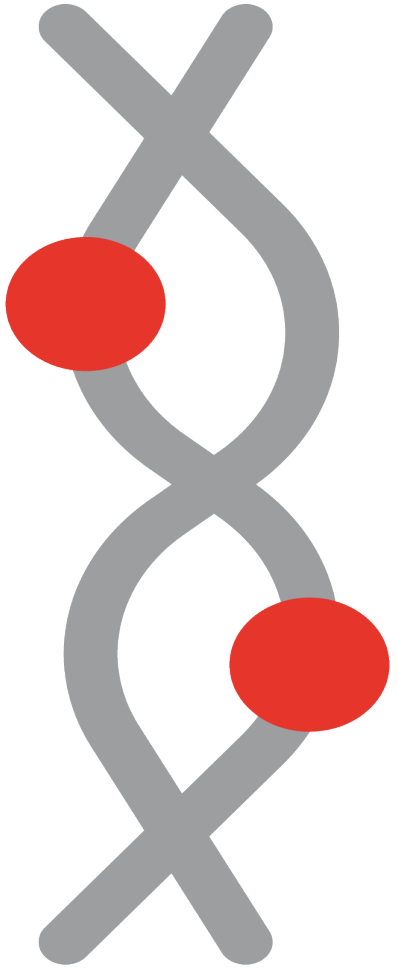
LIFE EXTENSION®

The Science of a Healthier Life™



Gene Comprehensive Nutrigenomic Report

Accession Number: NUG2026-00215
Specimen Collected: January 5, 2026
Specimen Received: January 14, 2026
Report Generated: January 14, 2026
Specimen Type: Buccal Swab
Provider: Derrick Bowling
Patient Name: Example Testing
Patient DOB: 08/08/2000
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.

Summary for Detoxification

Lifestyle Recommendations	Laboratory Recommendations
DETOXIFICATION	
• Herbicide and Pesticide Avoidance • Caution with Long Duration Anesthesia	• Plasma Homocysteine
• Consume Antioxidant Rich Diet	

Fagron Genomics US | 844-258-5564 | FagronGenomicsUS.com
Lab | 807 Las Cimas Pkwy, Suite 145 | Austin, TX 78746
Laboratory Director: James W. Jacobson, Ph.D

Example Testing – 25 – Male

(-/-) Normal Risk | (-/+) Medium Risk | (+/+) High Risk

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					
rs6721961	NFE2L2	G/G (-/-)	Pterostilbene, Green Tea (Epigallocatechin Gallate), Tumeric, Sulforaphane, Endurance Exercise		
rs8190955	GSR	G/G (-/-)	Riboflavin, Reduced Glutathione		
rs13043752	AHCY	G/G (-/-)	N-Acetyl Cysteine (NAC), Glutathione	Herbicide and Pesticide Avoidance Caution with Long Duration Anesthesia	Plasma Homocysteine
rs234706	CBS	G/G (+/+)	Methyltetrahydrofolate, Methylcobalamin, Pyridoxal 5'-Phosphate (B6), Choline, Trimethylglycine, Serine, N-Acetyl Cysteine		
rs1021737	CTH	G/G (-/-)	N-Acetyl Cysteine (NAC), Glutathione		

Fagron Genomics US | 844-258-5564 | FagronGenomicsUS.com
Lab | 807 Las Cimas Pkwy, Suite 145 | Austin, TX 78746
Laboratory Director: James W. Jacobson, Ph.D

Example Testing – 25 – Male

(-/-) Normal Risk | (-/+) Medium Risk | (+/+) High Risk

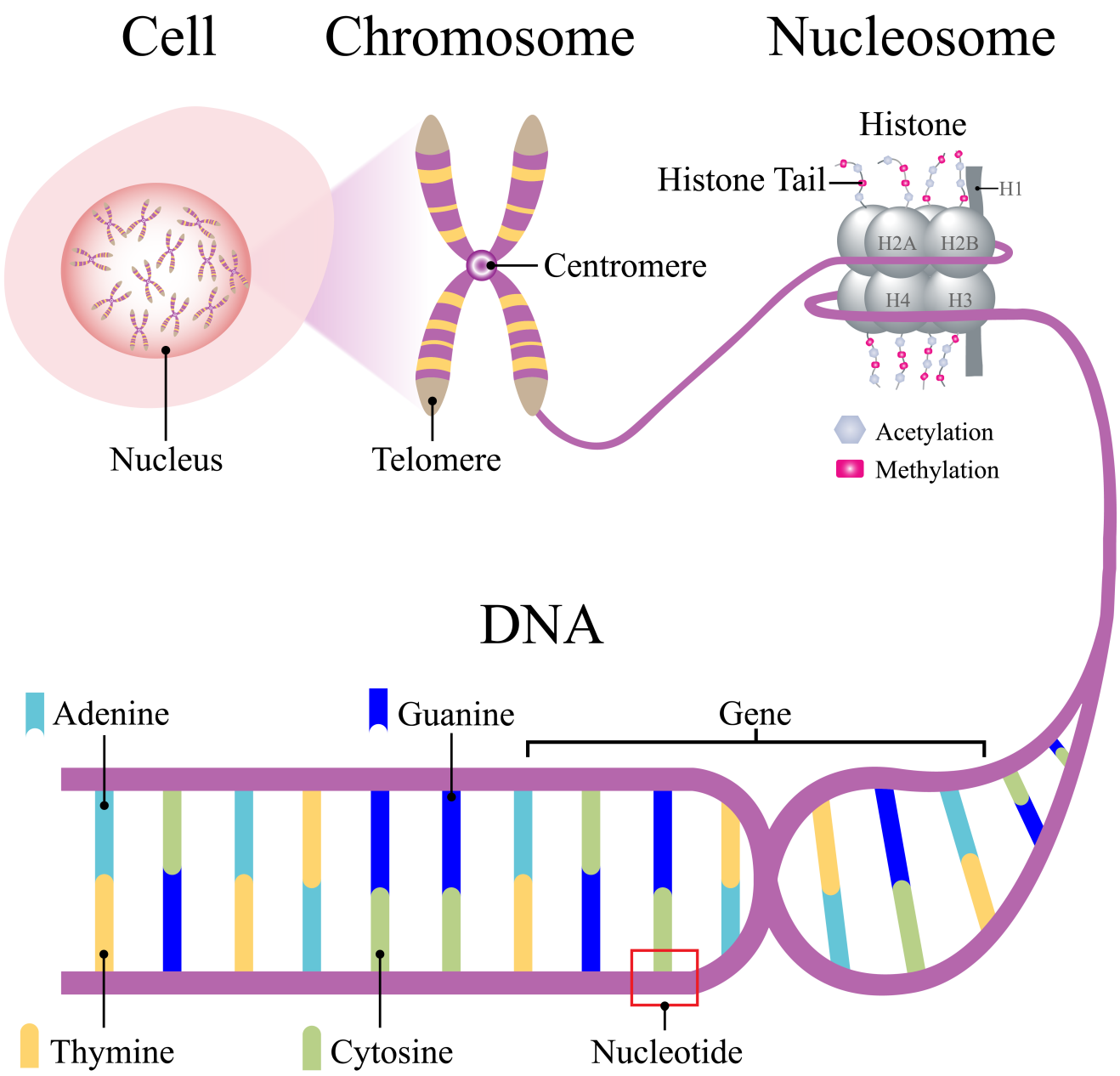
rsID	Gene	Genetic Result	This column contains the targeted ingredients to support healthy gene activity of the specific genes listed.	Lifestyle Recommendations	Laboratory Recommendations
DETOXIFICATION					
rs17883901	GCLC	G/G (-/-)	Glutathione		
rs1332018	GSTM3	G/T (+/-)	Glutathione		
rs1695	GSTP1	A/A (-/-)			
rs1050450	GPX1	G/G (-/-)	Glutathione, Selenium		

Fagron Genomics US | 844-258-5564 | FagronGenomicsUS.com
Lab | 807 Las Cimas Pkwy, Suite 145 | Austin, TX 78746
Laboratory Director: James W. Jacobson, Ph.D

Example Testing – 25 – Male

(-/-) Normal Risk | (-/+) Medium Risk | (+/+) High Risk

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					
rs2070424	SOD1	A/G (+/-)	High Dose Antioxidants, Curcumin, Sulforaphane, Vitamin C	Consume Antioxidant Rich Diet	
rs4880	SOD2	A/A (+/+)			
rs2536512	SOD3	A/A (-/-)			
rs1801280	NAT2	T/T (-/-)	Silymarin, Alpha Lipoic Acid (ALA), P-5-P, Catechins		


Cell
Chromosome
Nucleosome
Nucleus
Telomere
Centromere
Histone
Histone Tail
H1
H2A
H2B
H4
H3
Acetylation
Methylation
DNA
Adenine
Guanine
Gene
Thymine
Cytosine
Nucleotide

DETOXIFICATION

GLUTATHIONE IN DETOXIFICATION

Relevant genes for production are AHCY, CTH, GSTP1, GSTM1, GSTM3, GSR, MTRR & MTR

WHY IS IT IMPORTANT?

Maintains health by protecting the body from toxins

Regulates cell production and programmed cell death

Critical role in chemical detoxification

Vital for proper mitochondrial function

WAYS TO INCREASE GLUTATHIONE

- Limit alcohol intake
- N-acetyl-cysteine (NAC)
- Glutathione therapies
- (ie. IV Glutatione, Glutatione suppository, Lipsomal Glutatione)
- Include whey in diet, unless allergic or intolerant
- Methylation Support - if necessary

SUPEROXIDES & ANTIOXIDANTS

- SOD1, SOD2, SOD3 genes are important to transform superoxides to protect against mitochondrial damage
- Reactive Oxygen Species (ROS) can damage mitochondria and cause cell death.
- Antioxidants such as Vitamin A, Vitamin C and Vitamin E act as a defense against ROS

DEFICIENCY CAUSES

- Auto-immune diseases
- Cardiovascular diseases
- Neurodegenerative diseases
- Cell death
- Poor mitochondrial function

HIGH ANTIOXIDANT DIET

BENEFITS

Protection from oxidative stress

Helps reduce risk of heart disease, cancers & diabetes

Helps maintain functions of the liver, kidney, brain and digestive system

FOODS HIGH IN ANTIOXIDANTS

Dark chocolate

Spices/herbs (cinnamon, oregano, turmeric, cumin, sage, thyme)

Fruit (berries, red grapes, prunes, apples, cherries, black plums)

Whole grains (unless gluten free)

Vegetables (artichokes, beets, dark leafy greens)

Nuts (pecans, walnut, hazelnut, pistachios, almonds, cashews, macadamias)

Beans (pinto, red, kidney, black)

Beverages: juices (apple, tomato, pomegranate, pink grapefruit juice), teas (green, black)

SELENIUM

WAYS TO INCREASE LEVELS

Brazil nuts

Low-fat milk products

Meats & seafood – fish (tuna, halibut, sardines), ham, shrimp, beef, liver, chicken, turkey

Boiled eggs

Wheat germ, Brewer's yeast

Whole grains (unless gluten free)

Supplements

FUNCTIONS

Role in proper thyroid function & thyroid hormone metabolism

Role in DNA synthesis

Role in reproduction

Protection from infection & oxidative damage

DEFICIENCY VS HIGH INTAKE

Deficiency

- Cardiovascular disorders
- Developmental issues
- Thyroid disorders
- Joint & bone issues
- Infertility issues
- Cancers

High intake

- Metallic taste in mouth
- Garlic odor of breath
- Hair and nail loss or brittleness
- Nervous system abnormalities
- Nausea
- Diarrhea
- Skin rashes
- Fatigue
- Irritability

Gene Information Key

rsID	Gene	"-" variant	"+" variant
rs13043752	AHCY	G	A
rs234706	CBS	A	G
rs1021737	CTH	G	T
rs17883901	GCLC	G	A
rs1050450	GPX1	G	A
rs8190955	GSR	G	A
rs1332018	GSTM3	T	G
rs1695	GSTP1	A	G
rs1801280	NAT2	T	C
rs6721961	NFE2L2	G	T
rs2070424	SOD1	G	A
rs4880	SOD2	G	A
rs2536512	SOD3	A	G

Definitions

NFE2L2 rs6721961	The NFE2L2 (NFE2 like bZIP transcription factor 2) gene encodes a transcription factor, known as NRF2, that has a crucial role in the regulation of a network of antioxidant genes. NRF2 activates expression of genes with a conserved promoter sequence called the antioxidant response elements (ARE). Genes with an ARE include superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPX), etc. Therefore, NRF2 is a master regulator of oxidant and antioxidant balance. The polymorphism rs6721961 occurs in the promoter region of NFE2L2, and mechanistic studies have found that the variant encoded by the T allele has reduced promoter activity and mRNA levels. Consistent with these findings, carriers of the T allele have been shown to have lower total antioxidant capacity. T allele carriers had less SOD, CAT, GPX, and glutathione activity. Furthermore, T allele carriers are at increased risk for insulin resistance and vascular stiffness.
GSR rs8190955	The GSR (glutathione-disulfide reductase) gene encodes a riboflavin-dependent enzyme that reduces oxidized glutathione (GSSH) to its antioxidant form (GSH). Therefore, GSR is essential for maintaining adequate glutathione levels and cellular antioxidant capacity. The polymorphism rs8190955 results in a cysteine substitution for an arginine residue at position 153. Mechanistic studies have shown that the A allele, which encodes a cysteine residue, produces an enzyme that is less stable than the version produced by the G allele. Furthermore, the instability was predicted to reduce enzyme function, and the A allele has been associated with obstructive heart defects and hereditary anemia.
AHCY rs13043752	The AHCY (adenosylhomocysteinase) gene encodes an enzyme that catalyzes the reversible hydrolysis of S-adenosylhomocysteine (SAH) to adenosine and homocysteine. Therefore, this enzyme, sometimes referred to as S-adenosylhomocysteine hydrolase (SAHH) regulates intracellular SAH concentrations, which acts as an inhibitor of most transmethylation enzymes. Deficiency in this protein can lead to increased levels of methionine. The polymorphism rs13043752 results in a tryptophan substitution for an arginine residue at position 38 in the enzyme. Mechanistic studies have found that the variant produced by the A allele, which encodes a tryptophan residue, has decreased enzyme activity, suggesting the A allele may result in a reduced methylation index or less methylation capacity.
CBS rs234706	The CBS (cystathionine beta-synthase) gene encodes an enzyme that catalyzes the first step in the transsulfuration pathway. More specifically, CBS, a pyridoxal 5'-phosphate-dependent enzyme, consumes serine to convert homocysteine to cystathionine, which is further catabolized to generate substrate for glutathione synthesis. Therefore, homocysteine clearance and glutathione synthesis converge on the function of CBS. The polymorphism rs234706 results in a nucleotide substitution in exon 8. Carriers of the G allele have been found to have higher levels of homocysteine and lower levels of cystathionine and betaine, consistent with reduced CBS activity. Furthermore, individuals with the GG genotype had higher plasma homocysteine following the ingestion of a methionine load, and individuals with the GG genotype were less responsive to folate supplementation to lower homocysteine levels. Lastly, the GG genotype is associated with increased risk for coronary artery disease.
CTH	The CTH (cystathionine gamma-lyase) gene encodes an enzyme that catalyzes the last step in the transsulfuration of L-methionine to L-cysteine. More specifically, it converts cystathionine, derived from methionine, into cysteine, which is utilized in the liver to synthesis glutathione, a ubiquitous antioxidant. As a results, CTH has an important role in glutathione production. The polymorphism rs1021737 results in an isoleucine substitution for a serine residue in the enzyme at position 403. The T allele, which encodes the isoleucine variant, has been associated with an accumulation of homocysteine.
GCLC rs17883901	The GCLC (glutamate-cysteine ligase catalytic subunit) gene encodes the first and rate-limiting enzyme in glutathione biosynthesis. Glutathione is a potent, nonprotein antioxidant that has an important role in protecting cells from oxidative stress and xenobiotics. Therefore, a reduction in biosynthetic capacity through reduction of GCLC activity results in reduced antioxidant capacity and activity of enzyme that use glutathione as a cofactor, such as glutathione transferase and glutathione peroxidase. The polymorphism rs17883901 occurs in the promoter region of the gene, and mechanistic studies have found that the variant encoded by the A allele reduces promoter activity by as much as 60% in cell models. Furthermore, A allele carriers had significantly increased risk for coronary heart disease and heart attack. Lastly, plasma glutathione levels were reduced in individuals with the AA genotype.
GSTM3 rs1332018	The GSTM3 (glutathione S transferase mu 3) gene encodes a cytosolic enzyme that has a keystone role in cellular detoxification. It conjugates cytotoxic and carcinogenic substances to glutathione for elimination, thereby aiding in antioxidant defense and preserving DNA integrity. It’s highly expressed in brain, kidneys, and testes. The polymorphism rs1332018 occurs in the 5’ untranslated region of the gene, suggesting that it has a regulatory impact on GSTM3 expression or translation to enzyme. The variant encoded by the C allele has been shown to produce reduced levels of GSTM3 enzyme. Furthermore, the C allele is associated with risk for Alzheimer's disease and dysregulated cellular growth, indicating limited protection against cytotoxic substances.
GSTP1	The GSTP1 (glutathione S?transferase pi 1) gene encodes a cytosolic enzyme that has a keystone role in cellular detoxification. It conjugates cytotoxic and carcinogenic substances to glutathione for elimination, thereby aiding in antioxidant defenses and preserving DNA integrity. It's ubiquitously expressed; however, it's notably abundant in epithelial tissue and liver. The polymorphism rs1695 results in a valine substitution for an isoleucine residue in the enzyme at position 105, which is a region of the protein that is known to undergo several post-translational modifications. Mechanistic studies have shown that the protein produced by the G allele, which encodes a valine residue, has reduced substrate binding capacity and enzymatic activity. Numerous clinical studies have shown that the GG genotype is a risk factor for asthma, especially when individuals are exposed to environmental toxins, such as cigarette smoke or traffic-related air pollution. Additionally, the G allele is associated with increased risk for heart failure, and the frequency of the G allele is decreased in populations of older, living adults, suggesting it does not confer increased longevity.
GPX1 rs1050450	The GPX1 (glutathione peroxidase 1) gene encodes an antioxidant enzyme that consumes glutathione to protect cells from hydrogen peroxides. GPX1 is the most abundant enzyme in the GPX family, and its antioxidant activity is dependent on selenium status. The polymorphism rs1050450 results in a leucine substitution for a proline residue at position 200. The A allele, which encodes a leucine residue, is associated with reduced enzyme activity, resulting in less protection against oxidative stress. Additionally, the enzyme encoded by the A allele is less responsive to selenium supplementation. Consistent with reduced antioxidant capacity, the A allele is associated with higher levels of lipoperoxides in LDL and increased risk for coronary artery disease. The A allele is also associated with a longer duration of migraine attacks, and individuals in the AA genotype may have increased risk for inflammatory bowel disease, which is coupled with high levels of oxidative stress.

SOD1 rs2070424	The SOD1 (superoxide dismutase 1) gene encodes a copper and zinc-dependent enzyme that detoxifies superoxide radicals. The enzyme is soluble, and it primarily functions in the cytoplasm where it acts as a homodimer to convert naturally-occurring oxidants to molecular oxygen and hydrogen peroxide. Moreover, SOD enzymes participate in phase 1 detoxification to initiate the transformation of highly reactive oxygen species to a less reactive intermediary metabolite. Hydrogen peroxide, the intermediary metabolite produced by SOD activity, requires further detoxification by phase 2 enzymes, such as catalase or glutathione peroxidase. Nevertheless, SOD1 function is crucial to initiate the detoxification process of reactive oxygen species in the cytoplasm, aiding in protection against oxidative damage. The polymorphism rs2070424 occurs in the third intron, and carriers of the G allele were shown to have increased SOD1 activity in red blood cells. This increased activity was also associated with decreased mortality due to septic shock. Furthermore, the G allele was found to be protective against Alzheimer's disease and ulcerative colitis. Lastly, the A allele is associated with increased risk of type 2 diabetes and possibly PCOS, suggesting that the variant encoded by the A allele has decreased antioxidant function.
SOD2	The SOD2 (superoxide dismutase 2) gene encodes a mitochondrial matrix enzyme that uses iron and manganese to covert superoxide, a byproduct of the electron transport chain, to hydrogen peroxide and oxygen. Moreover, SOD2 participates in phase 1 detoxification to initiate the transformation of highly reactive oxygen species to a less reactive intermediary metabolite. Hydrogen peroxide, the intermediary metabolite produced by SOD2 activity, requires further detoxification by phase 2 enzymes, such as catalase or glutathione peroxidase. Nevertheless, SOD2 function is crucial to initiate the detoxification process of reactive oxygen species in the mitochondria, aiding in protection against oxidative damage. The polymorphism rs4880 results in a valine substitution for an alanine residue in the enzyme at amino acid position 16, which occurs in the mitochondrial targeting sequence. Mechanistic studies have shown that the A allele, which encodes a valine residue, has incomplete transfer to the mitochondria due to a conformational change in the targeting sequence. Furthermore, studies in animal models have shown that the enzyme encoded by the A allele has decreased formation of active enzyme in the mitochondrial matrix, and clinical studies have found individuals with the AA genotype to have less SOD2 activity. Consistently, individuals with the AA genotype have been shown to have decreased plasma total antioxidant status and increased markers of oxidative stress and lipid peroxidation. However, implementation of a healthy diet and exercise intervention has been shown to reduce markers of lipid peroxidation in those with the AA genotype. Lastly, the AA genotype was associated with increased risk for coronary heart disease.
SOD3 rs2536512	The SOD3 (superoxide dismutase 3) gene encodes a copper and zinc-dependent enzyme that detoxifies superoxide radicals. SOD3 is a soluble enzyme that primarily functions in extracellular spaces to covert naturally-occurring oxidants to molecular oxygen and hydrogen peroxide. Moreover, SOD enzymes participate in phase 1 detoxification to initiate the transformation of highly reactive oxygen species to a less reactive intermediary metabolite. Hydrogen peroxide, the intermediary metabolite produced by SOD activity, requires further detoxification by phase 2 enzymes, such as catalase or glutathione peroxidase. Nevertheless, SOD3 function is crucial to initiate the detoxification process of extracellular reactive oxygen species, aiding in protection against oxidative damage. The polymorphism rs2536512 results in a threonine substitution for an alanine residue at position 58. The A allele, which encodes a threonine residue, was associated with increased levels of protein, whereas individuals with the GG genotype were found to have reduced enzyme activity. Additionally, the GG genotype was associated with hypertension, and the G allele was associated with decreased lung function, suggesting that the G allele may be associated with decreased antioxidant function.
NAT2 rs1801280	The NAT2 (N-acetyltransferase 2) gene encodes an enzymes that catalyzes the transfer of an acetyl group from acetyl coenzyme A to compounds with aromatic amines, hetrocyclic amines, or hydrazine structures. Therefore, NAT2 has an important role in the metabolism and elimination of a large number of pharmaceutical drugs and environmental toxins. The polymorphism rs1801280 results in a threonine substitution for an isoleucine residue at position 114. The C allele, which encode a threonine residue, defines the NAT2*5B haplotype, which has been found to have slow acetylation activity. Consistent with this status, carriers of the C allele are at increased risk for various types of cancer and adverse drug reactions. Additionally, increased toxin exposure, such as frequent or intense smoking, can further increase these risks.

Disclaimers

METHODOLOGY AND LIMITATIONS DISCLAIMER:

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, LLC d/b/a Fagron Genomics US ("Fagron Genomics US") (807 Las Cimas Pkwy, Suite 145, Austin, TX. 78746). 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 Fagron Genomics US's laboratory (Laboratory Director: James Jacobson, PhD) pursuant to Clinical Laboratory Improvement Amendments (CLIA) requirements (CLIA #: 45D2144988).

MEDICAL DISCLAIMER:

This test was developed and its performance characteristics determined by Fagron Genomics US. 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 and educational purposes. It should not be regarded as investigational or for research. The Reference SNP Cluster IDs (rsIDs) for the alleles being tested were obtained from the Single Nucleotide Polymorphism Database (dbSNP) (Build 142). These products are not approved by the Food and Drug Administration and are not intended to diagnose, treat, cure, or prevent disease. These recommendations are for report purposes only and an individual is not required to use such products. These are recommendations only and do not replace the advisement of your own healthcare practitioner.

LEGAL DISCLAIMER:

Report contents and report recommendations are created based on the consultation, advice, and direction of Dr. Kendal Stewart, the Medical Director for Fagron Genomics US. Report contents and report recommendations are intended to be informational only. Report contents and report recommendations are not intended and should not be interpreted to make claims regarding the use, ef?cacy, or safety of products, formulas, and/or services listed herein. Only a doctor or other appropriately licensed health care practitioner can determine if a formula, product, or service described herein is appropriate for a speci?c patient. Sole risk for the use of all Fagron Genomics US lab test orders and test interpretation results rests with the reader. Implementation or experimentation with any supplements, herbs, dietary changes, medications, and/or lifestyle changes, etc. is done so at the patient's sole risk and responsibility and should be discussed with the patient or the patient's personal licensed healthcare practitioner prior to implementation. Fagron Genomics US and its affiliates, employees, associates, vendors, principals or partners, do not accept legal, moral, or ethical responsibility for any problems arising from experimentation with the information described in test results. Fagron Genomics US expressly reserves all legal rights and remedies in case of an inappropriate, negligent, or incorrect use or interpretation of the results of its tests.

UND RESULT DISCLAIMER:

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. You may request your sample to be run again by emailing info@fagrongenomicsus.com

SNP References:

https://acrobat.adobe.com/id/urn:aaid:sc:VA6C2:e0c9dc90-bba1-420f-b1ff-18e36d9654d7