Nordic Laboratories

♀dna oestrogen

GENOTYPE REPORT

Patient Name:

Date of Birth:

Sample Number:

Date Reported:

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BACKGROUND TO THE ANALYSIS

The importance of both oestrogen and progesterone in breast cancer development is well established. However, considerable inter-individual variability has been observed in carcinogen metabolism, metabolism of steroid hormones, and phase I and phase II detoxification. Variations in genes involved in these biological processes help identify a sub-population of women with higher lifetime exposure to oestrogens, oestrogen metabolites and other carcinogens. Understanding an individuals' genetic variability will allow for targeted diet, lifestyle and hormone intervention.

The DNA Oestrogen Metabolism and Detoxification test includes 10 genes involved in oestrogen biosynthesis, oestrogen metabolism, and phase I and phase II detoxification. The results provide unique information to guide personalised diet, lifestyle, hormone and nutraceutical recommendations.

To make a holistic assessment of disease risks, environmental factors (diet and lifestyle) need to be considered in conjunction with the accompanying genetic profile.

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.

SUMMARY GENOTYPE REPORT

SUMMARY RESULTS

The combination of gene variants identified in this analysis places you in the MEDIUM risk category

GENE NAME	GENETIC VARIATION	YOUR RESULTS	GENE IMPACT
COMT	472 G>A (Val158Met)	GA	
SULT1A1	638 G>A Arg213His	GG	No Impact
CYP17A	34 T>C	TC	
CYP1A1	Msp1 T>C	TT	No Impact
CYP1A1	A>G Ile462Val	AA	No Impact
CYP1B1	C>G Val432Leu	CG	
GSTM1	Insertion/Deletion	Present	No Impact
GSTT1	Insertion/Deletion	Present	No Impact
MTHFR	677 C>T	CC	No Impact
MnSOD	47 T>C Ala16Val	CT	

 Low Impact

 Medium Impact

 High Impact

GENE ASSOCIATIONS

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

COMT

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. 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.

CYP17A

CYP17 mediates both steroid 17a-hydroxylase and 17,20-lyase activities, and catalyses a rate-limiting step in ovarian and adrenal biosynthesis leading to the precursor, dehydroepiandrosterone. 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 such as increasing insoluble fibre, avoiding refined CHO, increasing phytoestrogen intake, losing weight, and increasing exercise.

CYP1B1

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

NUTRITION AND OESTROGEN

If a moderate or high impact gene variant is present for COMT, SULT1A1 or CYP17A, the following nutritional support is recommended to effectively reduce estrogen load by supporting preferred estrogen pathways.

- Increase intake of cruciferous vegetables (cauliflower, broccoli, cabbage, Brussels sprouts). Indole-3-carbinol (I3C) found in these vegetables actively promote the break down of oestrogen to the beneficial metabolite 2-OH.

- Include phytoestrogens in the diet for their many beneficial influences on oestrogen synthesis and metabolism. These include isoflavones and lignins. Isoflavones are found most commonly in soy products, but also include legumes, alfalfa, clover, licorice root, and kudzu root, and include genistein, daidzein, equol and puerarin. Lignins are an insoluble dietary fibre found in flaxseeds, whole grains, beans and seeds.

- Ensure adequate intake of magnesium and Vitamin E.

- Other beneficial micro and phyto-nutrients that impact oestrogen metabolism include calcium D-glucarate, curcumin, green tea polyphenols and D-limonene.