



dnahealth[®]

optimal health for life

Welcome

SUMMER

to your dna health[®] report

Date of Birth: 30 Mar

Date Reported: 12 Jul 2023

Sample Number: M23001760

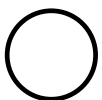
Referring Practitioner:

Introduction

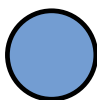
From your DNA sample we have used a process called the Polymerase Chain Reaction (PCR), which copies the DNA of your genes many times over so that we can generate sufficient quantities to analyse your genetic material. We then identify unique DNA sequences in some of your genes. Certain changes (polymorphisms) 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

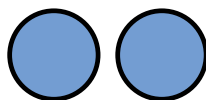
You will find your genetic results in the following pages. On the left side you will see the gene name and description. On the right side you will find your specific result and an explanation of the results, associated risks, and diet and lifestyle recommendations. The impact can be identified by the following:



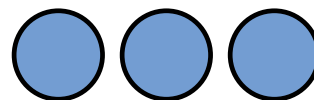
No Impact



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	
Methylation	
Detoxification	
Inflammation	
Oxidative Stress	
Bone Health	
Insulin Sensitivity	

Report summary



Food responsiveness summary



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	MTHFR	677 C>T	CT	
		1298 A>C	CA	
	MTR	2756 A>G	AA	
	MTRR	66 A>G	GG	
	CBS	699 C>T	TC	
	COMT	472 G>A	AG	
Detoxification	CYP1A1	Msp1 T>C	TT	
		Ile462Val A>G	AA	
	GSTM1	Insertion/Deletion	Insertion	
	GSTP1	313 A>G	GG	
	GSTT1	Insertion / Deletion	Insertion	
	NQO1	C>T	CC	
Inflammation	IL-6	-174 G>C	GG	
	TNFA	-308 G>A	AG	
	IL-1A	4845 G>T	GG	
	IL-1A	-889 C/T	CC	
	IL-1B	3954 C>T	CC	
	IL-1B	-511 A>G	AA	
	IL-1RN	2018 C>T	CT	
Oxidative Stress	eNOS	894 G>T	GT	
	MnSOD/SOD2	-28 C>T	TT	
	CAT	-262 C>T	CT	
	GPX1	C>T	CT	
Bone Health	VDR	Fok1 T>C	TC	
		Bsm1 G>A	AA	
		Taq1 C>T	CC	
	COL1A1	1546 G>T	GG	
Insulin Sensitivity	PPARG	Pro12Ala or C>G	CC	
	TCF7L2	rs7903146 C>T	CC	
	SLC2A2	Thr110Ile	CC	
	FTO	rs9939609 T>A	AT	
Iron overload	HFE	C282Y & H63D	282CC & 63HD	
Lactose Intolerance	MCM6	-13910C>T	TT	
Caffeine Sensitivity	CYP1A2	A>C	AA	
PUFA Metabolism	FADS1	rs174537 G>T	GG	
Salt Sensitivity	ACE	I/D	ID	
	AGT	T>C	TT	
Bitter Taste	TAS2R38	145 C>G 785 C>T 886 G>A	Medium Taster	
Alcohol Metabolism	ALDH2	rs671 G>A	GG	

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

YOUR RESULT: 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.

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
MTHFR	677 C>T	CT	
	1298 A>C	CA	
MTR	2756 A>G	AA	
MTRR	66 A>G	GG	
CBS	699 C>T	TC	
COMT	472 G>A	AG	

MTHFR 677 C>T

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

YOUR RESULT: 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 individuals. In addition to folate-rich foods, a supplement may be recommended.

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.

Methylation continued

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: TC

The variant 699T allele is associated with decreased risk of CAD and an increased responsiveness to the homocysteine lowering effects of folic acid. Check dietary folate intake and homocysteine levels and supplement if necessary.

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: AG

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.

Detoxification

The detoxification process in the body is governed primarily by the GST family of enzymes. Glutathione S-transferases 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	Insertion	
GSTP1	313 A>G	GG	
GSTT1	Insertion / Deletion	Insertion	
NQ01	NQ01 C>T	CC	

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: **Insertion**

No deletion was detected.

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: **GG**

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

NQO1 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: **CC**

The analysis identified no genetic variation at the 209 C>T locus.

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	AG	
IL-1	IL-1A 4845 G>T	GG	
	IL-1A -889 C>T	CC	
	IL-1B 3954 C>T	CC	
	IL-1B -511 A>G	AA	
	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: GG

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

TNF-A -308 G>A

Tumour necrosis factor- α (TNF α), 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 TNF α 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-1B and IL-1RN lead to a more active inflammatory response, and have been associated with increased risk for a number of chronic diseases.

YOUR RESULT:

These specific IL-1 genotypes are not associated with increased risk for inflammation.

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	GT	
MnSOD/SOD2	-28 C>T	TT	
CAT	-262 C>T	CT	
GPX1	Pro198Leu	CT	

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: GT

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

MnSod/SOD2 -28 C>T

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: CT

Compared to the CC genotype, individuals with the T allele (CT genotype) have been associated with decreased CAT activity. Ensure a polyphenol-rich diet with a high intake of vegetables. Decrease dietary and environmental carcinogen exposure (pollution, pesticides, smoked foods and nitrates used as a food preservative). Cessation of smoking should be strongly encouraged.

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 conversion 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: CT

The CT 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.

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.

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	AT	

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 β cell. 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: AT

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

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 responsiveness covered in this panel include: Lactose intolerance, polyunsaturated Fat (PUFA) metabolism, caffeine sensitivity, salt sensitivity and iron overload, as well as bitter taste and alcohol metabolism.

	Gene Name	Genetic Variation	Your Result	Gene Impact
Iron overload	HFE	C282Y & H63D	282CC & 63HD	
Lactose intolerance	MCM6	-13910C>T	TT	
Caffeine sensitivity	CYP1A2	A>C	AA	
PUFA metabolism	FADS1	rs174537 G>T	GG	
Salt sensitivity	ACE	I/D	ID	
	AGT	T>C	TT	
Bitter taste	TAS2R38	Pro49Ala Ala262Val Val296Iso	Medium Taster	
Alcohol metabolism	ALDH2	rs671 G>A	GG	

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.

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: **TT**

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

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: **AA**

Individuals with the AA genotype are fast metabolisers of caffeine.

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 -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: **GG**

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: ID

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: TT

No variant was detected.

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.

