

GENOTYPE REPORT

Patient Name:

Date of Birth:

Sample Number:

Referring Practitioner:

Date Reported:

WELCOME TO YOUR DNA OESTROGEN REPORT

From your buccal swab 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 colour of the circle (please see the key below).

EXAMPLE RESULT:

GENE NAME & DESCRIPTION	YOUR RESULT & EXPLANATION
GENE NAME Genetic Variation A brief description of the gene.	YOUR RESULT:  GENE IMPACT COLOUR KEY A brief explanation of the diet, nutrition and lifestyle factors relevant to the particular gene variant being identified.

GENE IMPACT COLOUR KEY:



BENEFICIAL



LOW/NO
IMPACT



MEDIUM
IMPACT



HIGH
IMPACT

CYP1A1

Genetic Variation: 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. CYP1A1 enzyme catalyses the 2-hydroxylation of oestradiol (E1 and E2) in several extra hepatic tissues including breast tissue. It is also involved in activating cigarette smoke, diet and environmental pollutants, and producing carcinogens.

YOUR RESULT:



TT

No variant was detected at the Msp1 T>C locus.

CYP1A1

Genetic Variation: 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.

CYP1B1

Genetic Variation: 1294 C>G, (Leu432Val)

CYP1B1 enzymes catalyses the 4-hydroxylation of oestradiol, it also activates many PAHs and arylamines.

YOUR RESULT:



CG

This SNP has been found to have the most profound impact on the catalytic properties of CYP1B1, with the 4-hydroxylase activity of the G allele displaying three-fold higher activity compared to the C allele.

In the presence of the G allele it is important to reduce exposure to all diet and environmental procarcinogens such as PAH, aromatic amines, nitrates, and smoking of any kind. In addition attention should be paid to optimising phase 2 detoxification.

CYP17A

Genetic Variation: 34 T>C

CYP17 mediates both steroid 17 α -hydroxylase and 17,20-lyase activities, and catalyses a rate-limiting step in ovarian and adrenal biosynthesis leading to the precursor, dehydroepiandrosterone.

YOUR RESULT:



TC

The C allele increases enzyme activity, thereby increasing the amount of bioavailable oestrogen.

For individuals with the C allele beneficial modulation of oestrogen metabolism can be accomplished through dietary and lifestyle modifications. Key interventions include increasing insoluble fibre, avoiding refined CHO, increasing phytoestrogen intake, losing weight, and increasing exercise. In addition, select nutrients and micronutrients effectively reduce oestrogen load by supporting preferred oestrogen pathways. These are included at the end of the report.

MnSOD

Genetic Variation: Ala16Val or -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:



CT

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 breast cancer.

Women with the C allele who had ever used HRT or smoked were at a higher risk of breast cancer. It is therefore important for individuals with the C allele to ensure adequate fruit and vegetable intake. Supplementation with ant-oxidant nutrients can reduce the oxidation of catechols and promote greater excretion of these metabolites through the methylation pathway.

GSTM1

Genetic Variation: 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. These enzymes are involved in the phase 2 conjugation of oestrogen quinones to glutathione.

YOUR RESULT:



PRESENT

The GSTM1 gene is present.

GSTT1

Genetic Variation: Insertion/Deletion

Glutathione S-transferases (GSTs) are a family of multifunctional enzymes involved in the metabolism of a variety of xenobiotic compounds, including mammary carcinogens. These enzymes are involved in the conjugation of oestrogen quinones to glutathione.

YOUR RESULT:

 **PRESENT**

The GSTT1 gene is present.

COMT

Genetic Variation: 472 G>A or Val158Met

Soluble catechol-O-methyltransferase (S-COMT) helps control the levels of certain hormones and is involved in methylation and inactivation of catechol oestrogens. Accumulation of oestrogen metabolites appears to confer increased risk of breast cancer via oxidative DNA damage.

YOUR RESULT:

 **GA**

The A allele is associated with a 3-4 fold reduction in the methylation activity of the COMT enzyme.

For A allele carriers beneficial modulation of oestrogen metabolism can be accomplished through dietary and lifestyle modifications. Key interventions include increasing insoluble fibre, managing the quality of dietary fat intake, increasing phytoestrogen intake, losing weight, and increasing exercise. In addition, select nutrients and micronutrients effectively reduce oestrogen load by supporting preferred oestrogen pathways. These are included at the end of the report.

MTHFR

Genetic Variation: 677 C>T

Methylenetetrahydrofolate Reductase (MTHFR) is a key enzyme in the folate metabolic pathway. Reduced activity influences the balance between DNA synthesis, repair and methylation processes.

YOUR RESULT:

 **CC**

No variant was detected at the 677 C>T locus.

SULT1A1

Genetic Variation: 638 G>A

Sulfotransferase 1A1 (SULT1A1) is involved in the inactivation of oestrogens and bio-activation of heterocyclic amines and polycyclic aromatic hydrocarbons.

YOUR RESULT:



No variant was detected at the 638 G>A locus.

Risks and Limitations

DNAllysis Biotechnology has a laboratory with standard and effective procedures in place for handling samples and effective protocols in place to protect against technical and operational problems. However as with all laboratories, laboratory error can occur; examples include, but are not limited to, sample or DNA mislabelling or contamination, failure to obtain an interpretable report, or other operational laboratory errors. Occasionally due to circumstances beyond DNAllysis Biotechnology's control it may not be possible to obtain SNP specific results.