such as DNA damage, and nutrient deprivation.

Autophagy

Autophagy is the natural, regulated, destructive mechanism of the cell that disassembles unnecessary or dysfunctional components. Autophagy allows for the orderly degradation and recycling of cellular components such as misfolded or aggregated proteins, damaged organelles, and intracellular pathogens.

Gene Name	Variants	Metrics
ULK1		
ULK1 (rs7487166)		GG 66.9%
ULK1 (rs377181421)		GG 99.9%
ULK1 (rs1134574)	1	AG 14.4%
ULK1 (rs12425431)		CC 94.6%
ULK2		
ULK2 (rs112759293)		CC 95.5%
ULK2 (rs111325162)		TT 91.9%
ULK2 (rs199558748)		GG 100%
ULK2 (rs34670978)		GG 94.8%
ULK2 (rs117513963)		GG 87.4%
ULK2 (rs117500794)		TT 94.1%
ULK2 (rs146758486)		TT 99.6%
ULK2 (rs2306271)		AA 99.9%
ULK2 (rs55730189)		CC 99.9%
ULK2 (rs112406545)		CC 94.8%
ULK2 (rs186533439)		CC 99.9%
ULK2 (rs281354)	1	CT 6.9%

ULK1 is part of the ULK1 Complex. The ULK1 Complex plays a central role in starvation-induced autophagy.

If there are many variants here, your health professional may suggest supplementation, diet, and eating patterns appropriate for you.

ULK2 is known to regulate autophagy.

If there are many variants here, your health professional may suggest supplementation, diet, and eating patterns appropriate for you.

ATG13		
ATG13 (rs35619591)		GG 97.6%
ATG13 (rs140660960)		AA 99.8%
ATG13 (rs117605660)		CC 94.6%
ATG13 (rs74807297)		CC 96.3%

The protein encoded by ATG13 is essential for autophagosome formation and mitophagy.

If there are many variants here, your health professional may suggest supplementation, diet, and eating patterns appropriate for you.

DNA Repair

DNA repair genes code the proteins whose normal function is to correct errors that arise when cells duplicate their DNA prior to cell division. These errors in the DNA can occur from things such as ultraviolet light, inhaled cigarette smoke, or endogenous weak mutagens.

Mutations in the DNA repair genes can lead to a failure in correcting the DNA, which in turn may allow subsequent mutations to accumulate.

If the rate of DNA damage exceeds the capacity of the cell to repair itself, the buildup of errors can overwhelm the cell.

Gene Name	Variants	Metrics
mutL homolog 1		
MLH1 (rs1800734)	1	GA 35.7%
MLH1 (rs35045067)		AA 99.9%

The MLH1 gene provides the instructions for making a protein that plays an essential role in DNA repair. This protein helps fix mistakes that are made when DNA is copied in DNA replication in preparation for cell division.

Ataxia telangiectasia mutated		
ATM (rs1801516)		GG 74.3%
ATM (rs664143)		GG 35%
ATM (rs1801673)		AA 98.2%
ATM (rs1800058)		CC 96.8%
ATM (rs1800056)		TT 97.3%
ATM (rs3092856)		CC 99.4%
ATM (rs3092857)		AA 99.8%

The main role of ATM is to repair double-stranded DNA breaks.

The Urea Cycle

Ammonia is the product of oxidative deamination reactions and is a toxin even in small amounts and must be removed from the body. The urea cycle facilitates the removal of ammonia as urea. The ammonia is first converted into urea in the liver. After conversion, the urea is then transported to the kidneys where it is excreted.

Your health professional may use this data to decide if testing ammonia levels could be helpful.

Gene Name	Variants	Metrics
Carbamoyl-Phosphate Synthase 1		
CPS1 (rs918233)	1	TC 45.3%
CPS1 (rs981024)		GG 36.4%
CPS1 (rs3821135)		TT 76.5%
CPS1 (rs12468557)		CC 41.1%
CPS1 (rs2302909)		GG 84.4%
CPS1 (rs2287598)	2	AA 3%
CPS1 (rs2270476)	1	GA 11.8%
CPS1 (rs4567871)	1	CT 21.9%
CPS1 (rs1047891)	1	CA 42.7%
CPS1 (rs111491997)		GG 96.9%
CPS1 (rs112826830)		GG 97.5%
CPS1 (rs113317681)		TT 95.3%
CPS1 (rs12694205)		AA 25.8%
CPS1 (rs114798794)		AA 97.3%
CPS1 (rs115837354)		TT 92.2%
CPS1 (rs10184633)		CC 20.2%
CPS1 (rs115897023)		GG 100%
CPS1 (rs117065979)		CC 99.8%
CPS1 (rs13033773)		AA 96.8%
CPS1 (rs13399140)		CC 92.7%
CPS1 (rs141481633)		GG 100%
CPS1 (rs141945326)		CC 99.7%
CPS1 (rs146430797)		AA 100%
CPS1 (rs148654695)		GG 99.8%
CPS1 (rs17825520)		TT 93.7%
CPS1 (rs186441487)		CC 96.7%
CPS1 (rs189008232)		GG 99.9%
CPS1 (rs200214298)		GG 99.8%
CPS1 (rs201111970)		GG 99.9%
CPS1 (rs2371004)		TT 53.7%
CPS1 (rs34449727)		GG 39.1%
CPS1 (rs4363965)		AA 95.2%
CPS1 (rs71422705)		CC 83.5%
CPS1 (rs715)	2	CC 9.8%
CPS1 (rs74566181)		AA 96.1%
CPS1 (rs74982911)		CC 93.4%
CPS1 (rs75266462)		AA 96.8%
CPS1 (rs753571186)		CC 99.9%
CPS1 (rs75395645)		CC 94.6%
CPS1 (rs7599931)	1	TG 40.3%
CPS1 (rs77268067)		AA 89.2%
CPS1 (rs778958318)		TT 100%
CPS1 (rs78365831)		CC 92.1%

The CPS1 gene is responsible for providing the instructions for making the enzyme carbamoyl phosphate synthetase I. The specific role of carbamoyl phosphate synthetase I is to control the first step of the urea cycle. In this step, excess nitrogen compounds are incorporated into the cycle to be processed.

Ornithine Transcarbamylase			
OTC (rs12557315)	1	CT 28.9%	The OTC gene is responsible for providing the instructions for making the enzyme ornithine transcarbamylase Ornithine transcarbamylase controls the reaction between carbamoyl phosphate (From the first step of the urea cycle) with ornithine to form citrulline.
OTC (rs4621959)		GG 36.5%	
OTC (rs68026851)		GG 100%	
OTC (rs1554993)		GG 80.8%	
OTC (rs5917575)		CC 36.6%	
OTC (rs72558473)		CC 100%	
OTC (rs72558451)		CC 98.7%	
OTC (rs146910727)		AA 99.7%	
Argininosuccinate synthase 1			
ASS1 (rs79576332)		GG 94.5%	The ASS1 gene is responsible for providing the instructions for making the enzyme argininosuccinate synthase 1. Argininosuccinate synthase 1 controls the reaction between the two amino acids citrulline (From the second step of the urea cycle) and aspartate to form argininosuccinic acid.
ASS1 (rs75912463)		TT 97.7%	
ASS1 (rs474330)		GG 47.6%	
ASS1 (rs11243414)		AA 65.2%	
ASS1 (rs62582568)		GG 79.3%	
ASS1 (rs7860909)	2	GG 12.5%	
ASS1 (rs640181)		CC 78.2%	
ASS1 (rs74332768)		GG 96.8%	
ASS1 (rs118129357)		CC 96%	
ASS1 (rs727503814)		GG 99.9%	
ASS1 (rs117997457)		CC 91.7%	
ASS1 (rs1215980)		AA 62.7%	
ASS1 (rs11244382)		CC 92.6%	
ASS1 (rs141365191)		GG 99.5%	
ASS1 (rs507351)		GG 94.3%	
ASS1 (rs10901080)		GG 74.8%	
ASS1 (rs602924)	2	TT 71.5%	
Argininosuccinate Lyase			
ASL (rs201523601)		GG 100%	The ASL gene is responsible for providing the instructions for making the protein argininosuccinate lyase. Argininosuccinate lyase creates arginine and fumarate from argininosuccinate acid (From the third step of the urea cycle). The arginine is later broken down into urea and is excreted from the body.
ASL (rs759952363)		GG 100%	
ASL (rs199938613)		CC 100%	
ASL (rs28941472)		AA 99.8%	
Arginase 1			
ARG1 (rs117272946)		TT 96.6%	The ARG1 gene is responsible for providing the instructions for making the enzyme arginase. Arginase controls the last step of the urea cycle. In this step, arginase removes nitrogen from arginine (From the fourth step in the urea cycle) and converts this nitrogen into urea to be excreted from the body. Ornithine is also produced in this reaction which is then used to repeat the cycle.
ARG1 (rs138541090)		AA 99.9%	
ARG1 (rs3850245)		CC 76.3%	

Electrical Sensitivity Potential

Variants in these genes may impact the potential to have negative effects from high levels of electrical field exposure.

Gene Name	Variants	Metrics
CACNA1C		
CACNA1C (rs216013)		AA 70.4%
CACNA1C (rs2159100)		CC 45.9%
CACNA1C (rs1006737)		GG 46%
CACNA1C (rs2302729)		CC 67.6%

Copper

Copper is a mineral that can be found throughout your body. Copper is essential to the proper functioning of organs and metabolic processes. Copper may also act as an antioxidant, and help your body absorb iron.

Foods that contain copper include oysters, liver, whole grain breads and cereals, shellfish, dark green leafy vegetables, dried legumes, nuts, and chocolate.

Dysregulation of copper may cause inflammation throughout your body.

Gene Name	Variants	Metrics	
SLC31A1			
SLC31A1 (rs10817465)		TT 32.8%	SLC31A1 encodes a copper transporter that is found in cell membranes.
SLC31A1 (rs10981694)		TT 78.3%	
SLC31A1 (rs7851395)	1	GA 49.3%	
SLC31A1 (rs117452400)		CC 97.7%	
SLC31A1 (rs7851623)		CC 58.5%	
SLC31A1 (rs58201577)	1	CA 22.2%	
SLC31A2			
SLC31A2 (rs4263842)	1	TC 44.3%	SLC31A2 encodes a copper transporter that is found in cell membranes.
SLC31A2 (rs7851648)		CC 30.8%	
SLC31A2 (rs10121981)	1	CT 35.9%	
SLC31A2 (rs117725512)		AA 94.8%	
SLC31A2 (rs4246897)	1	GA 28.4%	
SOD1			
SOD1 (rs1041740)	1	CT 41.6%	SOD1 enzymes deal with the superoxide radical by adding or removing an electron from a superoxide molecule.
SOD1 (rs4816407)		AA 85.3%	
ATOX1			
ATOX1 (rs28917210)		CC 93.9%	ATOX1 delivers copper from the cytosol to copper transporters ATP7A and ATP7B. This protein also functions as an antioxidant against superoxide and hydrogen peroxide.
ATOX1 (rs114216087)		CC 98.3%	
ATP7A			
ATP7A (rs72554640)		CC 100%	The ATP7A protein is a transmembrane protein and is expressed in the intestine and all tissues except liver. Copper is exported from the enterocytes into the blood by ATP7A. ATP7A is a copper transporter which uses the energy from ATP to transport Cu(I) across cell membranes.
ATP7A (rs72554645)		CC 100%	
ATP7A (rs72554649)		CC 100%	
ATP7A (rs72554650)		CC 100%	
ATP7A (rs5959130)		GG 100%	
ATP7A (rs72554639)		GG 99.9%	
ATP7A (rs72554644)		GG 100%	
ATP7A (rs72554652)		GG 100%	
ATP7A (rs2228447)		AA 100%	
ATP7A (rs150526992)		AA 100%	
ATP7A (rs138958687)		AA 99.8%	
ATP7A (rs143907597)		AA 99.9%	
ATP7A (rs61742278)		AA 99.9%	
ATP7A (rs192424860)		CC 100%	
ATP7A (rs139902461)		GG 100%	
ATP7A (rs2227291)		GG 66.8%	

ATP7B		
ATP7B (rs137853283)		CC 100%
ATP7B (rs137853282)		CC 100%
ATP7B (rs76151636)		GG 99.7%
ATP7B (rs17479855)		GG 95.2%
ATP7B (rs60986317)		GG 99.6%
ATP7B (rs60431989)		AA 100%
ATP7B (rs28942076)		CC 100%
ATP7B (rs28942075)		CC 100%
ATP7B (rs28942074)		CC 100%
ATP7B (rs1801249)	1	GA 48.3%
ATP7B (rs1801248)		CC 92.3%
ATP7B (rs1061472)	1	CT 48.7%
ATP7B (rs189601972)		CC 100%
ATP7B (rs115508314)		CC 45.4%
ATP7B (rs117498962)		GG 99.1%
ATP7B (rs118189338)		TT 96.2%
ATP7B (rs144246373)		TT 99.8%
ATP7B (rs184405818)		TT 99.8%
ATP7B (rs184868522)		AA 99.8%
ATP7B (rs192957846)		CC 97.8%
ATP7B (rs193922102)		AA 99.9%
ATP7B (rs193922107)		GG 100%
ATP7B (rs35206614)		AA 95.5%
ATP7B (rs4941716)	1	CT 18.9%
ATP7B (rs587783318)		CC 100%
ATP7B (rs72552255)		GG 99.9%
ATP7B (rs73184327)		CC 95.8%
ATP7B (rs7334118)		TT 97.5%
ATP7B (rs747781)		CC 25.6%
ATP7B (rs7999812)		AA 30.6%
ATP7B (rs9535826)		TT 24.1%
ATP7B (rs9535828)		GG 29%

The ATP7B protein is a transmembrane protein and is expressed in the brain and liver.

ATP7B protein is located in the trans-Golgi network of the liver and brain and works to balance the copper level in the body by excreting excess copper into bile and plasma.

CP		
CP (rs13098532)		TT 97.8%
CP (rs13072552)		GG 84.4%
CP (rs13095262)		AA 79.1%
CP (rs187293972)		CC 99.9%
CP (rs35198307)		AA 98.4%
CP (rs35904683)		AA 66.3%
CP (rs56033670)		GG 98.7%
CP (rs11924961)		GG 96.7%
CP (rs1053709)		TT 88.3%
CP (rs188643164)		GG 100%
CP (rs200156117)		TT 100%
CP (rs386134124)		GG 100%
CP (rs34386552)		GG 99.9%
CP (rs75633237)		TT 96.7%
CP (rs9841442)	2	CC 22.9%
CP (rs115552500)		CC 98.4%
CP (rs200864206)		GG 100%
CP (rs61733458)		GG 96.7%
CP (rs150303869)		TT 99.9%
CP (rs73866999)		GG 99.9%
CP (rs115154252)		CC 94%
CP (rs55773387)		GG 88%
CP (rs772908)		GG 56.9%
CP (rs386134123)		AA 100%
CP (rs200683433)		CC 99.1%
CP (rs7652826)	2	GG 29.8%

The CP protein encoded by this gene binds most of the copper in plasma.

Iron

If you have more iron than your body needs to satisfy your hemoglobin requirement (for cell oxygenation), the excess becomes a dangerous surplus.

Because iron has a limited capacity to be excreted by the body, it can easily build up in organs like the liver, heart and pancreas; this is potentially problematic because iron is a potent oxidizer that can damage your body tissues.

In vivo, Fenton reactions are initiated by by-products of aerobic respiration, such as hydrogen peroxide (H2O2) and superoxide. Many in vitro experiments have indicated that H2O2 can oxidize Fe2+ to produce hydroxide (OH−) and the highly reactive hydroxyl radical, and this is called the Fenton reaction.

Gene Name	Variants	Metrics
SLC48A1		
SLC48A1 (rs4760653)		TT 73.6%
SLC48A1 (rs73107911)		GG 67.7%
SLC48A1 (rs4760731)		GG 87.4%

Iron can exist in heme, and ferric forms. Heme is a Fe(2+) (ferrous) ion. The non-heme dietary iron ferric is a Fe(3+) ion. Fe(3+) must that be reduced to the ferrous form (Fe(2+)) before it is absorbed.

The protein encoded by SLC48A1 transports heme into the intestinal cells.

SLC11A2		
SLC11A2 (rs17125155)	1	TC 3.7%
SLC11A2 (rs149411)		AA 17.8%
SLC11A2 (rs12227734)		GG 90.9%
SLC11A2 (rs115874705)		CC 99.8%
SLC11A2 (rs118034836)		GG 99.1%
SLC11A2 (rs139984159)		CC 100%
SLC11A2 (rs144863268)		GG 99.6%
SLC11A2 (rs147259871)	2	AA 93.4%
SLC11A2 (rs224574)		AA 88%
SLC11A2 (rs2630362)		AA 88.4%
SLC11A2 (rs445520)		GG 88%

The SLC11A2 gene provides instructions for making a protein called divalent metal transporter 1 (DMT1). The DMT1 protein is found in all tissues, where its primary role is to transport positively charged iron atoms within cells. The DMT1 protein is located within fingerlike projections called microvilli in the duodenum of the small intestine.

SLC40A1		
SLC40A1 (rs10188785)	1	GT 47.3%
SLC40A1 (rs1123110)	1	AG 46.1%
SLC40A1 (rs199683014)		CC 100%
SLC40A1 (rs34206448)		TT 56.4%
SLC40A1 (rs35623329)		TT 55.8%
SLC40A1 (rs387907377)		CC 99.6%
SLC40A1 (rs7586757)	1	CT 43.2%
SLC40A1 (rs7596205)		GG 83.7%

The SLC40A1 gene contains the instructions for making a protein called ferroportin. Ferroprtin is found in all cells and tissues where iron is regulated and is the only cellular iron exporter.

Ferroportin transports iron from the small intestine into the bloodstream.

FTL		
FTL (rs201319635)		TT 100%

The FTL gene provides instructions for making the ferritin light chain. Ferritin is the major intracellular iron storage protein in eukaryotes. Each ferritin molecule can hold as many as 4,500 iron atoms. This storage capacity allows ferritin to regulate the amount of iron in cells and tissues. Iron is needed for the body to produce red blood cells.

Variation in ferritin subunit composition may affect the rates of iron uptake and release in different tissues. Variation in the ferritin subunit is also associated with several neurodegenerative diseases and hyperferritinemia-cataract syndrome.

HFE		
HFE C282Y (rs1800562)		GG 89.4%
HFE H63D (rs1799945)		CC 74.2%
HFE S65C (rs1800730)		#N/A
HFE (rs62625346)		GG 100%
HFE (rs140080192)		GG 99.8%
HFE (rs2071302)		TT 97.6%
HFE (rs9366637)		CC 84.5%

The HFE protein encoded by the HFE gene interacts with other proteins on the cell surface to detect the amount of iron in the body.

The HFE protein regulates the production of a protein called hepcidin. Hepcidin is produced by the liver, and determines how much iron is absorbed from the diet and released from storage sites in the body. When the proteins involved in iron sensing and absorption are functioning properly, iron absorption is tightly regulated

HMOX			
HMOX1 (rs141730669)		CC 100%	Heme oxygenase is an essential enzyme in heme catabolism. Heme oxygenase cleaves heme to form biliverdin. Biliverdin is then converted to bilrubin by biliverdin reductase, and carbon monoxide. Bilirubin is a compound that breaks down heme in vertebrates. This catabolism is a necessary process in the body's clearance of waste products that are produced from the breakdown of aged red blood cells. Under physiological conditions, the activity of heme oxygenase is highest in the spleen.
HMOX1 (rs148193694)		CC 100%	
HMOX1 (rs199554283)		CC 100%	
HMOX1 (rs200856037)		CC 100%	
HMOX1 (rs4820192)		AA 46.7%	
HMOX1 (rs75125910)		AA 97.9%	
HMOX1 (rs77672261)		GG 100%	
HMOX2 (rs17884699)		TT 98.3%	
HMOX2 (rs146912339)		CC 99.7%	
HMOX2 (rs140056309)		CC 99.8%	
HMOX2 (rs118181434)		GG 93.2%	
HMOX2 (rs11643057)	1	TC 41.7%	
HMOX2 (rs10500325)		TT 92.2%	
ACO1			
ACO1 (rs10970961)		CC 41.9%	The protein encoded by ACO1 is a cytosolic protein that functions as an essential enzyme in the Krebs cycle and also interacts with mRNA to control the levels of iron inside cells. When cellular iron levels are high, this protein can function as an aconitase. Aconitases are iron-sulfur proteins that function to catalyze the conversion of citrate to Isocitrate. Variations in this gene have been associated with higher iron levels.
ACO1 (rs10813805)		AA 27.4%	
ACO1 (rs4879586)	1	AC 34.9%	
ACO1 (rs77643348)		TT 91.9%	
ACO1 (rs77465798)		CC 94.7%	
ACO1 (rs7026133)		CC 75.8%	
ACO1 (rs4878497)	1	GA 48.9%	
ACO1 (rs3780474)	1	TG 45.6%	
ACO1 (rs2274721)		TT 99.8%	
ACO1 (rs2026739)	1	TG 38.8%	
ACO1 (rs1467713)	1	TC 44.9%	
ACO1 (rs11793098)	1	AG 42.4%	
ACO1 (rs117856719)		GG 91.3%	
ACO1 (rs117242326)		AA 99.8%	
ACO1 (rs113309164)		TT 94.7%	
ACO1 (rs10813818)	1	CT 48.5%	
ACO1 (rs10758139)	1	AG 45.4%	
ACO1 (rs10117433)		GG 76.6%	
TFR2			
TFR2 (rs7385804)		AA 39.6%	The protein encoded by TFR2 mediates the cellular uptake of transferrin-bound iron, and may be involved in iron metabolism.
TFR2 (rs200287731)		AA 83.1%	
TFR2 (rs41295933)		AA 94%	
TFR2 (rs200053955)		CC 99.8%	
TFR2 (rs202221581)		CC 99.8%	
TFR2 (rs80338885)		CC 99.8%	
TFR2 (rs187119131)		TT 99.6%	
TFR2 (rs41295900)		TT 100%	
TFR2 (rs41302360)		TT 99.3%	
TFR2 (rs4729597)		TT 42.5%	

TF		
TF (rs1799899)		GG 90.3%
TF (rs3811647)	1	GA 44.5%
TF C34378T (rs1049296)		CC 69.8%
TF (rs121918680)		GG 100%
TF (rs144143295)		GG 100%
TF (rs1799852)		CC 79.9%
TF (rs1800277)		CC 90.3%
TF (rs1880669)		CC 33.6%
TF (rs200493748)		GG 99.9%
TF (rs41295792)		GG 97%
TF (rs41296598)		CC 100%
TF (rs4459901)	1	TC 42.8%
TF (rs8177189)		GG 93.6%
TF (rs8177191)		GG 69.3%
TF (rs8177197)	1	GA 41.9%
TF (rs8177217)		GG 68.6%
TF (rs8177235)		GG 86.5%
TF (rs8177240)	1	TG 44.1%
TF (rs8177253)	1	CT 43.9%
TF (rs8177271)	1	GA 43.9%

The function of the protein encoded by the TF gene is to transport iron from the intestine, reticuloendothelial system, and liver parenchymal cells to all proliferating cells in the body.

Magnesium

Magnesium is a cofactor for many enzyme systems that regulate a multitude of diverse biochemical reactions in the body. These biochemical reactions include protein synthesis, muscle and nerve function, blood glucose control, and blood pressure regulation.

Magnesium is also required for energy production, oxidative phosphorylation, glycolysis, synthesis of DNA, RNA, and glutathione.

Gene Name	Variants	Metrics
Magnesium Transporters		
SLC41A1 (rs823156)	1	AG 30.5%
SLC41A1 (rs823066)	1	GA 13.4%
SLC41A1 (rs708730)	1	AG 29.7%
SLC41A1 (rs76951503)		GG 97.5%
SLC41A1 (rs73080391)		CC 91.7%
SLC41A1 (rs115519405)		CC 92.2%
SLC41A1 (rs115027058)		CC 96.6%
SLC41A2 (rs2453166)		TT 50.4%
SLC41A2 (rs77030943)		CC 98.1%
SLC41A2 (rs61129422)		AA 97%
SLC41A2 (rs190094757)		CC 100%
SLC41A2 (rs117456044)		CC 93.8%
SLC41A2 (rs78529822)		GG 97%
SLC41A2 (rs183218971)		GG 100%
SLC41A2 (rs117286618)		GG 99.3%
SLC41A2 (rs116185014)		GG 97.1%
SLC41A2 (rs9669285)	1	TC 20.5%
SLC41A2 (rs76245845)		TT 97.8%
SLC41A2 (rs145274729)		TT 99.7%
SLC41A2 (rs117912612)		TT 95.6%
SLC41A2 (rs113064473)		TT 92%
SLC41A2 (rs11112218)		TT 86.3%

Magnesium plays a role in the transport of calcium and potassium ions across cell membranes. The SLC41A1 and SLC41A2 genes encode enzymes that acts as a magnesium transporters.

TRPM6		
TRPM6 (rs3750425)		CC 82.3%
TRPM6 (rs111602408)		GG 94.3%
TRPM6 (rs1333343)	2	TT 60.5%
TRPM6 (rs11144085)	2	GG 31.3%
TRPM6 (rs35804026)		TT 95.8%
TRPM6 (rs145791687)		TT 99.9%
TRPM6 (rs72730940)		GG 94.8%
TRPM6 (rs62569673)		GG 93%
TRPM6 (rs56290308)		GG 99.7%
TRPM6 (rs191772517)		GG 100%
TRPM6 (rs148912866)		GG 99.7%
TRPM6 (rs139586014)		GG 100%
TRPM6 (rs121912625)		GG 100%
TRPM6 (rs79289883)		CC 97.9%
TRPM6 (rs7045949)	1	TC 49.1%
TRPM6 (rs66591564)		TT 91.1%
TRPM6 (rs6560408)	1	CT 48.5%
TRPM6 (rs2254229)		TT 82.1%
TRPM6 (rs7859201)		AA 38.1%
TRPM6 (rs117743586)		TT 97.5%
TRPM6 (rs143164660)		CC 99.6%
TRPM6 (rs77826848)		CC 100%
TRPM6 (rs79101189)	1	AG 12.3%
TRPM6 (rs77967152)		AA 96.1%
TRPM6 (rs2274925)	1	AG 14.2%
TRPM6 (rs182809758)		AA 99.8%
TRPM6 (rs4991745)		GG 70.9%
TRPM6 (rs13299138)		GG 60.2%
TRPM6 (rs58586447)		CC 92%
TRPM6 (rs182530243)		CC 100%
TRPM6 (rs180963446)		CC 100%
TRPM6 (rs150874152)		CC 99.3%
TRPM6 (rs142043309)		CC 100%
TRPM6 (rs149123085)		AA 99.9%

The TRPM6 gene encodes a protein that contains an ion channel that is critical for magnesium homeostasis. This gene is expressed predominantly in the kidneys and colon and plays a crucial role in epithelial magnesium transport and magnesium absorption in the gut and kidneys.

ATP2B1		
ATP2B1 (rs2854371)	1	GA 42.3%
ATP2B1 (rs1050395)		TT 65.5%
ATP2B1 (rs17381194)		TT 72.8%
ATP2B1 (rs2681492)		TT 68.3%
ATP2B1 (rs2681472)		AA 67.9%
ATP2B1 (rs116935590)		GG 99.8%
ATP2B1 (rs36010888)		AA 88.1%
ATP2B1 (rs957525)		TT 92.9%
ATP2B1 (rs77518567)		TT 98.7%
ATP2B1 (rs147096096)		TT 98.8%

The enzyme encoded by the ATP2B1 gene plays a critical role in intracellular calcium homeostasis.

The ATP2B1 gene has an indirect effect on blood magnesium levels via its function in calcium homeostasis regulation.

Glutamate and Glutamine

Glutamate plays a vital role in cognitive function but may cause anxiety or inflammation in excess. Your health professional may use this data with symptoms and labs to support health/glutamate.

Gene Name	Variants	Metrics	
SLC1A1			
			SLC1A1 encodes a member of the high-affinity glutamate transporters that play an essential role in transporting glutamate across plasma membranes. In the brain, these transporters are crucial in terminating the postsynaptic action of the neurotransmitter glutamate, and in maintaining extracellular glutamate concentrations below neurotoxic levels. This transporter also transports aspartate. All SLC1A1 SNPs can be found in the gene report.
SLC1A5			
SLC1A5 (rs1644343)		AA 61.4%	Glutamine is transported into cells through SLC7A5.
SLC1A5 (rs3027957)	1	TC 30.8%	
SLC1A5 (rs313853)		TT 44.3%	
SLC1A5 (rs8105903)		AA 29.9%	
SLC1A5 (rs139657571)		AA 99.9%	
SLC1A5 (rs138508383)		CC 97.5%	
SLC1A5 (rs201671774)		CC 99.2%	
SLC1A5 (rs56385874)		CC 71.3%	
SLC7A5			
SLC7A5 (rs11117303)		AA 97.7%	Glutamine is transported into cells through SLC7A5.
SLC7A5 (rs11865049)		GG 91.6%	
SLC7A5 (rs146583737)		CC 100%	
SLC7A5 (rs149350851)		CC 82.7%	
SLC7A5 (rs151257488)		CC 99.3%	
SLC7A5 (rs16943300)		GG 87.3%	
SLC7A5 (rs4240803)		GG 48.3%	
SLC7A5 (rs4465613)		CC 36.5%	
SLC7A5 (rs4843719)	1	CA 44.1%	
SLC7A5 (rs59237738)		CC 90.5%	
SLC7A5 (rs74319154)		CC 96.5%	
SLC7A5 (rs75220135)		GG 98.2%	
SLC7A5 (rs78174881)		CC 93.7%	
SLC7A5 (rs8051149)		GG 53.3%	
SLC7A5 (rs9935894)		TT 56.4%	
SLC7A5 (rs997761)	1	GT 41.6%	

SLC38A9			
SLC38A9 (rs10056287)		TT 67.8%	SLC38A9 transports glutamine, arginine and leucine as substrate.
SLC38A9 (rs112657890)		TT 93.3%	
SLC38A9 (rs191559769)		TT 83.5%	
SLC38A9 (rs72758226)		TT 97.7%	
SLC38A9 (rs7704138)		TT 44%	
SLC38A9 (rs112087862)		GG 97.9%	
SLC38A9 (rs11956514)		CC 50.5%	
SLC38A9 (rs7716219)		CC 62.9%	
SLC38A9 (rs11958779)		AA 47.6%	
SLC38A9 (rs35361432)		AA 93%	
SLC38A9 (rs3846506)		AA 63.7%	
SLC38A9 (rs72760041)		AA 97.6%	
SLC38A9 (rs78500873)		AA 95.2%	
SLC3A2			This gene is a member of the solute carrier family and encodes a cell surface, transmembrane protein. Glutamine is transported out of the cells through SLC3A2.
SLC7A11			
SLC7A11 (rs4131888)	1	CT 32.6%	This gene encodes a member of a heteromeric, sodium-independent, anionic amino acid transport system that is highly specific for cysteine and glutamate. Glutamine derived glutamate can also be exchanged through the SLC7A11 and SLC3A2 antiporter for cystine.
SLC7A11 (rs4602539)	1	TG 42.3%	
SLC7A11 (rs111500641)		TT 97.9%	
SLC7A11 (rs112913374)		TT 94.5%	
SLC7A11 (rs186693425)		GG 89.2%	
SLC7A11 (rs199779027)		GG 99.9%	
SLC7A11 (rs201460766)		GG 99.4%	
SLC7A11 (rs34757167)		GG 99.8%	
SLC7A11 (rs41280523)		GG 97.7%	
SLC7A11 (rs56061714)		GG 77.4%	
SLC7A11 (rs6830952)		AA 97.4%	
SLC7A11 (rs6851845)		CC 86%	
SLC7A11 (rs72712323)		CC 95%	
SLC7A11 (rs74674034)		TT 89.9%	
SLC7A11 (rs74968293)		TT 91.2%	
SLC7A11 (rs77316790)		GG 98.1%	
SLC7A11 (rs77562268)		TT 98.7%	
GLS			
GLS (rs116894218)		AA 100%	GLS or Glutaminase encodes a protein that catalyzes the hydrolysis of glutamine to glutamate and ammonia.
GLS (rs3771316)		AA 82%	
GLS (rs115647663)		CC 97%	
GLS (rs116681266)		GG 92%	
GLS (rs140284772)		GG 99.8%	
GLS (rs6758866)	1	GA 47.2%	
GLS (rs72907217)		GG 94.5%	
GLS (rs867637)	1	GA 45.4%	
GLS (rs115557657)		TT 97.4%	
GLS (rs1517354)		TT 86.4%	

GLS2		
GLS2 (rs2638315)		GG 65.3%
GLS2 (rs2657879)		AA 65.6%
GLS2 (rs11171863)		CC 48.3%
GLS2 (rs117449436)		TT 97.4%

GLS2 or Glutaminase 2 encodes a protein that catalyzes the hydrolysis of glutamine to stoichiometric amounts of glutamate and ammonia.

GLUL		
GLUL (rs12136955)	2	AA 10.5%

GLUL or Glutamate-ammonia Ligase encodes a protein that catalyzes the synthesis of glutamine from glutamate and ammonia in an ATP-dependent reaction.

Glutamate to AlphaKetoglutarate Conversion		
GLUD1 (rs80171587)		TT 99.8%
GLUD1 (rs200813784)		TT 99%
GLUD1 (rs2296063)	1	CT 45%
GLUD1 (rs185770189)		CC 100%
GLUD1 (rs113973335)		CC 94.6%
GOT1 (rs79694820)		GG 98.1%
GOT1 (rs12253861)		GG 77.9%
GOT1 (rs10748775)		GG 82.8%
GOT1 (rs35546038)		TT 82.4%
GOT1 (rs113309820)		TT 93.1%
GOT1 (rs76850691)		GG 99.7%
GOT1 (rs200430334)		GG 100%
GOT1 (rs77609090)		AA 98.5%
GOT1 (rs79162286)		AA 99.6%
GOT1 (rs4919308)		AA 97.2%
GOT1 (rs11190087)	2	GG 32%
GOT1 (rs181756022)		CC 100%
GOT2 (rs11076256)		CC 85.8%
GOT2 (rs118080449)		GG 96.3%
GOT2 (rs140747876)		TT 99.9%
GOT2 (rs257633)		AA 44.1%
GOT2 (rs30839)	2	CC 41.7%
GOT2 (rs30842)		CC 48.8%
GOT2 (rs35298154)		AA 96.3%
GOT2 (rs78623058)	1	TC 6.3%
GOT2 (rs9921563)		GG 92.5%
GPT (rs201783570)		GG 99.8%
GPT (rs201413052)		CC 99.9%
GPT (rs200479839)		GG 100%
GPT (rs200088103)		CC 100%
GPT (rs149505691)		GG 99.1%
GPT (rs147998249)		GG 99.6%
GPT (rs143462595)		GG 83.5%
GPT (rs138238489)		GG 99.7%
GPT (rs112574791)		GG 97.8%
GPT (rs1063739)		CC 28.8%

GLUD1 or Glutamate Dehydrogenase 1 encodes glutamate dehydrogenase which catalyzes the oxidative deamination of glutamate to alpha-ketoglutarate and ammonia. This enzyme has an important role in regulating amino acid-induced insulin secretion.

Glutamic-oxaloacetic transaminase is a pyridoxal phosphate-dependent enzyme which exists in cytoplasmic and inner-membrane mitochondrial forms, GOT1 and GOT2, respectively. GOT plays a role in the conversion of glutamate to alpha-ketoglutarate.

Glutamic-Pyruvate Transaminase also plays a role in the conversion of glutamate to alphaketoglutarate.

KRAS			
KRAS (rs9266)		GG 30.4%	KRAS encodes a protein that is a member of the small GTPase superfamily. Variations in this gene can cause increases in aminotransferases and decreases in GLUD mRNA.
KRAS (rs35081958)		GG 95%	
KRAS (rs61759623)		TT 94.3%	
KRAS (rs61764370)		AA 80.8%	
KRAS (rs61759637)		AA 94.7%	
KRAS (rs61761088)		AA 96.2%	
KRAS (rs61763587)		CC 96.7%	
KRAS (rs56375810)		CC 72.5%	
KRAS (rs187995827)		CC 94.5%	
MYC			
MYC (rs4645963)		CC 96.4%	Studies have shown that the MYC oncogene has been most associated with upregulated glutamine metabolism.
MYC (rs4645948)		CC 94%	
MYC (rs186663828)		CC 99.9%	
MYC (rs4645959)	1	AG 6.7%	
PYCR1			
PYCR1 (rs281875319)		CC 99.7%	PYCR1 encodes an enzyme that catalyzes the NAD(P)H-dependent conversion of pyrroline-5- carboxylate to proline. In a reaction independent of transamination, proline can be synthesized by conversion of glutamate to pyrroline-5-carboxylate (P5C) by PYCR1.
PYCR2			
PYCR2 (rs56362902)		GG 93.3%	PYCR2 belongs to the pyrroline-5-carboxylate reductase family. The encoded mitochondrial protein catalyzes the conversion of pyrroline-5-carboxylate to proline. This is the last step in proline biosynthesis. In a reaction independent of transamination, proline can be synthesized by conversion of glutamate to pyrroline-5-carboxylate (P5C) by PYCR2.
PSAT1			
PSAT1 (rs944514)		TT 59.8%	PSAT1 encodes a member of the class-V pyridoxal-phosphate-dependent aminotransferase family. PSAT1 is the major source of glutamine-dependent α-ketoglutarate.
PSAT1 (rs7470974)		TT 78%	
PSAT1 (rs3758201)		TT 41.8%	
PSAT1 (rs10735532)		TT 53.2%	
PSAT1 (rs10116267)		TT 27.4%	
PSAT1 (rs74451333)		GG 97.8%	
PSAT1 (rs3824361)		GG 80.9%	
PSAT1 (rs112128348)		GG 96.1%	
PSAT1 (rs11137591)		GG 72.8%	
PSAT1 (rs41277899)		CC 78.3%	
PSAT1 (rs11137606)		CC 70%	
PSAT1 (rs11137607)		AA 32.3%	
GPT			
GPT (rs1063739)		CC 28.8%	Glutamic-Pyruvate Transaminase also plays a role in the conversion of glutamate to alphaketoglutarate.
GPT (rs112574791)		GG 97.8%	
GPT (rs138238489)		GG 99.7%	
GPT (rs143462595)		GG 83.5%	
GPT (rs147998249)		GG 99.6%	
GPT (rs149505691)		GG 99.1%	
GPT (rs200088103)		CC 100%	
GPT (rs200479839)		GG 100%	
GPT (rs201413052)		CC 99.9%	
GPT (rs201783570)		GG 99.8%	

GPT2			
GPT2 (rs114467444)		CC 97.5%	Glutamate-pyruvate transaminase transfers nitrogen from glutamate to pyruvate to make alanine and α-ketoglutarate. GPT2 encodes mitochondrial alanine transaminase, a pyridoxal enzyme that catalyzes the reversible transamination between alanine and 2-oxoglutarate to generate pyruvate and glutamate. Alanine transaminases play roles in gluconeogenesis and amino acid metabolism in many tissues.
GPT2 (rs114708202)		AA 100%	
GPT2 (rs145807385)		CC 99.9%	
GPT2 (rs200427767)		GG 99.9%	
GPT2 (rs2290317)		GG 99.6%	
GPT2 (rs34454412)		GG 96.5%	
GPT2 (rs77435714)		GG 96.4%	
GPT2 (rs8044153)		CC 94.3%	
ASNS			
ASNS (rs148111963)		AA 100%	The protein encoded by ASNS is involved in the synthesis of asparagine. Glutamine will sometimes act as a nitrogen donor for asparagine synthesis through the ASNS gene.
ASNS (rs3735557)	1	TC 50%	
ASNS (rs41278824)		AA 95.5%	
ASNS (rs4727377)		AA 85.4%	
ASNS (rs754043007)		GG 99.9%	
ASNS (rs7797354)	1	TC 47%	
ASNS (rs7810919)		CC 45.4%	
TSC1			
TSC1 (rs1073123)		AA 75.8%	TSC1 encodes a growth inhibitory protein thought to play a role in the stabilization of tuberin. Studies have shown that TSC1 increased glutamine uptake and metabolism.
TSC1 (rs1076160)		CC 27.1%	
TSC1 (rs11243931)		AA 72.7%	
TSC1 (rs116917669)		AA 93.7%	
TSC1 (rs116974823)		TT 98.5%	
TSC1 (rs118203400)		GG 100%	
TSC1 (rs118203402)		CC 100%	
TSC1 (rs118203493)		GG 99.9%	
TSC1 (rs118203532)		GG 99.9%	
TSC1 (rs118203631)		GG 100%	
TSC1 (rs118203699)		TT 99.9%	
TSC1 (rs118203723)		GG 99.9%	
TSC1 (rs118203750)		CC 100%	
TSC1 (rs151097777)		AA 99.9%	
TSC1 (rs199620268)		AA 99.9%	
TSC1 (rs199755731)		CC 99.9%	
TSC1 (rs201738258)		TT 99.9%	
TSC1 (rs7020175)		GG 83.1%	
TSC1 (rs72619325)		AA 95%	
TSC1 (rs77464996)		GG 100%	
TSC1 (rs78136408)		GG 97.8%	
TSC1 (rs7862221)		TT 73.8%	
TSC2			
			TSC2 is a protein coding gene. All TSC2 SNPs can be found in the gene report. Studies have shown that TSC2 increased glutamine uptake and metabolism.

SIRT3			
SIRT3 (rs11246007)	1	CT 25.2%	SIRT3 encodes a member of the sirtuin family of proteins. SIRT3 can deacetylate GLS2 to promote increased activity. SIRT3 supports SOD production and NADPH production.
SIRT3 (rs12576565)		CC 99.9%	
SIRT3 (rs181924090)		CC 100%	
SIRT3 (rs28365927)	1	GA 23.8%	
SIRT3 (rs367869057)		GG 99.2%	
SIRT3 (rs3782118)	1	CT 41.3%	
SIRT3 (rs536715)		CC 77%	
SIRT3 (rs538053)		TT 68%	
SIRT3 (rs7104764)	1	AG 37.8%	
SIRT5			
SIRT5 (rs143092270)		CC 99.8%	SIRT5 encodes a member of the sirtuin family of proteins. SIRT5 desuccinylates and reduces GLS activity, this causes a reduction in ammonia production and autophagy activation.
SIRT5 (rs188775956)		GG 100%	
SIRT5 (rs2328676)		TT 49.3%	
SIRT5 (rs2804921)		GG 55%	
SIRT5 (rs34162626)		AA 87.8%	
SIRT5 (rs75603749)		CC 97.6%	
SIRT5 (rs7747037)		TT 45.6%	
SIRT5 (rs79562910)		AA 91.4%	
HIF1A			
HIF1A (rs41508050)		CC 98.8%	HIF1A encodes the alpha subunit of transcription factor hypoxia-inducible factor-1 (HIF-1). HIFA can also promote the conversion of glucose to lactate, keeping it from the TCA cycle. Decreased glucose in the TCA cycle can be compensated for by glutamine-fueled production.
HIF1A (rs2057482)		CC 71.1%	
HIF1A (rs61755705)		GG 99.3%	
HIF1A (rs188461135)		CC 99.9%	
HIF1A (rs2301113)		AA 56.4%	
HIF1A (rs11549467)		GG 98.3%	
HIF1A (rs61755706)		CC 100%	
HIF1A (rs79510556)		AA 99.1%	
HIF1A (rs11549465)		CC 79.7%	
GSS			
GSS (rs28936396)		GG 100%	The protein encoded by GSS functions as a homodimer to catalyze the second step of glutathione biosynthesis. This step is the ATP-dependent conversion of gamma-L-glutamyl-L-cysteine to glutathione.
GSS (rs199658514)		CC 100%	
GSS (rs35416056)		GG 91.1%	
GSS (rs138659144)		TT 100%	
GSS (rs28938472)		TT 100%	
GSS (rs34239729)		CC 99.9%	
GSS (rs193267972)		CC 100%	
CD4			
CD4 (rs28917476)		CC 98.5%	CD4 encodes a membrane glycoprotein of T lymphocyte. The CD4 gene is expressed in T lymphocytes, B cells, macrophages, and granulocytes. It is also expressed in specific regions of the brain. CD4 functions to initiate the early phase of T-cell activation. Glutamine metabolism is increased when there is T cell activation.
CD4 (rs7957426)		GG 42%	
CD4 (rs743600)		GG 47.6%	
CD4 (rs11064393)		TT 74.2%	
CD4 (rs11064407)		AA 91.5%	
CD4 (rs11064410)		AA 91.7%	
CD4 (rs7971576)		GG 27.5%	
CD4 (rs138218083)		CC 98.9%	