р	р	c/up	sprints	р	р	s + :	30 b/c
Weight							
Energy							
DAY	11	12	13	14	15	16	17
eggs	5	3	4	4	3	2	4
spinach	100		100	150			100
bacon	3	4	4		4		3
tomato	1	1	1		1	1	1
greek yoghurt	100	200	75	150	150	50	150
berries	50	100	100	100	100	100	100
whey protein con	С				30		30
ostrich stew							
ostrich burger							
mixed veg			5				
roasted peppers							
aubergines							
carrots							
cauliflower						100	
onion	0.5	0.5					
mushrooms					4 large	2 lai	rge
broccoli					150	100	
chicken liver parf	ait						
apple					,		
banana	_				1	1	1
green salad	40	40	40		40		
avocado	1	1	1		0.5	1	1
sweet potato			_				
small potato			2				
beetroot				4	75		
butter	1		20	1	1	1	1
cream			30				
cream - whipped		a a	4	2			1
full fat flat whi	1	1	1	2			7
coffee black							

feta cheese mozarella cheese			30				
blue cheese basil tuna			50				
chocolate 85% tea black	50	50	75	50	40	40	20
red wine	300	300	400	100		100	100
macadamia nı	100	150	150	150	200	150	100
honey cheddar cheese	1	1			1		1
chicken	150	150 250	150		250		250
chicken curry beef	150	150		350	150		
chili con carne pork belly						350	
smoked salmon				100			
lean burger calamari		250					
Fish						300	
olive oil herbs, spices	1	1	2		1	1	2
cinnamon coconut oil garlic	0.5	0.5	0.5	0.5	0.5		0.5
wheat free roll white rice		1	100				
hollandaise sa table	spoon		100	4			

.

Tel: 021 551 6372 Fax

021 551 6379

VAT No.: 4540241041



Smartsury House, 1st Floor, 32 Century Blvd, Century City 7441 Practice No: 5202507

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Labno WHI 0334319 (27/06/2012) Patient O NEILL, D, DONAL 606 FORTUNE Address JAMIE SMITH 109 BEACH ROAD PREVENTATIVE MEDICINE MOUILLE POINT 8001 AND EXECUTIVE WELLNESS SPORTS SCIENCE INSTITUTE OF SA Tel No (C) 0794550773 NEWLANDS Age (Sex) 41y (M) DoB 13/05/1971 FAX->021 659 5633 STAT Ref Dr JAMIE SMITH Practice SMITH, JAMIE Taken 27/06/12 00:01 Recd 27/06/12 10:12

## LABORATORY REPORT (E-MAIL)

Report

Specimen

Blood

Tests ordered

FBC & Plt, Diff, ESR (West), S-U&E, Creat, Uric Acid, S-Chol, HDL, Trig, LDL2,CRP,LFT,VITD,eGFR,COM

27/06/12 11:48

FBC & PLATELETS		Flags	RefInterval
WBC Count	4.6 x10^9/L		4.0 - 11.0
Red Blood Cell Count	4.99 x10^12/L		4.50 - 6.50
<b>Th</b>	15.3 g/dL		13.0 - 18.0
Het	45.3 %		40.0 - 54.0
NCV	91 fl	•	80 - 100
NCH	30.7 pg		27.0 - 32.0
мснс	33.8 g/dL		32.0 - 36.0
RDW	13.3 %		10.0 - 14.0
Platelets	. 248 x10^9/L		140 - 450
			1 10 29
HIFFEBENTIAL COUNT	•	Flags	RefInterval
Neutrophils	55.30 %		50.00 - 80.00
Neutrophils (Abs)	2.57 x 10^9/L		2.00 - 7.40
Monocytes	9 10 %		2.00 - 10.00
Monocytes (Abs)	0.42 x 10^9/L		0.10 - 0.84
Lymphocytes	31.90 %	•	25.00 - 50.00
Lymphocytes (Abs)	1.48 x 10^9/L		1.00 - 4.50
Rosinophils	1.30 %		0.00 - 5.00
Eosinophils (Abs)	0.06 x 10^9/L		0.04 - 0.60
Basophils	2.40 %	K	0.00 - 2.00
Basophils (Abs)	0.11 x 10^9/L		0.00 - 0.25
•			
ESR (WESTERGREN)		Flags	RefInterval
KSR (Westergren)	2 mm/h	_	0 - 12

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Labno WHI 0334319 (27/06/2012)	Patient	o ni	HLL,D,DO	NAL
KLECTROLYTES & URKA			Flans	RefInterval
S-Sodium	134	mm ol/L		135 - 145
S-Potassium		•		aemolysis
S-Chloride		mmol/L		98 - 107
S-Total CO2				22.0 - 30.0
S-Urea		mmol/L		3.2 - 7.2
Remarks :				
Sample not haemolysed. No colle	ction ti	me oor dat	te stated	i on form.
Please treat results with rese				
CREATININE			Flags	RefInterval
S-Creatinine	71	$\mu$ mol/L		53 - 115
WRIC ACID			Flags	RefInterval
S-Uric Acid	0.30	mmol/L		0.21 - 0.51
LIPIDS			Flags	RefInterval
S-Cholesterol 6.5	7 18	mmol/L	W	3.10 - 5.20
S-HDL 2:50		mmol/L	11	0.90 - 1.45
S-Triglyceride		mmol/L	m so	0.50 - 2.00
S-IDL		maol/L	W	1.00 - 3.00
Bud Mandad tiled ( a a a a s s s s s s s s s s s s s s s	.AC # #50°	man is and	***	
June 1904 Aller Hall Service County Street, Table 300, Part Service County Street				
C-REACTIVE PROTEIN			Flags	RefInterval.
S-CRP	< 0.6	mg/L	Flags	<b>RefInterval</b> 0.0 - 5.0
S-CRP	< 0.6	mg/L	<del></del>	0.0 - 5.0
S-CRP		•	Flags	0.0 - 5.0 <b>RefInterval</b>
S-CRP LIVER FUNCTIONS S-Total Protein	72	g/L	<del></del>	0.0 - 5.0 <b>RefInterval</b> 60 - 85
S-CRP LIVER FUNCTIONS S-Total Protein S-Albumin	72 48	g/L	<del></del>	0.0 - 5.0 <b>RefInterval</b> 60 - 85 38 - 54
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins	72 48 24	ä∖r à\r à\r	Flags	0.0 - 5.0 <b>RefInterval</b> 60 - 85 38 - 54 18 - 36
S-CRP LIVER FUNCTIONS S-Total Protein S-Albumin S-Globulins S-Total Bilirubin	72 48 24 8.8	hwol/F d/F d/F	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin	72 48 24 8.8 2.70	g/L g/L g/L mol/L	Flags	0.0 - 5.0 <b>RefInterval</b> 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin  S-Unconjugated Bilirubin	72 48 24 8.8 2.70 6.1	g/L g/L pmol/L pmol/L pmol/L	Flags	0.0 - 5.0 <b>RefInterval</b> 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin  S-Unconjugated Bilirubin  S-Aspartate Transaminase	72 48 24 8.8 2.70 6.1 24	g/L g/L pmol/L pmol/L pmol/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin  S-Unconjugated Bilirubin  S-Aspartate Transaminase  S-Alanine Transferase	72 48 24 8.8 2.70 6.1 24 28	g/L g/L pmol/L pmol/L pmol/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41
S-CRP  LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase	72 48 24 8.8 2.70 6.1 24 28	g/L g/L pmol/L pmol/L pmol/L UU/L UU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin  S-Unconjugated Bilirubin  S-Aspartate Transaminase  S-Alanine Transferase	72 48 24 8.8 2.70 6.1 24 28	g/L g/L pmol/L pmol/L pmol/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin  S-Unconjugated Bilirubin  S-Aspartate Transaminase  S-Alanine Transferase  S-Alkaline Phosphatase  S-Gamma-Glutamyltransferase	72 48 24 8.8 2.70 6.1 24 28	g/L g/L pmol/L pmol/L pmol/L UU/L UU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50
LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase S-Gamma-Glutamyltransferase	72 48 24 8.8 2.70 6.1 24 28 61	g/L g/L pmol/L pmol/L IU/L IU/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50  RefInterval
S-CRP  LIVER FUNCTIONS  S-Total Protein  S-Albumin  S-Globulins  S-Total Bilirubin  S-Conjugated Bilirubin  S-Unconjugated Bilirubin  S-Aspartate Transaminase  S-Alanine Transferase  S-Alkaline Phosphatase  S-Gamma-Glutamyltransferase	72 48 24 8.8 2.70 6.1 24 28 61	g/L g/L pmol/L pmol/L pmol/L UU/L UU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50
LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase S-Gamma-Glutamyltransferase	72 48 24 8.8 2.70 6.1 24 28 61	g/L g/L pmol/L pmol/L IU/L IU/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50  RefInterval
LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase S-Gamma-Glutamyltransferase  VITAMIN D Vitamin D	72 48 24 8.8 2.70 6.1 24 28 61	g/L g/L pmol/L pmol/L IU/L IU/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50  RefInterval
LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase S-Gamma-Glutamyltransferase WITAMIN D Vitamin D  Reference Ranges for Vitamin D	72 48 24 8.8 2.70 6.1 24 28 61 17	g/L g/L g/L pmol/L pmol/L IU/L IU/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50  RefInterval
S-CRP  LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase S-Gamma-Glutamyltransferase  VITAMIN D  Vitamin D  Reference Ranges for Vitamin D < 10 ng/ml Deficiency	72 48 24 8.8 2.70 6.1 24 28 61 17	g/L g/L g/L pmol/L pmol/L IU/L IU/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50  RefInterval
LIVER FUNCTIONS  S-Total Protein S-Albumin S-Globulins S-Total Bilirubin S-Conjugated Bilirubin S-Unconjugated Bilirubin S-Aspartate Transaminase S-Alanine Transferase S-Alkaline Phosphatase S-Camma-Glutamyltransferase VITAMIN D  Vitamin D  Reference Ranges for Vitamin D < 10 ng/ml Deficiency 10 - 30 ng/mL Relative Insa	72 48 24 8.8 2.70 6.1 24 28 61 17	g/L g/L g/L g/L pmol/L pmol/L IU/L IU/L IU/L	Flags	0.0 - 5.0  RefInterval 60 - 85 38 - 54 18 - 36 3.0 - 22.0 0.00 - 5.00 0.0 - 19.0 9 - 36 10 - 41 40 - 129 0 - 50  RefInterval

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Labno WHI 0334319 (27/06/2012) Patient

112.3

O NEILL, D, DONAL

Please note: Change in reference range due to new method

ECFR

9 . . . .

Flags

RefInterval

Glomerular Filtration Rate ...

-See below-

Reference Ranges for Glomerular Filtration Rate Stages of Chronic Kidney Disease

Stage:	Description:	GFR:
1	Normal	>90
2	Mild decrease	60-80
3	Moderate decrease	30 <i>-</i> 59
4	Severe decrease	15-29
5	Kidney failure	<15
(GFR U	$mits = mL/min/1.73m^{\circ}$	2)

COMMENT

Flags RefInterval

General Text

Please repeat specimen for accurate potassium result.

THERON, AMELIA MS Authorised by :

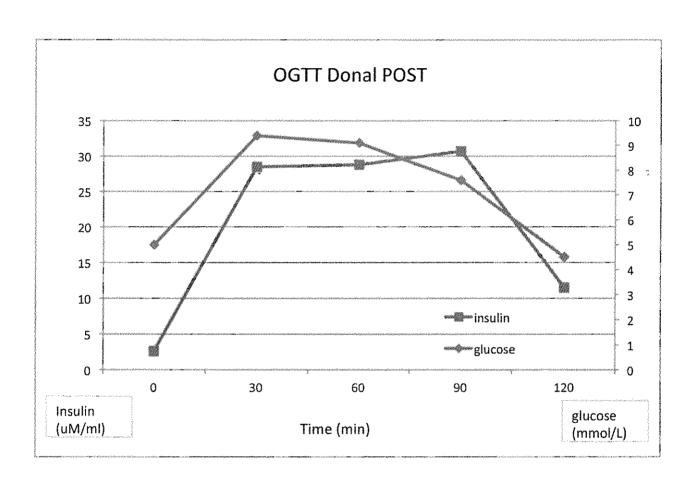
Test(s): FBC & Plt, Diff, RSR (West), S-U&R, Creat, Uric Acid, S-Chol, HDL, Trig, LDL2, CRP, LFT, VITD, eGFR, COM

Prof F Taljaard 083 627 1949

--- Rnd of Laboratory Report ---

Donal Oniell post 26/06/2012 Time

glu	cose insi	ulin	
0	5	2.6	2.5
30	9.4	28.5	<i>\( \)</i>
60	9.1	28.8	18-1
90	7.6	30.7	54.3
120	4.5	11.5	28 6
			10.9



# & dnaheath

PATIENT GENOTYPE REPORT - STRICTLY CONFIDENTIAL

PATIENT NAME: D. O'NEILL

SAMPLE ID: HH01000877ZA

DATE OF BIRTH: 13-05-1970

SAMPLE TYPE: BUCCAL SWAB

GENDER: MALE

**DATE COLLECTED: 04-06-2012** 

REFERRING DOCTOR: DR G. PRINSLOO

**DATE REPORTED: 20-06-2012** 



## **BACKGROUND TO THE ANALYSIS**

DNAlysis received your swab sample and used special molecular techniques to amplify your DNA for further analysis. This process, called the Polymerase Chain Reaction (PCR), 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, and evidence has emerged that correlates these polymorphisms with an individual's risk of developing certain chronic disease conditions or altering metabolic processes. Having identified the presence or absence of these polymorphisms, we are able, qualitatively, to assess particular health risks related to the specific genes. To make a holistic assessment of disease risks, environmental factors (diet and lifestyle) need to be considered in conjunction with the accompanying genetic profile.

#### **REQUESTED ANALYSES**

PANEL	ANALYSED
Lipid Profile	<b>✓</b>
B Vitamins / methylation	✓
Detoxification	✓
Inflammation	<b>✓</b>
Oxidative Stress	✓
Bone Health	✓
Insulin Resistance	<b>~</b>

In the following pages you will find a table of your genetic results, and an explanation of these results and associated risk including diet and lifestyle recommendations. Only gene variants that have a beneficial, moderate or high impact on metabolic processes or disease susceptibility have been described in detail, as gene variants that have no impact or a mild impact do not require diet or lifestyle intervention.

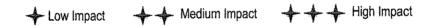
# \* Pillerot - IA conjust

# 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.

# **Summary Results**

GENE	GENETIC	YOUR	GENE
NAME	VARIATION	RESULTS	IMPACT
LPL	1595 C>G	CC	No impact
CETP	279 G>A	AA	Beneficial
APOA1	-75 G>A	GA	*
APOC3	3175 C>G	GG	**
APOE	158 Arg>Cys / 112 Cys>Arg	E3/E3	No impact



From the analysis of your genetic profile the following **BENEFICIAL**, **MEDIUM** or **HIGH IMPACT** gene variants were observed:

# CETP : 1

Cetp plays a key role in the metabolism of high-density lipoproteins (HDL), and mediates the exchange of lipids between lipoproteins, resulting in the eventual uptake of cholesterol by hepatocytes.

The A allele is associated with reduced plasma cetp, increased HDL-C and reduced risk. AA genotypes generally respond poorly to statin therapy. In GA & AA individuals, a diet enriched with ALA and low in cholesterol is effective in decreasing VLDL-cholesterol and LDL-cholesterol.

Choke - In eleme acid = 5.3

# APOC3 & cambolism of choi

APOC3 plays an important role in cholesterol metabolism, where it inhibits lipoprotein lipase and hepatic lipase, therefore delaying catabolism of triglyceride-rich particles.

The G allele is associated with elevated plasma triacylglycerol, cholesterol, and Apo C-III concentrations. Individuals with the G allele have a 4-fold increased risk for hypertriglyceridaemia. The G allele influences dietary responsiveness; where changing from a low-fat diet to a high-MUFA diet, LDL-cholesterol decreases. It is important to shift fat from saturated fat to unsaturated fat, especially MUFA, if the G allele present.

Responsive a diet: Swifer -> 7 MUFA

Free radicals damage DNA. Methylanon is involved in DNA report.

If this is inacliqued a kado is "holeo" - 1 nik of currer +

B Vitamins/methylation

- Useo B unemins.

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

#### **Summary Results**

4 Major enzyme in DNA repair.

GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT
MTHFR	677 C>T	ТТ	***
WITTK	1298 A>C	CA	* /
MTR	2756 A>G	AA	No impact
MTRR	66 A>G	AG	+
CBS	699 C>T	ст	Beneficial

From the analysis of your genetic profile the following **BENEFICIAL**, **MEDIUM** or **HIGH IMPACT** gene variants were observed:

## MTHFR

Mthfr is a key enzyme in DNA methylation and conversion of homocysteine to methionine.

Enzyme activity is decreased by the SNP. Enzyme functions at about 60% of optimal in individuals with the CT genotype, and about 30% of optimal in the TT genotype. A decrease in mthfr enzyme function leads to an increase in homocysteine and a decrease in DNA methylation and thus an increase in DNA adducts. Those with the T allele have greater folate, B6 and B12 requirements. In addition to folate rich foods, these individuals may require a supplement. When dietary intake of B vitamins, especially folate is adequate, the T allele has no effect on homocysteine.

# CBS 7 methylation

Cystathionine beta synthase catalyses the conversion of homocysteine to cystathione.

The variant T allele is associated with a decreased risk of CAD and increased responsiveness to the homocysteine lowering effects of folic acid.

\* Need Folda. B6 + BIL, B5 > In everything but in small amounts.

1. Opinmize diet 7 Goal for him = 800 pag Folda (MTHF) At hoor pub gening @ 300 pg.

2. Supplement \_ Multib (always supplement all logelle)

#### 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.

## **Summary Results**

			GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT	
Moir	NB	Photoc 11	GSTM1	Present/Absent	Absent	+++ 1.	Ma
			GSTP1	313 A>G	AA	No impact	
			GSTT1	Present/Absent	Present	No impact 7	

From the analysis of your genetic profile the following **BENEFICIAL**, **MEDIUM** or **HIGH IMPACT** gene variants were observed:

#### GSTM1

Gstm1 is the most biologically active member of the gst super-family and is involved in Phase II detoxification in the liver.

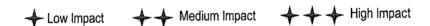
Absence of the enzyme results in reduced hepatic detoxification, which is associated with increased risk for various cancers, chemical sensitivity, atopic asthma and altered lung function. Gst enzyme activities are induced in part by the breakdown products of cruciferous and allium vegetables. These should be increased significantly in the diet to increase activity of other gst enzymes to compensate for a deletion.

#### 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.

## **Summary Results**

GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT
IL-6	-174 G>C	CC	+++
TNFA	-308 G>A	AG	++



From the analysis of your genetic profile the following **BENEFICIAL**, **MEDIUM** or **HIGH IMPACT** gene variants were observed:

# 11-6 / Small cell-signaling probain

II-6 is a <u>pro-inflammatory cytokine</u> playing a crucial role in inflammation and tissue injury – low grade inflammation is associated with raised hsCRP levels, obesity and insulin resistance.

Carriers of the C allele have increased circulating levels of il-6 and raised hsCRP compared to GG individuals. The C allele associated with inflammation and increased risk of CVD. A synergistic effect with smoking has been reported, which emphasizes the importance of smoking cessation in those with the C allele. Weight management is also important.

#### **TNFA**

Tumour necrosis factor is a multifunctional pro-inflammatory cytokine, with effects on lipid metabolism, coagulation, insulin resistance and endothelial function.

The A allele results in a two-fold increase in TNFA transcription and subsequent increase in tnfa levels. The A allele shows a greater responsiveness to dietary fat intake, and is associated with increased risk for obesity, adiposity and dyslipidaemia, especially when dietary fat intake is high. It is important to decrease saturated fat and increase n-3 fatty acids, as well as to manage weight.

#### **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 vegetables and fruits, as well as green tea and red wine.

#### **Summary Results**

GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT	
eNOS	894 G>T	TT .	-	77
SOD2	16 A>V	CC	***	]*
SOD3	760 C>G	CC	No impact	



From the analysis of your genetic profile the following BENEFICIAL, MEDIUM or HIGH IMPACT gene variants were observed:

Endothelium-derived nitric oxide (NO) plays a key role in the regulation of vascular tone, peripheral resistance.

The T allele effects proteolytic cleavage of the enzyme, reducing nitric oxide bio-availability in the blood vessel wall, thus promoting atherosclerosis, and is associated with increased risk of atherosclerosis, essential hypertension, end-stage renal disease and pre-eclampsia. Carriers of the T allele are associated with a better response to Omega-3 fatty acids 7 n-3

#### SOD2

The sod2 enzyme destroys the radicals which are normally produced within cells and which are toxic to biological systems.

There is evidence that people without the variant, and with lower consumption of fruits and vegetables, are at increased risk of developing disease, including the risk of developing certain cancers. It is important for individuals with the CC genotype to ensure a high intake of fruit and vegetables and adequate anti-oxidant intake.

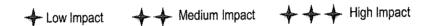
- Ensure adaquate interla in abot: berrico, small red becons, frue + vegles (red/puple / dark green), red wine, green tea, oats, dark chocolate
  May need to supplement

#### 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.

#### **Summary Results**

GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT
VDR	Fok1	СТ	**
	Bsm1	Т	No impact
	Taq1	СС	No impact
COL1A1	1546 G>T	TG	++



From the analysis of your genetic profile the following **BENEFICIAL**, **MEDIUM** or **HIGH IMPACT** gene variants were observed:

#### COL1A1

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

Individuals with the T allele show reduced bone strength and reduced inorganic content. Osteoblasts produce an abnormal ratio of collagen alpha I chains relative to collagen alpha I, impairing their ability to form mineralized bone. The T allele influences ratio but not total amount of collagen type I alpha chains produced by bone cells, hence leading to abnormal mineralization. GG individuals respond better to bisphosphonate therapy compared to GT and TT individuals. GT and TT genotypes have an increased risk of fracture and greater bone loss when calcium is low. Women with the TT genotype are at significantly increased risk of excess rates of bone loss at the spine, but this effect may be nullified by the use of HRT.

Ensure adequate dowly calcum: 19 dowly - if not getting enough in diet - supplement

## Insulin Sensitivity

Insulin is a hormone that stimulates the uptake of glucose from the diet into the blood. 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.

## **Summary Results**

GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT
PPAR-γ	Pro12Ala	СС	+++
Low Impact		→ High Impact	

From the analysis of your genetic profile the following **BENEFICIAL**, **MEDIUM** or **HIGH IMPACT** gene variants were observed:

#### **PPARG**

PPARG is a transcription factor activated by fatty acids which has a major role in adipogenesis and expression of adipocyte-specific genes.

Pro12Pro (CC) genotype individuals are highly sensitive to the type and amount of fat in their diet, with regards susceptibility to obesity and diabetes. An increase in total dietary fat and saturated fat is associated with greater waist circumference in CC individuals. It is important to manage total dietary fat intake, as well as quality of fat. The CC genotype does not offer the protection seen in those with the G allele, thus all diet and lifestyle variables that impact insulin sensitivity should be addressed.