dnahealth®

optimal health for life

Welcome

Matt Ooi

to your dna health® report

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Referring Practitioner: **R N LABS**		

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	LOW
Methylation	HIGH
Detoxification	HIGH
Inflammation	HIGH
Oxidative Stress	LOW
Bone Health	LOW
Insulin Sensitivity	LOW

Insulin Sensitivity LOW

Report summary

RESULTS	DO	WHAT SHOULD I DO?	AVOID
Methylation / B-Vitamin Requirements Genetic variants in this essential life process can influence our requirements for B-vitamins & may increase the risk of having high levels of homocysteine, which is an indicator of poor health. HIGH PRIORITY AREA	• Increase intake of vitamin B-rich foods, including dark green leafy vegetables, lentils, whole grains, nuts & seeds • Ensure adequate intake of magnesium rich foods • Supplementation may be required • Manage stress		• Limit alcohol
Detoxification The detoxification process in the body aids the removal of harmful substances, such as pollution, alcohol & drugs, from your body. HIGH PRIORITY AREA	• Increase intake of a variety of cruciferous vegetables (broccoli, cauliflower, kale), preferably organic, to a portion per day • Speak to your healthcare practitioner about relevant supplementation that may be required for added detoxification support such as DIM, sulforaphane & ashwagandha, green tea & milk thistle		• Reduce exposure to environmental toxins such as cigarette smoke, smoked foods, air pollution, pesticides & plastic
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

Food responsiveness summary

RESULTS	DO	WHAT SHOULD I DO?	AVOID
Salt Sensitivity Salt sensitivity is, to a large extent, genetically determined. The gene variants tested in this section give insight to your body's responsiveness to salt intake & whether this might spike your blood pressure levels.	HIGH PRIORITY AREA 	If you suffer from high blood pressure, it is essential to severely restrict salt & all sodium rich foods Use a variety of herbs & spices instead of salt to flavour food	Avoid adding extra salt to food Don't eat processed meats Decrease intake of high sodium condiments Avoid ready made meals & fast foods

Vitamin metabolism summary

RESULTS	WHAT SHOULD I DO?
Vitamin B12 Vitamin B12 (cobalamin) is an essential nutrient for brain and neural functioning as well as many metabolic processes including homocysteine metabolism. **INCREASED REQUIREMENT**	Increase intake of vitamin B12-rich foods such as fatty fish, liver, beef and eggs. Supplementation may be required. Strict vegans, if you have gut health problems or take heartburn medication, your absorption of vitamin B12 may be decreased. Limit alcohol intake.

Summary table

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

		Taq1 C>T	TC	●
	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	CC	○
	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	II	●●●
	AGT	T>C	TC	●●
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	DQ8	●●
Vitamin A	BCO1	G>T	GT	●●
		Ala379Val C>T	CC	○
Vitamin D	CYP2R1	A>G	AA	○
	GC	T>G	TT	○
		1296 G>T	TG	●●
Vitamin B12	FUT2	Gly258Ser G>A	GA	●●
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	CG	✓
CETP	279 G>A	AG	●
APOC3	3175 C>G	CC	○
APOE	E2/E3/E4	E3/E3	○
PON1	A>G	GA	●

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: **CG** ✓

In individuals who carry the G allele, plasma VLDL-C and triglyceride levels are lower and HDL-C levels higher, compared to individuals carrying the C allele. These individuals also tend to have lower blood pressure.

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: **AG** ●

The 279 A allele is associated with reduced plasma CETP levels, increased HDL-C levels and reduced risk of cardiovascular disease.

An alpha-linoleic acid-enriched (ALA) -enriched, low cholesterol diet is effective in decreasing VLDL-C and LDL-C levels in GA and AA individuals.

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: **E3/E3**

E3 is the neutral isoform.

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: **GA**

The G allele is associated with lower concentrations of PON1 and decreased PON1 activity. The SNP has been linked to increased risk of atherosclerosis and certain cancers. Increase mono-unsaturated fat intake and encourage a high intake of a variety of vegetables and fruit.

Priority level: LOW

Recommendation:

Based on your genes tested in the lipid metabolism panel, your genotypes do not contribute toward an increased risk for an abnormal lipid profile and risk for cardiovascular disease. Manage weight, exercise and follow a healthy balanced diet as prescribed by your healthcare practitioner.

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 (CH_3). 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	AA	●●●
MTHFR	677 C>T	CT	●●
	1298 A>C	CA	●
MTR	2756 A>G	AA	○
MTRR	66 A>G	GG	●●
CBS	699 C>T	CC	○
COMT	472 G>A	GG	○

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: **AA** ●●●

MTHFD1 A allele carriers have a decreased enzyme function and have been shown to develop signs of choline deficiency and organ (liver and muscle) dysfunction compared to those with the GG genotype. Individuals with the AA genotype may require an increased intake of choline-rich foods and supplementation where necessary.

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: **CT** ●●

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 & B12 requirements. Enzyme function is only 70% of optimal in CT

requirements. – Enzyme function is only 70% of optimal in CT individuals. In addition to folate-rich foods, a supplement may be recommended.

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: **GG**

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.

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: **GG**

No variation was detected at the 472 G>A locus.

Priority level: HIGH

Recommendation:

Based on your genes tested in the methylation panel, your genotype combination contributes toward an increased risk for decreased methylation processes and increased homocysteine levels, and makes this a **high priority** area to focus on. It is important to increase intake of B vitamin-rich foods with an emphasis on vitamin B2, B6, B9 and B12 sources. Supplementation with a vitamin B complex that contains L-5-methyltetrahydrofolate and methylcobalamin, is recommended. Decrease alcohol intake and implement stress management strategies.

Because of the MTHFD1 A allele, ensure adequate intake of choline-rich foods or supplement where necessary.

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	AG	●
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: **AG**

The G allele decreases activity of the enzyme. Conjugation activity is around 80% for carriers of one G allele, and 70% for the GG genotype individuals.

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 DIM may be required.

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: HIGH

Recommendation:

Based on your genes tested in the detoxification panel, your genotype combination contributes toward a decreased detoxification ability and therefore an increased risk for DNA damage, making this a **high priority** area to focus on. 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, preferably organic, with a specific emphasis on daily intake of cruciferous and allium vegetables. Specific nutrients known to support phase two detoxification include, DIM, sulforaphane, resveratrol and curcumin. Supplementation may be required for added support.

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	GG	○
TNFA	-308 G>A	GG	○
IL-1	IL-1A 4845 G>T	TG	●●
	IL-1A -889 C>T	TC	●●
	IL-1B 3954 C>T	CT	●●
	IL-1B -511 A>G	GA	●
	IL-1RN 2018 C>T	TT	●●

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: **GG** ○

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

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: **GG** ○

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

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	CC	○

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** ●●

TT genotype carriers may have lower longevity in comparison with CC genotype carriers. Moderate intenisty exercise has been shown to improve SOD2 activity and protect from oxidative stress.

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: **CC**

No variation was detected. The CC genotype is associated with normal glutathione peroxidase function. Individuals with the CC genotype are more responsive to improving GPX activity with dietary selenium intake.

Priority level: LOW

Recommendation:

Based on your genes tested in the oxidative stress panel, your genotypes do not contribute toward an increased risk for poor anti-oxidant status and related oxidative stress-driven disorders.

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	GA	●
	Taq1 C>T	TC	●
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: **GA** ●

The T (A) allele is associated with reduced BMD in a dose-dependent manner, and predisposes to osteoporosis, especially when calcium intake is low.

YOUR RESULT: **TC** ●

The variation does not lead to an increased risk for osteoporosis.

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: LOW

Recommendation:

Based on your genes tested in the bone health panel, your genotypes do not contribute toward an increased risk for a low bone mineral density and increased risk for osteoporosis. It is still important to ensure adequate vitamin D and calcium intake, and include load bearing exercises to maintain adequate bone mineral density.

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	CC	○
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: **CC** ○

No variant was detected.

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

YOUR RESULT: **CC** ○

The analysis detected no variant.

regulation.

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	II	●●●
	AGT	T>C	TC	●●
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	DQ8	●●

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

YOUR RESULT: **282CC & 63HD** ○

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

pigmentation.

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: **II**

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: **TC**

Individuals who carry the C 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.

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: **DQ8**

The analysis detected the presence of the DQ8 genotype. This result suggests that you have a 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	CC	○
Vitamin D	CYP2R1	A>G	AA	○
	GC	T>G	TT	○
		1296 G>T	TG	●●
Vitamin B12	FUT2	Gly258Ser G>A	GA	●●
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

YOUR RESULT: **CC** ○

The CC genotype appears to have normal enzymatic activity and thus standard dietary recommendations would be advised.

carotenoids compete for oxidation to vitamin A, with the enzyme favouring β-carotene over α-carotene, β-cryptoxanthin and β-apo-8′-carotenal.

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: **AA**

The AA genotype leads to increased enzyme production and thus improved ability to convert calcidiol to calctriol - the active form of vitamin D. Standard dietary recommendations for vitamin D would be advised.

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: **TT**

The TT genotype is associated with higher vitamin D levels compared to individuals carrying the variant. Vitamin D supplementation also seems to show a greater incremental increase in serum levels in TT individuals compared to those who carry the variant.

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: **TG**

The TG 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: **GA**

There is an increased risk for lower vitamin B12 levels in AG genotype carriers, thus possibly increasing risk for anaemia, neurological conditions and altered homocysteine metabolism. Increased vitamin B12 may be required through dietary sources such as meat, fish, poultry and eggs or through supplementation where indicated.

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

From the laboratories of:

DNALYSIS Biotechnology

Distributed by:

dnalife

Nordic Laboratories

APPROVED BY:
Thenusha Naidoo - Medical Scientist
Larisa Naguriah - Medical Technologist

info@dnalife.healthcare
www.dnalife.healthcare

Danny Meyersfeld (PhD) - Laboratory Director
Denmark Office: Nygade 6, 3.sal • 1164 Copenhagen K • Denmark
South Africa Office: North Block • Thrupps Centre • 204 Oxford Rd • Illovo 2196 • South Africa

Tlf: +45 33 75 10 00
Tel: +27 (0) 11 268 0268

UK Office: 11 Old Factory Buildings • Battenhurst Road • Stonegate • E. Sussex • TN5 7DU • UK Tel: +44 (0) 1580 201 687

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