

**Patient: Eric Ehle**

## Variants that Impact Gut Health & Digestion

For those with health challenges, gut inflammation, dysbiosis and digestive disturbances are often common. If there are issues here, this may be step number one of many steps in supporting the patient/client. Proper function of the intestinal tract is critical for the absorption of nutrients. Unfortunately, there are many genetic variants that can impact digestive function.

Inflammation from peroxynitrite can damage the delicate intestinal lining. SNPs that reduce glutathione, SOD, NOS and BH4, as well as the CBS and BHMT SNPs that will increase ammonia, will increase the peroxynitrite and cause damage to the gut.

When there are low methyl groups as a result of MTHFR, along with SNPs in HNMT and ABP1 (that both degrade histamine) the high histamine will create higher levels of zonulin, which irritates the intestinal tract and potentially contributes to candida and leaky gut.

Variants in the HLA genes may contribute to gluten intolerance, and further 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 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 supporting the patient/client. This would include, but are not limited to, reducing histamine, eliminating gluten if an issue, reducing peroxynitrite by supporting variants in SOD, GSH, NOS, CBS, BHMT, and creating BH4.

Gene Name	Variants	Metrics
<b>HLA</b>		
HLA-DQA2 (rs2858331)		AA 34.8%
HLA-DQA1 (rs2187668)		CC 78.9%
HLA-DQA2 (rs7454108)	1	TC 19.3%
HLA-DQB1 (rs7775228)		TT 74.2%
HLA-DRA (rs2395182)	2	TT 62.6%
HLA Enzymes	70%	
<b>KIAA1109</b>		
KIAA1109 (rs6822844)	1	GT 24.6%
KIAA1109 (rs13119723)	1	AG 25.1%
KIAA1109	50%	

Product Name	SNP Total	Lab Total	Symptoms
Histamine Scavenger	1.46	#N/A	4

Variants in these genes may increase the chances of Celiac Disease or gluten intolerance. Other factors that may impact gut health are FUT variants that impact probiotics, HNMT and ABP1 variants that lessen histamine degradation and consequently cause zonulin production, low folate or high peroxynitrite.

With three HLA variants, there is a high likelihood of gluten intolerance/sensitivity, especially if the HLA DQA1 is homozygous. Additionally, if the gut is damaged due to peroxynitrite and zonulin, gluten sensitivity can be worse.

The KIAA1109 gene is associated with susceptibility to celiac disease. Celiac disease is a common small intestinal inflammatory condition induced by dietary wheat, rye, and barley. Variants in this gene may increase the chances of Celiac Disease.

Studies have found that the T allele of rs6822844 at the IL2-IL21 region is associated with multiple autoimmune diseases in individuals of European descent. These include rheumatoid arthritis, type-1 diabetes, autoimmune disease, Inflammatory Bowel Disease, psoriasis, and ulcerative colitis.

MCM6		
MCM6 (rs182549)	1	CT 41.6%
MCM6 (rs4988235)	1	GA 42.3%
<p>The MCM6 gene is a protein coding gene. Single nucleotide polymorphisms in this gene can impact the neighboring LCT gene. The LCT gene provides instructions for making an enzyme called lactase.</p> <p>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.</p> <p>Variations in the MCM6 genes cause the LCT gene to remain active during adulthood. Because of this, individuals with increased variants are more likely able to digest the lactose found in milk and dairy products.</p>		
Lactose Intolerance	50%	
<p>There are 2 variants in the MCM6 gene. With two variants, there is a likelihood of being lactose tolerant.</p>		
Peanut Allergy		
HLA-DQA2 (rs9275596)	1	TC 44.2%
HLA-DRA (rs7192)	1	GT 46.0%
<p>Studies have shown that peanut allergies are one of the most common food allergies.</p> <p>Peanuts are not the same as tree nuts such as almonds, cashews, and walnuts. Peanuts grow underground and are part the legume family. Other examples of legumes include beans, peas, lentils and soybeans.</p> <p>Variants in rs9275596 and rs7192 are associated with the increased susceptibility of developing a peanut allergy in individuals with European ancestry.</p>		
Peanut Allergy	50%	
<p>With two variants, this individual has an increased risk of developing a peanut allergy.</p>		
Caffeine Consumption		
AHR (rs4410790)	1	TC 46.9%
CYP1A2 (rs2472297)	1	CT 31.9%
<p>The AHR gene contains the instructions for a protein that helps regulate the amount of certain proteins. One of these proteins includes an enzyme, called CYP1A2.</p> <p>The CYP1A2 gene contains the instructions for an enzyme that breaks down many substances, including caffeine. This enzyme is one of the many cytochrome P450 enzymes.</p> <p>Studies have shown that variants in these SNPs related to a higher consumption of caffeine.</p>		
Caffeine Consumption	50%	
<p>With 2 variants it is possible that this individual consumes an increased amount of caffeine</p>		
Caffeine Metabolization		
CYP1A2 C164A (rs762551)	2	AA 50.2%
<p>The CYP1A2 gene encodes a member of the cytochrome p450 family of proteins. These proteins metabolize nutrients and drugs. One well known substrate of CYP1A2 is caffeine.</p> <p>Caffeine is a bitter substance that can be found in coffee, tea, soft drinks, chocolate, kola nuts, and certain medicines. It has many effects on the body's metabolism, including stimulating the central nervous system.</p> <p>Studies have shown that individuals with the A allele in this gene are faster metabolizers of caffeine and therefore will feel less of a stimulating effect from caffeine.</p>		
Caffeine Metabolization	0%	
<p>With 2 variants this individual is likely a fast caffeine metabolizer.</p>		

BCMO1		
BCMO1 A379V (rs7501331)	1	CT 34.5%
BCMO1 R267S (rs12934922)		AA 31.6%
BCMO1 (rs4889294)		TT 31.0%
BCMO1 (rs11643312)	1	GT 42.7%
BCMO1 (rs6564862)	1	CT 43.7%
BCMO1 (rs7192178)	1	AG 48.0%
BCMO1 (rs8046134)		GG 60.1%
BCMO1 (rs6564863)	1	TC 43.9%
BCMO1 (rs117523015)		AA 97.5%
BCMO1 (rs7202895)		AA 91.3%
BCMO1 (rs117887860)		CC 99.5%
BCMO1 (rs4889298)	1	CT 49.8%
BCMO1 (rs11865869)	1	AG 34.5%
BCMO1 (rs3803651)		AA 58.2%
BCMO1 (rs11647597)		TT 58.0%
<b>BCMO1</b>	<b>81%</b>	

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 I in Females.

Our Phase II Lyme study also determined that variants in BCMO1 R267S rs12934922, and BCMO1 rs4889294 were much higher in patients with Lyme Disease.

FUT2		
FUT2 (rs492602)	1	AG 49.2%
FUT2 (rs601338)	1	GA 49.0%
FUT2 (rs602662)	1	GA 49.1%
FUT2 (rs16982241)		GG 73.4%
FUT2 (rs281377)	1	CT 48.5%
FUT2 (rs1800022)		CC 98.0%
FUT2 (rs1047781)		AA 98.6%
FUT2 (rs1800027)		CC 86.9%
FUT2 (rs1800028)		CC 99.9%
FUT2 (rs485186)	1	AG 49.1%
FUT2 (rs603985)	1	TC 49.1%
FUT2 (rs504963)	1	GA 49.3%
<b>FUT2</b>	<b>73%</b>	

Product Name	SNP Total	Lab Total	Symptoms
Pro Flora Max Plus	2.69	0	0

Variants in the FUT2 enzyme may lead to disruptions in the good intestinal bacteria. This enzyme variant may cause a predisposition to Crohn's disease. Monitor gut health with this variant. FUT2 may also be related to lowered immune function.

Approximately 20% of individuals of European descent represent the non-secretor phenotype, which is caused by the FUT2 SNP rs601338 (W143X, G428A).

Studies demonstrate convincing evidence supporting a recessive association between Type 1 Diabetes and rs601338.

Studies indicate women with the homozygous rs492602 G allele had higher B12 level.

ABP1 (Histamine Breakdown)		
ABP1 (rs1049793)	1	CG 41.8%
ABP1 (rs10156191)	1	CT 38.0%
ABP1 (rs1049742)		CC 86.0%
ABP1 (rs35070995)		AA 99.9%
<b>ABP1</b>	<b>80%</b>	
<b>ABP1 (Most Relevant)</b>	<b>50%</b>	

Product Name	SNP Total	Lab Total	Symptoms
Histamine Scavenger	1.46	#N/A	4

This is the gene that makes the DAO enzyme that helps degrade histamine. SNPs with this gene, combined with HNMT genes, and low methyl groups, may result in high histamine and high zonulin.

Eating less histamine containing and histamine reducing foods may be needed.

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.

With only two variants in the APB1 gene, it would seem likely the production of the DAO enzyme is good. However, at this time, we do not know which SNP is most relevant, and homozygosity of the most important one could be clinically relevant.

HNMT (Histamine Transferase)			Product Name	SNP Total	Lab Total	Symptoms
			Histamine Scavenger	1.46	#N/A	4
HNMT (rs1020678)		TT 36.3%	<p>HNMT produces the enzyme that uses a methyl group to degrade histamine in the body. The ABP1 gene also clears histamine with the DAO enzyme.</p> <p>If there are many SNPs, and low methyl groups, there is the potential for high histamine. This can result in high levels of zonulin, which can cause gut inflammation and the potential for leaky gut. Over time, this may contribute to autoimmune disorders.</p> <p>Avoiding high histamine foods (alcoholic beverages and fermented foods) may be helpful as well as taking high amounts of Histamine Scavenger. Sometimes dosages need to be 9 to 12 per day in the beginning, and then can reduce over time.</p> <p>Histamine Scavenger may need Pro SAME if there are low methyl groups.</p> <p>If there is a lot of histamine and zonulin, and if they also have an HLA gene, gluten sensitivity may be a problem as well.</p>			
HNMT (rs1050891)		AA 61.7%				
HNMT (rs1349992)	1	GA 47.5%				
HNMT (rs1378321)		AA 61.5%				
HNMT (rs1455157)		TT 60.5%				
HNMT (rs1455158)		CC 60.5%				
HNMT (rs1455162)		AA 60.6%				
HNMT (rs1455164)	2	AA 59.9%				
HNMT (rs1455167)	2	GG 60.4%				
HNMT (rs1580111)		CC 36.4%				
HNMT (rs16840064)		GG 98.9%				
HNMT (rs2198652)		CC 60.5%				
HNMT (rs2737385)		TT 61.4%				
HNMT (rs3100701)		GG 35.0%				
HNMT (rs3100725)		GG 60.5%				
HNMT (rs3791235)		CC 62.2%				
HNMT (rs3828168)		CC 61.8%				
HNMT (rs4245861)		CC 61.7%				
HNMT (rs4646322)		CC 69.2%				
HNMT (rs4646333)		GG 61.6%				
HNMT (rs4954941)		GG 61.6%				
HNMT (rs60444277)		GG 99.9%				
HNMT (rs993891)	2	GG 60.0%				
Histamine Clearing (HNMT)	85%					
GRHPR			<p>GRHPR provides instructions for making the enzymes glyoxylate, and hydroxypyruvate reductase. This enzyme plays a role in preventing the buildup glyoxylate by converting it into glycolate. Glycolate can be easily eliminated from the body. This enzyme can also convert hydroxypyruvate to D-glycerate. D-glycerate is eventually converted into glucose, by other enzymes, and can be used for energy.</p> <p>Variations in this gene can 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. Calcium oxalate is a hard compound that is the main component of kidney and bladder stones.</p> <p>A diet of low oxalate is suggested if there are variants present.</p> <p>We are not aware of these SNPs being clinically relevant for Oxylate issues, but put them here as a consideration for someone has health challenges that cannot be found. If there are SNPs here, verification though OAT testing or other methods would be in order, rather than just relying on these SNPs.</p>			
GRHPR (rs2768659)	2	GG 43.7%				
GRHPR (rs309455)		CC 82.9%				
GRHPR (rs309453)		TT 44.2%				
GRHPR	67%					

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Oxalate Genes		
SPP1 (rs2853744)		GG 85.0%
SPP1 (rs11728697)	2	TT 33.1%
SPP1 (rs6840362)	1	CT 40.6%
SPP1 (rs139555315)		GG 99.8%
SPP1 (rs4754)	1	TC 39.1%
SPP1 (rs35382133)		TT 96.4%
SPP1 (rs1126616)	1	CT 39.1%
SPP1	64%	

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.

## Krebs Cycle - Genes that support the production of Acetyl-CoA and ATP

For the body to function properly, fats, carbs and proteins need to be carried into the cell and to be converted into Acetyl-CoA, the first step of the Citric Acid Cycle, for the production of ATP. These genes play a role in this process. If inadequate Acetyl-CoA is made, the individual may present with fatigue. Since ATP is needed for many functions, other parts of the body may suffer as a result with low ATP.

If there are a lot of SNPs here, this very well may be one of the first things that need to be addressed with the gut. If gut issues exist as well, you can work on both the gut and cellular energy at the same time.

Gene Name	Variants	Metrics
<b>Carnitine Transportation</b>		
SLC22A5 (rs13180043)		CC 92.2%
SLC22A5 (rs2631367)	1	CG 50.0%
SLC22A5 (rs13180186)		GG 83.5%
SLC22A5 (rs2631361)		CC 37.6%
SLC22A5 (rs2631362)		AA 48.1%
SLC22A5 (rs2631363)		AA 37.8%
SLC22A5 (rs17622208)	1	GA 48.0%
SLC22A5 (rs17689550)		CC 79.1%
SLC22A5 (rs2073642)		CC 84.7%
SLC22A5 (rs2073643)	1	TC 49.0%
SLC22A5 (rs2074610)		TT 99.7%
SLC22A5 (rs2631359)		CC 48.1%
SLC22A5 (rs274549)	1	AC 26.6%
SLC22A5 (rs274550)	1	GT 27.6%
SLC22A5 (rs274551)	1	TC 26.7%
SLC22A5 (rs274557)		TT 36.9%
SLC22A5 (rs274558)		AA 36.7%
SLC22A5 (rs274567)		CC 37.6%
SLC22A5 (rs274570)		CC 48.2%
SLC22A5 (rs274571)		AA 48.1%
SLC22A5 (rs4646301)		GG 84.8%
SLC22A5 (rs635619)		GG 48.2%
SLC22A5 (rs671473)		CC 48.1%
SLC22A5 (rs1045020)		CC 79.0%
SLC22A5 (rs2631366)		CC 99.8%
SLC22A5 (rs72552726)		GG 99.7%
SLC22A5 (rs274548)	1	TC 26.7%
<b>Carnitine Transportation</b>	<b>90%</b>	

Product Name	SNP Total	Lab Total	Symptoms
Fatty Acid Assist	1	0	4
Mitochondrial & Energy Assist	8.89	0	0
CBS / BHMT Assist	6.86	0	10

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.

Carnitine is an amino acid derivative that is synthesized in the human body. Carnitine is primarily synthesized in the liver and is stored in the tissues that use fatty acids as their primary fuel (Such as skeletal and cardiac muscle). Carnitine is required for mitochondrial & beta;-oxidation of long-chain fatty acids for energy production.

Variations in the SLC22A5 gene can result in a dysfunctional OCTN2 protein. This can cause a shortage of carnitine within cells. Without carnitine, fatty acids cannot enter mitochondria. This may cause muscle weakness and hypoglycemia. Fatty acids may also build up in cells and damage the heart, liver, and muscles.

Under certain conditions, the demand for Carnitine may exceed an individual's capacity to synthesize it, making it a conditionally essential.

High levels of Adipate, Suberate or Ethylmalonate in urine organic acid testing may also confirm lack of carnitine.

Consequently, if there are too many variants, supplementation with Acetyl-L Carnitine and other nutrients to support fat transportation/utilization may be needed to consumed with meals.

PANK		
PANK1 (rs12412483)		GG 94.6%
PANK1 (rs2038921)		AA 19.8%
PANK1 (rs10509577)		AA 88.0%
PANK1 (rs10160034)		CC 80.0%
PANK1 (rs10881606)	1	TC 44.3%
PANK1 (rs6586201)	1	CT 39.9%
PANK1 (rs17482070)		AA 82.3%
PANK1 (rs7921294)	1	GT 48.3%
PANK1 (rs7091402)	1	TC 48.3%
PANK1 (rs997456)		GG 61.0%
PANK2 (rs6107373)		GG 94.3%
PANK2 (rs6084513)	2	AA 27.3%
PANK2 (rs6084506)	1	CT 47.0%
PANK2 (rs4815628)	2	CC 28.4%
PANK2 (rs4815621)	2	GG 50.4%
PANK3 (rs11952767)		CC 99.0%
PANK4 (rs7535528)		GG 41.3%
PANK4 (rs2246732)		AA 58.0%
PANK4 (rs2236395)		AA 58.0%
PANK4 (rs1980789)	1	AC 8.3%
PANK1	83%	
PANK2	50%	
PANK3	100%	
PANK4	88%	
Total PANK	73%	

Product Name	SNP Total	Lab Total	Symptoms
Fatty Acid Assist	1	0	4
A-L-O Formula	0	#N/A	#N/A

This gene encodes members of the pantothenate kinase family. Pantothenate kinase catalyzes the ATP-dependent phosphorylation of pantothenate (vitamin B5) to give 4&prime;-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.

PANK1 encodes a member of the pantothenate kinase family.

PANK2 is the only member of the pantothenate kinase family to be expressed in mitochondria.

PANK3 is expressed most abundantly in the liver

PANK4 is most abundant in muscle but is expressed in all tissues.

ACAT		
ACAT1-02 (rs3741049)	2	AA 1.4%
ACAT-1 (rs10890819)		CC 46.3%
ACAT-2 (rs3798211)	1	AC 48.1%
ACAT-1 (rs2280332)	2	CC 4.8%
ACAT-2 (rs9347340)	1	TC 37.9%
ACAT-2 (rs25683)	1	AG 48.2%
ACAT-2 (rs3465)		GG 38.7%
ACAT - (Single SNP Most Relevant)	0%	
ACAT (All Genes)	50%	
SLC16A1		
SLC16A1 (rs7169)		GG 17.9%
SLC16A1 (rs76612089)		CC 96.7%
SLC16A1 (rs11585690)		AA 95.0%
SLC16A1 (rs71659381)		GG 86.6%
SLC16A1 (rs3849174)		TT 60.8%
SLC16A1 (rs12028967)		TT 44.0%
SLC16A1 (rs4301628)		CC 44.5%
SLC16A1	100%	

Product Name	SNP Total	Lab Total	Symptoms
Fatty Acid Assist	1	0	4
Fatty Acid Liquesence	1	0	#N/A
Mitochondrial & Energy Assist	8.89	0	0
Gastrogest	11.5	#N/A	0
ACAT Assist	11.5	#N/A	0
Adenosyl-Cobalamin B12 Assist	11.5	0	5

The ACAT Gene may be one of the most important, as it supports the conversion of fats and proteins into Acetyl-CoA. This may be one of the first variants to support, as it slows the production of ATP from the Citric Acid Cycle. Checking the Fatty Acid Metabolism Markers in a Urine Organic Acid test may verify how serious of a problem ACAT is creating.

Unfortunately, this person has two variants in the most clinically significant ACAT gene. This may likely be one of the most important things you address with them. It is recommended to do the Urine Organic Acids test to see how this is impacting fats, protein and the citric acid cycle.

This variant will likely need lifetime support.

There are seven variants in the ACAT enzyme. If the variant is the first one listed, the ACAT1-02, then support for ACAT is needed. This is the most significant SNP for ACAT. If there are no variants in ACAT1-02 but seven other variants, support may be needed.

If you want to find out if these SNPs are impacting the utilization of fats and proteins, run the Genova Urine Organic Acids, and see if the markers for fat usage and protein usage indicate a problem.

Product Name	SNP Total	Lab Total	Symptoms
ACAT Assist	11.5	#N/A	0
Carb Assist	0	0	3

The protein encoded by this gene modulates the cellular levels of lactate and pyruvate.

Pyruvate is the end product of glycolysis, which is then converted into acetyl coA that enters the Krebs cycle when there is sufficient oxygen present. When the oxygen is insufficient, pyruvate is broken down anaerobically, creating lactate.

Lactate is produced by almost all tissues in the body, with the highest level of production found in muscle tissues. Under normal conditions, lactate is rapidly cleared by the liver.

Variants in this gene may lead to metabolic myopathy and exercise-induced hyperinsulinemic hypoglycemia.



ACSL1		
ACSL1 (rs9997745)		GG 73.0%
ACSL1 (rs4862417)	1	AG 37.8%
ACSL1 (rs13120078)	1	GA 44.6%
ACSL1 (rs12503643)		GG 34.9%
ACSL1 (rs41278587)		GG 94.7%
ACSL1 (rs6552828)	1	AG 48.0%
ACSL1 (rs72695682)		CC 90.3%
ACSL1 (rs72695685)		TT 86.3%
ACSL1	81%	
TALDO1		
TALDO1 C749776T (rs11246300)		CC 62.8%
TALDO1	100%	
OGDH		
OGDH (rs142839706)		GG 96.8%
OGDH (rs17133537)	1	TC 49.5%
OGDH (rs740094)	1	GA 49.2%
OGDH (rs2268308)		CC 92.1%
OGDH (rs757702)		GG 92.3%
OGDH (rs10951768)		GG 83.9%
OGDH (rs799434)	2	CC 80.9%
OGDH (rs12155014)		TT 84.7%
OGDH (rs10247064)		CC 84.4%
OGDH (rs710887)	2	CC 47.8%
OGDH (rs3735474)		AA 83.9%
OGDH (rs3801401)		CC 94.3%
OGDH (rs7805156)		CC 93.2%
OGDH (Alpha-Ketoglutarate to Succinyl-CoA and CO2)	77%	
PDHB		
PDHB (rs28933391)		GG 100.0%
PDHB (rs28935769)		TT 100.0%
PDHB	100%	

Product Name	SNP Total	Lab Total	Symptoms
Fatty Acid Assist	1	0	4
A-L-O Formula	0	#N/A	#N/A

The protein encoded by this gene is an isozyme of the long-chain fatty-acid-coenzyme A ligase family. Although differing in substrate specificity, subcellular localization, and tissue distribution, all isozymes of this family convert free long-chain fatty acids into fatty acyl-CoA esters, and thereby play a key role in lipid biosynthesis and fatty acid degradation.

At this time, no particular SNPs have been specifically identified as having the greatest impact on lipids, so these genes are added for general information and may mean that more weight should be given to ACAT or carnitine issues when these genes have high amounts of variants.

If there are many variants, be aware of fat utilization impairments.

Product Name	SNP Total	Lab Total	Symptoms
A-L-O Formula	0	#N/A	#N/A

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.

In our Phase II Lyme study, we found that variants in TALDO1 were much higher in patients with Lyme Disease

Product Name	SNP Total	Lab Total	Symptoms
Pro Alpha Ketoglutarate Plus	0	#N/A	#N/A

OGDH or Oxoglutarate (Alpha-Ketoglutarate) Dehydrogenase (Lipoamide) encodes one subunit of the 2-oxoglutarate dehydrogenase complex. This complex catalyzes the overall conversion of alpha-ketoglutarate to succinyl-CoA and CO2.

Studies have shown that variants in OGDH lead to hypotonia, metabolic acidosis, and hyperlactatemia.

Product Name	SNP Total	Lab Total	Symptoms
ACAT Assist	11.5	#N/A	0

PDHB catalyzes the overall conversion of pyruvate to acetyl-CoA and CO2 and provides the primary link between glycolysis and the tricarboxylic acid (TCA) cycle.

PDK4		
PDK4 (rs2073978)	1	CT 46.0%
PDK4 (rs10247649)	1	GA 46.3%
PDK4 (rs4729201)	1	GA 49.3%
PDK4 (rs17626204)		CC 93.7%
PDK4 (rs12668651)		TT 51.4%
PDK4 (rs3779478)		AA 85.6%
PDK4 (rs9791957)	1	GT 44.3%
<b>PDK4</b>	<b>71%</b>	

Product Name	SNP Total	Lab Total	Symptoms
ACAT Assist	11.5	#N/A	0

PDK4 is a member of the PDK/BCKDK protein kinase family and encodes a mitochondrial protein with a histidine kinase domain located in the matrix of the mitochondria. PDK4 inhibits the pyruvate dehydrogenase complex by phosphorylating one of its subunits. This inhibits pyruvate dehydrogenase activity, and thereby regulates metabolite flux through the tricarboxylic acid cycle.

Inhibition of pyruvate dehydrogenase decreases glucose utilization and increases fat metabolism in response to prolonged fasting and starvation. This also plays an important role in maintaining normal blood glucose levels under starvation.

## Electron Transport Chain

The electron transport chain consists of a series of redox reactions in which electrons are transferred from a donor molecule to an acceptor molecule.

Each electron donor passes electrons to a more electronegative acceptor. The electronegative acceptor then donates these electrons to another acceptor until the electrons are passed to oxygen, the most electronegative and terminal electron acceptor in the electron transport chain. Passage of electrons between donor and acceptor releases energy, which is used to generate a proton gradient across the mitochondrial membrane by “pumping” protons into the intermembrane space. The resulting proton gradient is used to make ATP via ATP synthase.

NADH → Complex I → Q → Complex III → cytochrome c → Complex IV → O<sub>2</sub>

Complexes I, III and IV are the proton pumps, while Q and cytochrome c are mobile electron carriers.

Gene Name	Variants	Metrics
<b>Complex I</b>		
<b>Complex I Total</b>	<b>56%</b>	

Product Name	SNP Total	Lab Total	Symptoms
Mitochondrial & Energy Assist	8.89	0	0
Pro NADH	5.39	0	2

NDUFA1, NDUFA, NDUFA, NDUFA5, NDUFA6, NDUFA8, NDUFA9, NDUFA10, NDUFA11, NDUFA12, NDUFAB1, NDUFB1, NDUFB2, NDUFB4, NDUFB5, NDUFB6, NDUFB7, NDUFB8, NDUFB9, NDUFB10, NDUFB11, NDUFC1, NDUFC2, NDUFS1, NDUFS2, NDUFS3, NDUFS4, NDUFS5, NDUFS6, NDUFS7, NDUFS8, NDUFV2, and NDUFV3 encode proteins that are part of the subunits for Complex I. All SNPs related to encoding Complex I can be found in the Gene Report. All Enzymes related to encoding Complex I can be found in the Enzyme Report.

Complex I is the first enzyme of the mitochondrial electron transport chain. Complex I is also the largest and most complicated enzyme of the electron transport chain. There are over 40 subunits found in Complex I. Complex I translocates four protons across the inner membrane per molecule of oxidized NADH, helping to build the electrochemical potential difference used to produce ATP.

Variations in these genes may cause Complex I to be deficient.

Complex II			
SDHA (rs142441643)		CC 100.0%	<p>SDHA, SDHB, and SDHC encode proteins that are part of the subunits for Complex II.</p> <p>Complex II is the only enzyme that participates in both the citric acid cycle and the electron transport chain.</p> <p>Complex II is composed of four subunits.</p> <p>In the citric acid cycle, Complex II catalyzes the oxidation of succinate to fumarate with the reduction of ubiquinone to ubiquinol.</p> <p>In the electron transport chain, Complex II binds succinate and a hydride which is then transferred to FAD to generate FADH2 and fumarate.</p> <p>The final step of Complex II is to transfer 2 electrons to coenzyme Q to produce CoQH2.</p> <p>Variations in these genes may cause Complex 2 to be deficient.</p>
SDHA (rs6555059)		GG 6.9%	
SDHB (rs2871775)	2	GG 30.8%	
SDHB (rs978528)	1	CT 19.7%	
SDHB (rs33927012)		AA 97.7%	
SDHB (rs7550829)		CC 81.2%	
SDHB (rs4920653)		TT 55.0%	
SDHB (rs732679)	2	TT 40.5%	
SDHB (rs2295059)	2	AA 28.9%	
SDHB (rs2647145)		TT 68.4%	
SDHC (rs4272646)		AA 79.8%	
SDHC (rs9330294)		CC 87.9%	
SDHC (rs11585941)		AA 79.7%	
SDHC (rs12140361)		TT 94.2%	
Complex II Total	75%		
SDHA	100%		
SDHB	56%		
SDHC	100%		

Complex III		
CYC1 (rs2070688)		TT 97.3%
UQCR10 (rs16988025)	1	CT 14.8%
UQCR10 (rs112717334)		AA 100.0%
UQCR10 (rs201266199)		TT 100.0%
UQCRB (rs35895613)		AA 100.0%
UQCRC2 (rs117955262)		TT 86.5%
UQCRC2 (rs11648723)		GG 90.7%
UQCRC2 (rs4850)		GG 89.7%
UQCRFS1 (rs8109749)	2	GG 83.8%
UQCRH (rs41292543)		AA 80.7%
UQCRH (rs11588062)	1	CT 36.4%
UQCRH (rs4660920)	1	GC 36.5%
UQCRQ (rs11544803)		CC 100.0%
Complex III Total	81%	
CYC1	100%	
UQCR10	83%	
UQCRB	100%	
UQCRC2	100%	
UQCRFS1	0%	
UQCRH	67%	
UQCRQ	100%	

CYC1, UQCR10, UQCRB, UQCRC2, UQCRFS1, UQCRH, and UQCRQ encode proteins that are part of the subunits for Complex III.

Complex III is composed of 11 subunits.

Complex III passes the electrons from CoQH2 to cytochrome c through a very unique electron transport pathway called the Q-cycle.

In the Q cycle, two protons are consumed from the matrix, four protons are released into the inter membrane space, and two electrons are passed to cytochrome c.

Variations in Complex III can cause exercise intolerance.

Complex IV		
COX4I1 (rs2733954)		TT 61.5%
COX4I2 (rs119455950)		GG 100.0%
COX5A (rs8042694)	2	AA 46.8%
COX5B (rs41280591)		TT 100.0%
COX6A2 (rs12240)		GG 85.6%
COX6B1 (rs7254601)	1	AG 37.3%
COX6C (rs4626565)		TT 66.1%
COX7A1 (rs753420)	1	TG 40.7%
COX7A2 (rs75996601)		GG 94.4%
COX7B2 (rs4395475)	1	TC 22.2%
COX7B2 (rs4478161)	1	TC 45.2%
COX7B2 (rs6447514)	2	GG 36.9%
COX7B2 (rs11726563)	1	AC 23.9%
COX7B2 (rs12511771)	1	GA 41.8%
COX7B2 (rs13119057)	1	CT 36.1%
COX7C (rs13167616)		GG 94.9%
Complex IV Total	66%	
COX4I1	100%	
COX4I2	100%	
COX5A	0%	
COX5B	100%	
COX6A2	100%	
COX6B1	50%	
COX6C	100%	
COX7A1	50%	
COX7A2	100%	
COX7B2	42%	
COX7C	100%	

COX4I1, COX4I2, COX5A, COX5B, COX6A2, COX6B1, COX6C, COX7A1, COX7A2, COX7B2, and COX7C encode proteins that are part of the subunits for Complex IV.

Complex IV is composed of 14 subunits.

Complex IV is the last enzyme in the respiratory electron transport chain of mitochondria.

Complex IV receives an electron from each of four cytochrome c molecules, and transfers them to one oxygen molecule, converting molecular oxygen to two molecules of water.

Variations in these genes may cause Complex IV to be deficient.

Complex V		
ATP5A1 (rs8089150)	2	GG 18.8%
ATP5A1 (rs7244921)	2	CC 18.1%
ATP5B (rs11542644)		CC 100.0%
ATP5C1 (rs1244414)		CC 78.4%
ATP5E (rs6026648)		GG 100.0%
ATP5H (rs148887046)		GG 100.0%
ATP5F1 (rs12040764)		TT 55.4%
ATP5F1 (rs1264898)		GG 35.6%
ATP5F1 (rs1264897)		CC 35.2%
ATP5G2 (rs12422531)		CC 75.4%
ATP5G3 (rs36089250)		TT 99.8%
ATP5G3 (rs1802622)		CC 100.0%
ATP5G3 (rs8106)		AA 88.4%
ATP5H (rs10512598)		GG 87.7%
ATP5H (rs4435292)	1	CT 42.6%
ATP5H (rs1466681)		AA 83.3%
ATP5O (rs2834297)		TT 27.2%
ATPIF1 (rs8559)	1	AG 46.1%
ATP5A1	0%	
ATP5B	100%	
ATP5C1	100%	
ATP5E	100%	
ATP5F1	100%	
ATP5G2	100%	
ATP5G3	100%	
ATP5H	88%	
ATP5O	100%	
ATPIF1	50%	
Complex V Total	83%	

ATP5A1, ATP5B, ATP5C1, ATP5E, ATP5F1, ATP5G2, ATP5G3, ATP5H, ATP5O, and ATPIF1 encode proteins that are part of the subunits for mitochondrial ATP synthase.

Complex V is composed of 2 main subunits.

ATP synthase is an important enzyme that creates the energy storage molecule adenosine triphosphate (ATP).

Variations in these genes may cause Complex V to be deficient.

## Glutathione

Glutathione (GSH) is often referred to as the body's master antioxidant. Composed of three amino acids - cysteine, glycine, and glutamic acid - glutathione can be found in every cell of the human body. The highest concentrations of glutathione are found in the skin and liver, making it critical in the body's detoxification process. Glutathione is used by the liver to detoxify many toxins including formaldehyde, acetaminophen, benzpyrene and many other compounds. It plays a key role in Phase I and Phase II detoxification reactions.

Studies have shown those with the highest glutathione live the longest. If there is insufficient glutathione, you will age prematurely, and be prone to lowered ability to

Patient: Eric Ehle

detox. Individuals with low glutathione often report an inability to tolerate strong smells and are very prone to inflammatory conditions, especially when this is combined with other variants that cause inflammation.

Glutathione is a powerful antioxidant because it neutralizes free radicals and prevents their formation. It has an important role in immune function via white blood cell production and is one of the most potent anti-viral agents known.

We all know the benefits of vitamin C, vitamin E and selenium and other antioxidants, however, it's not well known that as antioxidants donate their electron to the free radical (thus neutralizing the bad free radical), they can become a pro-oxidant and potentially cause damage. However, glutathione recharges other antioxidants so they can continue to do their job.

Glutathione easily restores them to their reduced form so they can resume the free radical scavenging activity again. It also has the amazing ability to recycle itself via the enzymes glutathione reductase (GSR).

Glutathione Accelerator has NAC and enzyme support, while GSH Assist has glycine when this is needed, or NAC is contraindicated. Nrf2 Accelerator supports the production of Glutathione. Always make sure you have supported Glutathione before giving folate.

Methionine & rarr; Homocysteine & rarr; CBS & rarr; Cystathionine & rarr; CTH + Pyridoxal 5'-phosphate & rarr; Cysteine + Glutamate & rarr; GCLM + GCLC & rarr; γ-Glu-Cys + Glycine & rarr; GSS + ATP & rarr; GSH & rarr; GLRX & rarr; GSSG & rarr; GSR & rarr; GSH

Gene Name	Variants	Metrics
<b>CTH</b>		
CTH (rs1021737)		GG 50.7%
CTH (rs6413471)		AA 88.2%
CTH (rs3767205)		GG 86.1%
CTH A11886G (rs1145920)		GG 55.1%
CTH A32114G (rs515064)	2	GG 10.8%
CTH G25229T (rs663649)	2	TT 8.3%
CTH G6010A (rs10889869)		GG 85.2%
CTH T16147C (rs12723350)		TT 86.8%
CTH T8763C (rs681475)		CC 44.5%
CTH (Total SNPs)	78%	
CTH ( Most Relevant)	100%	
<b>SHMT</b>		
SHMT1 (rs9902498)		CC 97.4%
SHMT1 (rs2273026)		CC 81.2%
SHMT1 (rs17806333)		TT 96.7%
SHMT2 (rs34095989)	2	AA 15.1%
Glycine / SHMT	75%	

Product Name	SNP Total	Lab Total	Symptoms
Glutathione Accelerator	4.39	0	3
Peroxynitrite Scavenger	4	0	2
S Acetyl Glutathione	4.39	0	3
Peroxynitrite Scavenger P.M.	4	0	2
GSH Assist	4.39	0	2
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

The CTH gene catalyzes the last step in the trans-sulfuration pathway from methionine to cysteine. Cysteine is needed for glutathione. Glutathione synthesis in the liver is dependent upon the availability of cysteine. Variants in this gene may reduce Glutathione, especially when combined with Glycine issues (SMHT) and Glutathione enzymes.

CTH + Pyridoxal 5'-phosphate & rarr; Cysteine

CTH rs1021737 has been found to be the most significant. All other CTH SNPs are included for research purposes.

With no variants on the CTH gene, Cysteine levels should be normal, as long as Homocysteine is being properly brought down the transsulfuration pathway by the CBS gene.

Product Name	SNP Total	Lab Total	Symptoms
SHMT Assist	10	1	#N/A

Glycine is one of the nutrients needed to make the master antioxidant glutathione. Since the SHMT gene is responsible for making glycine.

SHMT Assist and GSH Assist may be helpful with low glycine production.

With 1 SHMT2 variant, there is a possible glutathione deficiency due to lack of glycine, and methylation is likely impaired. 2 SHMT Assist would be recommended. Pro Cell Health is likely. However, make sure you have supported B12, if needed, before adding this.

GCL		
GCLC (rs2066509)		GG 99.0%
GCLC (rs2066511)		CC 54.7%
GCLC (rs13437395)		TT 84.5%
GCLC (rs2277108)		GG 83.4%
GCLC (rs34925335)		GG 100.0%
GCLC (rs642429)		TT 74.9%
GCLC (rs574389)	1	CT 49.0%
GCLC (rs742529)		AA 98.1%
GCLC (rs553822)	1	TC 48.0%
GCLC (rs617066)		GG 60.0%
GCLC (rs761141)		CC 60.3%
GCLC (rs1555906)		GG 59.5%
GCLC (rs2268327)		AA 96.3%
GCLC (rs4715407)		GG 82.9%
GCLC (rs3799696)		GG 64.8%
GCLC (rs6934367)		GG 82.9%
GCLC (rs502862)	1	TC 48.4%
GCLC (rs2284650)		AA 88.5%
GCLM (rs3827715)	1	TC 38.0%
GCLM (rs718875)		TT 72.1%
GCLM (rs2301022)	1	CT 43.6%
GCL	88%	
GCLC	92%	
GCLM	67%	
GSS		
GSS (rs28938472)		TT 100.0%
GSS (rs6088655)	1	GA 47.5%
GSS A18836C (rs2273684)	1	TG 49.3%
GSS A5997G (rs6088659)	1	CT 27.7%
GSS G11705T (rs6060124)	1	CA 37.9%
GSS	60%	

Product Name	SNP Total	Lab Total	Symptoms
Peroxynitrite Scavenger	4	0	2
S Acetyl Glutathione	4.39	0	3
Peroxynitrite Scavenger P.M.	4	0	2
GSH Assist	4.39	0	2
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

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) also known as gamma-glutamylcysteine synthetase. GCL is composed of two subunits. These subunits include catalytic GCLC and modifier GCLM.

Glutamate + Cysteine → GCLM + GCLC → γ-Glu-Cys + Glycine

Product Name	SNP Total	Lab Total	Symptoms
Glutathione Accelerator	4.39	0	3
Peroxynitrite Scavenger	4	0	2
S Acetyl Glutathione	4.39	0	3
Peroxynitrite Scavenger P.M.	4	0	2
GSH Assist	4.39	0	2
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

The protein encoded by GSS catalyzes the second step of glutathione biosynthesis. This step is the ATP-dependent conversion of gamma-L-glutamyl-L-cysteine to glutathione.

γ-Glu-Cys + Glycine → GSS + ATP → GSH



GLRX		
GLRX (rs4561)	1	AG 48.2%
GLRX (rs3777209)		TT 90.0%
GLRX	75%	
GSR		
GSR (rs201693439)		GG 100.0%
GSR (rs8190996)	1	GA 49.3%
GSR (rs3779647)	1	CT 49.3%
GSR (rs2978663)	1	TC 46.9%
GSR (rs2978662)	1	AG 30.8%
GSR (rs2911670)		CC 87.9%
GSR (rs17557435)	1	TC 20.6%
GSR (rs2551698)		AA 85.8%
GSR (rs8190898)		CC 97.8%
GSR (rs8190893)		CC 87.2%
GSR A43851G (rs2551715)	1	CT 47.3%
GSR	73%	

Product Name	SNP Total	Lab Total	Symptoms
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

GLRX catalyzes the reversible reduction of GSH to GSSG.

GSH &rarr; GLRX &rarr; GSSG

Product Name	SNP Total	Lab Total	Symptoms
S Acetyl Glutathione	4.39	0	3
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

GSR is a central enzyme in cellular antioxidant defense, and reduces oxidized glutathione disulfide (GSSG) to GSH.

GSSG &rarr; GSR &rarr; GSH

GSTs																																																		
GSTM1 (rs1056806)		CC 87.8%																																																
GSTP1 A114V (rs1138272)		CC 84.7%																																																
GSTP1 I105V (rs1695)		AA 44.0%																																																
<table border="1"> <thead> <tr> <th>GSTs Total</th> <th>90%</th> <th></th> </tr> </thead> <tbody> <tr><td>GSTA1</td><td>100%</td><td></td></tr> <tr><td>GSTA2</td><td>100%</td><td></td></tr> <tr><td>GSTA3</td><td>90%</td><td></td></tr> <tr><td>GSTA4</td><td>68%</td><td></td></tr> <tr><td>GSTA5</td><td>75%</td><td></td></tr> <tr><td>GSTK1</td><td>100%</td><td></td></tr> <tr><td>GSTM1</td><td>97%</td><td></td></tr> <tr><td>GSTM2</td><td>100%</td><td></td></tr> <tr><td>GSTM3</td><td>83%</td><td></td></tr> <tr><td>GSTM4</td><td>100%</td><td></td></tr> <tr><td>GSTM5</td><td>100%</td><td></td></tr> <tr><td>GSTO1</td><td>100%</td><td></td></tr> <tr><td>GSTO2</td><td>75%</td><td></td></tr> <tr><td>GSTP1</td><td>100%</td><td></td></tr> <tr><td>GSTT1</td><td>100%</td><td></td></tr> </tbody> </table>			GSTs Total	90%		GSTA1	100%		GSTA2	100%		GSTA3	90%		GSTA4	68%		GSTA5	75%		GSTK1	100%		GSTM1	97%		GSTM2	100%		GSTM3	83%		GSTM4	100%		GSTM5	100%		GSTO1	100%		GSTO2	75%		GSTP1	100%		GSTT1	100%	
GSTs Total	90%																																																	
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GSTT1	100%																																																	

Product Name	SNP Total	Lab Total	Symptoms
Glutathione Accelerator	4.39	0	3
Peroxynitrite Scavenger	4	0	2
S Acetyl Glutathione	4.39	0	3
Peroxynitrite Scavenger P.M.	4	0	2
GSH Assist	4.39	0	2
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

GSTs include the following classes:

A- (alpha-), P- (pi-), M- (mu-), O- (omega), T- (theta), and Z - (Zeta)

These genes encode enzymes that add glutathione to target electrophilic compounds such as therapeutic drugs, environmental toxins, and products of oxidative stress. This action is an important step in detoxification of these compounds.

All the GST SNPs can be found in the Gene Report.

The enzymes GSTA1, GSTA2, GSTA3, GSTA4, GSTA5, GSTK1, GSTM1, GSTM2, GSTM3, GSTM4, GSTM5, GSTO1, GSTO2, GSTP1, GSTT1, and GSTZ1 can all be found in the Enzyme Report.

Patient: Eric Ehle

GSTZ1	79%	
<b>TALDO1</b>		
TALDO1 C749776T (rs11246300)		
		CC 62.8%
TALDO1	100%	

Product Name	SNP Total	Lab Total	Symptoms
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

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.

## Detoxification Capacity - SOD, (Phase 2 Liver Detox) and CYP (Phase 1 Liver Detox)

SOD (Superoxide Dismutase), CYP (cytochrome P-450) and PON1 represent the body's ability to neutralize free radicals and to detox properly. The more variants here, the less ability to deal with free radicals, which may increase inflammation, aid in the eventual breaking down of the body, and lower the ability to clear toxins. After supporting the gut and ATP production, supporting the neutralizing of free radicals and detoxifying may be the next most important part of the body to support.

Superoxide Dismutase turns the free radical Superoxide into H2O2, which is then turned into water and oxygen by glutathione and catalase. If SOD does not neutralize the free radical, it combines with nitric oxide and creates the very strong oxidizing agent peroxynitrite.

If there is low glutathione, and folate is given, the folate can stimulate Phase 1 detox but overwhelm Phase 2. This can cause inflammation. This is why many people have negative reactions to folate, even when they have MTHFR and folate deficiency. Always make sure you have adequately supported Phase 2 Liver Detox before proceeding with folate.

Variants in PON1 will reduce the ability to clear herbicides and pesticides, further straining glutathione levels.

Gene Name	Variants	Metrics
<b>Detox Ability - SOD</b>		
SOD2 (rs2758331)		
	1	CA 49.4%
SOD2 A16V (rs4880)		
	1	AG 49.5%
SOD3 (rs2855262)		
	2	CC 41.3%
<b>SOD</b>		
	33%	

Product Name	SNP Total	Lab Total	Symptoms
Pro SOD/Catalase Support	7.33	0	2
Nutrition & Anti-Oxidant Accelerator	7.67	#N/A	2

The free radical Super Oxide, may be created 5% of the time when the cells create ATP, and is made in large quantities with NOS uncoupling, and thus making the very dangerous oxidizing agent Peroxynitrite. Since inflammation may be one of the major causes of premature aging and disease, controlling the superoxide free radical is critical. Superoxide Dismutase turns the superoxide free radical into H2O2, so glutathione and catalase can turn them into water and oxygen. The SOD2 genes make superoxide dismutase (SOD) inside the cells, while SOD3 make the SOD outside the cells. Nutrition & Anti-Oxidant Accelerator supports the production of SOD, while Pro SOD/Catalase contains the actual enzymes in a capsule that only opens in the intestinal tract.

With 4 SOD variants, Nutrition & Anti-Oxidant Accelerator will likely not be enough superoxide dismutase protection. Consequently, use 3 Nutrition & Anti-Oxidant Accelerator capsules and at least 2 Pro SOD/Catalase. This can be increased to 3 if there are other factors that increase the peroxynitrite. Pro SOD will be a permanent supplement for this individual. Nrf2 Accelerator would also be likely needed.

Catalase		
CAT (rs1049982)	2	CC 42.7%
CAT (rs11032703)		CC 83.6%
CAT (rs2300181)	1	CT 37.8%
CAT (rs480575)		AA 48.9%
CAT (rs494024)	2	CC 39.3%
CAT (rs484214)		AA 49.2%
CAT (rs17881734)		GG 97.2%
CAT (rs2284369)		AA 58.3%
CAT (rs1408036)		AA 80.5%
CAT (rs769218)		GG 58.2%
CAT (rs17881288)		AA 97.3%
CAT (rs7933285)	1	CT 37.7%
CAT (rs2073058)	1	AG 37.8%
CAT (rs12273124)	1	AG 10.0%
CAT (rs769217)		CC 58.2%
CAT (rs17881586)		GG 96.6%
CAT (rs511895)	2	CC 39.2%
CAT (rs10488736)	2	TT 9.4%
CAT	67%	

Product Name	SNP Total	Lab Total	Symptoms
Pro SOD/Catalase Support	7.33	0	2

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.

Studies have hypothesized that oxidative stress plays a role in the development of many chronic or late-onset conditions such as diabetes, asthma, Alzheimer's disease, and rheumatoid arthritis.

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.

SULT		
SULT1A1 (rs36043491)		CC 99.7%
SULT1A1 (rs60749306)		TT 99.9%
SULT1A1 (rs35728980)		TT 52.8%
SULT1A1 (rs35497673)		GG 100.0%
SULT1A1 (rs4149394)		CC 56.7%
SULT1A1 (rs4149393)		AA 55.6%
SULT1A1 (rs2925628)		TT 47.9%
SULT1A1 (rs141343888)		GG 100.0%
SULT1A1 (rs60701883)		CC 100.0%
SULT1A1 (rs11639918)		TT 100.0%
SULT1A1 (rs4149378)		GG 100.0%
SULT1A1 (rs72483420)		TT 88.8%
SULT1A1 (rs7192559)		CC 98.6%
SULT1A1 (rs79527462)		CC 99.6%
SULT1A1 (rs2411453)		GG 38.5%
SULT1A1 (rs8049739)		GG 100.0%
SULT1A1 (rs7189373)		AA 100.0%
SULT1A1 (rs7500452)		TT 100.0%
SULT1A1 (rs4149385)		CC 99.9%
SULT1A1 (rs4149381)		TT 94.5%
SULT1A1 (rs1042157)		GG 43.4%
SULT1C3 (rs112050262)		GG 97.6%
SULT1C3 (rs201793819)		GG 100.0%
SULT1C3 A108878711G (rs1470874)	1	GA 44.3%
SULT1C3 C13545841T (rs13392744)		CC 87.9%
SULT1C3 G535A (rs2219078)		GG 62.5%
SULT1C3 M194T (rs6722745)		TT 49.6%
SULT2A1 (rs296364)	1	AG 49.3%
SULT2A1 (rs11569680)		TT 100.0%
SULT2A1 (rs11083907)		GG 99.5%
SULT2A1 A20117G (rs296366)	1	CT 34.9%
SULT2A1 G17136A (rs4149452)		CC 53.4%
SULT2A1 G781A (rs11569679)		CC 99.5%
SULT2A1 G9598T (rs2547231)	1	AC 26.5%
SULT2A1 G9696A (rs4149449)		CC 78.3%
SULT1A1	100%	
SULT1C3	92%	
SULT2A1	81%	

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 varied SULT SNPs may have slowed detoxification and may be sensitive to toxins, hormones, xenobiotics, and heavy metals.

Nrf2			Product Name	SNP Total	Lab Total	Symptoms
			Nrf2 Accelerator	4	0	2
NFE2L2 (rs10183914)		CC 44.0%	The NFE2L2 gene has major involvement in the defense against oxidative stress in vitro and in vivo. The NFE2L2 gene encodes a transcription factor that 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.			
NFE2L2 (rs2001350)		TT 80.7%				
NFE2L2 (rs6726395)	2	GG 30.8%	Under normal conditions, Nrf2-dependent transcription is repressed by a negative regulator Keap1. When cells are exposed to oxidative stress, or electrophiles, Nrf2 escapes Keap1-mediated repression and activates ARE to maintain cellular redox homeostasis.			
NFE2L2 (rs1962142)		GG 80.3%				
NFE2L2 (rs1806649)		CC 58.0%	NQO1 is a cytosolic enzyme that catalyzes the two or four electron reduction of many environmental quinones using flavin adenine dinucleotide (FAD) as a cofactor.			
NFE2L2 (rs2364722)		AA 47.2%				
NFE2L2 (rs2886161)		TT 47.3%	NQO1 is expressed in many tissues, and its expression is regulated by the antioxidant response element both in basal and during oxidative stress conditions.			
KEAP1 (rs11085735)		CC 86.7%				
KEAP1 (rs8113472)		CC 83.1%	This enzyme is generally considered to be a detoxification enzyme due to its ability to diminish reactive quinones and quinoneimines to its less reactive and less toxic hydroquinones forms and because of its response to antioxidants, xenobiotics, electrophiles, heavy metals, and radiations.			
KEAP1 (rs9676881)		GG 38.2%				
NQO1 (rs1063556)		AA 100.0%	The enzyme encoded by GSTA2 plays a role in the detoxification of electrophilic compounds, including environmental toxins, and products of oxidative stress, by conjugation with glutathione.			
NQO1 (rs1050873)		TT 100.0%				
NQO1 (rs3191214)		GG 100.0%	Variations in this gene can change an individual's susceptibility to toxins.			
NQO1 (rs117363962)		CC 98.2%				
NQO1 (rs141820737)		CC 100.0%	The enzyme encoded by GSTA2 also exhibits glutathione peroxidase activity and thereby protects the cells from reactive oxygen species and the products of peroxidation.			
NQO1 (rs1131341)		GG 92.5%				
NQO1 (rs35572901)		GG 99.5%				
NQO1 C494+ (rs10517)		GG 74.0%				
NQO1 C609T (rs1800566)		GG 64.8%				
NQO1 G13070C (rs689452)		GG 75.7%				
NQO1 G13161A (rs689453)		CC 85.8%				
NQO1 G13528A (rs34755915)		CC 97.0%				
NQO1 T6314C (rs2917669)		GG 75.3%				
NQO1 T7706C (rs1437135)		AA 64.6%				
GSTA2 (rs1803682)		CC 100.0%				
GSTA2 (rs60332313)		TT 100.0%				
GSTA2 (rs2234951)		GG 92.8%				
GSTA2 (rs142078893)		CC 100.0%				
GSTA2 (rs2608632)		GG 49.4%				
NFE2L2	86%					
NQO1	100%					
GSTA2	100%					
Nrf2 Total	96%					
KEAP1	100%					

Detox Ability - CYP		
CYP1A1 (rs4986883)		TT 99.9%
CYP1A1*2C A4889G (rs1048943)	1	TC 8.6%
CYP1A1*4 C2453A (rs1799814)		GG 91.4%
CYP1A2 C164A (rs762551)	2	AA 50.2%
CYP1B1 L432V (rs1056836)	1	CG 48.0%
CYP1B1 R48G (rs10012)	1	GC 66.5%
CYP1B1 N453S (rs1800440)		TT 67.7%
CYP2A6*2 A1799T (rs1801272)		AA 95.1%
CYP2C19 (rs12248560)		CC 62.4%
CYP2C9*3 A1075C (rs1057910)	1	AC 11.8%
CYP2C9*2 A C430T (rs1799853)		CC 76.9%
CYP2D6 T100C (rs1065852)	1	GA 34.6%
CYP2D6 (rs1135840)	1	GC 46.1%
CYP2D6 T2850C (rs16947)		GG 45.5%
CYP2E1*1B A10023G (rs55897648)		GG 99.6%
CYP2E1*1B G9896C (rs2070676)	2	CC 75.8%
CYP2E1*4 A4768G (rs6413419)		GG 94.4%
CYP3A4*1B (rs2740574)	2	TT 91.6%
CYP3A4*3 M445T (rs4986910)		AA 98.6%
CYP - Phase 1 Liver Detox	71%	
ABP1		
ABP1 (rs10156191)	1	CT 38.0%
NSAID Sensitivity	50%	

Product Name	SNP Total	Lab Total	Symptoms
Nrf2 Accelerator	4	0	2
Detox Liquesense	5	0	1

Inside the liver cells there are sophisticated mechanisms that break down toxic substances. Every drug, artificial chemical, pesticide, and hormone is broken down by enzyme pathways inside the liver cells.

Many of the toxic chemicals that enter the body are fat-soluble, which means they dissolve only in fatty or oily solutions and not in water. This makes them difficult for the body to excrete. The body's primary defense against metabolic poisoning is carried out by the liver. The liver has two mechanisms designed to convert fat-soluble chemicals into water soluble chemicals so that they may then be easily excreted from the body via watery fluids such as bile and urine.

There are two detoxification pathways inside the liver cells, which are called the Phase 1 and Phase 2 detoxification pathways. Phase one detoxification consists of oxidation reduction and hydrolysis. Phase one detoxification is catalyzed by enzymes referred to as the cytochrome P450 enzyme. These enzymes reside on the membrane system of the liver cells (called Hepatocytes). Human liver cells possess the genetic code for many isoenzymes of P-450 whose synthesis can be induced upon exposure to specific chemicals. This provides a mechanism of protection from a wide variety of toxic chemicals.

This pathway converts a toxic chemical into a more harmful chemical. This is achieved by various chemical reactions (such as oxidation, reduction and hydrolysis), and during this process free radicals are produced which, if excessive, can damage the liver cells. Antioxidants (such as vitamin C and E and natural carotenoids) reduce the damage caused by these free radicals. If antioxidants are lacking and toxin exposure is high, toxic chemicals become far more dangerous.

The more CYP variants, the more difficulty there may be in detoxification of toxins and drugs.

We may develop a supplement to support CYP, but in the meantime if there are many variants, support Nrf2 and glutathione.

Non-steroidal anti-inflammatory drugs (NSAIDs) are the drugs most frequently involved in hypersensitivity drug reactions. Histamine is released in the allergic response to NSAIDs and is responsible for some of the clinical symptoms.

Studies have shown that individuals with variants in SNP rs10156191 have a hypersensitivity to NSAIDS.

With 1 variant this individual may be hypersensitive to NSAIDS.

PON1 - Paraoxonase		
PON1 Q192R (rs662)		TT 48.5%
PON1 (rs854555)	2	CC 40.6%
PON1 (rs3917550)		GG 76.8%
PON1 (rs3917548)		AA 88.4%
PON1 (rs3917542)		CC 60.5%
PON1 (rs2074354)		GG 79.5%
PON1 (rs854561)	2	TT 12.8%
PON1 (rs3917498)		GG 42.9%
PON1 (rs2272365)		AA 71.6%
PON1 (rs2049649)		AA 44.9%
PON1 (rs2299260)		TT 66.9%
PON1 (rs2299262)	1	CT 46.4%
PON1 (rs854569)	2	GG 58.7%
PON1 (rs2237584)	1	CT 13.3%
PON1 (rs3917478)		TT 79.4%
PON1 (rs854566)	2	GG 66.5%
PON1 (Single Most Relevant)	100%	
PON1 ( All Genes)	75%	

Product Name	SNP Total	Lab Total	Symptoms
PON1 Assist	0	0	0
Addex	0	#N/A	0

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.

Consider using Addex Homeopathic Spray and PON1 Assist for those with this genetic variant.

Although there are no PON1 rs662 variants, if there are many others, support may be needed. It is unknown how the other PON1 variants may impact detoxification.



NAT Genes		
NAT1 (rs4986782)		GG 96.3%
NAT1 (rs7017402)	2	GG 76.8%
NAT1 (rs11203943)		GG 81.5%
NAT1 (rs4921581)	2	GG 45.3%
NAT1 (rs13253389)	2	GG 42.8%
NAT1 (rs17693103)		GG 71.9%
NAT1 (rs9325827)		TT 71.8%
NAT1 (rs6586714)		AA 6.2%
NAT1 (rs17126350)		AA 86.5%
NAT1 (rs8190837)		AA 82.8%
NAT1 (rs8190844)		CC 97.8%
NAT1 (rs8190845)		GG 72.2%
NAT1 (rs8190847)		GG 94.2%
NAT1 (rs4987076)		GG 94.2%
NAT1 (rs4986990)		GG 94.3%
NAT1 (rs4986783)		TT 94.2%
NAT1 (rs56172717)		AA 99.4%
NAT1 (rs15561)	2	CC 51.9%
NAT1 (rs4986993)	2	GG 52.0%
NAT2 (rs11780272)	1	TC 47.8%
NAT2 (rs2087852)	1	AG 41.1%
NAT2 (rs1390358)	1	TC 47.0%
NAT2 (rs2410556)		TT 76.3%
NAT2 (rs1961456)		AA 48.8%
NAT2 (rs973874)	2	CC 98.7%
NAT2 (rs7832071)	1	CT 47.6%
NAT2 (rs56011192)		CC 99.3%
NAT2 (rs2552)		TT 91.5%
NAT2 C282T (rs1041983)	1	CT 44.1%
NAT2 C481T (rs1799929)	1	CT 47.8%
NAT2 G286E (rs1799931)		GG 94.1%
NAT2 I114T (rs1801280)	1	TC 64.3%
NAT2 K268R (rs1208)	1	GA 47.7%
NAT2 R197Q (rs1799930)	1	GA 41.4%
NAT2 R64Q (rs1801279)		GG 99.6%
NAT1	74%	
NAT2	66%	

Product Name	SNP Total	Lab Total	Symptoms
Nrf2 Accelerator	4	0	2

The NAT1 and NAT2 genes encode an enzyme that catalyzes the transfer of an acetyl group from acetyl-CoA to various arylamine and hydrazine substrates. This enzyme helps in the metabolism of drugs, and functions in folate catabolism.

Variations in these genes are associated with higher incidences of drug toxicity

## Folate Creation & Pathways

For the methylation cycle to work, there needs to be adequate amounts of folate. Variants along the pathway will reduce the folate in the body. In addition to many other roles in the body, folate is needed to work with B12 to convert homocysteine into methionine, so more SAMe can be made.

Before supporting folate, always make sure there is adequate B12, that the transsulfuration pathway is not going too fast and thus creating glutamate, and glutathione levels are adequate. If there is not enough B12, you can get folate trapping. If CBS is variated, you can create anxiety by making more glutamate, and if phase II (glutathione) is not adequate, the folate can stimulate Phase I and cause inflammation. It is usually best to add folate LAST, after inflammation, CBS, and B12

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is properly addressed.

FOLR -> DHFR -> DHF (dihydrofolic acid) -> DHFR -> THF (tetrahydrofolic acid) -> MTHFD1 -> 10-FORMYL THF -> MTHFD1 -> 5-10 Methenyl THF (a form of tetrahydrofolate) MTHFD1 -> 5-10 Methenyl THF (a form of tetrahydrofolate) -> MTHFD1 -> 5-10 Methylene THF (the substrate used by the enzyme methylenetetrahydrofolate reductase to generate 5-methyltetrahydrofolate) - MTHFR -> 5 -MTHF

Gene Name	Variants	Metrics
<b>Folate Receptor Sites</b>		
FOLR1 (adult) (rs2071010)		GG 88.1%
FOLR2 (fetal) (rs651933)	1	GA 49.0%
FOLR3 (gamma) (rs7925545)	1	AG 8.8%
SLC19A1 (rs1051266)		TT 18.7%
<b>Folate Assimilation</b>		
	75%	
<b>DHFR</b>		
DHFR (rs1643649)	1	TC 38.7%
DHFR (rs1650697)	2	GG 55.7%
DHFR (rs865646)	1	GT 42.9%
DHFR A20965G (rs1643659)	1	TC 38.7%
DHFR C19483A (rs1677693)	1	GT 38.7%
DHFR	40%	
<b>MTHFR</b>		
MTHFD1 C105T (rs1076991)	2	CC 21.1%
SHMT2 (rs34095989)	2	AA 15.1%
MTHFS (rs6495446)	1	CT 38.2%
MTHFR A1298C (rs1801131)		TT 47.7%
MTHFR C677T (rs1801133)	1	GA 45.2%
MTHFR (C677T & A1298C)	75%	
<b>Overall Folate</b>		
	50%	

Product Name	SNP Total	Lab Total	Symptoms
Detox Accelerator	5	0	0
Methylation Assist Liquescence	5.66	1	12

Folate plays many critical roles in the body, and the first step of folates is the folate receptor sites. Variants in the folate receptor sites will likely reduce the amount of folate absorbed for usage, and increase the need for supplementation. Methylation Assist Liquescence may support the absorption of Folate.

With 2 variants, some folate supplementation may be in order, and assimilation support may be needed as well.

Product Name	SNP Total	Lab Total	Symptoms
BH4 Assist	7.81	3	14
Pro NADH	5.39	0	2

The DHFR gene is a protein coding gene. DHFR converts dihydrofolate into tetrahydrofolate. DHFR has a key role in cell growth.

Variants here will indicate the need for methyl folate and PRO NADH. BH4 Support and Glutathione Support may also be needed.

Product Name	SNP Total	Lab Total	Symptoms
BH4 Assist	7.81	3	14
Pro Bioactive Folate	5	1	0
MTHFR/BHMT Assist	9.48	1	0
MTHFR/MTR/MTRR/BHMT Assist	9.48	1	0

It is currently theorized that the C677T impacts the methionine cycle more significantly while the A1298 impacts the BH4 cycle. If this theory is correct, those with C677 would need more support in reducing Homocysteine while A1298C may need more support with creating BH4 and preventing NOS uncoupling. Nonetheless, there is usually a need for folate with these variants. However, to be sure, checking the urine organic acids can confirm, and can also be used as a measure when adequate levels are reached when supplementing.

With 1 heterozygous MTHFR variant, there is a possible need for folate, methylation, and possibly circulation support. Folate production may be about 70%. However, doing the Genova Urine Organic Acid test will verify if there is a need for folate. In some instances, they are compensating OK.

With 9 folate production variants, folate supplementation may be extremely important.

## Methionine Cycle

The Methionine Cycle takes the amino acid methionine, uses the MAT gene to make SAME. SAME is the methyl donor that gives a methyl group where it is needed for well over 100 functions. The GAMT gene takes SAME to make creatine.

After donating a methyl group and making creatine, SAME turns into SAH and then the AHCY gene turns it into homocysteine.

Variants in MTRR, MTR, BHMT, PEMT will slow the conversion of homocystine into methionine.

Gene Name	Variants	Metrics
<b>MTR (upregulation)</b>		
MTR A2756G (rs1805087)	1	AG 30.7%
MTR	50%	
<b>MTRR</b>		
MTRR A66G (b12) (rs1801394)	1	AG 48.7%
MTRR	50%	
<b>All B12 Factors</b>		
MTR A2756G (rs1805087)	1	AG 30.7%
MTRR A66G (b12) (rs1801394)	1	AG 48.7%
FUT2 (rs492602)	1	AG 49.2%
FUT2 (rs601338)	1	GA 49.0%
FUT2 (rs602662)	1	GA 49.1%
GIF (TCN3) (rs558660)	1	AG 28.6%
TCN1 (rs526934)		GG 7.5%
TCN2 C766G (rs1801198)	2	CC 31.9%
B12	50%	
<b>Choline</b>		
PEMT (rs4244593)	1	TG 48.5%
PEMT (rs4646406)	1	TA 48.9%
PEMT (rs7946)	2	TT 48.8%
Choline	33%	

Product Name	SNP Total	Lab Total	Symptoms
Pro Hydroxocobalamin	5	0	6
Methylation Assist	5	0	6

MTR combines folate, Methyl B12 and Homocysteine into Methionine. Variants in MTR are upregulations, so it tries to go faster. MTRR attaches a methyl group to B12, and variants here will slow the process. When both MTR and MTRR exist, dysfunction can occur.

With one MTR variants, the gene may be upregulated, meaning it's trying to go faster than normal. If there are MTRR variants (less methyl B12), and MTHFR variants (less folate), this process may be impaired. Make sure there is adequate folate and methyl B12 with this variant.

Product Name	SNP Total	Lab Total	Symptoms
Pro Hydroxocobalamin	5	0	6
Methylation Assist	5	0	6
Methylation Assist Liquesence	5.66	1	12

THE MTRR enzyme places a methyl group on B12 so it can be used by MTR to convert Homocysteine into Methionine. Variants here may hamper this function. When combined with other variants that impact the absorption and transport of B12, and if the MTR variant exists (which is trying to make it go faster), this function may be impaired. Supplementation with Methyl B12 is needed (Methylation Assist), unless the individual has excess methyl groups due to other variants such as GAMT and COMT.

There is one MTRR variant. This may reduce the available methyl B12, so the MTRR enzyme can covert Homocysteine into Methionine. This can be worse, if there are other B12 variants, such as GIF, TCN1 and TCN2. If there is an MTR variant (see enzyme above), this potential upregulation could exacerbate the situation.

Product Name	SNP Total	Lab Total	Symptoms
Pro Hydroxocobalamin	5	0	6
Methylation Assist	5	0	6

Variants in the FUT genes may decrease probiotics, and hence decrease the absorption of B12. The MTR variant is an upregulation, creating a higher demand for B12, while the MTRR variants reduces the ability to put methyl groups on B12, thus reducing availability of methyl B12.

GIF (gastric intrinsic factor) reduces the absorption of B12, while TCN1 and TCN2 limit the transport of B12. Any combination of higher demand, less absorption and transport will impair the functions dependent upon B12.

FUT variants may create a need for immune support as well.

With eight variants of the SNPs related to B12, supplementation is likely needed, especially if both the MTR and MTRR have variants.

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger/Calmng Formula	2.5	0	12
CBS / BHMT Assist	6.86	0	10
A-L-O Formula	0	#N/A	#N/A

Variants in PEMT can impede choline production. Choline is needed by the liver and brain. PEMT variants have been tied to fatty liver. When there are PEMT variants, use CBS/BHMT with meals. The CBS variants, especially the CBS C699T, will cause homocysteine to rush downstream too quickly, potentially causing high glutamate and ammonia.

With four variants in PEMT, there is a likely and ongoing need for choline support. CBS/BHMT Assist taken with meals provides choline and other digestive support. 2 per meal is suggested.

PNPLA3		
PNPLA3 (rs738409)		CC 57.9%
PNPLA3	100%	
BHMT		
BHMT (rs6875201)	1	AG 18.0%
BHMT R239Q (rs3733890)	1	GA 42.4%
BHMT-02 (rs567754)	1	CT 44.7%
BHMT-08 (rs651852)	1	CT 49.2%
BHMT	50%	
AHCY		
AHCY-01 (rs819147)		TT 75.4%
AHCY-19 (rs819171)		TT 75.9%
AHCY	100%	
GAMT (Creatine)		
GAMT (rs17851582)		GG 82.7%
GAMT (rs55776826)	1	CT 23.8%
GAMT (rs80338734)	1	CG 1.3%
GAMT (Creatine)	67%	
MAT Gene		
MAT1 (rs11595587)		GG 93.3%
MAT1 (rs12242871)	2	AA 29.9%
MAT1 (rs1819684)		GG 83.3%
MAT1 (rs1985908)	2	GG 11.3%
MAT1 (rs2993763)	2	AA 21.2%
MAT1 (rs4934028)	2	AA 18.9%
MAT1 (rs7081756)		GG 13.6%
MAT1 (rs756208)	2	GG 47.9%
MAT	38%	

Product Name	SNP Total	Lab Total	Symptoms
Fatty Acid Assist	1	0	4
Nrf2 Accelerator	4	0	2

Variants in this gene may cause a predisposition for fatty liver.

Variants in the BHMT gene will slow the conversion of homocysteine into methionine. Be aware of BHMT-08 as this may push the homocysteine down faster through the transsulfuration pathway, potentially causing excess glutamate, anxiety attacks, high levels of stress, high cortisol and adrenal fatigue.

With four variants in BHMT support is likely needed, especially if there are variants in BHMT-08. This variant will push the homocysteine down through transsulfuration, potentially causing high ammonia, glutamate and anxiety. Also, look at this variant in conjunction with PEMT, which makes the choline needed to be used by the BHMT enzyme to turn homocysteine into methionine.

AHCY variants slow the conversion of SAH into homocysteine with no predictable results. It may lower homocysteine and consequently glutathione, but not always. The Doctor's Data serum methylation pathway blood test is quite helpful when these variants are present. SAME and amino acids with methionine might be contraindicated and N-Acetylcysteine in Glutathione Accelerator may be helpful if cysteine blood levels are low.

With no AHCY variants, it would be likely that S-adenosylhomocysteine would convert properly to homocysteine.

Product Name	SNP Total	Lab Total	Symptoms
GAMT Assist	3.33	#N/A	0

GAMT is the gene that converts SAME and other cofactors into creatine, needed for muscle strength. Variants here could lead to muscle weakness. GAMT Assist contains Creatine in a capsule that only opens in the intestinal tract for better absorption. However, use this with caution in kidney disease and hypertension.

Creatine supplementation may be in order, especially if they report muscle weakness.

The MAT Gene turns methionine into SAME. Variants here may decrease the production of SAME and create high methionine. This can cause some serious health problems, including neurological issues. If there are a lot of variants, consider doing the Doctor's Data Methylation Plasma test. This is especially true when there are AHCY and GAMT variants as well. If there is high methionine, supporting BHMT may be contraindicated. Glycine (GSH Assist) and reducing foods high in methionine may be helpful.

With ten variants in the MAT gene, there is a chance that Methionine is not being converted effectively into SAME. To find out for sure, you may want to do the Doctors Data Blood Plasma test to measure Methionine, SAME, SAH, and Homocysteine. Glycine, and supporting ATP production may support the production of SAME. Be cautious with supporting folate, B12 and choline, because if there is high methionine, this could make their conditions worse.

## Transsulfuration Pathway

The transsulfuration pathway takes homocysteine, and pulls it down into glutathione, ammonia, cortisol, sulfites and sulfates.

If there are variants that cause less than optimal conversion of homocysteine back into methionine, and then if there are variants in the CBS genes, especially the CBS699, then homocystine can travel too fast down the transsulfuration pathway and create glutamate, which can cause stress and anxiety. Variants in the GAD genes can worsen the problem.

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CBS variants can also create excess ammonia, that can be worse if the urea cycle is less than optimal. The excess ammonia can cause mental stress, sleeping problems, and deplete the much needed BH4, needed for neurotransmitter production.

The excess glutamate can also raise cortisol levels, and eventually lead to adrenal fatigue.

To support this function, you need to support both pathways that convert homocysteine into methionine. One can use Calming Formula/Glutamate Scavenger, reducing the glutamate.

Check sulfites and sulfates to see if SUOX is overwhelmed.

Gene Name	Variants	Metrics
<b>Transsulfuration</b>		
CBS A13637G (rs2851391)		TT 22.1%
CBS C19150T (rs4920037)		GG 61.5%
CBS C699T (rs234706)		GG 45.8%
CBSA360A (rs1801181)		GG 41.3%
CTH (rs1021737)		GG 50.7%
CBS	100%	
<b>Ammonia &amp; Glutamate Production Estimates</b>		
BHMT-08 (rs651852)	1	CT 49.2%
CBS C699T (rs234706)		GG 45.8%
Potential Ammonia & Glutamate Clearing Ability	75%	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger/Calming Formula	2.5	0	12
CBS / BHMT Assist	6.86	0	10
Ammonia Scavenger	7.11	0	5

The CBS gene is similar to a brake, governor, or a dam in the river. It allows homocysteine to move down the transsulfuration pathway at an appropriate pace. Although still being researched, it is believed that some variants in CBS, and especially the CBS 699, cause the homocysteine to move down too quickly, potentially to stress SUOX, and to create excess glutamate that could create anxiety, ammonia and adrenal stress. Checking the urine sulfite and sulfate levels may give clues to what is occurring.

With no variants in the CBS genes, it is likely that homocysteine is coming down the Transsulfuration Pathway at an appropriate pace.

A possible exception may be that if the conversion of homocysteine into methionine is impaired by variants in PEMT, BHMT, MTR, MTRR and MTHFR, CBS may be overwhelmed. If these variants exist, checking homocystine levels may be in order. B6 can be used to stimulate CBS if needed.

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger/Calming Formula	2.5	0	12
CBS / BHMT Assist	6.86	0	10
Ammonia Scavenger	7.11	0	5

Estimated production of ammonia and glutamate in this calculation is based on variants in BHMT-08 and CBS 699, thus potentially creating glutamate and ammonia. Measuring sulfites and sulfates can give some clues (higher levels would go along with higher glutamate and ammonia levels). The Genova urine organic acids test can give estimates of ammonia and blood tests can measure ammonia as well. Excitability, anxiety and high cortisol levels would go along with high glutamate. Checking cortisol levels may be helpful in the assessment.

With one variant in CBS699 and BHMT-08, there is a chance for excess glutamate and ammonia from excessive Homocysteine being pulled down transsulfuration pathway. However, ammonia can also be high from a weakened Urea Cycle and digestive issues. If they present with a lot of ammonia symptoms, consider checking the Genova Urine Organic Acids.

## Neurotransmitters - Serotonin, Dopamine, Glutamate, GABA

Neurotransmitters impact many functions beside emotions. Serotonin and GABA are generally considered relaxing, while dopamine, norepinephrine and epinephrine are considered excitatory.

Variants in MAO may be sparing to serotonin, and may be helpful if there is low production due to low BH4. Variants in COMT can cause a myriad of issues, as the COMT enzyme uses methyl groups to break down dopamine, and is also involved in other detox functions. Variants in COMT has the potential to cause excess methyl groups in the body, thus negative reactions to methyl folate and methyl B12.

The GAD genes convert glutamate to GABA. If there is an overproduction of glutamate, as well as variants in GAD (especially homozygous), the patient/client may experience severe anxiety.

DAO variants may also create overexcitement in the brain, and may contribute to ammonia production as well.

BH4 is needed to create neurotransmitters. See the next page for BH4 production estimates, as low BH4 may impact neurotransmitter production.

Gene Name	Variants	Metrics
<b>MAOA</b>		
MAOA (R297R) (rs6323)	1	GT 50.0%
MAOA (rs3027397)	1	AG 48.4%
MAOA (rs2283724)	1	GA 50.5%
MAOA (rs2179098)		GG 96.6%
MAOA (rs3027407)	1	AG 38.4%
MAOA (rs1800466)		AA 99.9%
MAOA (rs2235185)	1	AG 50.0%
MAOA (rs979605)	1	AG 50.2%
MAOA (rs5905418)		AA 93.1%
MAOA (rs1803986)		GG 100.0%
MAOA (rs1800464)		AA 91.3%
MAOA (rs1800659)	1	GA 50.1%
MAOA (rs58524323)		GG 100.0%
MAOA (rs1799835)		TT 100.0%
MAOA (rs3027399)	1	GC 10.5%
MAOA A16535C (rs5906883)	1	AC 49.9%
MAOA A85020G (rs2235186)	1	AG 50.0%
MAOA C42794T (rs909525)	1	CT 50.5%
MAOA G3638A (rs5953210)	1	GA 49.9%
MAOA T1011C/1460C (rs1137070)	1	TC 50.3%
MAOA T89113C (rs2072743)	1	TC 50.7%
<b>MAOA</b>	<b>62%</b>	

MAOA is one of two neighboring gene family members that encode mitochondrial enzymes which catalyze the oxidative deamination of amines, such as dopamine, norepinephrine, and serotonin.

Variants in this gene will actually preserve serotonin. This can be helpful when there is low BH4 and poor availability of amino acids that are the precursors to high peroxynitrite.

Variations in this gene have also been associated with antisocial behavior.

<b>Dopamine</b>		
COMT (MIR4761) (rs6269)	1	AG 46.9%
COMT H62H (MIR4761) (rs4633)	1	CT 49.2%
COMT V158M (MIR4761) (rs4680)	1	GA 49.0%
COMT-61 P199P (mood swings) (rs769224)		GG 95.5%
<b>COMT</b>	<b>63%</b>	

COMT is involved in breaking down excitatory neurotransmitters and detox reactions. Click on the enzyme rating for more information.

<b>Glutamate Production Factors</b>		
BHMT-08 (rs651852)	1	CT 49.2%
CBS C699T (rs234706)		GG 45.8%
<b>Potential Glutamate Reduction Ability</b>	<b>75%</b>	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger/Calming Formula	2.5	0	12
Glutamate Scavenger II	2.06	#N/A	1

If the theory is correct that BHMT-08 and CBS699T causes Homocysteine to be converted into Glutamate, this estimate may give some clues if this needs support. Checking sulfite and sulfate urine levels, and cortisol will give additional information. Glutamate Scavenger/Calming Formula may help with the excess glutamate, SUOX Assist may be needed for supporting the sulfite to sulfate process, and Ammonia Scavenger may be needed if the urea cycle is overwhelmed and cannot clear all the ammonia. CBS/BHMT Assist will support the conversion of Homocysteine into Methionine.

There is one variant that may increase the glutamate levels. This may cause excess ammonia production, excess glutamate and higher cortisol to stress the adrenals.

GABA (Glutamate to GABA)		
GAD1 (rs3749034)		GG 59.5%
GAD1 (rs2241165)		TT 54.6%
GAD1 (rs769407)		GG 55.9%
GAD1 (rs2058725)	1	TC 37.4%
GAD1 (rs3791851)		TT 55.7%
GAD1 (rs3791850)	1	GA 36.7%
GAD1 (rs12185692)	1	CA 48.2%
GAD1 (rs3791878)	1	GT 41.0%
GAD1 (rs10432420)		GG 49.6%
GAD1 (rs3828275)	1	CT 49.7%
GAD1 (rs701492)		CC 52.5%
GAD1 (rs16858988)		GG 62.6%
GAD2 (rs2236418)		AA 64.6%
GAD2 (rs8190612)		CC 77.4%
GAD2 (rs7079102)		GG 98.2%
GAD2 (rs8190645)	1	GA 13.4%
GAD2 (rs8190646)	1	AG 16.4%
GAD2 (rs11015008)		GG 62.8%
GAD2 (rs8190650)	1	AG 16.9%
GAD2 (rs2368160)	1	GA 41.5%
GAD2 (rs7906725)	1	GA 41.5%
GAD2 (rs11015025)		CC 81.3%
GAD2 (rs4749107)	1	AG 41.4%
GAD2 (rs3781108)		TT 64.2%
GAD2 (rs3781107)		CC 74.9%
Glutamate to GABA Conversion	78%	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger II	2.06	#N/A	1

The GAD enzyme converts glutamate to GABA. When someone has high glutamate and a lot of variants in GAD, it creates conditions that may have high glutamate and low GABA that could increase stress and conditions related to high glutamate. It has been observed, that Homozygous variants in GAD have more impact than many Heterozygous. SER-GAB Assist and GABA Assist may be helpful if there is low GABA.

DAO		
DAO (rs2070586)		GG 68.7%
DAO (rs3741775)	1	AC 49.4%
DAOA (rs2391191)	1	GA 46.5%
DAO	67%	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger II	2.06	#N/A	1

The name of this gene is D-amino-acid oxidase and DAO is the gene's official symbol. Health conditions observed with this variant are: Schizophrenia, Bipolar Disorder, Primary Hyperoxaluria, ALS (Type 18), Autism and Crohn's Disease.

Studies have found that the A allele in rs2391191 is a possible genetic feature of certain health conditions such as Schizophrenia, and Bipolar Disorder.

With two variants, there may be some stress/anxiety. When combined with high glutamate and GAD variants, even more potential for stress/anxiety.

Patient: Eric Ehle

Oxytocin Receptor		
OXTR (rs2139184)		CC 96.2%
OXTR (rs11706648)	2	CC 11.0%
OXTR (rs237888)		TT 88.0%
OXTR (rs2268492)	1	CT 40.0%
OXTR (rs2268494)		TT 83.5%
OXTR (rs35498753)		TT 78.1%
OXTR (rs237893)	1	AG 49.2%
OXTR (rs11711703)	1	AG 29.2%
OXTR (rs237901)		GG 100.0%
OXTR (rs237902)		GG 48.4%
OXTR (rs189386)	1	CA 13.9%
OXTR (rs237906)		CC 100.0%
OXTR (rs237907)		CC 100.0%
OXTR (rs237908)		CC 99.9%
OXTR (rs237915)		TT 51.4%
OXTR (rs35413809)		GG 82.1%
OXTR (rs2301261)		CC 82.5%
OXTR (rs9860869)		TT 78.7%
OXTR (rs237897)	1	AG 45.5%
OXTR (rs237887)	2	AA 33.6%
OXTR (rs53576)	1	AG 43.0%
OXTR (rs7632287)		GG 59.0%
OXTR (rs2268491)		CC 76.4%
OXTR (rs2254298)		GG 76.1%
OXTR (rs1042778)	2	TT 14.9%
OXTR (rs13316193)	1	TC 45.9%
OXTR (rs4686302)		CC 78.0%
OXTR	76%	

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.

Variants in this gene can lead to a higher sensitivity to stress, and conduct disorders.

OXTR Empathy		
OXTR (rs53576)	1	AG 43.0%
OXTR Empathy	50%	

For rs53576, 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.

There is one variant in the OXTR rs53576. Variants in this gene have been shown to be associated with people who are more empathetic, feeling less lonely, employ more sensitive parenting techniques, and have lower rates of autism

## BH4 Cycle, Nitric Oxide & Peroxynitrite (Inflammation) Estimates

The NOS enzyme uses BH4 and L-Arginine to create Nitric Oxide, the critical molecule needed for vasodilation and many other factors. If there is inadequate BH4 or variants in NOS, the arginine may instead create the free radical superoxide. Superoxide then combines with nitric oxide to create the very strong oxidizing agent peroxynitrite. This is called NOS uncoupling. NOS uncoupling causes inflammation and may weaken the immune system.

The more factors that lessen BH4, (A1298C, DHFR, QDPR) and the more NOS variants, and the more SOD variants, the higher the likelihood of peroxynitrite production.

Urea cycle dysfunction will contribute to lowering BH4, because BH4 is needed to clear ammonia not removed by the Urea Cycle.



Gene Name	Variants	Metrics
<b>Nitric Oxide &amp; NOS</b>		
NOS2 (rs2297518)		GG 64.4%
NOS2 (rs2274894)		TT 14.8%
NOS2 (rs2248814)		AA 16.4%
NOS3 (rs1800779)	2	AA 39.7%
NOS3 (rs3918188)	1	CA 45.7%
NOS3 D298E (rs1800783)	2	TT 38.2%
NOS	57%	
<b>BH4 Production Factors</b>		
CBS C699T (rs234706)		GG 45.8%
BHMT-08 (rs651852)	1	CT 49.2%
DHFR (rs1643649)	1	TC 38.7%
SHMT2 (rs34095989)	2	AA 15.1%
MTHFR A1298C (rs1801131)		TT 47.7%
BH4	60%	
<b>BH2 to BH4 Conversion</b>		
QDPR (rs1031326)	2	CC 39.6%
QDPR (rs11722315)		CC 67.1%
QDPR (rs12645938)		GG 91.7%
QDPR (rs3796809)	1	GA 38.2%
GCH1 (rs2878169)		GG 82.3%
QDPR	70%	

Product Name	SNP Total	Lab Total	Symptoms
NOS Assist	4.17	#N/A	0
Pro SOD/Catalase Support	7.33	0	2

The NOS enzymes convert L-Arginine and BH4 into Nitric Oxide. Variants in the NOS enzymes and if along with low BH4 will result in the free radical Superoxide being created instead. If there is not enough Superoxide Dismutase to neutralize the superoxide, the superoxide molecules combines with Nitric Oxide to create the very dangerous and damaging Peroxynitrite, in a process called NOS uncoupling.

NOS Assist supports the NOS Enzyme, while Nitric Oxide Accelerator does as well, but has L Arginine. L Arginine may be contraindicated with NOS variants and low BH4. NOS3 D298 may be the most important NOS variant that impacts Nitric Oxide Production.

If there a lot of NOS variants, supporting SOD and Glutathione while scavenging Peroxynitrite may be needed as well. Checking inflammation markers in Urine Organic Acids may be beneficial, to determine if there is excess inflammation.

There are 5 NOS variants. NOS support is likely needed, especially if one is the D298E. Peroxynitrite Scavenger may be needed as well.

Product Name	SNP Total	Lab Total	Symptoms
BH4 Assist	7.81	3	14
Pro NADH	5.39	0	2

BH4 is critical for neurotransmitter production and making nitric oxide. Low BH4 can lead to impaired neurotransmitter production and NOS uncoupling, thus resulting in the creation of the very dangerous, peroxynitrite. These variants may lower the production or recycling of BH4.

With five variants that support the production of BH4, levels may be compromised. If one of the variants is A1298C, it may impact BH4 levels more significantly. Also, check QDPR genes for recycling of BH2 to BH4.

Product Name	SNP Total	Lab Total	Symptoms
BH4 Assist	7.81	3	14
Pro NADH	5.39	0	2

QDPR produces the enzyme quinoid dihydropteridine reductase that recycles BH2 to BH4. Variants here, along with other variants that impact BH4 production, may contribute to NOS uncoupling, where the dangerous Peroxynitrite oxidizing agent is created.

With three variants in QDPR, BH2 to BH4 conversion may be slightly compromised. However, DHFR also impacts BH2 to BH4 and MTHFR1298C supports the folinic acid needed for BH4. All of these need to be taken into consideration.

Peroxynitrite Factors		
MTHFR A1298C (rs1801131)		TT 47.7%
SHMT2 (rs34095989)	2	AA 15.1%
DHFR (rs1643649)	1	TC 38.7%
QDPR (rs1031326)	2	CC 39.6%
QDPR (rs11722315)		CC 67.1%
QDPR (rs12645938)		GG 91.7%
QDPR (rs3796809)	1	GA 38.2%
BHMT-08 (rs651852)	1	CT 49.2%
CBS C699T (rs234706)		GG 45.8%
CTH (rs1021737)		GG 50.7%
GSTM1 (rs1056806)		CC 87.8%
GSTP1 A114V (rs1138272)		CC 84.7%
GSTP1 I105V (rs1695)		AA 44.0%
SOD2 (rs2758331)	1	CA 49.4%
SOD2 A16V (rs4880)	1	AG 49.5%
SOD3 (rs1799895)		CC 97.7%
SOD3 (rs2855262)	2	CC 41.3%
NOS2 (rs2274894)		TT 14.8%
NOS2 (rs2248814)		AA 16.4%
NOS3 (rs3918188)	1	CA 45.7%
NOS2 (rs2297518)		GG 64.4%
NOS3 (rs1800779)	2	AA 39.7%
NOS3 D298E (rs1800783)	2	TT 38.2%
Peroxynitrite Reduction Efficiency	60%	

Product Name	SNP Total	Lab Total	Symptoms
NOS Assist	4.17	#N/A	0
Glutathione Accelerator	4.39	0	3
Peroxynitrite Scavenger	4	0	2
S Acetyl Glutathione	4.39	0	3
Ammonia Scavenger	7.11	0	5
Peroxynitrite Scavenger P.M.	4	0	2
Pro SOD/Catalase Support	7.33	0	2
GSH Assist	4.39	0	2
Nrf2 Accelerator	4	0	2
Pro NADH	5.39	0	2

The Peroxynitrite Support Estimate is a summation of all the variants that could contribute to the creation of peroxynitrite. Reducing peroxynitrite may be the most important step you take nutritionally.

The variants listed here are related to those that reduce the creation of BH4 (MTHFR A1298C, SHMT2), those that would slow the recycling of BH2 to BH4 (DHFR and QDPR), those that would reduce BH4 by creating excess ammonia (BHMT 08 and CB 699) and the variants that would reduce SOD and glutathione. Also, look at the NOS variants that would make superoxide rather than nitric oxide.

Reviewing this list may give you clues as to how severe peroxynitrite production is, and how suited they are to reduce it with glutathione and SOD and the most appropriate strategies to reduce the peroxynitrite.

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, Cell Membrane, Intestinal Bacteria, SHBG & Cardiovascular, Iron

These SNPs may be reflective of need for Vitamin D, prebiotics, hormonal support and cardiovascular support.

Gene Name	Variants	Metrics
<b>Vitamin D Receptor</b>		
VDR BSM (rs1544410)	1	CT 47.9%
VDR Fok (blood sugar) (rs2228570)		AA 14.1%
VDR Taq (methy group) (rs731236)	1	AG 47.5%
Vitamin D (TAQ Only)	50%	
<b>Cell Membrane Protection</b>		
G6PD (rs1050828)		CC 99.7%
G6PD (rs1050829)		TT 99.0%
G6PD	100%	
<b>SHBG</b>		
SHBG (rs1799941)	1	GA 36.0%
SHBG (rs9898876)		GG 69.1%
SHBG (rs13894)		GG 86.9%
SHBG (rs6257)		TT 80.6%
SHBG (rs143609002)		GG 100.0%
SHBG (rs12150660)	1	GT 26.3%
SHBG (rs6258)		CC 98.8%
SHBG	86%	
<b>Cardiovascular Genes</b>		
ACE Del 16 (rs4343)		GG 28.0%
ADD1 G460W (rs4961)		GG 65.1%
AGT M235T/C4072T (rs699)	2	GG 20.4%
MTHFR C677T (rs1801133)	1	GA 45.2%
Cardio Protection	63%	

Product Name	SNP Total	Lab Total	Symptoms
Vitamin D3 5000	5	#N/A	#N/A

Variants in the VDR (Vitamin D receptor) Taq may lower the Vitamin D in the body and supplementation is needed. More information will be coming on the VDR Fok and VDR BSM. The Vitamin D rating, is only calculated based upon the TAQ, and not the other Vitamin D genes. More information will be added here on the others in the future.

There is 1 variant. Measure Vitamin D, and consider 5,000 IU/day supplementation.

G6PD encodes glucose-6-phosphate dehydrogenase. This protein is a cytosolic enzyme whose main function is to produce NADPH.

Variants in the SHBG gene may cause dysregulation in testosterone and estrogen levels and lowered progesterone. Hormone testing may be in order if hormonal symptoms exist. For men (especially older men), SHBG variants may indicate more circulating SHBG resulting in lowered testosterone levels. For women, SHBG variants may indicate less SHBG resulting in higher androgen levels overall.

There is one variant in the SHBG gene. This increases the chance of higher estrogen and testosterone, with lower progesterone, and for women, this may be a contributing factor in PCOS or other hormonal issues related to low Progesterone. If there are hormonal issues, doing a hormone test may be advisable. For men, this can lead to lower testosterone later in life.

Product Name	SNP Total	Lab Total	Symptoms
Circulation Accelerator	5.07	#N/A	0

Variants in these genes may contribute to circulatory issues. More information coming soon.

The more SNPs in these genes, the higher the risk for cardiovascular issues, especially when combined with carnitine and ACAT variants.

HFE		
HFE C282Y (rs1800562)		GG 89.3%
HFE H63D (rs1799945)	1	CG 23.7%
HFE S65C (rs1800730)		AA 97.3%
HFE (rs1572982)	2	AA 22.0%
HFE 6382T>G (rs2794719)	1	TG 46.9%
HFE 8828T>C (rs2071303)	2	CC 11.2%
HFE		
	50%	
SLC40A1		
SLC40A1 (rs4667287)		AA 80.4%
SLC40A1 (rs137979680)	1	CT 3.1%
SLC40A1 (rs28939076)		GG 100.0%
SLC40A1 (rs1123109)	1	TC 32.6%
SLC40A1 (rs11539983)		TT 94.3%
SLC40A1 (rs13404407)		TT 98.5%
SLC40A1 (rs16831652)		TT 98.6%
SLC40A1	86%	

Product Name	SNP Total	Lab Total	Symptoms
HFE Assist	14	#N/A	3

H63D represents a SNP that accounts for a mild form of hereditary hemochromatosis (HH), an iron overload condition in which mutations of certain genes involved in iron metabolism disrupt the body's ability to regulate uptake of iron, causing increased intestinal iron absorption. The most common form is caused by mutations in the HFE gene, which are inherited recessively.

A mutation at amino acid 282 (C282Y) was found to be homozygous in 83 percent of patients with HH. This is a point mutation from guanine to adenine, resulting in a missense mutation from cysteine to tyrosine. Such mutations are commonly found in people with European ancestry.

The three most common HH-causing mutations in the HFE gene are C282Y and S65C. At least 17 other mutations in the HFE gene have been linked to HH. 60-90% of people with HH have two copies of the C282Y mutation. The H63D mutation is also quite common, about 20% of people carry a copy of the mutation, and about 3% have two copies. This mutation is not as severe as the C282Y mutation, and only causes symptoms when someone has both the H63D and the C282Y mutations. Even then, only a small fraction of people with one copy of each mutation actually exhibit evidence of iron overload. Additionally, those who have two copies of H63D do not exhibit any symptoms and are not at risk for iron overload. The S65C mutation is less common, and will also only cause symptoms if in combination with C282Y. For both H63D/C282Y and S65C/C282Y single mutation individuals, symptoms are usually mild if they develop at all.

The SLC40A1 gene contains the instructions for making a protein called ferroportin. Ferroportin 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. Ferroportin also plays a role in the metabolism of iron. Different variants of the SLC40A1 gene affect the ferroportin protein in different ways which in turn can alter the export and metabolism of iron.

Iron oxidation Potential		
BHMT-08 (rs651852)	1	CT 49.2%
CBS C699T (rs234706)		GG 45.8%
CTH (rs1021737)		GG 50.7%
GSTM1 (rs1056806)		CC 87.8%
GSTP1 A114V (rs1138272)		CC 84.7%
GSTP1 I105V (rs1695)		AA 44.0%
HFE C282Y (rs1800562)		GG 89.3%
HFE H63D (rs1799945)	1	CG 23.7%
HFE S65C (rs1800730)		AA 97.3%
HFE 8828T>C (rs2071303)	2	CC 11.2%
HFE (rs1572982)	2	AA 22.0%
HFE 6382T>G (rs2794719)	1	TG 46.9%
SOD2 (rs2758331)	1	CA 49.4%
SOD2 A16V (rs4880)	1	AG 49.5%
SOD3 (rs1799895)		CC 97.7%
SOD3 (rs2855262)	2	CC 41.3%
SLC40A1 (rs4667287)		AA 80.4%
SLC40A1 (rs137979680)	1	CT 3.1%
SLC40A1 (rs28939076)		GG 100.0%
SLC40A1 (rs1123109)	1	TC 32.6%
SLC40A1 (rs11539983)		TT 94.3%
SLC40A1 (rs13404407)		TT 98.5%
SLC40A1 (rs16831652)		TT 98.6%
Iron Oxidation Potential	65%	

Product Name	SNP Total	Lab Total	Symptoms
HFE Assist	14	#N/A	3
Pro SOD/Catalase Support	7.33	0	2
GSH Assist	4.39	0	2
Pro NADH	5.39	0	2

HFE SNPs, in combination with these others, may increase the potential for Oxidized Iron. More information coming soon.

Patient: Eric Ehle

APOE		
APOE (rs429358)		TT 76.1%
APOE (rs7412)		CC 88.4%
APOE	100%	

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
CT	CT	E2/E4
TT	CC	E3/E3
CT	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.

## 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 allows 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
<b>mutL homolog 1</b>		
MLH1 (rs1800734)	1	GA 35.4%
MLH1 (rs35045067)		AA 99.9%
MLH1	75%	

Product Name	SNP Total	Lab Total	Symptoms
Cellular Health Assist	9.91	0	0

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.

Patient: Eric Ehle

Ataxia telangiectasia mutated		
ATM (rs1801516)		GG 73.8%
ATM (rs664143)		AA 17.0%
ATM (rs664677)		CC 17.3%
ATM (rs1801673)		AA 98.3%
ATM (rs1800058)		CC 96.4%
ATM (rs1800056)		TT 97.4%
ATM (rs1800054)		CC 97.8%
ATM (rs3218707)		GG 99.8%
ATM (rs3092856)		CC 99.6%
ATM (rs623860)		CC 17.1%
ATM (rs2235006)		TT 99.8%
ATM (rs3092857)		AA 99.8%
ATM (rs227060)		CC 44.8%
ATM (rs227062)		GG 18.4%
ATM (rs17412803)		AA 92.5%
ATM (rs227092)		GG 24.4%
ATM (rs600931)		CC 18.4%
ATM (All Genes)	100%	
ATM (Most Relevant)	100%	

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

The first 9 are shown to be the most relevant, and the last 9 are included for informational research purposes.

Studies have shown that variants in the most relevant genes listed can increase chances of cells being damaged from oxidative stress and not repairing as quickly. It would be advantageous for individuals with these variants to reduce exposure to free radical producing agents and support antioxidant protection.

For now, we have no suggested protocols, other than adequately controlling oxidative stress. This information is just being presented now for research purposes.

## 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.

A urea cycle disorder can occur if there is a mutation that results in a deficiency of CPS1, OTC, ASS1, ASL, or ARG1 which could result in higher ammonia concentration in the blood.

Gene Name	Variants	Metrics
<b>Carbamoyl-Phosphate Synthase 1</b>		
CPS1 (rs918233)	1	CT 45.0%
CPS1 (rs1509821)		CC 81.4%
CPS1 (rs981024)	1	GA 47.9%
CPS1 (rs2012564)	1	AG 47.9%
CPS1 (rs17773128)		CC 85.4%
CPS1 (rs6749597)		GG 74.4%
CPS1 (rs2887913)	1	AC 47.8%
CPS1 (rs9789405)		CC 74.3%
CPS1 (rs2287603)		AA 64.1%
CPS1 (rs2287602)		AA 74.7%
CPS1 (rs10515951)		GG 85.5%
CPS1 (rs6714124)	1	CT 50.3%
CPS1 (rs7573258)	1	GA 49.1%
CPS1 (rs2371000)	1	TC 49.2%
CPS1 (rs2371001)	1	AG 50.3%
CPS1 (rs3821135)		TT 76.6%
CPS1 (rs7607205)	1	TG 48.1%
CPS1 (rs12468557)	1	CT 45.7%
CPS1 (rs2302909)		GG 84.6%
CPS1 (rs2371011)	1	AG 40.1%
CPS1 (rs13010236)		TT 82.4%
CPS1 (rs2287598)	2	GG 68.0%
CPS1 (rs6435580)	1	CT 43.8%
CPS1 (rs2270476)		GG 88.0%
CPS1 (rs12997383)		CC 75.6%
CPS1 (rs4672587)	1	AG 41.0%
CPS1 (rs4567871)		CC 75.7%
CPS1	72%	
<b>Ornithine Transcarbamylase</b>		
OTC (rs72554348)		GG 99.9%
OTC (rs7056866)		GG 13.5%
OTC (rs5917584)		CC 64.9%
OTC (rs5963418)		GG 78.7%
OTC (rs5963419)		TT 47.6%
OTC (rs12557315)		CC 66.4%
OTC	100%	

Product Name	SNP Total	Lab Total	Symptoms
Ammonia Scavenger	7.11	0	5
A-L-O Formula	0	#N/A	#N/A

The enzyme encoded by this gene catalyzes the synthesis of carbamoyl phosphate from ammonia and bicarbonate. This synthesis is the first step in the Urea Cycle.

Carbamoyl phosphate is an intermediary metabolite in nitrogen disposal.

A mutated CPS1 gene may result in a carbamoyl phosphate synthetase I enzyme that is smaller than normal, not correct in shape, or the enzyme may not be produced at all.

Studies have shown that polymorphisms in the CPS1 gene have been associated with pulmonary hypertension. Polymorphisms in CPS1 may also reduce the production of nitric oxide (NO). A reduced amount of nitric oxide can also lead to circulatory problems.

Product Name	SNP Total	Lab Total	Symptoms
Ammonia Scavenger	7.11	0	5
A-L-O Formula	0	#N/A	#N/A

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.

A mutated OTC gene will not be able to control the reaction between carbamoyl phosphate and ornithine correctly. This in turn can cause a buildup of ammonia in the body.



Argininosuccinate synthase 1		
ASS1 (rs12554609)		TT 84.6%
ASS1 (rs11243372)	1	AG 49.0%
ASS1 (rs4740158)		TT 7.8%
ASS1 (rs914983)	2	GG 45.1%
ASS1 (rs1615006)	1	GA 44.5%
ASS1 (rs1653332)		GG 16.3%
ASS1 (rs1215988)		GG 38.9%
ASS1 (rs1215985)	1	CT 37.6%
ASS1 (rs590086)	1	CT 16.9%
ASS1 (rs12551145)	1	GA 13.5%
ASS1 (rs10901072)		CC 77.5%
ASS1 (rs652313)	2	GG 74.8%
ASS1 (rs1215972)		GG 2.0%
ASS1 (rs41302903)		GG 88.3%
ASS1 (rs75912463)		TT 97.8%
ASS1 (rs540140)		GG 52.1%
ASS1 (rs480313)		GG 51.9%
ASS1 (rs11243474)		GG 75.2%
ASS1 (rs474330)		GG 48.1%
ASS1 (rs17147023)	2	CC 5.3%
ASS1 (rs553696)		AA 45.8%
ASS1 (rs12375699)		CC 34.8%
ASS1 (rs634432)	2	TT 71.7%
ASS1 (rs544701)		AA 76.2%
ASS1	73%	

Product Name	SNP Total	Lab Total	Symptoms
Ammonia Scavenger	7.11	0	5
A-L-O Formula	0	#N/A	#N/A

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.

A mutated ASS1 gene can prevent the liver from processing excess nitrogen into urea. This in turn can cause a buildup of ammonia and other byproducts of the urea cycle (for example citrulline) in the bloodstream.

Argininosuccinate Lyase		
ASL (rs12530898)		GG 91.9%
ASL (rs313830)	2	CC 55.4%
ASL (rs313829)	2	GG 48.1%
ASL	33%	

Product Name	SNP Total	Lab Total	Symptoms
Ammonia Scavenger	7.11	0	5
A-L-O Formula	0	#N/A	#N/A

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.

A mutated ASL gene may not be able to form arginine and fumarate properly. This could lead to a buildup of ammonia in the blood.

Arginase 1		
ARG1 (rs2246012)		TT 70.5%
ARG1	100%	

Product Name	SNP Total	Lab Total	Symptoms
Ammonia Scavenger	7.11	0	5
A-L-O Formula	0	#N/A	#N/A

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.

A mutated ARG1 gene may not be able to form a stable arginase enzyme. This can cause a build up of ammonia and arginine in the body.

## Variants that Impact Exercise and Fitness Potential

Gene Name	Variants	Metrics
<b>Muscle Fiber Composition</b>		
ACTN3 (rs1815739)	1	CT 49.0%
Muscle Fiber Composition	50%	
<b>Aerobic Exercise Potential</b>		
ADRB2 (rs1042713)	1	AG 46.3%
ADRB2 (rs1042714)		CC 36.0%
PPARGC1A (rs8192678)	1	CT 45.3%
VEGF (rs833069)	2	TT 42.9%
Aerobic Exercise Potential	50%	
<b>Exercise Recovery Speed</b>		
CRP (rs1205)		TT 11.5%
IL6 (rs1800795)	1	GC 45.8%
IL6R (rs4129267)		TT 15.9%
SOD2 A16V (rs4880)	1	AG 49.5%
TNFA (rs1800629)		GG 72.3%
Exercise Recovery Speed	80%	

Muscles are made up of two main types of muscle fibers, "fast-twitch" and "slow-twitch." Endurance athletes tend to have more slow-twitch muscle, while sprinters tend to have more fast-twitch muscle. Some of the variation in muscle fibers is dependent on a protein called alpha-actinin-3.

The ACTN3 gene contains instructions for making alpha-actinin-3. The alpha-actinin-3 protein can be found in certain types of fast-twitch muscle fibers. People who make this protein tend to have a greater proportion of fast-twitch muscle and are better sprinters than people who do not make this protein.

With 1 variant in the ACTN3 gene, this person has a mixture of both fast-twitch and slow-twitch muscle fibers.

Our bodies need oxygen while exercising. VO2 max is a test that can be used by scientist to measure the optimum rate at which someone's body can effectively use oxygen when exercising. There are certain genes that can help at better understanding someone's natural VO2 max capacity.

Studies have shown that individuals with a higher number of variants in these genes are less responsive to endurance training.

Research has shown that certain genetic factors can determine whether or not someone can quickly recover after workouts.

Studies have shown that individuals with variations in these genes require longer recovery times due to higher levels of inflammation during strenuous exercise.

Exercise Injury Risk		
COL1A1 (rs1800012)	2	CC 67.7%
COL5A1 (rs12722)		CC 28.7%
GDF (rs224329)	1	CT 47.8%
Exercise Injury Risk	50%	
FTO		
FTO	83%	
FADS		
FADS1 (rs174546)	1	CT 43.7%
FADS1 (rs174547)	1	TC 43.6%
FADS1 (rs174548)	1	CG 41.4%
FADS1 (rs174549)	1	GA 40.6%
FADS1 (rs174550)	1	TC 43.6%
FADS1 (rs174556)	1	CT 40.4%
FADS2 (rs174570)		CC 73.0%
FADS2 (rs1535)	1	AG 43.9%
FADS2 (rs174575)	1	CG 37.4%
FADS2 (rs174576)	1	CA 44.7%
FADS2 (rs2072114)		AA 77.4%
FADS2 (rs174579)	1	CT 32.2%
FADS2 (rs2851682)		AA 81.7%
FADS2 (rs174592)	1	AG 46.3%
FADS2 (rs174602)	1	TC 33.0%
FADS2 (rs498793)	1	TC 47.0%
FADS2 (rs174611)	1	TC 39.9%
FADS2 (rs482548)		CC 82.2%
FADS3 (rs174450)	1	GT 49.6%
FADS3 (rs1000778)	1	AG 38.2%
FADS Total	62%	
FADS1	56%	
FADS2	67%	
FADS3	50%	

Research has shown that certain genetic factors can determine an individuals exercise injury risk. Studies have shown that individual's with variations in these genes are at higher risk for tendon and ligament injuries.

FTO or Fat Mass and Obesity Associated, is a Protein Coding gene. Variations in this gene may cause growth delay, developmental delay, facial dysmorphism and overnutrition. All 63 of the FTO SNPs can be viewed in the Gene Report.

Product Name	SNP Total	Lab Total	Symptoms
A-L-O Formula	0	#N/A	#N/A

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.

## Electrical Sensitivity Potential

Gene Name	Variants	Metrics	
<b>CACNA1C</b>			
CACNA1C (rs216013)		AA 70.7%	This gene encodes an alpha-1 subunit of a voltage-dependent calcium channel. Calcium channels mediate the influx of calcium ions into the cell upon membrane polarization.
CACNA1C (rs2159100)	1	CT 43.4%	
CACNA1C (rs1006737)	1	GA 43.4%	Variants in these genes may impact the potential to have negative effects from high levels of electrical field exposure.
CACNA1C (rs2302729)		CC 67.3%	
CACNA1C	75%		

## Glutamate and Glutamine

Gene Name	Variants	Metrics	
<b>SLC1A1</b>			
			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 70 SLC1A1 SNPs can be found in the gene report.
SLC1A1	63%		
<b>SLC1A5</b>			
SLC1A5 (rs1060043)	1	GA 18.1%	The SLC1A5 gene encodes a sodium-dependent neutral amino acid transporter.  Glutamine is transported into cells through SLC1A5.
SLC1A5 (rs2070246)		GG 61.4%	
SLC1A5 (rs3027957)	1	TC 30.9%	
SLC1A5 (rs313853)	1	TC 43.8%	
SLC1A5 (rs8105903)		AA 30.3%	
SLC1A5 (rs1862336)		CC 59.8%	
SLC1A5	75%		

<b>SLC7A5</b>			SLC7A5 is a Protein Coding gene.  Glutamine is transported into cells through SLC7A5.
SLC7A5 (rs3889228)	1	CA 39.2%	
SLC7A5 (rs16943315)	1	GA 37.9%	
SLC7A5 (rs9938601)		GG 34.8%	
SLC7A5 (rs1060251)		GG 99.9%	
SLC7A5 (rs750950)	1	AC 42.8%	
SLC7A5 (rs11865049)		GG 91.8%	
SLC7A5 (rs1060250)		GG 99.8%	
SLC7A5 (rs17853937)		TT 99.9%	
SLC7A5 (rs4843718)	1	GA 39.1%	
SLC7A5 (rs876985)	1	TC 44.6%	
SLC7A5 (rs731710)	1	AG 46.4%	
SLC7A5 (rs4240803)		GG 48.4%	
SLC7A5 (rs4843272)		CC 48.9%	
SLC7A5 (rs4465613)	1	CT 46.4%	
SLC7A5	75%		
<b>SLC38A9</b>			
SLC38A9 (rs2161504)		TT 37.6%	
SLC38A9 (rs2897834)		AA 76.7%	
SLC38A9 (rs79560556)		TT 94.9%	
SLC38A9 (rs4361476)		CC 44.4%	
SLC38A9 (rs10056287)		TT 67.8%	
SLC38A9 (rs79818066)		CC 97.4%	
SLC38A9 (rs2408208)		AA 44.4%	
SLC38A9 (rs3761766)		GG 44.8%	
SLC38A9 (rs11749532)	1	GA 43.7%	
SLC38A9 (rs7736177)		AA 48.5%	
SLC38A9	95%		
<b>SLC3A2</b>			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.
SLC3A2 (rs12794763)		TT 73.8%	
SLC3A2 (rs10897300)		AA 88.5%	
SLC3A2 (rs2070870)	1	TC 40.0%	
SLC3A2 (rs489381)		GG 78.0%	
SLC3A2 (rs4726)	1	CT 34.7%	
SLC3A2	80%		

<b>SLC7A11</b>			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 (rs7674870)	1	AG 48.7%	
SLC7A11 (rs13144383)		AA 69.1%	
SLC7A11 (rs4863771)		GG 33.8%	
SLC7A11 (rs4131888)		CC 63.2%	
SLC7A11 (rs4602539)		TT 48.6%	
SLC7A11 (rs6537244)	1	AG 49.4%	
SLC7A11 (rs11734488)	1	TC 49.3%	
SLC7A11 (rs6854381)	1	GA 49.4%	
SLC7A11 (rs7666936)		TT 69.5%	
SLC7A11 (rs7685529)	1	TC 49.4%	
SLC7A11	75%		
<b>GLS</b>			GLS or Glutaminase encodes a protein that catalyzes the hydrolysis of glutamine to glutamate and ammonia.
GLS (rs3771316)		AA 81.9%	
GLS (rs1921915)		AA 87.6%	
GLS (rs6758866)		GG 34.2%	
GLS (rs3771311)		TT 77.9%	
GLS (rs62179862)		AA 95.2%	
GLS (rs1517354)		TT 86.2%	
GLS (rs3088307)	2	GG 18.6%	
GLS (Glutamine to Glutamate Conversion)	86%		
<b>GLS2</b>			GLS2 or Glutaminase 2 encodes a protein that catalyzes the hydrolysis of glutamine to stoichiometric amounts of glutamate and ammonia.
GLS2 (rs2638315)		GG 65.1%	
GLS2 (rs6581096)		GG 48.3%	
GLS2 (Glutamine to Glutamate Conversion)	100%		
<b>GLUL</b>			GLUL or Glutamate-ammonia Ligase encodes a protein that catalyzes the synthesis of glutamine from glutamate and ammonia in an ATP-dependent reaction.
GLUL (rs12735664)		AA 82.2%	
GLUL (rs12403634)		CC 67.3%	
GLUL (Glutamate to Glutamine Conversion)	100%		

Glutamate to Alpha-Ketoglutarate Conversion			Product Name	SNP Total	Lab Total	Symptoms
			Pro Alpha Ketoglutarate Plus	0	#N/A	#N/A
GOT1 (rs201272543)		GG 100.0%	<p>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.</p> <p>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.</p> <p>Glutamic-Pyruvate Transaminase also plays a role in the conversion of glutamate to alpha-ketoglutarate.</p>			
GOT1 (rs9971274)		GG 84.5%				
GOT1 (rs9971275)		GG 84.5%				
GPT (rs1063739)	1	CA 49.0%				
GOT1 (rs4328160)		TT 80.7%				
GOT2 (rs30842)	1	CA 42.9%				
GOT2 (rs30838)	1	CT 42.9%				
GOT2 (rs863944)	2	AA 16.8%				
GLUD1 (rs1923939)		AA 60.1%				
GOT1 (rs11190083)		AA 84.5%				
GLUD1 (rs9421574)		CC 82.0%				
GLUD1 (rs9421580)		CC 61.7%				
GOT1 (rs12768505)		CC 90.3%				
Glutamate to Alpha-Ketoglutarate Conversion	73%					
<b>MTOR</b>			<p>The protein encoded by MTOR belongs to a family of phosphatidylinositol kinase-related kinases. These kinases facilitate cellular responses to stresses such as DNA damage, and nutrient deprivation. Glutamine controls mTOR activity.</p>			
MTOR (rs2536)		TT 94.2%				
MTOR (rs12139042)		GG 94.5%				
MTOR (rs17036350)		CC 93.1%				
MTOR (rs2275522)		GG 94.1%				
MTOR (rs11121691)	2	TT 6.2%				
MTOR (rs868080)		CC 93.1%				
MTOR (rs3737611)		AA 93.0%				
MTOR (rs1770344)		CC 99.9%				
MTOR (rs2275527)	2	AA 6.2%				
MTOR (rs1417131)	2	CC 6.0%				
MTOR (rs3730381)		GG 94.1%				
MTOR (rs1057079)	2	CC 8.6%				
MTOR (rs2275942)		AA 94.2%				
MTOR (rs2791643)	2	CC 6.4%				
MTOR (rs1770345)		CC 23.6%				
MTOR (rs17036458)		GG 94.5%				
MTOR (rs143435072)		CC 99.9%				
MTOR (rs28991014)		AA 89.0%				
MTOR (rs11121697)		AA 94.2%				
MTOR (rs2273127)		AA 94.4%				
MTOR (rs4845986)	2	GG 8.1%				
MTOR (rs1064261)	2	GG 7.8%				
MTOR (rs17229172)		AA 98.3%				
MTOR (rs7524202)	2	TT 7.8%				
MTOR (rs1135172)	2	AA 8.1%				
MTOR (rs12141961)		CC 94.4%				
MTOR (rs4845987)		CC 51.8%				
MTOR (rs12142905)		TT 93.9%				
MTOR (rs17229137)		TT 96.9%				
MTOR	69%					

<b>KRAS</b>		
KRAS (rs61764370)		AA 88.7%
KRAS (rs9266)	2	AA 21.2%
KRAS (rs712)		AA 35.7%
KRAS (rs1137282)		AA 62.9%
KRAS (rs12305513)	1	AG 18.8%
KRAS (rs4246229)	2	GG 21.3%
KRAS (rs6487461)	2	TT 20.9%
KRAS (rs200186819)		GG 100.0%
KRAS (rs10842508)	2	TT 5.7%
KRAS (rs12579073)	2	CC 22.9%
KRAS (rs11047901)		AA 26.2%
KRAS (rs17388148)	1	TG 16.9%
KRAS (rs17329025)		AA 30.5%
KRAS (rs4623993)	1	CT 24.1%
KRAS (rs11047912)	1	TC 39.2%
KRAS (rs7133640)		GG 62.7%
KRAS (rs17329424)	1	AC 22.6%
KRAS (rs6487464)	1	CT 45.0%
KRAS (rs10842514)		CC 30.0%
KRAS (rs10505980)	1	CT 45.2%
KRAS (rs10842515)		TT 62.6%
KRAS (rs17388893)	1	AC 11.0%
KRAS (rs12813551)	1	TC 46.2%
KRAS (rs2970532)	1	CT 24.6%
KRAS (rs11047917)		CC 88.7%
KRAS (rs11047918)	1	GA 24.5%
KRAS (rs17389103)		TT 62.6%
KRAS (rs12228277)	1	TA 22.9%
KRAS (rs11047919)	2	AA 20.3%
KRAS (rs10842518)	1	GT 45.2%
KRAS (rs7315339)	1	TC 39.3%
KRAS	57%	
<b>MYC</b>		
MYC (rs4645946)		GG 96.2%
MYC (rs3891248)	2	AA 3.0%
MYC (rs4645959)		AA 93.0%
MYC (rs28933407)		CC 100.0%
MYC	75%	

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.

Studies have shown that the MYC oncogene has been most associated with upregulated glutamine metabolism.



ME1		
ME1 (rs1180243)	1	GT 48.4%
ME1 (rs2300465)		CC 86.2%
ME1 (rs1180241)		GG 62.8%
ME1 (rs9449593)		CC 80.8%
ME1 (rs1012741)		GG 80.9%
ME1 (rs1180228)	1	GA 47.3%
ME1 (rs983087)	1	TC 42.9%
ME1 (rs2179847)		TT 89.4%
ME1 (rs1180195)	1	CT 46.7%
ME1 (rs1180187)		AA 39.0%
ME1 (rs13202010)		TT 82.9%
ME1 (rs1954537)		GG 82.9%
ME1 (rs767144)		GG 54.2%
ME1 (rs1145917)		TT 53.7%
ME1 (rs13192303)		GG 82.3%
ME1 (rs1170348)		TT 40.1%
ME1 (rs750385)		AA 69.9%
ME1 (rs1170484)		AA 43.7%
ME1 (rs1535588)		AA 43.6%
ME1 (rs12213544)		GG 95.3%
ME1 (rs78734745)		CC 98.7%
ME1 (rs3798890)		GG 46.4%
ME1 (rs3798886)		GG 40.1%
ME1 (rs3798883)		CC 94.7%
ME1	92%	

ME1 encodes a cytosolic, NADP-dependent enzyme that generates NADPH for fatty acid biosynthesis.

Glutamine-derived malate is transported out of the mitochondria, and is converted by ME1 into pyruvate, reducing one molecule of NADP+ to NADPH.

GABA (Glutamate to GABA)		
GAD1 (rs3791850)	1	GA 36.7%
GAD1 (rs12185692)	1	CA 48.2%
GAD1 (rs10432420)		GG 49.6%
GAD1 (rs3749034)		GG 59.5%
GAD1 (rs769407)		GG 55.9%
GAD1 (rs2058725)	1	TC 37.4%
GAD1 (rs3791851)		TT 55.7%
GAD1 (rs3791878)	1	GT 41.0%
GAD1 (rs3828275)	1	CT 49.7%
GAD1 (rs701492)		CC 52.5%
GAD1 (rs2241165)		TT 54.6%
GAD1 (rs16858988)		GG 62.6%
GAD2 (rs2236418)		AA 64.6%
GAD2 (rs8190612)		CC 77.4%
GAD2 (rs7079102)		GG 98.2%
GAD2 (rs8190645)	1	GA 13.4%
GAD2 (rs8190646)	1	AG 16.4%
GAD2 (rs11015008)		GG 62.8%
GAD2 (rs8190650)	1	AG 16.9%
GAD2 (rs2368160)	1	GA 41.5%
GAD2 (rs7906725)	1	GA 41.5%
GAD2 (rs11015025)		CC 81.3%
GAD2 (rs4749107)	1	AG 41.4%
GAD2 (rs3781108)		TT 64.2%
GAD2 (rs3781107)		CC 74.9%
Glutamate to GABA Conversion	78%	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger II	2.06	#N/A	1

The GAD enzyme converts glutamate to GABA. When someone has high glutamate and a lot of variants in GAD, it creates conditions that may have high glutamate and low GABA that could increase stress and conditions related to high glutamate. It has been observed, that Homozygous variants in GAD have more impact than many Heterozygous. SER-GAB Assist and GABA Assist may be helpful if there is low GABA.

PYCR1		
PYCR1 (rs149261551)		CC 94.2%
PYCR1	100%	

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 (rs14868)		TT 74.5%
PYCR2 (rs10915897)		CC 73.1%
PYCR2 (rs56362902)	1	GA 6.7%
PYCR2 (rs10915898)		GG 73.1%
PYCR2	88%	

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 (rs4877550)		AA 40.4%
PSAT1 (rs7849813)		GG 66.8%
PSAT1 (rs944514)		TT 59.3%
PSAT1 (rs10116267)	1	TC 49.6%
PSAT1 (rs7874921)	1	TC 36.9%
PSAT1 (rs11137595)	1	GA 36.9%
PSAT1 (rs7875271)		GG 95.9%
PSAT1 (rs7858423)	1	CT 21.0%
PSAT1 (rs3780193)		CC 65.3%
PSAT1 (rs10735532)	1	TC 39.3%
PSAT1 (rs11137607)	2	GG 19.3%
PSAT1 (rs867376)	1	CT 38.3%
PSAT1 (rs1411916)	1	GA 17.2%
PSAT1 (rs3758203)		AA 82.6%
PSAT1	68%	
GPT		
GPT (rs1063739)	1	CA 49.0%
GPT	50%	
GPT2		
GPT2 (rs8044153)		CC 94.5%
GPT2 (rs754043)		GG 94.0%
GPT2 (rs115352435)		CC 100.0%
GPT2	100%	
ASNS		
ASNS (rs10486011)		CC 72.8%
ASNS (rs7792744)	1	TC 46.1%
ASNS (rs10263979)	1	GT 42.7%
ASNS (rs17345759)		AA 88.1%
ASNS (rs7790127)	1	GA 48.1%
ASNS	70%	

PSAT1 encodes a member of the class-V pyridoxal-phosphate-dependent aminotransferase family.

PSAT1 is the major source of glutamine-dependent  $\alpha$ -ketoglutarate.

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

Glutamate-pyruvate transaminase transfers nitrogen from glutamate to pyruvate to make alanine and  $\alpha$ -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

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.

<b>TSC1</b>			<p>TSC1 encodes a growth inhibitory protein thought to play a role in the stabilization of tuberin.</p> <p>Studies have shown that TSC1 increased glutamine uptake and metabolism.</p>
TSC1 (rs1050700)	1	CT 41.2%	
TSC1 (rs10491534)		TT 79.8%	
TSC1 (rs739441)	2	TT 65.8%	
TSC1 (rs739442)	1	GA 48.9%	
TSC1 (rs2809244)	1	AC 37.6%	
TSC1 (rs4962081)		GG 84.7%	
TSC1 (rs11243929)		TT 61.2%	
TSC1 (rs1076160)	1	CT 49.9%	
TSC1 (rs11243931)		AA 72.5%	
TSC1 (rs10901219)		CC 82.6%	
TSC1 (rs2519757)	1	TC 12.4%	
TSC1 (rs2809246)	2	GG 93.1%	
TSC1 (rs10901220)		GG 72.8%	
TSC1 (rs147614350)		TT 98.8%	
TSC1 (rs13295430)		GG 79.9%	
TSC1 (rs3761840)	1	TC 50.0%	
TSC1 (rs7874234)		CC 59.3%	
TSC1	71%		
<b>TSC2</b>			<p>TSC2 is a protein coding gene. All 421 TSC2 SNPs can be found in the gene report.</p> <p>Studies have shown that TSC2 increased glutamine uptake and metabolism.</p>
TSC2	100%		
<b>SIRT3</b>			<p>SIRT3 encodes a member of the sirtuin family of proteins.</p> <p>SIRT3 can deacetylate GLS2 to promote increased activity.</p>
SIRT3 (rs12226402)	1	GA 8.0%	
SIRT3 (rs10714)	1	GA 8.1%	
SIRT3 (rs3847648)	1	GA 9.5%	
SIRT3 (rs511744)	1	CT 42.6%	
SIRT3 (rs4758633)	2	GG 28.6%	
SIRT3 (rs4980335)		GG 62.9%	
SIRT3 (rs3782115)	1	GA 42.0%	
SIRT3 (rs1023430)	1	AG 31.3%	
SIRT3 (rs7946716)		CC 62.8%	
SIRT3 (rs7946581)		CC 62.8%	
SIRT3 (rs7934919)		TT 62.9%	
SIRT3 (rs547025)		TT 86.2%	
SIRT3 (rs11246020)		CC 62.8%	
SIRT3 (rs11555236)		CC 63.5%	
SIRT3 (rs12365010)		TT 63.2%	
SIRT3 (rs11246025)		AA 62.8%	
SIRT3 (rs9795476)		GG 54.8%	
SIRT3 (rs28365927)		GG 74.1%	
SIRT3 (rs7118852)		GG 99.3%	
SIRT3	79%		

<b>SIRT5</b>			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 (rs2804919)	1	GA 42.3%	
SIRT5 (rs2841512)		TT 75.2%	
SIRT5 (rs145857339)		CC 100.0%	
SIRT5 (rs4712047)	1	AG 48.5%	
SIRT5 (rs7759452)	1	GA 36.3%	
SIRT5 (rs3757261)	1	CT 34.9%	
SIRT5 (rs2841523)		GG 31.6%	
SIRT5	71%		
<b>HIF1A</b>			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 (rs2301106)		TT 75.2%	
HIF1A (rs1951795)		CC 62.9%	
HIF1A (rs12435848)		GG 61.3%	
HIF1A (rs8005745)		AA 80.6%	
HIF1A (rs4899056)		CC 79.7%	
HIF1A (rs1957757)		CC 81.5%	
HIF1A (rs12434438)		AA 59.8%	
HIF1A (rs12885226)		CC 98.4%	
HIF1A (rs966824)		CC 91.0%	
HIF1A (rs2301113)		AA 57.0%	
HIF1A (rs34005929)		GG 99.3%	
HIF1A (rs11549465)		CC 79.6%	
HIF1A (rs11549467)		GG 98.3%	
HIF1A	100%		
<b>GSS</b>			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 (rs28938472)		TT 100.0%	
GSS (rs6088655)	1	GA 47.5%	
GSS A18836C (rs2273684)	1	TG 49.3%	
GSS A5997G (rs6088659)	1	CT 27.7%	
GSS G11705T (rs6060124)	1	CA 37.9%	
GSS	60%		

CD4		
CD4 (rs2707212)	2	TT 11.0%
CD4 (rs2707210)	2	TT 22.1%
CD4 (rs2707209)		TT 40.5%
CD4 (rs1075835)		CC 58.7%
CD4 (rs10849517)		CC 77.1%
CD4 (rs2255301)	2	TT 13.6%
CD4 (rs7957426)		GG 42.1%
CD4 (rs11064404)	1	TC 11.2%
CD4 (rs11064410)		AA 91.7%
CD4 (rs10774451)	1	GA 48.1%
CD4 (rs3782736)	1	AC 49.9%
CD4 (rs1055141)	1	CT 49.0%
CD4 (rs3213427)	1	TC 49.1%
CD4 (rs1045261)	1	TC 26.4%
CD4	56%	
DAO		
DAO (rs2070586)		GG 68.7%
DAO (rs3741775)	1	AC 49.4%
DAOA (rs2391191)	1	GA 46.5%
DAO	67%	

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.

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger II	2.06	#N/A	1

The name of this gene is D-amino-acid oxidase and DAO is the gene's official symbol. Health conditions observed with this variant are: Schizophrenia, Bipolar Disorder, Primary Hyperoxaluria, ALS (Type 18) , Autism and Crohn's Disease.

Studies have found that the A allele in rs2391191 is a possible genetic feature of certain health conditions such as Schizophrenia, and Bipolar Disorder.

With two variants, there may be some stress/anxiety. When combined with high glutamate and GAD variants, even more potential for stress/anxiety.

## Lyme Study Phase I SNPs

These are the SNPs that were found to be most prevalent for individuals with chronic Lyme for our Phase I Study, and is not a test for Lyme. Inherited genetic mutations when expressed may reduce enzyme production. This can lead to, nutrient deficiencies, an increased production of free radicals or other toxic substances, or a slow clearing of toxic substances. Any one of these or a combination of may have the potential to allow Lyme to be resistant to traditional treatment by suppressing the immune system or susceptible to creating toxic conditions.

Gene Name	Variants	Metrics
<b>HFE and Potential Hydroxyl Radical Production SNPs</b>		
HFE C282Y (rs1800562)		GG 89.3%
HFE H63D (rs1799945)	1	CG 23.7%
CBS C699T (rs234706)		GG 45.8%
BHMT-08 (rs651852)	1	CT 49.2%
SOD2 (rs2758331)	1	CA 49.4%
SOD2 A16V (rs4880)	1	AG 49.5%
GSTP1 A114V (rs1138272)		CC 84.7%
GSTP1 I105V (rs1695)		AA 44.0%
CTH (rs1021737)		GG 50.7%
PEMT (rs4244593)	1	TG 48.5%
PEMT (rs7946)	2	TT 48.8%
PEMT (rs4646406)	1	TA 48.9%
HFE and Potential Hydroxyl Radical SNPs	67%	
<b>Mitochondrial Function SNPs</b>		
SLC22A5 (rs17622208)	1	GA 48.0%
SLC22A5 (rs2073643)	1	TC 49.0%
SLC22A5 (rs1045020)		CC 79.0%
ACAT-2 (rs3465)		GG 38.7%
ACAT-2 (rs3798211)	1	AC 48.1%
ACAT-2 (rs25683)	1	AG 48.2%
NDUFS7 (rs1142530)	2	TT 37.4%
Mitochondrial Function SNPs	56%	
<b>Methylation Cycle SNPs</b>		
MTHFR C677T (rs1801133)	1	GA 45.2%
MTHFR A1298C (rs1801131)		TT 47.7%
Methylation Cycle SNPs	75%	

Product Name	SNP Total	Lab Total	Symptoms
HFE Assist	14	#N/A	3
Pro SOD/Catalase Support	7.33	0	2
GSH Assist	4.39	0	2
Pro NADH	5.39	0	2

The following SNPs may increase the potential of the Fenton Reaction and those with Lyme had a higher number of SNPs in each of the genes. CBS699 and BHMT-08 may increase the cysteine, while the glutathione variants may slow the conversion of cysteine into glutathione. Variants in SOD genes may slow the ability to neutralize the hydroxyl radicals.

Further research is needed to determine if iron oxidation from the Fenton Reaction is a contributing factor to those with chronic Lyme, and if nutritional interventions with nutrients that may slow iron absorption, regulate iron, support cysteine to glutathione conversion and NADH to recycle glutathione and superoxide dismutase may be an appropriate holistic support.

Product Name	SNP Total	Lab Total	Symptoms
Mitochondrial & Energy Assist	8.89	0	0
Pro NADH	5.39	0	2

The following SNPs relate to mitochondrial function.

These findings may suggest that lowered energy production in the Krebs Cycle, may be a contributing factor to Chronic Lyme. Further studies of these findings are needed to confirm if these observations are clinically relevant, and if nutritional intervention with carnitine, choline, NADG, CoQ10 and pantethene may be a useful therapy when these variants are present.

These findings may suggest that an increased amount of SNPs in the MTHFR gene, in particular, and the entire Methylation pathway, may be a contributing factor in chronic Lyme. Further studies of these findings are needed to confirm if these observations are clinically relevant.

As a result of these observations, further analysis on a larger scale, and other lab testing may be warranted to see if these observed variants play a role in Chronic Lyme Disease and if supplementation of methyl folate, methyl B12, choline, B6, TMG and SAME may be helpful holistic therapies.

Urea Cycle SNPs		
CPS1 (rs1509821)		CC 81.4%
CPS1 (rs6435580)	1	CT 43.8%
CPS1 (rs12468557)	1	CT 45.7%
CPS1 (rs7607205)	1	TG 48.1%
ASS1 (rs12375699)		CC 34.8%
ARG2 (rs3742879)		AA 52.0%
ARG2 (rs742869)	1	GA 47.8%
Urea Cycle SNPs	71%	

Product Name	SNP Total	Lab Total	Symptoms
Ammonia Scavenger	7.11	0	5

The following SNPs relate to the Urea Cycle.

As a result of these observations, larger scale testing and associated lab work may be needed to see if these variants create increased ammonia burden and are clinically significant in those with Chronic Lyme Disease, and if supporting the Urea Cycle and ammonia clearance would be an appropriate nutritional therapy. Digestive support therapies that reduce ammonia may be appropriate as well.

Detoxification SNPs		
CYP1A1*4 C2453A (rs1799814)		GG 91.4%
CYP1B1 N453S (rs1800440)		TT 67.7%
PON1 (rs854561)	2	TT 12.8%
SOD2 (rs2758331)	1	CA 49.4%
GSTP1 A114V (rs1138272)		CC 84.7%
Detoxification SNPs	70%	

Product Name	SNP Total	Lab Total	Symptoms
PON1 Assist	0	0	0
Detox Accelerator	5	0	0
Pro SOD/Catalase Support	7.33	0	2
GSH Assist	4.39	0	2

The following SNPs relate to detoxification.

As a result of these observations, larger scale testing and associated lab work may be needed to see if these variants are clinically significant in those with Chronic Lyme Disease, and if supporting the detox mechanisms controlled by CYP, PON1, SOD, and glutathione would be an appropriate nutritional therapy. Additional nutritional therapies that scavenge peroxynitrite should be investigated as well.

Glutamate SNPs		
GAD1 (rs3791850)	1	GA 36.7%
GAD1 (rs3828275)	1	CT 49.7%
GAD1 (rs12185692)	1	CA 48.2%
GAD1 (rs3791878)	1	GT 41.0%
Glutamate SNPs	50%	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger II	2.06	#N/A	1

The following SNPs relate to glutamate.

As a result of these findings, future research may be needed to see if higher glutamate levels and peroxynitrite are associated with symptoms related to Lyme Disease, or if supporting the conversion into GABA may be a part of a holistic treatment plan.

DNA Repair SNPs		
ATM (rs1801516)		GG 73.8%
DNA Repair SNPs	100%	

Product Name	SNP Total	Lab Total	Symptoms
Cellular Health Assist	9.91	0	0

If those with chronic Lyme disease have higher rates of oxidative stress due to mitochondrial dysfunction, lowered ability to detox, iron oxidation, etc., higher rates of variants in the ATM genes may also play a contributing role. Further research may be warranted.

Total Lyme Study SNPs		
Total Lyme Study Phase I SNPs	65%	

## Lyme Study Phase II SNPs

These are the SNPs that were found to be most prevalent for individuals with chronic Lyme in our Phase II Study, and is not a test for Lyme. Inherited genetic mutations when expressed may reduce enzyme production. This can lead to, nutrient deficiencies, an increased production of free radicals or other toxic substances, or a slow clearing of toxic substances. Any one of these or a combination of may have the potential to allow Lyme to be resistant to traditional treatment by suppressing the immune system or susceptible to creating toxic conditions.



Gene Name	Variants	Metrics
<b>Allergic Response</b>		
FCER1A (rs2251746)		TT 55.8%
Allergic Response	100%	
<b>Antioxidant Detox</b>		
CAT (rs11032703)		CC 83.6%
Antioxidant Detox	100%	
<b>Beta-Carotene Metabolism</b>		
BCMO1 (rs4889294)		TT 31.0%
BCMO1 R267S (rs12934922)		AA 31.6%
Beta-Carotene Metabolism	100%	
<b>Drug Metabolization</b>		
NAT2 (rs2410556)		TT 76.3%
Drug Metabolization	100%	
<b>Fatty Acid Desaturase</b>		
FADS2 (rs174611)	1	TC 39.9%
Fatty Acid Desaturase	50%	
<b>Fatty Acid Lipid Biosynthesis</b>		
TALDO1 C749776T (rs11246300)		CC 62.8%
Fatty Acid Lipid Biosynthesis	100%	
<b>Peanuts Allergy</b>		
HLA-DQA2 (rs9275596)	1	TC 44.2%
Peanuts Allergy	50%	

The protein encoded by FCER1A represents the alpha subunit of the immunoglobulin epsilon receptor. This receptor is the initiator of an allergic response.

Product Name	SNP Total	Lab Total	Symptoms
Pro SOD/Catalase Support	7.33	0	2

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.

Studies have hypothesized that oxidative stress plays a role in the development of many chronic or late-onset conditions such as diabetes, asthma, Alzheimer's disease, and rheumatoid arthritis.

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 NAT2 gene encodes an enzyme that catalyzes the transfer of an acetyl group from acetyl-CoA to various arylamine and hydrazine substrates. This enzyme helps in the metabolization of drugs. Variations in these genes are associated with higher incidences of drug toxicity.

Product Name	SNP Total	Lab Total	Symptoms
Fatty Acid Assist	1	0	4

The protein encoded by the FAD2 gene is a member 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. Variations in these genes may affect long-chain polyunsaturated fatty acids metabolism.

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.

Studies have shown that peanut allergies are one of the most common food allergies.

Peanuts are not the same as tree nuts such as almonds, cashews, and walnuts. Peanuts grow underground and are part the legume family. Other examples of legumes include beans, peas, lentils and soybeans.

<b>Gluten Intolerance/Celica's Disease</b>			Variants in these genes may increase the chances of Celiac Disease or gluten intolerance. Other factors that may impact gut health are FUT variants that impact probiotics, HNMT and ABP1 variants that lessen histamine degradation and consequently cause zonulin production, low folate or high peroxynitrite.								
KIAA1109 (rs6822844)	1	GT 24.6%									
Gluten Intolerance/Celica's Disease	50%										
<b>Hydrolysis of Paroxon</b>			<table border="1"> <thead> <tr> <th>Product Name</th> <th>SNP Total</th> <th>Lab Total</th> <th>Symptoms</th> </tr> </thead> <tbody> <tr> <td>PON1 Assist</td> <td>0</td> <td>0</td> <td>0</td> </tr> </tbody> </table> <p>PON1 (Paraoxonase) plays a large role in removing pesticides. It is also involved with supporting HDL function, crucial for healthy circulation.</p>	Product Name	SNP Total	Lab Total	Symptoms	PON1 Assist	0	0	0
Product Name	SNP Total	Lab Total		Symptoms							
PON1 Assist	0	0		0							
PON1 (rs854561)	2	TT 12.8%									
Hydrolysis of Paroxon	0%										
<b>Immune System</b>			HLA-DRB1 belongs to the HLA class II of beta chain paralogs. It plays a central role in the immune system by presenting peptides derived from extracellular proteins.								
HLA-DRB1 (rs35445101)	1	AG 42.1%									
Immune System	50%										
<b>Histamine Inactivation</b>			<table border="1"> <thead> <tr> <th>Product Name</th> <th>SNP Total</th> <th>Lab Total</th> <th>Symptoms</th> </tr> </thead> <tbody> <tr> <td>Histamine Scavenger</td> <td>1.46</td> <td>#N/A</td> <td>4</td> </tr> </tbody> </table> <p>HNMT produces the enzyme that uses a methyl group to degrade histamine in the body.</p>	Product Name	SNP Total	Lab Total	Symptoms	Histamine Scavenger	1.46	#N/A	4
Product Name	SNP Total	Lab Total		Symptoms							
Histamine Scavenger	1.46	#N/A		4							
HNMT (rs4646322)		CC 69.2%									
Histamine Inactivation	100%										
<b>Lactose</b>			The MCM6 gene is a protein coding gene. Single nucleotide polymorphisms in this gene can impact the neighboring LCT gene. The LCT gene provides instructions for making an enzyme called lactase. Variations in the MCM6 genes cause the LCT gene to remain active during adulthood. Because of this, individuals with increased variants are more likely able to digest the lactose found in milk and dairy products.								
MCM6 (rs4988235)	1	GA 42.3%									
MCM6 (rs182549)	1	CT 41.6%									
Lactose	50%										

Mitochondria			Product Name	SNP Total	Lab Total	Symptoms
			Mitochondrial & Energy Assist	8.89	0	0
			Pro NADH	5.39	0	2
NDUFS4 (rs4147740)		TT 67.7%	Mitochondria -ATP Production			
UQCRC2 (rs4850)		GG 89.7%	NDUFS4 encodes a protein that is part of a subunit for Complex I. Complex I is the first enzyme of the mitochondrial electron transport chain. There are over 40 subunits found in Complex I.			
PANK1 (rs10509577)		AA 88.0%	Mitochondria -Complex III			
PANK1 (rs997456)		GG 61.0%	The protein encoded by UQCRC2 is located in the mitochondrion, where it is part complex III. This complex is part of the mitochondrial respiratory chain.			
PANK4 (rs7535528)		GG 41.3%	Mitochondria-CoA Synthesis			
			This gene encodes members of the pantothenate kinase family. Pantothenate kinase catalyzes the ATP-dependent phosphorylation of pantothenate (vitamin B5) to give 4&prime;-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.			
			PANK1 encodes a member of the pantothenate kinase family.			
			PANK4 is most abundant in muscle but is expressed in all tissues.			
Mitochondria - ATP	100%					
Mitochondria - CoA Synthesis	100%					
Mitochondria - Complex III	100%					
Total Phase II Mitochondria SNPs	100%					
Sex Hormone Binding Globulin						
SHBG (rs1799941)	1	GA 36.0%	Variants in the SHBG gene may cause dysregulation in testosterone and estrogen levels and lowered progesterone. Hormone testing may be in order if hormonal symptoms exist. For Men (especially older men), SHBG variants may indicate more circulating SHBG resulting in lowered testosterone levels. For women, SHBG variants may indicate less SHBG resulting in higher androgen levels overall.			
Sex Hormone Binding Globulin	50%					
Interfero Activation						
IRF5 (rs4728142)	1	GA 49.0%	The IRF5 gene encodes a member of the interferon regulatory factor (IRF) family. The role of this factor includes modulation of cell growth, differentiation, apoptosis, and immune system activity.			
Interfero Activation	50%					
Vitamin D Receptor						
VDR G14442A (rs3890733)	1	CT 43.0%	VDR is a protein coding gene. This gene encodes the nuclear hormone receptor for vitamin D3. This receptor also functions as a receptor for the secondary bile acid lithocholic acid.			
VDR G48288246A (rs11574026)		GG 80.6%				
VDR G48293716T (rs11168293)	1	GT 42.9%				
Vitamin D Receptor	67%					

Cannabinoid Receptors			The CNR1 gene encodes one of two cannabinoid receptors. The cannabinoid receptors are members of the guanine-nucleotide-binding protein (G-protein) coupled receptor family.
CNR1 (rs806380)		AA 45.0%	
CNR1 (rs806378)		CC 55.1%	
CNR1 (rs12205430)		TT 62.8%	
CNR1 T453T (rs1049353)		CC 55.7%	
Cannabinoid Receptors	100%		
Dopamine			<p>The protein encoded by ANKK1 belongs to the Ser/Thr protein kinase family, and protein kinase superfamily involved in signal transduction pathways. This gene is closely linked to DRD2 gene.</p> <p>The protein encoded by the DBH gene is an oxidoreductase belonging to the copper type II, ascorbate-dependent monooxygenase family. This protein converts dopamine to norepinephrine.</p> <p>DDC is a protein coding gene. The encoded protein catalyzes the decarboxylation of L-3,4-dihydroxyphenylalanine (DOPA) to dopamine, L-5-hydroxytryptophan to serotonin and L-tryptophan to tryptamine.</p> <p>DRD2 and DRD3 genes encode the D2 and D3 subtypes of the dopamine receptor. These G-protein coupled receptors inhibit adenylyl cyclase activity.</p> <p>The GCH1 gene encodes a member of the GTP cyclohydrolase family. The encoded protein is the first and rate-limiting enzyme in tetrahydrobiopterin (BH4) biosynthesis.</p>
ANKK1 G318R (rs11604671)		GG 33.1%	
DBH T8114C (rs2519155)	1	TC 42.6%	
DBH T13150C (rs2519152)	1	TC 48.1%	
DDC C166017G (rs1470750)	2	GG 16.7%	
DRD2 (rs17529477)	1	GA 42.6%	
DRD2 (rs12363125)	1	CT 46.8%	
DRD3 (rs11706283)		CC 82.2%	
DRD2 (rs4630328)	1	GA 45.6%	
GCH1 (rs2878169)		GG 82.3%	
DRD2 (rs2734839)	1	CT 47.0%	
DRD2 (rs2734838)	1	AG 46.9%	
DRD2 (rs2234690)	1	TA 46.1%	
DRD2 (rs1800498)	1	GA 46.9%	
DRD2 (rs1107162)	1	GA 46.8%	
DRD2 (rs1076563)	1	AC 46.3%	
DRD3 (rs963468)		GG 38.5%	
DRD2 (rs6277)	1	GA 48.9%	
Dopamine	59%		

Glutamate		
GLS (rs3088307)	2	GG 18.6%
GLS (rs6758866)		GG 34.2%
GOT1 (rs9971274)		GG 84.5%
GOT1 (rs9971275)		GG 84.5%
GOT1 (rs11190083)		AA 84.5%
GRIA1 (rs889062)	2	CC 22.8%
GRIA1 (rs1381119)		GG 63.9%
GRIA1 (rs1463747)	1	GT 48.2%
GRIA1 (rs1493383)		CC 67.6%
GRIA1 (rs1864205)		TT 48.8%
GRIA1 (rs2910263)	2	AA 30.8%
GRIA1 (rs2910266)	2	AA 7.1%
GRIA1 (rs7719292)	1	AG 32.6%
GRIA1 (rs11746246)		CC 51.7%
GRIA1 (rs11741511)	1	TC 37.6%
GRIA1 (rs11748500)		GG 51.7%
GRIA2 (rs17243330)		GG 70.4%
GAD1 (rs3791850)	1	GA 36.7%
GAD1 (rs3791878)	1	GT 41.0%
Glutamate	66%	
<b>Total Lyme Study Phase II SNPs</b>		
Total Lyme Study Phase II SNPs	70%	

Product Name	SNP Total	Lab Total	Symptoms
Glutamate Scavenger II	2.06	#N/A	1

GLS or Glutaminase encodes a protein that catalyzes the hydrolysis of glutamine to glutamate and ammonia.

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

GRIA1 and GRIA2 are Protein Coding genes and are glutamate receptors. Glutamate receptors are the predominant excitatory neurotransmitter receptors in human brains and are activated in a variety of normal neurophysiologic processes.

The GAD enzyme converts glutamate to GABA. When someone has high glutamate and a lot of variants in GAD, it creates conditions that may have high glutamate and low GABA that could increase stress and conditions related to high glutamate. It has been observed, that Homozygous variants in GAD have more impact than many Heterozygous. SER-GAB Assist and GABA Assist may be helpful if there is low GABA.