dnahealth®

optimal health for life

Welcome

[redacted]

to your dna health® report

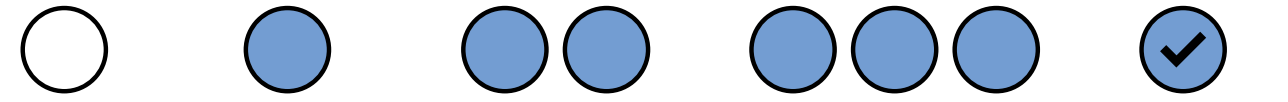
Date of Birth: [redacted]	Date Reported: 09 Mar 2022	Sample Number: [redacted]
Referring Practitioner: Karen Leggett		

Introduction

From your DNA sample we have used 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 analyse your genetic material. We then 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. The impact can be identified by the following:



No Impact | Low Impact | Moderate Impact | High Impact | Beneficial Impact

Priority table

Each biological area has been allocated a priority rating of either low, medium or high priority, in order for you to understand where your focus areas should be.

Based on the genes tested, a low priority biological area means that there is no need for increased support compared to standard health recommendations. A moderate or high priority biological area means that the particular area will require increased support with regards to appropriate diet, lifestyle and nutraceutical interventions to off-set the imbalances in that pathway caused by the genetic variants you carry.

Biological Area	Priority
Lipid metabolism	MODERATE
Methylation	MODERATE
Detoxification	MODERATE
Inflammation	HIGH
Oxidative Stress	MODERATE
Bone Health	HIGH
Insulin Sensitivity	LOW

Report summary

RESULTS		DO	AVOID
Inflammation An increasing number of disorders, such as obesity, heart disease, arthritis & diabetes have been associated with chronic low-grade inflammation, which is influenced by the genes you carry.	HIGH PRIORITY AREA 	• Manage weight • Incorporate aspects of a Mediterranean style diet • Try to eat a portion of red/blue fruit (e.g. blueberries) & vegetables daily • Use ginger & turmeric in cooking • Other beneficial nutrients, where supplementation may be considered, include anthocyanins & trans-resveratrol	• Avoid all refined grains & high sugar foods • Decrease intake of saturated fats, such as fat on meat & full cream dairy products including cheese • Decrease intake of omega 6 fatty acids such as sunflower & vegetable oil. Focus on nuts & seeds instead
Bone Health Both nutrition & environmenntal, as well as genetic factors play an important role in determining bone health & bone mineral density.	HIGH PRIORITY AREA 	• Ensure adequate vitamin D (mushrooms, fatty fish, egg yolks) & calcium (low fat dairy, fatty fish, almonds) intake, as well as other 'bone-building' nutrients such as phosphorous, magnesium, boron, vitamin K, zinc & manganese • Include load bearing exercises to help maintain adequate bone mineral density • Depending on dietary intake, supplementation may be required	• Limit caffeine intake to less than 300mg (3 cups of coffee) per day

Food responsiveness summary

RESULTS	DO	WHAT SHOULD I DO?	AVOID
Gluten Intolerance Coeliac disease (CD) is a common, autoimmune disorder in which the small intestine is damaged in response to a severe gluten intolerance. Non-coeliac gluten sensitivity is also related to the genes tested in this area. Gluten is a component of many grains.	HIGH PRIORITY AREA 	You have an increased risk for coeliac disease and non-coeliac gluten sensitivity. If you find you suffer from related symptoms, consider a gluten free diet. Gluten free grains include quinoa and buckwheat.	Avoid gluten-containing foods including grains such as wheat, rye, oats and barley.

Vitamin metabolism summary

RESULTS	WHAT SHOULD I DO?
Vitamin A High dietary carotenoid intake and elevated plasma concentrations are correlated with a decreased risk of several chronic diseases. It is also known that dietary carotenoids and retinoids play important roles in innate and acquired immunity and in the body's response to inflammation. Vitamin A is also essential for embryonic development, as well as in eye and skin health.	INCREASED REQUIREMENT 	Increase intake of carotenoid-rich foods such as carrots, tomatoes, pumpkin and butternut as well as oranges, grapefruit and apricots. Speak to your healthcare provider before taking an active vitamin A supplement.
Vitamin D Vitamin D is a fat-soluble vitamin that is required for many life processes including the absorption of calcium, phosphate and magnesium and is essential in healthy bone development. Active vitamin D has potent cell signalling abilities and vitamin D deficiency has been associated with an increased incidence as well as the progression of a broad range of diseases.	INCREASED REQUIREMENT 	Increase intake of vitamin D rich foods such as fatty fish, liver, and egg yolks and ensure adequate sun exposure. Supplementation may also be required.

Summary table

Biological Area	Gene Name	Genetic Variation	Your Result	Gene Impact
Lipid metabolism	LPL	1595 C>G	CC	○
	CETP	279 G>A	GG	●●
	APOC3	3175 C>G	CC	○
	APOE	E2/E3/E4	E4/E3	●●●
	PON1	A>G	AA	○
Methylation	MTHFD1	1958 G>A	GG	○
	MTHFR	677 C>T	CC	○
		1298 A>C	CA	●
	MTR	2756 A>G	AA	○
	MTRR	66 A>G	AA	○
	CBS	699 C>T	CC	○
	COMT	472 G>A	AA	●●●
Detoxification	CYP1A1	Msp1 T>C	TT	○
		Ile462Val A>G	AA	○
	GSTM1	Insertion/Deletion	Deletion	●●●
	GSTP1	313 A>G	AA	○
	GSTT1	Insertion / Deletion	Insertion	○
	NQ01	C>T	TC	●●
Inflammation	IL-6	-174 G>C	CG	●●
	TNFA	-308 G>A	AG	●●
	IL-1A	4845 G>T	TG	●●
	IL-1A	-889 C/T	TC	●●
	IL-1B	3954 C>T	CC	○
	IL-1B	-511 A>G	GA	●
	IL-1RN	2018 C>T	CT	●
Oxidative Stress	eNOS	894 G>T	GG	○
	MnSOD/SOD2	47 T>C (Val16Ala)	TT	○
	CAT	-262 C>T	CC	✓
	GPX1	C>T	TT	●●●
Bone Health	VDR	Fok1 T>C	TC	●
		Bsm1 G>A	AA	●●●
		Taq1 C>T	CC	●●●
	COL1A1	1546 G>T	GG	○

Summary table continued

Biological Area	Gene Name	Genetic Variation	Your Result	Gene Impact
Insulin Sensitivity	PPARG	Pro12Ala or C>G	CC	●●
	TCF7L2	rs7903146 C>T	CT	●
	SLC2A2	Thr110Ile	CC	○
	FTO	rs9939609 T>A	TT	○
Iron overload	HFE	C282Y & H63D	282CC & 63HD	○
Caffeine Sensitivity	CYP1A2	A>C	CA	●●
PUFA Metabolism	FADS1	rs174537 G>T	GT	●●
Salt Sensitivity	ACE	I/D	DD	○
	AGT	T>C	CC	●●●
Bitter Taste	TAS2R38	145 C>G 785 C>T 886 G>A	Medium Taster	●●
Alcohol Metabolism	ALDH2	rs671 G>A	GG	○
Lactose Intolerance	MCM6	–13910C>T	TC	●
Gluten Intolerance	HLA	DQ2/DQ8	DQ2.2 & DQ2.5	●●●
Vitamin A	BCO1	G>T	GT	●●
		Ala379Val C>T	CT	●●
Vitamin D	CYP2R1	A>G	AG	●●
	GC	T>G	GT	●●
		1296 G>T	TT	●●●
Vitamin B12	FUT2	Gly258Ser G>A	AA	○
Vitamin C	GSTT1	Insertion / Deletion	Insertion	○

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.

Gene Name	Genetic Variation	Your Result	Gene Impact
LPL	1595 C>G	CC	○
CETP	279 G>A	GG	●●
APOC3	3175 C>G	CC	○
APOE	E2/E3/E4	E4/E3	●●●
PON1	A>G	AA	○

LPL 1595 C>G

Lipoprotein lipase is anchored to the vascular endothelium and removes lipids from the circulation by hydrolysing 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: **CC** ○

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

CETP 279 G>A

Cholesterol esther 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: **GG** ●●

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

APOC3 3175 C>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: **CC** ○

The analysis identified no genetic variation at the 3175 C>G locus.

Lipid metabolism continued

APOE E2/E3/E4

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: **E4/E3**

The E4 isoform contributes toward a 40 to 50% increased risk of CVD, which is due to higher levels of total- and LDL 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 anti-oxidant requirement.
Reduce the total fat, specifically saturated fat, intake in the diet.
Increase anti-oxidant intake and reduce oxidative stress (Decrease alcohol intake, cessation of smoking, weight loss).

PON1 A>G

PON1 encodes the glycoprotein enzyme paraoxonase. PON1 protects LDL and HDL from oxidation possibly by hydrolysing phospholipid or cholesteryl ester hydroperoxides, thus protecting against atherogenesis. Low serum PON activity has been associated with increased risk for coronary artery disease.

YOUR RESULT: **AA**

No variant was detected. The AA genotype is associated with normal PON1 activity.

Priority level: MODERATE

Recommendation:

Based on your genes tested in the lipid metabolism panel, your genotype combination contributes toward a moderately increased risk for an abnormal lipid profile and risk for cardiovascular disease.
It is important to manage weight, and replace saturated fats with mono-unsaturated fats, and increase intake of vegetables and fruit. Match diet and lifestyle interventions to the genotype specific recommendations.

Take note that in APOE E4 carriers, it is important to focus on avoiding environmental pro-carcinogens, significantly increase intake of phytonutrient rich foods, and keep saturated fat intake low but ensure adequate intake of omega 3 fatty acids (oily fish).

Next steps:

Consider the following tests: CardioMetabolic Profile I ***(Insulin, hsCRP, HbA1c, TG, CH, LDL, HDL, VLDL)*** for actual lipid levels or ***Liposcan (HDL & LDL Subfractions), Oxidised LDL*** or a combination; ***Oxidised LDL & Liposcan Panel*** for a more advanced lipid level evaluation, that includes LDL particle sizes and oxidised LDL.

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 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. B vitamins are also involved in turning many genes on and off, and also help repair DNA. The process of DNA repair is called methylation. Methylation uses the process of donating 'methyl groups' to a substrate. A methyl group consists of one carbon bound to three hydrogen atoms (CH3). Although B vitamins are only required in small amounts, they are crucial for methylation and in producing new DNA.

Gene Name	Genetic Variation	Your Result	Gene Impact
MTHFD1	1958 G>A	GG	○
MTHFR	677 C>T	CC	○
	1298 A>C	CA	●
MTR	2756 A>G	AA	○
MTRR	66 A>G	AA	○
CBS	699 C>T	CC	○
COMT	472 G>A	AA	●●●

MTHFD1 1958 G>A

MTHFD1 encodes the enzymes 5,10-methylenetetrahydrofolate dehydrogenase, cyclohydrolase and synthetase. The varying enzymatic reactions are important in the interconversion of 1-carbon derivatives of tetrahydrofolate, which are substrates for methionine, thymidylate, and de novo purine syntheses.

Choline, an essential nutrient, plays a central role in many physiological pathways in the body including homocysteine metabolism, as well as neurotransmitter synthesis, cell-membrane signalling and transport of bile and lipoproteins. Requirements for choline vary based on gender, age, physical activity level as well as genetics.

YOUR RESULT: **GG** ○

The GG genotype is associated with normal enzyme function and thus there are no increased requirements for choline.

MTHFR 677 C>T

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

YOUR RESULT: **CC** ○

The CC genotype shows normal function.

Methylation continued

MTHFR 1298 A>C

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: **CA**

The C allele is associated with decreased enzyme function.

Folate requirements are increased and supplementation of Folate, B2, B6 and B12 may be desirable.

MTR 2756 A>G

Methionine Synthase encodes the enzyme that catalyses the remethylation of homocysteine to methionine.

YOUR RESULT: **AA**

No variation was detected at the 2576 A>G locus.

MTRR 66 A>G

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

YOUR RESULT: **AA**

No variant was detected at the 66 A>G locus.

CBS 699 C>T

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

YOUR RESULT: **CC**

No variant was detected at the 699 C>T locus.

Methylation continued

COMT 472 G>A

Soluble catechol-O-methyltransferase (S-COMT) helps control the levels of certain hormones and is involved in the inactivation of the catecholamine neurotransmitters (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 catecholestrogens and catechol-containing flavonoids, are substrates of COMT.

YOUR RESULT: **AA**

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 oestrogen metabolism can be accomplished by increasing insoluble fibre, managing the quality of dietary fat intake, losing weight, and increasing exercise. In addition, ensure sufficient anti-oxidant and magnesium intake. Dietary components that inhibit COMT activity include quercetin and tea catechins.

Priority level: MODERATE

Recommendation:

Based on your genes tested in the methylation panel, your genotype combination contributes toward a moderately increased risk for decreased methylation processes and increased homocysteine levels. It is important to increase intake of B vitamin-rich foods with an emphasis on vitamin B9 and B12 sources. Supplementation may be required if dietary intake is not adequate.

Because of the COMT A allele, ensure adequate magnesium intake.

Next steps:

Consider the following tests: ***Methylation Profile – Plasma*** to evaluate methylation and transulfuration functions and/or ***Organix Basic (excl. Dysbiosis)*** or ***Organix Comprehensive***, which includes B-complex vitamins and methylation cofactor markers (B12 and folate).

Detoxification

The detoxification process in the body is governed primarily by the GST family of enzymes. Glutathione S-tranferases are responsible for catalysing 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.

Gene Name	Genetic Variation	Your Result	Gene Impact
CYP1A1	Msp1 T>C	TT	○
	Ile462Val A>G	AA	○
GSTM1	Insertion/Deletion	Deletion	●●●
GSTP1	313 A>G	AA	○
GSTT1	Insertion / Deletion	Insertion	○
NQ01	NQ01 C>T	TC	●●

Phase I Detoxification

CYP1A1 Msp1 T>C

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

YOUR RESULT: **TT** ○

No variation was detected.

CYP1A1 Ile462Val A>G

The CYP1A1 gene encodes a phase I cytochrome P-450 enzyme that converts environmental procarcinogens such as PAHs and aromatic amines to reactive intermediates having carcinogenic effects. In addition, CYP1A1 is involved in the oxidative metabolism of oestrogens, which may play a critical role in the aetiology of breast and prostate cancer.

YOUR RESULT: **AA** ○

No variant was detected.

Detoxification continued

Phase II Detoxification

GSTM1 Insertion/Deletion

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: **Deletion**

A deletion results in an absence of the enzyme, leading to reduced capacity for hepatic detoxification and increased risk of various cancers, chemical sensitivity, coronary artery disease in smokers, atopic asthma, and deficits in lung function. Recommend a diet rich in antioxidants and minimize exposure to toxins. Substantially increase intake of cruciferous and allium vegetables to increase activity of other GST enzymes. When dietary intake is inadequate a high quality supplement containing DIM may be required.

GSTP1 313 A>G

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: **AA**

No variant was detected

GSTT1 Insertion / Deletion

GSTT1 is a member of a super family of proteins that catalyse the conjugation of reduced glutathione to a variety of electrophilic and hydrophobic compounds.

YOUR RESULT: **Insertion**

No deletion was detected.

Detoxification continued

Phase II Detoxification continued

NQ01 609 C>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 oestrogen metabolism. NQO1 also protects cells from oxidative stress by maintaining the antioxidant forms of ubiquinone and vitamin E.

YOUR RESULT: TC

The variant is a C-to-T transition resulting in a proline to serine amino acid substitution at codon 187 in the protein. The variant T allele results in reduced enzymatic activity. Compared with the wild type CC genotype, the heterozygote variant (TC) has a three-fold decrease in enzyme activity. Individuals with the TC genotype show an increased risk for developing certain cancers including breast, colorectal and gastrointestinal cancers especially when there is exposure to cigarette smoke. The polymorphism has also been linked to benzene toxicity.

Priority level: MODERATE

Recommendation:

Based on your genes tested in the detoxification panel, your genotype combination contributes toward a moderately decreased detoxification ability and therefore an increased risk for DNA damage. Decrease the 'load' on phase one detoxification by decreasing exposure to environmental pro-carcinogens such as cigarette smoke, smoked and chargrilled foods, pesticides and other pollutants. To support phase two detoxification, increase intake of a variety of fruits and vegetables with a specific emphasis on daily intake of cruciferous and allium vegetables.

Next steps:

Consider the following tests: ***Hepatic Detox Profile (D-glucaric & Mercapturic Acids)*** for detoxification status or ***Organix Comprehensive***, which includes detoxification indicators and the 8-Hydroxy-2-deoxygaunosine marker for the evaluation of oxidative stress.

Inflammation

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.

Gene Name	Genetic Variation	Your Result	Gene Impact
IL-6	-174 G>C	CG	●●
TNFA	-308 G>A	AG	●●
IL-1	IL-1A 4845 G>T	TG	●●
	IL-1A -889 C>T	TC	●●
	IL-1B 3954 C>T	CC	○
	IL-1B -511 A>G	GA	●
	IL-1RN 2018 C>T	CT	●

IL-6 -174 G>C

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

YOUR RESULT: CG

The C allele of this functional SNP has been associated with raised IL-6 and CRP concentrations and has been associated with inflammation, obesity, insulin resistance, dyslipidaemia and raised systolic blood pressure. All of these are pronounced in smokers.

Individuals with the C allele should follow a diet to reduce inflammation that includes increasing n-3 fatty acids, decreasing saturated fatty acids, and increasing anti-oxidants. A healthy weight and avoidance of all smoking is also imperative in managing inflammation.

TNF-A -308 G>A

Tumour necrosis factor-α (TNFα), 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: AG

The A allele results in a two-fold increase in TNFA transcription, which leads to elevated levels of the circulating TNFα protein. The A allele is also associated with increased risk for obesity, adiposity, dyslipidaemia and insulin resistance, especially when dietary fat intake is high. In the presence of the A allele, increase intake of n-3 fatty acids and reduce pro-inflammatory saturated fatty acids. If dietary intake of n-3 fatty acids is inadequate, supplementation may be required. Weight management is also imperative in managing inflammation.

Inflammation (continued)

IL-1

IL-1 has been increasingly implicated as an important leverage point in the inflammatory cascade, and IL-1 expression is therefore key in the pathogenesis of several chronic diseases. The biological activity of IL-1 involves the two agonists – IL-1alpha (IL-1A) and IL-1beta (IL-1B), specific IL-1 receptors, and an IL-1 receptor antagonist (IL-1RN), which is a negative regulator of the pro-inflammatory response. Certain genetic variations in IL-1A, IL-B and IL-1 RN lead to a more active inflammatory response, and have been associated with increased risk for a number of chronic diseases.

YOUR RESULT:

Individuals with variations in IL-1A, IL-1B or IL-1RN have been associated with increased IL-1 plasma concentrations, and have been linked with a number of pro-inflammatory chronic diseases, including periodontitis, coronary artery disease, certain autoimmune diseases and cancers. Increase intake of nutrients known to inhibit secretion of pro-inflammatory markers. These include omega 3 fatty acids, curcumin, ginger, and phytonutrient rich foods including certain berries that contain compounds such as resveratrol, anthocyanins and dehydro-ascorbate.

Priority level: HIGH

Recommendation:

Based on your genes tested in the inflammation panel, your genotype combination contributes toward an increased risk for chronic low-grade inflammation and related inflammatory disorders, due to increased expression of these pro-inflammatory markers, making this a **high priority** area to focus on. It is important to manage weight and implement a Mediterranean style diet, which has been shown to be beneficial in improving markers of inflammation. Decrease intake of saturated fats, and moderate intake of omega 6 fatty acids. Increase intake of omega 3 fatty acids, and supplementation may be required. Other nutrients shown to have a beneficial effect on inflammation include ginger and curcumin, anthocyanins and trans-resveratrol from red berries.

Next steps:

Consider the following tests: ***Hs-CRP – DBS*** for the evaluation of current inflammation and/or Bloodspot ***Fatty Acids*** for the evaluation of dietary balance of omega 3 and 6 fatty acids to evaluate if diet is impacting the inflammatory state.

Oxidative stress

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. Anti-oxidants are free radical scavengers that interact with the free radical to ensure it is no longer a reactive molecule. Anti-oxidants are found naturally in the body in the form of enzymes, but can also be consumed in a wide variety of foods, especially from vegetables and fruit. However, the major role in anti-oxidant defense is fulfilled by the body's own anti-oxidant enzymes.

Gene Name	Genetic Variation	Your Result	Gene Impact
eNOS	894 G>T	GG	○
MnSOD/SOD2	47 T>C (Val16Ala)	TT	○
CAT	-262 C>T	CC	✓
GPX1	Pro198Leu	TT	●●●

eNOS 894 G>T

The endothelium-derived nitric oxide (NO) plays a key role in the regulation of vascular tone and peripheral resistance. It also has vasoprotective effects by suppressing platelet aggregation, leukocyte adhesion and smooth muscle cell proliferation.

YOUR RESULT: **GG** ○

No variant was detected at the 894 G>T locus.

MnSod/SOD2 47 T>C (Val16Ala)

The SOD2 enzyme destroys the free radicals which are normally produced within cells and which are damaging to biological systems. The enzyme thus has important anti-oxidant activity within the cell, especially within the mitochondria.

YOUR RESULT: **TT** ○

There is evidence that people without the variant, i.e. those with the C allele, and with a lower consumption of fruits and vegetables, are at increased risk of developing disease, including the risk of developing certain cancers. Individuals with the TT genotype have normal SOD2 function.

CAT -262 C>T

CAT encodes the antioxidant enzyme, catalase, which is most highly expressed in the liver, kidney and erythrocytes. The enzyme is responsible for the rapid conversion of hydrogen peroxide to water and oxygen, where one molecule of this enzyme can catalyse more than 1 million hydrogen peroxide molecules per second. Decreased CAT activity leads to increased concentrations of hydrogen peroxide, hence leading to increased oxidative stress.

YOUR RESULT: **CC** ✓

Individuals carrying the C allele, especially those with the CC genotype, have been associated with a decreased risk of cancer and better anti-oxidative balance. The protection offered by the C allele is further pronounced in individuals who have a high dietary intake of anti-oxidant and polyphenol rich foods.

Oxidative stress (continued)

GPX1 Pro198Leu

Glutathione peroxidase 1 (GPx1) is the most abundant of the selenoperoxidase enzymes, and is expressed in almost all tissues in the body. It is responsible for catalysing the coonversion of hydrogen peroxide into water, as well as reducing fatty acid hydroperoxides and peroxynitrite using glutathione as a substrate, and thus helps to maintain redox balance.

YOUR RESULT: TT

The TT genotype has been linked to a disturbed anti-oxidative balance and has been associated with increased risk for chronic diseases, including certain cancers and coronary artery disease, especially when fruit and vegetable intake is low. Ensure a polyphenol-rich diet, with a high intake of vegetables, and include good food sources of selenium (brazil nuts). Avoid toxin exposure from heavy metals and pesticides, and cessation of smoking should be strongly encouraged.

Priority level: MODERATE

Recommendation:

Based on your genes tested in the oxidative stress panel, your genotype combination contributes toward a moderately increased risk for poor anti-oxidant status and related oxidative stress-driven disorders. It is important to manage weight, and follow an exercise routine that includes low to moderate intensity exercises. Increase intake of a variety of vegetables and fruit daily, as well as other phytonutrient rich foods. Ensure adequate selenium intake to support GPX, as well as adequate omega 3 fatty acid intake for eNOS variant carriers.

Next steps:

Consider the following tests: ***Organix Comprehensive, DUTCH Comprehensive Urinary Hormone Test (UHT)*** or ***Oxidative Damage (8-OHdG)***.
All three tests measures 8-Hydroxy-2-deoxygaunosine, a marker for oxidative damage on DNA.

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 latest research both nutrition and genetic factors play an important role in determining bone health.

Gene Name	Genetic Variation	Your Result	Gene Impact
VDR	Fok1 T>C	TC	●
	Bsm1 G>A	AA	●●●
	Taq1 C>T	CC	●●●
COL1A1	1546 G>T	GG	○

VDR

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: TC ●

The T allele has poorer calcium absorption compared to the C allele.

YOUR RESULT: AA ●●●

The T (A) allele is associated with reduced BMD in a dose-dependent manner, and predisposes to osteoporosis, especially when calcium intake is low. There is also lower phosphorus re-absorption in the TT (AA) genotype when calcium is low in the diet, which results in lower calcium absorption and higher rates of hip fracture. Women with the TT (AA) genotype have a high bone loss when their caffeine intake is more than 300mg/day. 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.

YOUR RESULT: CC ●●●

Individuals with the CC genotype have higher bone turnover, increased bone loss and a higher risk of suffering osteoarthritis. This is highest when there is a low calcium intake. Individuals with the CC genotype have higher bone loss when caffeine intake is > 300 mg/d. 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.

Bone health continued

COL1A1 1546 G>T

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

YOUR RESULT: **GG**

No genetic variation was detected at the 1546 G>T locus.

Priority level: HIGH

Recommendation:

Based on your genes tested in the bone health panel, your genotype combination contributes toward an increased risk for a low bone mineral density and increased risk for osteoporosis, making this a **high priority** area to focus on. Ensure adequate vitamin D and calcium intake, as well as other 'bone-building' nutrients such as phosphorous, magnesium, boron, vitamin K, zinc and manganese. depending on dietary intake, supplementation may be required. Also include load bearing exercises to help maintain adequate bone mineral density. Ensure caffeine intake does not exceed 300mg per day.

Next steps:

Consider the following tests: ***Vitamin D - BLOODSPOT*** for the evaluation of vitamin D status and ***Bone Resorption Assessment*** for the evaluation of Pyridinium crosslinks for bone resorption status and deoxypyridinoline for possible bone loss.

Insulin sensitivity

Insulin is a hormone that stimulates the uptake of glucose from the diet into the cells. Those with lowered 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.

Gene Name	Genetic Variation	Your Result	Gene Impact
PPARG	Pro12Ala or C>G	CC	●●
TCF7L2	rs7903146 C>T	CT	●
SLC2A2	Thr110Ile	CC	○
FTO	rs9939609 T>A	TT	○

PPARG Pro12Ala or C>G

Peroxisome proliferator-activated receptor gamma 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 and has been identified as the nuclear receptor for the thiazolidinedione class of insulin-sensitizing drugs.

YOUR RESULT: **CC** ●●

The CC genotype is highly sensitive to the type and amount of fat in the diet, with regards susceptibility to obesity and diabetes. An increase in total dietary fat and saturated fat has been associated with increased waist circumference in CC individuals. Attention should be paid to the quality of fat intake, increasing MUFA's in the diet and decreasing SAT FAT. All diet and lifestyle variables that impact insulin sensitivity should be addressed.

TCF7L2 rs7903146 C>T

Transcription factor 7-like 2 (TCFL2) 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: **CT** ●

Individuals with the T allele have an increased risk for insulin resistance and type 2 diabetes, especially in obese individuals and those with low HDL-C. The T allele has also been associated with less weight loss in response to diet and lifestyle intervention, especially when fat intake is high. Individuals with the CT genotype require diet and lifestyle changes that impact insulin sensitivity.

SLC2A2 Thr110Ile

GLUT2, coded by the SLC2a2 gene, facilitates the first step in glucose induced insulin secretion, with the entry of glucose into the pancreatic βcell. Because of its low affinity for glucose, it has been suggested as a glucose sensor, and is considered to be important in the postprandial state, and is involved in food intake and regulation.

YOUR RESULT: **CC** ○

The analysis detected no variant.

Insulin sensitivity continued

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: **TT**

No variant was detected.

Priority level: LOW

Recommendation:

Based on your genes tested in the insulin sensitivity panel, your genotypes do not contribute toward an increased risk for insulin resistance and type 2 diabetes. It is still important to manage weight, and follow a healthy balanced diet as prescribed by your healthcare practitioner.

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 to how an individual might respond to a particular food component. The areas of food reponsiveness covered in this panel include: Lactose intolerance, polyunsaturated Fat (PUFA) metabolism, caffeine sensitivity, salt senitivity and iron overload, as well as bitter taste and alcohol metabolism.

In addition, many foodstuffs have been implicated in the condition irritable bowel syndrome (IBS). In this section, food responsiveness with regards to lactose intolerance and gluten sensitivity, which can be related to gut health and IBS symptoms, are reported.

	Gene Name	Genetic Variation	Your Result	Gene Impact
Iron overload	HFE	C282Y & H63D	282CC & 63HD	○
Caffeine sensitivity	CYP1A2	A>C	CA	●●
PUFA metabolism	FADS1	rs174537 G>T	GT	●●
Salt sensitivity	ACE	I/D	DD	○
	AGT	T>C	CC	●●●
Bitter taste	TAS2R38	Pro49Ala Ala262Val Val296Iso	Medium Taster	●●
Alcohol metabolism	ALDH2	rs671 G>A	GG	○
Lactose intolerance	MCM6	–13910C>T	TC	●
Gluten Intolerance	HLA	DQ2/DQ8	DQ2.2 & DQ2.5	●●●

Iron overload

HFE C282Y & H63D

Hereditary hemochromatosis is a genetic disorder in which there is excessive accumulation of iron in the body, leading to iron overload. In individuals with the 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 A>C

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

YOUR RESULT: **CA**

Individuals with the C allele are associated with a reduced ability to metabolise 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.

PUFA metabolism

FADS1 rs174537 G>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: **GT**

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.

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.

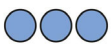
YOUR RESULT: **DD**

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

AGT T>C

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: **CC**



Individuals with the CC genotype are associated with increased risk for hypertension, however incidence of hypertension was found to be significantly lower among these individuals who reduced sodium intake.

Bitter taste

TAS2R38 Pro49Ala / Ala262Val / Val296Iso

Taste is an important determinant of food acceptance or rejection behaviour. Interindividual variability in bitter taste sensitivity can strongly influence food preferences, nutritional status, and health. TAS2R38 encodes the taste receptor responsible for the sensitivity to bitter compounds.

YOUR RESULT: **Medium Taster**

This combination of genotypes for the TAS2R38 gene results in a 'medium-taster' phenotype, meaning individuals are able to taste the bitter compounds in food. Medium tasters have been associated with having a decreased intake of vegetables, especially dark green leafy vegetables, and a preference for sweet foods. There has also been a link with medium tasters and an increased risk for having a higher BMI, and possibly colon cancer. Increase awareness of this preference, and encourage vegetable intake. More palatable vegetable options with the use of other ingredients may improve compliance.

Alcohol metabolism

ALDH2 rs671 G>A

Aldehyde dehydrogenase 2 (ALDH2) is an enzyme that is expressed in the liver, and is responsible for the detoxification of carcinogenic aldehydes to acetate. These toxic aldehydes include acetaldehyde - derived from ethanol (alcohol), as well as 4-hydroxynonenal and malondialdehyde - generated by lipid peroxidation. This enzyme is therefore important in protecting against oxidative stress. The SNP determines the activity of the enzyme, and thus blood acetaldehyde levels after alcohol consumption.

YOUR RESULT: **GG**

No variant was detected at the rs671 G>A locus. The GG genotype leads to a normal functioning aldehyde dehydrogenase enzyme.

Gut Health

Lactose intolerance

MCM6 –13910C>T

Adult lactase deficiency is a common condition with a decrease in the ability of the epithelial cells in the small intestine to digest lactose, owing to a physiological decline in the lactase enzyme. After ingestion of milk or other dairy products, Individuals who suffer from this condition may experience abdominal cramps, bloating, distension, flatulence and diarrhoea.

YOUR RESULT: **TC**

The TC genotype is associated lactase persistence in the Caucasian population.

Gluten intolerance

HLA DQ2 /DQ8

Coeliac disease (CD) is a common, autoimmune disorder in which the small intestine is damaged in response to a severe gluten intolerance. Specific Human Leukocyte Antigen (HLA) alleles represent the major genetic predisposition. A positive HLA test is indicative of genetic susceptibility but does not necessarily mean the disease will develop.

YOUR RESULT: DQ2.2 & DQ2.5

The analysis shows a positive result for both DQ2,2 and DQ2,5. This result suggests that you have a significantly greater chance of developing coeliac disease when on a diet high in gluten. This is not a diagnosis of coeliac disease, but coeliac disease cannot be excluded.
If you suffer from gastrointestinal symptoms, such as bloating, cramps, diarrhea, flatulence, as well as other general symptoms such as fatigue and joint pain, and have not excluded gluten from your diet, we recommend you discuss further coeliac testing with your dietitian or general practitioner.

Vitamin Metabolism

Vitamin requirements are dependent on a number of factors, from gender to age, as well as co-morbidities and genetics. The genes that are reported in this area are related to vitamin A, vitamin D, vitamin C and vitamin B12 requirements.

	Gene Name	Genetic Variation	Your Result	Gene Impact
Vitamin A	BCO1	G>T	GT	●●
		Ala379Val C>T	CT	●●
Vitamin D	CYP2R1	A>G	AG	●●
	GC	T>G	GT	●●
		1296 G>T	TT	●●●
Vitamin B12	FUT2	Gly258Ser G>A	AA	○
Vitamin C	GSTT1	Insertion/Deletion	Insertion	○

Vitamin A

BCO1 G>T

The BCO1 gene encodes the enzyme β-carotene 15,15'-oxygenase which is responsible for catalysing the oxidative cleavage of provitamin A carotenoids to yield retinal (vitamin A). It is highly expressed in retinal pigment epithelium, as well as in the kidney, testes, liver, brain, small intestine and colon. Its nutrient cofactor is iron (Fe).

It is important to note that these provitamin A carotenoids compete for oxidation to vitamin A, with the enzyme favouring β-carotene over α-carotene, β-cryptoxanthin and β-apo-8'-carotenal.

YOUR RESULT: **GT** ●●

Carriers of the GT genotype have been associated with higher levels of provitamin A carotenoids in the serum, including β-carotene. The G allele leads to a decrease in the BCO1 enzyme activity, which is associated with a decreased oxidation of many carotenoids, and a lower conversion rate of β-carotene and other provitamin A carotenoids to retinal.
In these individuals, personalised recommendations for pro-vitamin A carotenoids and active vitamin A may be required. Suggested recommended intake for β-carotene ranges between 2 - 4.8 mg/day, with higher intake from foods, over supplementation, being associated with favourable health effects. Food sources rich in B-carotene include: carrots, sweet potatoes, dark leafy greens.

BCO1 Ala379Val C>T

The BCO1 gene encodes the enzyme β-carotene 15,15'-oxygenase which is responsible for catalysing the oxidative cleavage of provitamin A carotenoids to yield retinal (vitamin A). It is highly expressed in retinal pigment epithelium, as well as in the kidney, testes, liver, brain, small intestine and colon. Its nutrient cofactor is iron (Fe).

It is important to note that these provitamin A carotenoids compete for oxidation to vitamin A, with the enzyme favouring β-carotene over α-carotene, β-cryptoxanthin and β-apo-8'-carotenal.

YOUR RESULT: **CT** ●●

Carriers of the BCO1 CT genotype may have a 30% reduced enzymatic conversion efficiency of β-carotene to retinal.
In these individuals, personalised recommendations for pro-vitamin A carotenoids and active vitamin A may be required. Suggested recommended intake for β-carotene ranges between 2 - 4.8 mg/day, with higher intake from foods, over supplementation, being associated with more favourable effects. Food sources rich in B-carotene include carrots, sweet potatoes, and dark leafy greens.

Vitamin D

CYP2R1 A>G

CYP2R1 is expressed in the liver, and encodes the enzyme 25-hydroxylase, which is involved in the conversion of vitamin D to 25(OH)D (calcidiol) - the first of two reactions to convert vitamin D to its active form (calcitriol).

YOUR RESULT: **AG**

The AG genotype is associated with a significant risk of having a low circulating vitamin D level.
It has also been found that individuals placed on cholecalciferol supplementation with the CYP2R1 AG genotype may be associated with a lower serum 25(OH)D concentration than expected. Ensure adequate vitamin D intake, UV exposure and supplementation of vitamin D when required.

GC T>G

GC, known as the group-specific component gene, is part of the albumin gene family and encodes the vitamin D binding protein (DBP), which binds vitamin D and transports it to its target tissues.

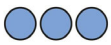
YOUR RESULT: **GT**

The GT genotype is associated with lower 25(OH)D concentrations. Supplementation may be associated with a lower incremental increase in serum levels in these individuals compared to those without the variant. Interventions for improving vitamin D levels include encouraging adequate dietary vitamin D intake, UV exposure and supplementation of vitamin D when required.

GC 1296 G>T

GC, known as the group-specific component gene, is part of the albumin gene family and encodes the vitamin D binding protein (DBP), which binds vitamin D and transports it to its target tissues.

YOUR RESULT: **TT**



The TT genotype is associated with lower D binding protein (DBP) levels and lower serum vitamin D levels. The T allele may also confer an increased risk for the development of metabolic syndrome, COPD, and certain cancers, especially when vitamin D levels are insufficient. Interventions for improving vitamin D levels include encouraging adequate dietary vitamin D intake, UV exposure and supplementation of vitamin D when required.

Vitamin B12

FUT2 Gly258Ser 772 G/A

FUT2 encodes the enzyme, fucosyltransferase 2, which is involved in vitamin B12 absorption and transport between cells.

YOUR RESULT: **AA**

The AA genotype is associated with normal functioning of the FUT2 enzyme. Genetically, there is no increased risk for lower serum vitamin B12 levels.

Vitamin C

GSTT1 Insertion/Deletion

GSTT1 encodes a member of the Glutathione S-transferase (GST) family, which are detoxifying enzymes that contribute to the glutathione-ascorbic acid (vitamin C) antioxidant cycle. Vitamin C is an essential antioxidant vitamin that aids in the reduction of free radical production.

YOUR RESULT: **Insertion**

The presence of the gene produces an active enzyme which is shown to protect against serum ascorbic acid deficiency when dietary vitamin C is insufficient.

Notes for practitioners

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