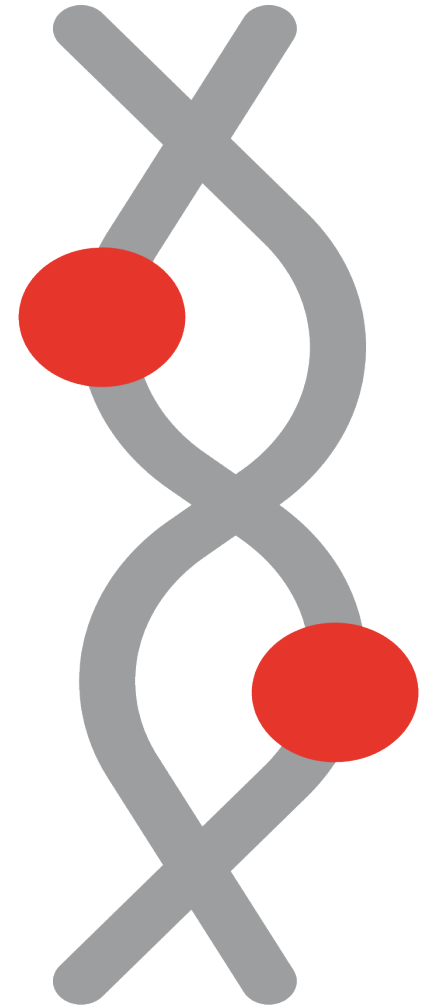




Gene Comprehensive Nutrigenomic Report

Accession Number: #####
Specimen Collected: ##/##/####
Specimen Received: ##/##/####
Report Generated: March 9, 2022
Specimen Type: Buccal Swab
Provider: #####
Patient Name: #####
Patient DOB: ##/##/####
Patient Gender: Male



Do not make any decisions about your health solely based on the information contained in this report.
Always consult with a licensed and experienced health practitioner when you receive this report.

– 57 – Male

(-/-) No clinical abnormality

(+/-) Heterozygous result

(+/+) Homozygous result

rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
METHYLATION					
rs2071010	FOLR1	-/-	Methyltetrahydrofolate (5-MTHF)		
rs651933	FOLR2	+/+			
rs1643649	DHFR	-/-			
rs6495446	MTHFS	+/-			
rs1076991	MTHFD1	+/-			
rs1801133	MTHFR C677T	-/-			
rs1801131	MTHFR A1298C	-/-			
rs1051266	SLC19A1	+/-			
rs1802059	MTRR A664A	-/-			
rs1801394	MTRR A66G	+/-			
rs526934	TCN1	-/-	Methyl B12, Adenosyl B12		
rs1801198	TCN2	+/+			
rs558660	GIF	+/-			

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NEUROTRANSMITTER					
rs4680	COMT V158M	+/-	B2 (Riboflavin), Methyl Donors (Taurine, Choline, Trimethylglycine (TMG), Dimethylglycine (DMG), Inositol, L-Methionine	Higher Risk of Depression / Anxiety	Consider PGx Testing
rs6323	MAO-A	-/NA			
rs1799836	MAO-B	-/NA			
rs769407	GAD1	+/-	Prescription Amantadine, Ketamine, Glycine, N-Acetyl-Cysteine (NAC), Zinc, Magnesium, Oxaloacetate, Elderberry, L-Theanine, Melatonin	Be cautious with MSG (monosodium glutamate) exposure and glutamine supplementation	
rs3828275	GAD1	-/-			

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rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
MITOCHONDRIA					
rs4147730	NDUFS3	-/-	CoQ 10, PQQ, L-Carnitine, Ornithine, Magnesium, NADH, Calcium		
rs809359	NDUFS7	-/-			
rs1051806	NDUFS8	-/-			
rs11648723	UQCRC2	-/-			
rs4850	UQCRC2	-/-			
rs8042694	COX5A	+/-			
rs4626565	COX6C	-/-			
rs1244414	ATP5C1	+/-			

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rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
DETOXIFICATION					
rs1021737	CTH	+/+	N-Acetyl Cysteine (NAC), Glutathione	Herbicide and Pesticide Avoidance	
rs819147	AHCY	-/-			
rs1056806	GSTM1	-/-	Glutathione		
rs7483	GSTM3	+/-			
rs1695	GSTP1 I105V	+/-			
rs1208	NAT2	+/+	Silymarin, Alpha Lipoic Acid (ALA), P-5-P, Catechins	Avoid Industrial Carcinogens	
rs4880	SOD2	+/+	High Dose Antioxidants, Curcumin, Sulforaphane, Vitamin C	Consider high antioxidant diet (fruits and vegetables)	

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rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
INFLAMMATORY					
rs2069812	IL5	+/-	Anti-Inflammatory Therapy: Curcumin, Omega 3s, Resveratrol, Quercetin, Low Dose Naltrexone (LDN), CBD Oil	Consider Low Inflammatory Diet	Consider Testing Pregnenolone, Cortisol, Progesterone, Testosterone
rs10402876	C3	+/-			
rs2569191	CD14	+/-			
rs1800925	IL13	+/-			
rs10181656	STAT4	+/-			
rs1800629	TNF	-/-			
rs231775	CTLA4	+/-			
rs2248814	NOS2	+/-	Anti-Infectives, Beta Glucans		

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rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
ENVIRONMENTAL INFLAMMATORY					
rs10156191	AOC1	-/-	Poor Ability To Break Down External Histamine		
rs492602	FUT2	+/-	Prebiotics and Probiotics Needed		
rs2187668	HLA DQA1	-/-	High Risk of Gluten Based Issues		
rs2858331	HLA DQA2	-/-			
rs10210302	ATG16L1	+/-	Curcumin, Lithium Orotate, D-Chiro-Inositol, Catechins, Resveratrol, 12-15 Hour Fasting	12-15 Hour Fasting	Routine Blood Sugar, Insulin and Hb A1c
rs2241880	ATG16L1	+/-			
rs510432	ATG5	-/-			
rs26538	ATG12	-/-			
rs731236	VDR Taq	+/+	Vitamin D, Vitamin K		Consider Checking Vitamin D Level

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rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
HEALTH PRECAUTIONS					
rs1867277	FOXE1	-/-	Iodine, Selenium, Increased Risk of Hypothyroidism		
rs4343	ACE	+/-	Increased risk of salt retention and hypertension		
rs1800440	CYP1B1	+/-	Increased Levels of 4-hydroxy Estrogen, Endometriosis and Osteoporosis		
rs6025	F5	-/-			
rs3211719	F10	+/-			

Summary for Pro7

Lifestyle Recommendations

- Higher Risk of Depression / Anxiety
- Be cautious with MSG (monosodium glutamate) exposure and glutamine supplementation
- Herbicide and Pesticide Avoidance
- Avoid Industrial Carcinogens
- Consider high antioxidant diet (fruits and vegetables)
- Consider Low Inflammatory Diet
- 12-15 Hour Fasting

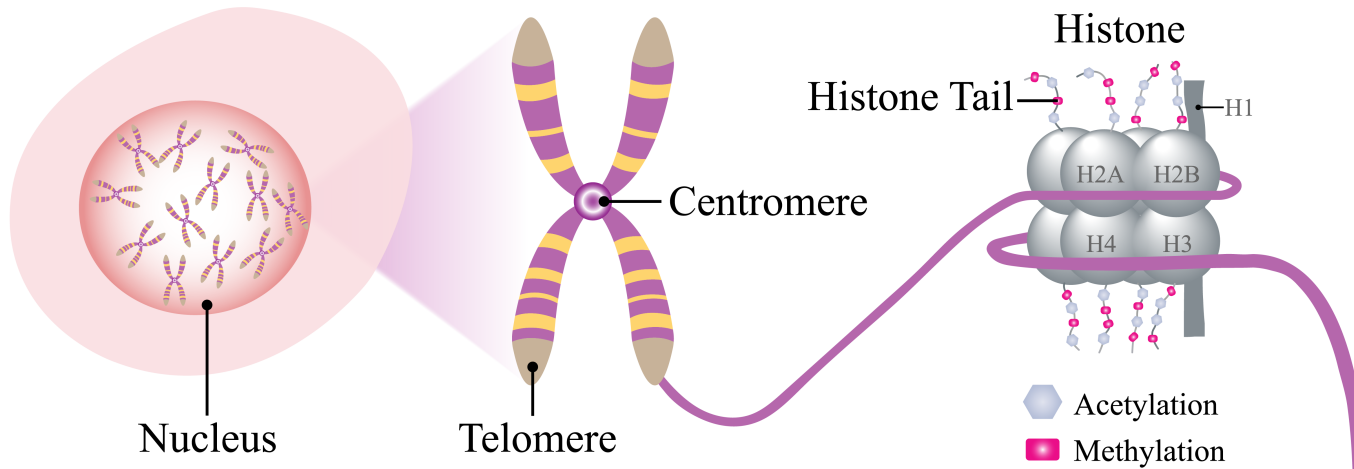
Laboratory Recommendations

- Consider Checking Plasma B12 Level
- Consider PGx Testing
- Consider Testing Pregnenolone
- Cortisol
- Progesterone
- Testosterone
- Routine Blood Sugar
- Insulin and Hb A1c
- Consider Checking Vitamin D Level

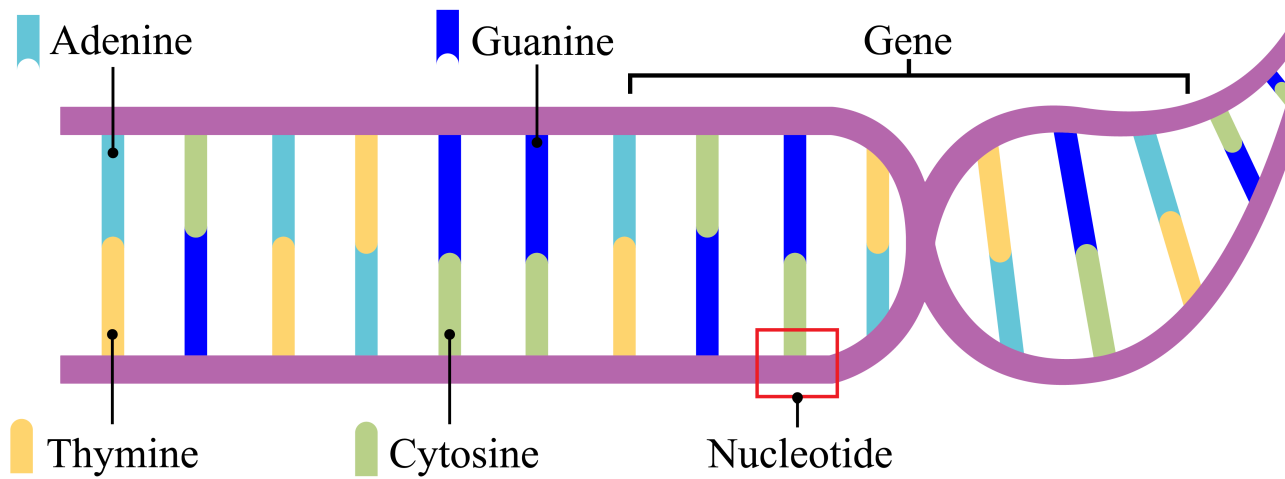
Cell

Chromosome

Nucleosome



DNA



Gene Information Key

rsID	Gene	"-" variant	"+" variant
rs4343	ACE	A	G
rs819147	AHCY	T	C
rs10156191	AOC1	C	T
rs26538	ATG12	T	C
rs2241880	ATG16L1	A	G
rs10210302	ATG16L1	C	T
rs510432	ATG5	C	T
rs1244414	ATP5C1	C	T
rs10402876	C3	G	C
rs2569191	CD14	T	C
rs4680	COMT V158M	G	A
rs8042694	COX5A	A	G
rs4626565	COX6C	T	C
rs1021737	CTH	G	T
rs231775	CTLA4	A	G
rs1800440	CYP1B1	T	C
rs1643649	DHFR	T	C
rs3211719	F10	A	G
rs6025	F5	C	T
rs2071010	FOLR1	G	A
rs651933	FOLR2	A	G
rs1867277	FOXE1	G	A
rs492602	FUT2	A	G
rs769407	GAD1	G	C
rs3828275	GAD1	C	T
rs558660	GIF	G	A
rs1056806	GSTM1	C	T
rs7483	GSTM3	C	T
rs1695	GSTP1:I105V	A	G

rsID	Gene	"-" variant	"+" variant
rs2187668	HLA-DQA1	C	T
rs2858331	HLA-DQA2	A	G
rs1800925	IL13	C	T
rs2069812	IL5	A	G
rs6323	MAO-A	T	G
rs1799836	MAO-B	T	C
rs1076991	MTHFD1	C	T
rs1801131	MTHFR:A1298C	T	G
rs1801133	MTHFR:C677T	G	A
rs6495446	MTHFS	C	T
rs1802059	MTRR:A664A	G	A
rs1801394	MTRR:A66G	A	G
rs1208	NAT2	A	G
rs4147730	NDUFS3	G	A
rs809359	NDUFS7	A	G
rs1051806	NDUFS8	C	T
rs2248814	NOS2	G	A
rs1051266	SLC19A1	T	C
rs4880	SOD2	A	G
rs10181656	STAT4	C	G
rs526934	TCN1	A	G
rs1801198	TCN2	C	G
rs1800629	TNF	G	A
rs4850	UQCRC2	G	A
rs11648723	UQCRC2	G	T
rs731236	VDR Taq	A	G

Definitions

CLOT RISK	The SNPs in this category define some areas of potential concern in the clotting mechanisms of the body. Polymorphisms in these proteins may need to be considered during pregnancy, surgery, trauma and/or certain forms of birth control
Factor V	A single nucleotide polymorphism in the F5 gene (rs6025) leads to a mutant Factor V protein. This mutant protein is associated with increased clotting, especially in the veins.
Factor X	The F10 gene encodes a protein, Factor X, involved in coagulation and wound healing. Mutations in the F10 gene predict for clot risk and anticoagulant drug sensitivity.
DETOXIFICATION	Detoxification enzymes are responsible for clearing environmental chemicals and metabolites from our body. Accumulation of these chemicals and by-products can damage intracellular biochemical functions. Alterations in these systems can have a significant negative effect on the nervous system and immune systems functions. These polymorphisms can result in decreased "quality of life" and even decreased "life-span".
AHCY	Adenosylhomocysteinase (AHCY) is an enzyme that breaks down S-adenosylhomocysteine (SAH) to homocysteine and adenosine. Polymorphisms in this gene will lead to lower levels of homocysteine and glutathione.
CTH	Glutathione production is dependent on the function of the enzyme cystathionine gamma-lyase (CTH). CTH converts cystathionine to cysteine. Individuals with mutations in the CTH gene are predicted to have decreased glutathione-mediated detoxification.
GSTM1	Glutathione S-transferase M1 (GSTM1) is an important enzyme in the body's detoxification pathway. GSTM1 conjugates glutathione to molecules (drugs, environmental toxins, carcinogens etc.) bound for excretion. GSTM1 is mainly responsible for binding toxins in joints and for binding carcinogens.
GSTM3	Glutathione S-transferase mu 3 is an enzyme that detoxifies drugs, environmental toxins, and carcinogens by conjugating toxins to glutathione and subsequent excretion by the kidneys. Mutations in GSTM3 are associated with decreased clearance of toxins, anesthetics and drugs from the nervous system.
GSTP1	Glutathione S-transferases (GSTs) are a family of enzymes that play an important role in detoxification. The glutathione S-transferase pi gene (GSTP1) functions in chemical clearance and anti-inflammatory properties. High concentration of GST-p are found in the skin, lungs, sinuses, bladder and the intestinal tract. Polymorphisms of this enzyme allow for increased inflammatory activity in these areas that include eczema, asthma, chronic sinusitis, IBS, "leaky" gut and interstitial cystitis.
NAT2	N-Acetyl Transferase 2 (NAT2) is a liver enzyme that functions to both activate and deactivate drugs and carcinogens. Polymorphisms in this gene are divided into rapid, intermediate, and slow acetylator phenotypes. The slow polymorphism phenotype of NAT2 are also associated with higher incidences of cancer and drug toxicity.
SOD2	Mitochondrial Superoxide Dismutase 2 (SOD2) is a member of the iron/manganese mitochondrial superoxide dismutase family. This protein transforms toxic superoxide, a byproduct of the mitochondrial electron transport chain, into hydrogen peroxide and oxygen. This function allows SOD2 to clear mitochondrial reactive oxygen species (ROS) and, as a result, confer protection against mitochondrial damage and cell death.
DEVELOPMENTAL	The SNPs in this category have been identified as potential areas of weakness in the recovery of developmental disorders.
ATG12	Autophagy-related 12 protein is part of the core autophagy machinery inside the cell. Autophagy, a form of cellular "recycling" is necessary for many cell functions. ATG12 is specifically involved in turning off the innate immune response. Mutations in the ATG12 gene are predicted to lead to increased activity of the innate immune response, and overall inflammation.
ESTROGEN METABOLISM AND CLEARANCE	The conversion of estrogen and its' metabolites is essential to effective safe estrogen treatment. These SNPs will identify your potential for increased production of possible carcinogenic forms of estrogen
CYP1B1	The CYP1B1 gene encodes a member of the cytochrome P450 family of enzymes. CYP1B1 is involved in metabolizing lipids, fats, cholesterol, and steroid hormones. SNPs in the CYP1B1 gene predict risk of hormone dependent diseases and efficacy of treatments of such diseases.
HYPERTENSION	The polymorphisms in this category will increase the risk of developing hypertension.
ACE	Angiotensin-converting enzyme (ACE) is an important target for therapeutic drugs treating hypertension and heart failure. The best studied single nucleotide polymorphism in the ACE gene (rs4343) has been linked to a wide variety of human phenotypes: nephropathy and renal disease, cancer, and even sports performance. Interestingly, rs4343 is a member of a large family of human mutations called Alu elements.
INFLAMMATORY	This Enzyme category has significant effects on the inflammatory state of a person's body. Polymorphisms in these specific enzymes will significantly increase the levels of inflammation in the body. By supplementing these enzyme deficiencies, the patient will effectively reduce inflammatory damage to the body.
AOC1	The SNP rs10156191 encodes a weaker form of the histamine degradation enzyme Amine Oxidase, Copper Containing 1 (AOC1). This mutation, Thr16Met, is predicted to produce an enzyme with less catalytic activity and associated higher levels of pro-inflammatory amines like histamine and putrescine.

ATG16L1 rs10210302	The ATG16L1 gene encodes a protein that is a vital component of a protein complex necessary for the cellular phenomena known as autophagy. Autophagy is the process of degrading and cleaning of inert debris of the cell. Weakness in autophagy leads to abnormal accumulation of cellular "garbage" that will eventually affect the cellular function and lead to autophagy-related disease states including many neurological and immunological diseases, DM Type 2 and fatty liver disease.
ATG5	Autophagy-related 5 protein (ATG5) is an important intracellular mediator of the autophagy response. ATG5 is involved in a wide range of "quality control" features inside the cell: autophagy vesicle formation, innate immune system signaling, consumption of damaged mitochondria, and apoptosis. Mutations in the ATG5 gene are associated with numerous neurological, immunological and endocrine syndromes.
C3	Essential for the immune response, C3 is a protein involved in initiation of the complement system. C3 polymorphisms are associated with susceptibility to asthma and other inflammatory disorders.
CD14	The CD14 protein is a macrophage cell surface receptor that binds bacterial cell wall components. As one of the initiators of the innate immune response, fully functional CD14 is necessary for normal response to potential pathogens. Mutations in the CD14 gene are associated with susceptibility to asthma and other allergen-mediated inflammatory processes.
CTLA4	Cytotoxic T-lymphocyte Associated protein 4 (CTLA4) is an important inhibitor of T-cell activity: CTLA4 is part of the signaling cascade that turns off overactive T cells. Mutations in the gene that encodes CTLA4 are associated with a host of diseases characterized by a heightened immune state.
FUT2	Fucosyltransferase 2 (FUT2) is responsible for producing specific sugar groups that are secreted by the intestinal cells into the bowel to attract "good bacteria" . Polymorphisms in this gene produce "poor secrete" status. Lack of these sugars allows for gut dysbiosis and a higher risk of inflammatory bowel disease.
HLA-DQA1	Major histocompatibility complex, DQ alpha 1 (HLA-DQA1) is a human gene responsible for a cell surface receptor essential to the function of the immune system. Patients with a polymorphism in this gene are at higher risk for auto-immune based inflammatory disease including Celiac disease, Crohn's, Ulcerative Colitis, and gluten sensitivity.
HLA-DQA2	Major histocompatibility complex, DQ alpha 2 (HLA-DQA2) is a human gene responsible for a cell surface receptor essential to the function of the immune system. Patients with a polymorphism in this gene are at higher risk for auto-immune based inflammatory disease including Celiac disease, Crohn's, Ulcerative Colitis, and gluten sensitivity.
IL13	IL13 (Interleukin 13) is a member of the interleukin family of chemical messengers of the immune system. Polymorphisms in this gene are associated with changes in IL13 gene expression and increase the risk of more severe inflammatory responses to allergens.
IL5	The protein product of the Interleukin 5 gene (IL5) is important for normal development of B lymphocytes and eosinophils (a pro-inflammatory white blood cell). Inactivating mutations in the IL5 gene are associated with susceptibility to certain viral infections and increased aggression of inflammatory response. These polymorphisms are also associated with increased aggression of allergies, asthma and eosinophilia.
NOS2	Nitric Oxide Synthase 2 (NOS2) is responsible for producing nitric oxide, a biologic mediator used by the nervous system, immune system and in blood vessel function. Polymorphisms in this enzyme can cause reduced immune system function, exercise intolerance and fatigue.
STAT4	The Signal Transducer and Activator of Transcription 4 (STAT4) gene encodes a transcription factor that responds to extracellular growth factors and cytokines. Mutations in the STAT4 gene are associated with inflammatory disorders like lupus and rheumatoid arthritis.
TNF	Tumor necrosis factor, TNF, is an important pro-inflammatory signaling molecule. Polymorphisms in the protein coding part of this gene are associated with more severe pro-inflammatory responses and require supplementation for inflammatory control.
VDR Taq1	The Vitamin D (calcitriol) Receptor is a member of the nuclear receptor family. Upon activation by vitamin D (a secosteroid), the VDR causes the activation or deactivation of protein production by the cell. Impaired vitamin D function can result in significant immune weakness and increased cancer risk, as well as, early bone loss, an increased risk of cognitive decline and mood disorders.
METABOLIC RISK FACTOR	The polymorphisms in this category relate to increase risk of developing metabolic syndromes including diabetes, fatty liver, hypothyroidism and insulin resistance.
FOXE1	FOXE1 (Forkhead Box Protein E1) is a gene that codes for a protein that is intimately involved in thyroid hormone synthesis. Polymorphisms in this gene most commonly lead to an increased risk of hypothyroidism due to a weakened ability to synthesize thyroid hormone.
METHYLATION	Methylation is a primary biochemical process in the body that involves the addition of a "methyl" chemical group to a vitamin or neurotransmitter. The addition of the "methyl" group allows for very specific biochemical interactions. Poor "methylation" function alters the effectiveness, delivery and function of many vitamins and important chemicals in the cell.
DHFR	Dihydrofolate reductase, or DHFR, is an enzyme that reduces dihydrofolic acid to tetrahydrofolic acid. This enzyme is the second enzyme in the folic acid conversion chain. Having a mutation in this enzyme can create a methylation deficiency with a MTHFR mutation.

FOLR1	Folate Receptor 1 (FOLR1) is a member of the folate receptor (FOLR) family. Members of this gene family have a high affinity for folate. Polymorphisms in this gene allow for poor delivery of folate to the interior of cells. This can create a high plasma folic acid. This polymorphism does create a methylation deficiency. This polymorphism is associated with many disorders of pregnancy.
FOLR2	Folate Receptor 2 (FOLR2) is a member of the folate receptor (FOLR) family. Members of this gene family have a high affinity for folic acid. Polymorphisms in this gene allow for poor delivery of folic acid to the interior of cells. This can create a high plasma folic acid. This polymorphism does create a methylation deficiency. This polymorphism is associated with many disorders of pregnancy. This receptor is found in high quantities on the placenta, thymus and bone marrow. Can be affiliated with immune disorders.
GIF	The glycoprotein product of the Gastric Intrinsic Factor (GIF) gene is secreted by the stomach lining. GIF protein is required for absorption of Vitamin B12. B12 is necessary for normal red blood cell maturation.
MTHFD1	Methylenetetrahydrofolate Dehydrogenase 1 enzyme handles 2 significant enzymes conversions in the production of L-MTHF. This common polymorphism causes a significant methylation deficiency due to the fact that it is utilized in two steps in methyl-folate production.
MTHFR A1298C	Methylenetetrahydrofolate reductase (MTHFR) catalyzes the conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, the bioactive form of folic acid. Two significant polymorphism variants exist in this gene, the A1298C and the C677T. The 1298 confers a conversion weakness of 10% for one copy and approximately 20% for two copies. In contrast, the 677 variant is much more severe and conveys a 40% conversion weakness for one copy and 70% for two copies. A reduced level of MTHFolate produces significant biochemical effects including poor production of dopamine and serotonin, pregnancy complications, poor healing of the nervous system, weak mitochondrial function, reduced production of glutathione, poor cell turnover and poor function of T cell lymphocytes.
MTHFR C677T	Methylene tetrahydrofolate reductase (MTHFR) catalyzes the conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, the bioactive form of folic acid. Two significant polymorphism variants exist in this gene, the A1298C and the C677T. The 1298 confers a conversion weakness of 10% for one copy and approximately 20% for two copies. In contrast, the 677 variant is much more severe and conveys a 40% conversion weakness for one copy and 70% for two copies. A reduced level of MTHFolate produces significant biochemical effects including poor production of dopamine and serotonin, pregnancy complications, poor healing of the nervous system, weak mitochondrial function, reduced production of glutathione, poor cell turnover and poor function of T cell lymphocytes.
MTHFS	MTHFS (methenyletetrahydrofolate synthase) is an enzyme that catalyzes the conversion of 5-formyltetrahydrofolate to 5,10-methenyletetrahydrofolate, a precursor of reduced folates. This polymorphism codes for a decreased function of the enzyme and results in poor utilization of Leucovorin (5-formyltetrahydrofolate)..
MTRR Ala637=	Methionine Synthase Reductase is an enzyme responsible for the production of methionine, a very important amino acid. Polymorphisms in this enzyme require an increased amount of Methyl B12 to help this reaction.
SLC19A1	The SLC19A1 gene encodes the reduced folate carrier (RFC) protein. Mutations in the RFC are associated with reduced plasma folate.
TCN1	The protein product of the transcobalamin 1 (TCN1) gene binds Vitamin B12 and protects it from the low pH environment of the human stomach. Individuals homozygous for the G allele of the TCN1 SNP, rs526934, are predicted to have lower serum B12.
TCN2	The protein product of the Transcobalamin 2 gene, TCN2, binds the active form of vitamin B-12. Individuals with the G/G phenotype at rs1801198 have decreased serum B-12 and increased homocysteine when compared to individuals with the C/C phenotype.
MITOCHONDRIA	The mitochondrial enzymes are responsible for energy production from the mitochondria. The mitochondria is known as the "powerhouse" of the cell and produces over 90% of the energy for a cell. The mitochondrial respiratory chain (also known as the electron transport chain) is where these 4 protein complexes are found. Polymorphic alterations in these enzymes reduce the energy output of the mitochondria and leads to symptoms of chronic fatigue, cognitive deficiency, exercise intolerance, low metabolic rate, muscle weakness, poor healing and higher rates of sleep disorders and mood abnormalities.
ATP5C1	ATPase 5c1 (ATP5C1) is an enzyme responsible for producing ATP (the energy component) in the mitochondria. This protein is known as Complex V (the 5th protein) in the mitochondrial respiratory chain. Polymorphisms in the gene confer a weakened energy production by the mitochondria.
COX5A	Cytochrome c oxidase subunit 5a (COX5A) is a protein in a subunit of the cytochrome c oxidase complex, also known as Complex IV of the mitochondrial electron transport chain. Polymorphisms in this enzyme produce a weakened energy production by the mitochondria.
COX6C	Cytochrome c oxidase subunit 6c (COX6C) is a protein in a subunit of the cytochrome c oxidase complex, also known as Complex IV of the mitochondrial electron transport chain. Polymorphisms in this enzyme produce a weakened energy production by the mitochondria.
NDUFS3	The NDUFS3 genes encodes a mitochondrial enzyme, NADH Dehydrogenase (Ubiquinone) Fe-S Protein 3. Like other NDUFS proteins, NDUFS3 is thought to require ubiquinone for full activity.
NDUFS7	NADH Dehydrogenase [ubiquinone] iron-sulfur protein 7 (NDUFS7) is a mitochondrial protein also know as Complex I of the mitochondrial respiratory chain. It is located in the mitochondrial inner membrane and is the largest of the five complexes of the electron transport chain. Polymorphisms in this enzyme produce a weakened energy production in the mitochondria.

NDUFS8	NADH Dehydrogenase (Ubiquinone) Fe-S Protein 8 (NDUFS8) encodes an enzyme in the mitochondrial respiratory chain. Mutations in the NDUFS8 gene are associated with Leigh Syndrome, osteoporosis, and mitochondrial complex I deficiency.
UQCRC2 Arg183Gln	Ubiquinol Cytochrome c Reductase (UQCR, Complex II) is a mitochondrial enzyme protein also known as Complex III of the electron transport chain. Polymorphisms in this enzyme produce a weakened energy production by the mitochondria.
NEUROTRANSMITTER	Neurotransmitters are chemicals that are used to produce specific effects in the nervous system. These specific neurotransmitter genomics assess a person's risk for anxiety, depression and dysphoria.
COMT V158M	Catechol-O-methyltransferase (COMT) is one of several enzymes that degrade catecholamine neurotransmitters such as dopamine, epinephrine, and norepinephrine. COMT's main function is to inactivate neurotransmitters (dopamine, epinephrine, and norepinephrine) by the addition of a methyl group to the catecholamine. Normal COMT function allows people to rapidly reverse feelings of anxiety or depression. COMT (+/-) patients have sluggish ability to alter anxiety or depression episodes. COMT (+/+) patients are more prone to prolonged episodes of anxiety, depression and OCD.
GAD1 rs3828275	Glutamic Acid Decarboxylase (GAD 1) is the enzyme responsible for conversion of glutamic acid (a stimulant neurotransmitter) to GABA (a calming neurotransmitter). Deficiency of GABA from polymorphisms in this enzyme are associated with sleep disorders, "half glass empty" syndrome, dysphoria, and spasticity.
MAOA	Monoamine oxidase A (MAOA) is one of the classic neurotransmitter degradation enzymes. By degrading serotonin, dopamine, epinephrine, and norepinephrine, MAO-A ends neuronal signaling induced by those neurotransmitters. Mutations in the MAO-A gene leads to decreased degradation of these neurotransmitters and can be associated with increased aggression, mood disorders and drug addiction.
MAOB	Monoamine Oxidase B (MAO B) catalyzes the neuroactive amines, such as dopamine, epinephrine, norepinephrine, and plays a role in the stability of mood in the central nervous system,. MAO B's primary purpose is to degrade dopamine. Patients who possess polymorphisms of MAO B have a higher risk of clinical depression and mood disorders.

Disclaimers

METHODOLOGY AND LIMITATIONS:

Testing for genetic variation/mutation on listed genes was performed using ProFlex PCR and Real-Time PCR with TaqMan® allele-specific probes on the QuantStudio 12K Flex. All genetic testing is performed by GX Sciences, 4150 Freidrich Lane, Ste H, Austin, TX. 78744. This test will not detect all the known alleles that result in altered or inactive tested genes. This test does not account for all individual variations in the individual tested. Test results do not rule out the possibility that this individual could be a carrier of other mutations/variations not detected by this gene mutation/variation panel. Rare mutations surrounding these alleles may also affect our detection of genetic variations. Thus, the interpretation is given as a probability. Therefore, this genetic information shall be interpreted in conjunction with other clinical findings and familial history for the administration of specific nutrients. Patients should receive appropriate genetic counseling to explain the implications of these test results. Details of assay performance and algorithms leading to clinical recommendations are available upon request. The analytical and performance characteristics of this laboratory developed test (LDT) were determined by GX Sciences' laboratory pursuant to Clinical Laboratory Improvement Amendments (CLIA) requirements.

CLIA #: 45D2144988 Laboratory Director: James Jacobson, PhD

DISCLAIMER:

This test was developed and its performance characteristics determined by GX Sciences. It has not been cleared or approved by the FDA. The laboratory is regulated under CLIA and qualified to perform high-complexity testing. This test is used for clinical purposes. It should not be regarded as investigational or for research. rsIDs for the alleles being tested were obtained from the dbSNP database (Build 142).

DISCLAIMER:

UND Result: If you have received the result Variant undetermined (UND) this indicates that we were not able to determine your carrier status based on your raw data. Please refer to the GX Sciences genetic knowledge database for more information: https://www.gxsciences.com/kb_results.asp

DISCLAIMER:

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