Health Report

OPTIMAL HEALTH FOR LIFE

GENE MATRIX

GENOTYPE REPORT

NAME	NGx Sample
DATE OF BIRTH	1/1/1900
REFFERRING PRACTITIONER	
DATE REPORTED	2/20/2023 11:28:57 AM
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WELCOME TO YOUR DNA HEALTH REPORT

From your buccal swab sample, we use a process called the Polymerase Chain Reaction (PCR), which copies the DNA of your genes many times over so that we can generate sufficient quantities to analyze your genetic material. Then, we identify unique DNA sequences in some of your genes. Certain changes (polymorphisms) in these genes have been studied in detail, with evidence that correlates these polymorphisms with an individual's risk of developing certain chronic disease conditions or altered metabolic processes. Having identified the presence or absence of these polymorphisms, we are able to qualitatively assess particular areas of health risk related to the specific genes.

To make a holistic assessment of health risks, environmental factors (diet and lifestyle) need to be considered in conjunction with the accompanying genetic profile.

HOW TO READ YOUR RESULTS

You will find your genetic results in the following pages. On the left side, you will see the gene name and description. On the right side, you will find your specific result and an explanation of the results, associated risks, and diet and lifestyle recommendations. Please see the key above to identify each impact level.

NO IMPACT
Genotype has no effects on the biological area in question.

LOW IMPACT
Genotype has mild effects on the biological area in question with a small change in responsiveness to environmental influences.

MODERATE IMPACT
Genotype has moderate effects on the biological area in question. Attention should be paid, and some dietary and lifestyle changes are recommended.

HIGH IMPACT
Genotype has significant impact on the biological area in question. Cohesive and intensive diet and lifestyle action should be taken.

BENEFICIAL IMPACT
Genotype result is advantageous to health.

BONE HEALTH

Our bones are not a fixed structure. Our cells work continuously to dissolve old bone and create new bone tissue. After the age of 30, both men and women start losing bone mass; the loss is particularly marked in women after menopause. According to the latest research, both nutrition and genetic factors play an important role in determining bone health.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Bone Health	COL1A1	1546G>T	A/A	
	VDR	Fok1 T>C	A/A	
		Taq1 C>T	T/T	
		Bsm1 G>A	G/G	

COL1A1 | 1546G>T

Type 1 Collagen is the major protein of bone and is formed from two collagen alpha 1- and one collagen alpha 2 chains.

YOUR RESULT: **A/A**

The COL1A1 T (A) allele influences the ratio of collagen alpha chains produced by bone cells, leading to abnormal mineralization of bone and reduced bone strength. Women with the TT (AA) genotype are at significantly increased risk of excess rates of spinal bone loss. This effect may be nullified by the use of HRT. Individuals with the T (A) allele have increased risk of fracture and greater bone loss when calcium is low. Ensure adequate calcium intake.

VDR | Fok1 T>C

Peak bone mass is, to a great extent, genetically determined. The vitamin D receptor (VDR) gene accounts for around 70% of the entire genetic influence on bone density, playing an important role in calcium homeostasis, bone cell growth and differentiation, and intestinal calcium absorption.

YOUR RESULT: **A/A**

The T (A) allele has poorer calcium absorption compared to the C (G) allele. The TT (AA) genotype has higher bone turnover and increased bone loss and is associated with a lower BMD and osteoporosis in the lumbar spine. In these individuals, ensure adequate calcium and vitamin D intake and reduce caffeine to less than 300 mg/d. It may be prudent to test vitamin D levels.

VDR | Taq1 C>T

Peak bone mass is, to a great extent, genetically determined. The vitamin D receptor (VDR) gene accounts for around 70% of the entire genetic influence on bone density, playing an important role in calcium homeostasis, bone cell growth and differentiation, and intestinal calcium absorption.

YOUR RESULT: **T/T**
The variation does not lead to an increased risk for osteoporosis.

VDR | Bsm1 G>A

Peak bone mass is, to a great extent, genetically determined. The vitamin D receptor (VDR) gene accounts for around 70% of the entire genetic influence on bone density, playing an important role in calcium homeostasis, bone cell growth and differentiation, and intestinal calcium absorption.

YOUR RESULT: **G/G**
No genetic variation was detected.

DETOXIFICATION

The detoxification process in the body is governed primarily by the GST family of enzymes. Glutathione S-tranferases are responsible for catalyzing reactions in which the products of Phase I metabolism are conjugated with glutathione, thus making them more water soluble and more easily excreted from the body through sweat and urine. Cruciferous and allium vegetables help increase the activity of your detoxification system, which aids the removal of harmful substances from your body.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Detoxification	CYP1A1	Msp1 T>C	T/T	
		2454A>G (Ile462Val)	T/T	
	GSTM1	519G>C	G/G	
	GSTP1	313A>G	A/G	
	GSTT1	15G>C	C/C	
	NQO1	609C>T	C/C	

Phase I Detoxification

CYP1A1 | Msp1 T>C

The CYP1A1 gene encodes a phase I cytochrome P450 enzyme that converts environmental procarcinogens such as polycyclic aromatic hydrocarbons (PAHs) and aromatic amines to reactive intermediates having carcinogenic effects. In addition, CYP1A1 is involved in the oxidative metabolism of estrogens, which may play a critical role in the etiology of breast and prostate cancers.

YOUR RESULT: **T/T**
No variation was detected.

CYP1A1 | 2454A>G (Ile462Val)

The CYP1A1 gene encodes a phase I cytochrome P450 enzyme that converts environmental procarcinogens such as polycyclic aromatic hydrocarbons (PAHs) and aromatic amines to reactive intermediates having carcinogenic effects. In addition, CYP1A1 is involved in the oxidative metabolism of estrogens, which may play a critical role in the etiology of breast and prostate cancers.

YOUR RESULT: **T/T**
No variant was detected.

NQO1 | 609C>T

NADP(H:) quinone oxidoreductase 1 (NQO1) often referred to as Quinone Reductase is primarily involved in the detoxification of potentially mutagenic and carcinogenic quinones derived from tobacco smoke, diet and estrogen metabolism. NQO1 also protects cells from oxidative stress by maintaining the antioxidant forms of ubiquinone and vitamin E.

YOUR RESULT: **C/C**
The analysis identified no genetic variation at the 209 C>T locus.

Phase II Detoxification

GSTP1 | 313A>G

Glutathione S-transferase P1 is a member of the GST super-family and is involved in phase II detoxification by conjugating xenobiotics to glutathione and thereby detoxifying cellular environments. Oxidative stress is a risk factor shared by most disorders implicating GST, and it appears that the efficiency of the GSTP1 enzyme may have an impact on the development and prognosis of diseases influenced by oxidative stress. GSTP1 is the most abundant GST subtype in the lungs and is known to metabolize many carcinogenic compounds.

YOUR RESULT: **A/G**

The G allele decreases activity of the enzyme. Conjugation activity is around 80% for carriers of one G allele and 70% for carriers of two G alleles. GST enzyme activities are induced in part by the products of cruciferous and allium vegetables. These should be increased significantly in the diet to increase activity of other GST enzymes to compensate for decreased activity. Daily intake is recommended. When dietary intake is inadequate, a high quality supplement containing diindolylmethane (DIM) may be required.

GSTM1 | 519G>C

Glutathione S-transferase M1 is the most biologically active member of the GST super-family and is involved in Phase II detoxification in the liver. It is responsible for the removal of xenobiotics, carcinogens, and products of oxidative stress.

YOUR RESULT: **G/G**

The absence of a genotype at the GSTM1 519G>C indicates that the gene is deleted.

GSTT1 | 15G>C

Glutathione S-transferase theta-1 (GSTT1) is a member of a super family of proteins that catalyzes the conjugation of reduced glutathione to a variety of electrophilic and hydrophobic compounds.

YOUR RESULT: **C/C**

This genotype indicates the presence of the GSTT1 gene.

FOOD RESPONSIVENESS

Particular nutrients and certain food components in different foodstuffs can affect individuals in different ways. With new research coming to light in this area, specific genes can be tested to give more insight into how an individual might respond to a particular food component. The areas of food responsiveness covered in this panel include: lactose intolerance, Polyunsaturated fat (PUFA) metabolism, caffeine sensitivity, salt sensitivity and iron overload.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
	ACE	I/D	G/C	

Food Responsiveness	AGT	Met235Thr	A/G	
	CYP1A2	-163C>A	C/A	
	HFE	H63D; C282Y	282CC/63HD	
	MCM6	-13910C>T	C/T	
	MYRF/FADS1	-592G>T	G/G	

Iron overload

HFE | H63D; C282Y

Hereditary hemochromatosis is a genetic disorder in which there is excessive accumulation of iron in the body, leading to iron overload. For individuals with this disorder, the daily absorption of iron from the intestines is greater than the amount needed to replace losses. Since the normal body cannot increase iron excretion, the absorbed iron accumulates in the body. Individuals who carry the genes for hereditary hemochromatosis may have no symptoms or signs and the disease is treatable, if detected early. Severe symptoms and signs of iron overload include sexual dysfunction, heart failure, joint pains, liver cirrhosis, diabetes mellitus, fatigue, and hypermelanotic pigmentation.

YOUR RESULT: **282CC/63HD**

The analysis detected no genetic variation increasing risk for the disorder.

Caffeine sensitivity

CYP1A2 | -163C>A

Coffee is a major source of caffeine, which is metabolized by the cytochrome P450 1A2 enzyme (CYP1A2) .

YOUR RESULT: **C/A**

Carriers of the C allele have a reduced ability to metabolize caffeine. A moderate to high intake of caffeinated beverages, such as coffee, is associated with increased risk of heart disease. It is recommended that these individuals opt for decaffeinated options.

Salt Sensitivity

ACE | I/D

ACE codes for the angiotensin-converting enzyme and is part of the renin-angiotensin system, which controls blood pressure by regulating the volume of fluids in the body.

YOUR RESULT: **G/C**

Studies show that patients with essential hypertension homozygous for the insertion allele of the ACE gene have a significantly higher blood pressure increase with high salt intake compared to DD (GG) individuals.

AGT | Met235Thr

Angiotensinogen is expressed in tissues involved in blood pressure regulation such as the kidneys, adrenals and brain. Increased angiotensinogen levels correlate with increased blood pressure. The gene also influences salt sensitivity of blood pressure.

YOUR RESULT: **A/G**

Individuals who carry the C (G) allele are associated with increased risk for hypertension. However, incidence of hypertension was found to be significantly lower among these individuals who reduced sodium intake.

Lactose intolerance

MCM6 | -13910C>T

A specific DNA sequence within the MCM6 gene called a regulatory element helps control the activity of a nearby gene called LCT gene which encodes an enzyme called lactase. This enzyme helps to digest lactose, a sugar found in milk and other dairy products. In most individuals, the expression of LCT gene decreases after infancy leading to lactase deficiency. After ingestion of milk or other dairy products, these individuals may experience abdominal cramps, bloating, distension, flatulence and diarrhea.

YOUR RESULT: **C/T**

The CT genotype is associated with lactase persistence in the Caucasian population.

Polyunsaturated fatty acids (PUFA) metabolism

MYRF/FADS1 | -592G>T

The delta 5 and delta 6 desaturases, encoded by FADS1 and FADS2 genes, are key enzymes in polyunsaturated fatty acid (PUFA) metabolism that catalyze the conversion of linoleic acid (LA) into arachidonic acid (AA) and that of alpha-linolenic acid (ALA) into eicosapentaenoic acid (EPA). SNPs in the FADS locus have been associated with blood concentrations of long-chain PUFAs as well as with cholesterol concentrations. Based on genetic variation, individuals may require different amounts of dietary PUFAs or LC-PUFAs to achieve comparable biological effects.

YOUR RESULT: **G/G**

The G allele is associated with enhanced conversion of DGLA to AA due to increased enzymatic efficiency, and thus appears to be associated with higher levels of AA, systemic inflammation and inflammatory disorders.

INFLAMMATION HEALTH

Inflammation is a normal immune response and an essential step in tissue healing. The release of these inflammatory substances is controlled by genes that govern inflammation. However, when these genes are not switched off, the inflammatory response continues. An increasing number of common disorders, such as obesity, heart disease, arthritis and inflammatory bowel disease have been associated with chronic low-grade inflammation.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Inflammation Health	IL6	-174G>C	G/G	
	TNF	-308G>A	G/G	

IL6 | -174G>C

Interleukin 6 is a pro-inflammatory cytokine that plays a crucial role in inflammation and regulates expression of C-reactive protein (CRP). Low-grade chronic inflammation is associated with obesity and visceral fat deposition, insulin resistance, dyslipidaemia and increased risk of cardiovascular disease.

YOUR RESULT: **G/G**

No variant was detected at the 174 G>C locus.

TNF | -308G>A

Tumor necrosis factor-a (TNFA), a proinflammatory cytokine secreted by both macrophages and adipocytes, has been shown to alter whole body glucose homeostasis, and has been implicated in the development of obesity, obesity-related insulin resistance and dyslipidaemia.

YOUR RESULT: **G/G**

No variant was detected at the 308 G>A locus.

INSULIN SENSITIVITY

Insulin is a hormone that stimulates the uptake of glucose from the diet into the blood. Those with lower sensitivity to insulin have a limited ability to respond to the hormone's action. The scientific literature suggests that insulin insensitivity or resistance may play an important role in some of the most common disorders, including obesity, type 2 diabetes, high blood pressure, heart disease and disrupted fat metabolism.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Insulin Sensitivity	FTO	rs9939609 T>A	A/A	
	PPARG	Pro12Ala	C/G	
	SLC2A2	Thr110Ile	C/C	
	TCF7L2	C>T	C/C	

FTO | rs9939609 T>A

Fat-mass-and-obesity-associated (FTO) gene is present at high levels in several metabolically active tissues, including heart, kidney, and adipose tissue, and is most highly expressed in the brain, particularly in the hypothalamus which is concerned with the regulation of arousal, appetite, temperature, autonomic function, and endocrine systems. It has been suggested that the FTO gene plays a role in appetite regulation and that it is associated with energy expenditure, energy intake, and diminished satiety.

YOUR RESULT: A/A

The A allele has been associated with higher body mass index (BMI), body fat percentage and waist circumference, especially in individuals with a sedentary lifestyle. Overweight individuals with the A allele are at increased risk for insulin resistance and diabetes, especially when there is a high fat intake. Modify the diet to include a moderate amount of carbohydrate, increase monounsaturated fatty acids (MUFA) intake and decrease satured fats (SAT FAT); manage the overall fat intake. Regular physical activity is recommended.

PPARG | Pro12Ala

Peroxisome proliferator-activated receptor gamma (PPARG) is believed to be involved in adipocyte differentiation. It is a transcription factor activated by fatty acids, which has a major role in adipogenesis and expression of adipocyte-specific genes. It is also involved in the regulation of glucose and lipid metabolism. This receptor is the target for the thiazolidinedione antidiabetic drugs.

YOUR RESULT: C/G

The G allele is associated with reduced promoter activation, reduced transcriptional activity and reduced adipocyte differentiation. As a result, the G allele has been associated with lower BMI and fasting insulin, improved insulin sensitivity and reduced risk of insulin resistance and diabetes.

SLC2A2 | Thr110Ile

GLUT2, coded by the SLC2A2 gene, is a member of the facilitative glucose transport protein (GLUT) family and is expressed in the pancreas, liver, small intestine, kidney, and brain. GLUT2 facilitates the first step in glucose induced insulin secretion, with the entry of glucose into the pancreatic ßcell. Due to its low affinity for glucose, it has been suggested as a glucose sensor and is considered to be important in the postprandial state. It is also involved in food intake and regulation.

YOUR RESULT: **C/C**
The analysis detected no variant.

TCF7L2 | C>T

Transcription factor 7-like 2 (TCF7L2) gene encodes a transcription factor that regulates blood glucose homeostasis. This SNP influences both insulin secretion and resistance and has been associated with an increased risk of insulin resistance and type 2 diabetes mellitus.

YOUR RESULT: **C/C**
No variant was detected.

LIPID METABOLISM

Heart health depends on a complex balance of environmental, dietary and genetic factors. Certain genes influence LDL and HDL cholesterol levels; higher levels of LDL, or 'bad' cholesterol, and lower levels of HDL, or 'good' cholesterol, are associated with a higher risk of heart disease.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Lipid metabolism	APOC3	3175C > G	C/G	
	APOE	388T>C; 526C>T	ε3/ε4	
	CETP	279G>A	G/G	
	LPL	1595C>G	C/C	

APOE | 388T>C; 526C>T

Apolipoprotein E has a multi-functional role in lipoprotein metabolism and is essential for the normal catabolism of triglyceride-rich lipoprotein constituents. Two SNPs result in three allelic isoforms, affecting the protein conformation, and thus the receptor binding activity and lipoprotein preference of the APOE protein.

YOUR RESULT: **ε3/ε4**

The E4 isoform contributes toward a 40 to 50% increased risk of CVD, due to higher levels of both LDL and total cholesterol. E4 carriers are hyper-responsive to toxins such as alcohol and smoking, as well as the total fat and fatty acid content of the diet. E4 individuals have a greater antioxidant requirement. Reduce the total fat, specifically saturated fat and intake in the diet. Increase antioxidant intake and reduce oxidative stress (e.g. alcohol intake reduction, cessation of smoking, weight loss).

APOC3 | 3175C > G

Apolipoprotein C3 plays an important role in cholesterol metabolism. It inhibits lipoprotein lipase and hepatic lipase, delaying catabolism of triglyceride-rich particles.

YOUR RESULT: **C/G**

The G allele is associated with elevated plasma triacylglycerol, cholesterol, and APOC3 concentrations. Carriers of the G variant have an approximate 4-fold increased risk of hypertriglyceridemia. However, they are responsive to dietary intervention. Decrease saturated fat and increase MUFA. If triglycerides are raised, modify carbohydrates intake. Carriers of the G variant may also show enhanced benefit to statin therapy.

CETP | 279G>A

Cholesterol ester transfer protein plays a key role in the metabolism of HDL and mediates the exchange of lipids between lipoproteins, resulting in the eventual uptake of cholesterol by hepatocytes (reverse cholesterol transport). High plasma CETP concentration is associated with reduced HDL-C concentrations. CETP is a strong and independent risk factor for CAD.

YOUR RESULT: **G/G**

The G allele is associated with increased plasma CETP, lower HDL-C and increased CVD risk. GG individuals respond well to statin therapy.

LPL | 1595C>G

Lipoprotein lipase is anchored to the vascular endothelium and removes lipids from the circulation by hydrolyzing triglycerides present in VLDL into free fatty acids. The 1595 C>G variant is a strong indicator of body fat, fat distribution, plasma lipids and insulin concentrations.

YOUR RESULT: **C/C**

The analysis identified no genetic variation at the 1595 C>G locus.

METHYLATION

B vitamins provide building blocks for growing cells, which are constantly being renewed, and play an important role in many physiological processes. B vitamins also supply some of the chemicals necessary for protecting our genes, so that our DNA doesn't accumulate damage from the wear and tear in the daily lives of our cells. These vitamins – including folate, vitamins B6 and B12 – help make new DNA for cells that are constantly growing and renewing themselves. Folate is also involved in turning many genes on and off, and also helps repair DNA. The process of DNA repair is called methylation. Although B vitamins are only required in small amounts, they are crucial for methylation and in producing new DNA.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Methylation	CBS	699C>T	G/A	
	COMT	472G>A (Val158Met)	A/G	
	MTHFR	1298A>C	TT	
		677C>T	AA	
	MTR	2576A>G	A/A	
	MTRR	66A>G	G/G	

MTHFR | 1298A>C

Methylenetetrahydrofolate Reductase (MTHFR) is a key enzyme in the folate metabolism pathway, directing folate from the diet either to DNA synthesis or homocysteine remethylation.

YOUR RESULT: **TT**

No genetic variation was detected at the 1298 A>C locus.

MTHFR | 677C>T

Methylenetetrahydrofolate Reductase is a key enzyme in the folate metabolism pathway, directing folate from the diet either to DNA synthesis or homocysteine remethylation.

YOUR RESULT: **AA**

The T allele lowers activity of the MTHFR enzyme, which results in an increase in homocysteine levels, a decrease in DNA methylation, and thus an increase in DNA adducts. T allele carriers have increased folate, vitamin B2, B6 and B12 requirements. In addition to folate-rich foods, a supplement may be recommended.

COMT | 472G>A (Val158Met)

Soluble catechol-O-methyltransferase (S-COMT) helps control the levels of certain hormones and is involved in the inactivation of the catecholamine neurotransmitters (e.g. dopamine, epinephrine, and norepinephrine). The enzyme introduces a methyl group to the catecholamine, which is donated by S-adenosyl methionine (SAM). Any compound having a catechol structure, like catechol estrogens and catechol-containing flavonoids, are substrates of COMT.

YOUR RESULT: **A/G**

The A allele is associated with a 3-4 fold reduction in the methylation activity of the COMT enzyme and is associated with increased risk for breast cancer. Key interventions for beneficial modulation of estrogen metabolism can be accomplished by increasing insoluble fiber, managing the quality of dietary fat intake, losing weight, and increasing exercise. In addition, ensure sufficient antioxidant and magnesium intake. Dietary components that inhibit COMT activity include quercetin and tea catechins.

CBS | 699C>T

Cystathionine beta synthase catalyzes the conversion of homocysteine to cystathione and is directly involved in the removal of homocysteine from the methionine cycle. Any alterations in its activity could affect homocysteine levels.

YOUR RESULT: **G/A**

The T (A) allele is associated with decreased risk of CAD and an increased responsiveness to the homocysteine-lowering effects of folic acid. Check dietary folate intake and homocysteine levels and supplement if necessary.

MTR | 2576A>G

MTR gene encodes the Methionine Synthase, an enzyme that catalyzes the remethylation of homocysteine to methionine.

YOUR RESULT: **A/A**

No variation was detected at the 25776 A>G locus.

MTRR | 66A>G

Methionine Synthase Reductase (MTRR) catalyzes methylcobalamin, an essential cofactor of methionine synthase (MTR), which is necessary for maintaining adequate intracellular pools of methionine and maintaining homocysteine concentrations at non-toxic levels.

YOUR RESULT: **G/G**

The G allele is associated with increased risk for premature CAD and the GG genotype is a significant risk factor for the development of premature CAD and Neural Tube Defects (NTDs) when cobalamin (vitamin B12) status is low. Ensure adequate intake of folate, vitamin B12 and vitamin B6.

OXIDATIVE STRESS HEALTH

Free radicals are a normal by-product of the body's energy-generating biochemical processes. They are highly reactive with other molecules, and can damage DNA, proteins and cellular membranes. The balance between oxidation and antioxidation is believed to be critical in maintaining healthy biological systems. Dietary antioxidants such as vitamin C, vitamin E, carotenoids and polyphenols are free radical scavengers that interact with the free radical to ensure it is no longer a reactive molecule, and play an essential role in many antioxidant mechanisms in living organisms. However, the major role in antioxidant defense is fulfilled by the body's own antioxidant enzymes.

AREA OF ACTIVITY	GENE	GENETIC VARIATION	RESULT	GENE IMPACT
Oxidative Stress Health	NOS3	894G>T	G/T	
	SOD2	-28C>T (Ala16Val)	C/C	

NOS3 | 894G>T

NOS3 gene encodes the endothelial nitric oxide synthase 3 (eNOs), an essential enzyme for a healthy cardiovascular system. eNOs produces nitric oxide (NO), a small gaseous molecule involved in several biological processes. In the vascular endothelium NO plays crucial roles in the regulation of vascular tone and peripheral resistance. It has vasoprotective effects by suppressing platelet aggregation, leukocyte adhesion and smooth muscle cell proliferation.

YOUR RESULT: **G/T**

The T allele affects proteolytic cleavage of the enzyme, thereby reducing nitric oxide bio-availability in the blood vessel wall and promoting atherosclerosis. As a result, it is associated with atherosclerosis, essential hypertension, end-stage renal disease and pre-eclampsia. Ensure adequate antioxidant and n-3 fatty acids intake.

SOD2 | -28C>T (Ala16Val)

The SOD2 gene encodes the superoxide dismutase 2, a mitochondrial enzyme involved in the elimination of free radicals which are normally produced within cells and which are damaging to biological systems. The enzyme thus has important antioxidant activity within the cell, especially within the mitochondria.

YOUR RESULT: **C/C**

Individuals with the C allele and with a lower consumption of fruits and vegetables may have an increased risk of experiencing the damaging effects of oxidative stress resulting from free radicals. These effects are also enhanced by the presence of additional risk factors such as smoking. Therefore, it is important for individuals with the C allele to ensure adequate fruit and vegetable intake. Supplementation with antioxidant nutrients can also be considered.

Approved By:

Name of Laboratory Director	Laboratory Director
Nutrigenomics Test Lab	CLIA: 123456789

NOTES FOR PRACTITIONERS

***Disclaimer**: These tests were developed and characterized by this laboratory. They have not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary.*

Only a qualified healthcare professional should advise a person on the use of information in this report.

All clinical decisions relative to test results should be directed by your qualified healthcare provider. The laboratory makes no representations or recommendations in regards to results.

***Methodology**: All SNP genotyping tests performed using Agena Bioscience MassARRAY technology. All PCR based methods are subject to rare interference such as inhibitors or quality or quantity of DNA. If present, the interference typically yields a no result requiring a repeat rather than an inaccurate one.*

Array based assays detect listed alleles, including all common and most rare variants with known clinical significance at analytical sensitivity and specificity >99%.

***Limitations**: This test will not detect all the known mutations that result in altered or inactive tested genes. Absence of a detectable gene mutation or polymorphism does not rule out the possibility that a person has intermediate or high sensitivity phenotypes due to the presence of an undetected polymorphism.*

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