

## Client Report

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**Venus deMilo**

## Opus23 Explorer

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Opus23 Explorer™ is a fully functional version of the well-regarded and widely used Opus23 Pro™ genomic exploration software designed and programmed by Dr. Peter D'Adamo and distributed under license by Diagnostic Solutions Lab (DSL) by Datapunk Bioinformatics LLC for use in the interpretation of genomic raw data produced by the DSL 'Opus' genomic microarray chip.

Opus23 Explorer scans over 20 peer-reviewed, evidence-based scientific databases and cross-references their information with the results of your raw data. This report summarizes the findings from your genomic data that have been curated by your clinical team into a human-understandable format. However, before we begin, let's introduce a few genetic concepts to set the stage and advance your understanding a bit.



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# Welcome to your owner's manual

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Opus23 Explorer is a very sophisticated computer program that looks for very simple things: variations in the code of DNA (the A, T, C, and G of the genetic alphabet) that can exist between people. Not all of our DNA varies from person to person, but about 9% of it can. The variations are called 'snips' (SNPs) which stands for single nucleotide polymorphism.

Although SNPs are the 'letters' of individuality, genes are in fact the words and vocabulary. After all, it is the genes that have to do the work, coding for the construction for a myriad of enzymes and proteins. Because gene function is central to any sort of biochemical prediction, Opus 23 Pro groups all the SNP outcomes under their parent gene, and presents its results as a reflection of their combined influence on the effectiveness of that gene. Although SNPs are pretty much unchangeable, our genes can be influenced (for better or worse) by lifestyle, diet, emotions and nutritional supplementation.

The DNA in our bodies is a double-stranded molecule, meaning that for every location that we might find a SNP there exists two letters, one for each strand. Taken together, these two letters comprise the **genotype** for that location. Over the years, much research has been done to examine whether a particular SNP variation (or mutation) can be shown to result in an effect on our health. For example, let's look at two different people, John and Jane. At location 12345678 on chromosome #1 most people, as does John, have the 'AA' genotype. It has been noticed that 15% of the population have one 'G' (genotype 'AG') while 5% of the population have genotype 'GG'. Separate studies show that people with at least one 'G' genotype have an increased risk of eczema. Jane's genotype at this location is 'GA' so she may have this susceptibility. As you might have noticed, genotypes come in two types: two identical letters ('GG', 'AA') known as *homozygous* and one of each letter ('GA' or 'AG') known as *heterozygous*.

Because the presence of a 'G' at this SNP location is associated with a condition, for this SNP 'G' is known as the *risk nucleotide* or *risk allele*. Most of the time, having the risk allele negatively impacts the function of its parent gene, but sometimes the mutations can convey a benefit or advantage.

Something like 99.6% of the human genome is identical in all people. This is true of everyone, regardless of race or heritage. However, it is at the SNP location that variation does take place. SNPs only make up a tiny portion of the genome (0.4%) but because the genome is so enormous, this equals over 12 million locations. It's the differences at these SNP locations that make each of us unique. If your genotype at SNP rs17822931 is TT, then you probably have dry earwax. If you have any other genotype at this SNP, then you have wet earwax.

By the way, you're **CT** for the rs17822931 SNP.

This owner's manual was produced by your clinician who, using the Opus23 Explorer software, has curated what, in the great sea of data that Opus23 Explorer provides, they believe is most important to your health care. It would be untrue (and unkind) to pretend that much of the material in this report is easy to understand. Although the editors of Opus23 Explorer try to provide explanations in layperson terminology when and where possible, things can get quite technical. Don't panic! Make note of your questions and remember to discuss these with your clinician next opportunity. Also, use online resources such as Google and Wikipedia as research tools.



Genetics can be complicated to the layperson. Sometimes a word is used to describe a gene function that you might not recognize. If *Opus23 Explorer* thinks that you might need some help with a technical term, 'Mr. Smart Owl' will try to explain it to you.

## Now, a few caveats

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Depending on how your health professional has decided to structure this report, you might find the information that follows to be intimidating or even potentially disturbing. For example, nobody enjoys hearing that they may have an increased risk for a disease or health complication. While Opus23 Explorer cannot guarantee that all of its findings will be of a positive nature, it's important to understand what this information can and cannot do. Let's discuss a few facts that you should keep in mind.

Advances in genetic technology have made the process of discovering new SNPs very easy. However the process of linking a SNP to particular trait or illness requires epidemiologic studies that are far more expensive and labor intensive. Thus there is a large gap between the SNPs we know and what in fact we know about them. Opus 23 Pro is constantly updated with new information and your health care provider can very easily update your data to include any new information as it arrives. Opus23 Pro strives to provide the most accurate possible data interpretation. As part of this mission, we constantly monitor and refine our data analysis algorithms. When an improvement is identified, the new algorithm becomes available immediately on creation. In that event, a corrected report will be available to your health care provider. Such re-analysis of patient data may lead to reclassification of your results.

### **Opus23 Explorer can only supply correlations and relationships**

Opus23 Explorer can only compare your genetic data with published data linking your results to the outcomes in the research. It can't diagnose disease. Nor should it. However, it can point the way to areas of possible further clinical interest, and perhaps guide both you and your health care professional in the process of developing a more evidence-based approach to prevention. The etiology (cause) of many diseases is multifactorial; that is, disease can occur as a result of various factors, including both inherited and acquired genetic variants, diet, lifestyle choices and age.

### **Opus23 Explorer results are as good as the starting data**

The interpretations given by Opus23 Explorer are the result of evaluated inherited genetic variants in data uploaded to our server, and interpretations are only as accurate as the data received from the genomic test. It is possible that inaccuracies in the genomic test results could lead to false interpretations. It is also possible that variants in genes and genetic regions not tested in the DNA sequencing test may contribute to an individual's risk for disease. Therefore, a negative result in a gene where no pathogenic variants are detected does not eliminate the individual's disease risk.

### **Genetic findings can only report the starting point**

Your genome is similar to the blueprint for a house that is yet to be built. If the builder follows the architect's instructions exactly, the house will match the blueprint perfectly. However, all throughout the construction process alterations will most certainly be made: For example, if the new owners are running short on funds, perhaps the original plans for an expensive slate roof may have to be altered to a less expensive, though still-functional, asphalt version. It's the same with genomics, although variations in your gene data may reflect an increased or decreased risk of a health issue, many of these risks may have been altered by environmental factors (such as your pre-existing lifestyle and health habits) acting epigenetically to control the expression of these genes. If you've carefully watched your diet over time and kept your weight at a healthy level, a finding that you are at risk for obesity might do nothing more than encourage you to continue what you are already doing.

## **Genetic findings can only reflect probabilities**

Very few gene mutations result in a direct, absolutely certain, health consequence. Most of the time, they instead reflect a change to your odds of developing a particular health condition. This is defined as the 'risk' for a certain event. This is usually expressed as an 'odds ratio' (OR). Understanding the meaning of an OR for a particular risk is a key to minimizing stress when encountering dire results. For example, being told you are 110% more likely to get struck by lightning (OR=1.1) is much less distressing when you realize that:

- This is a very small difference from normal
- Very few people get struck by lightning regardless

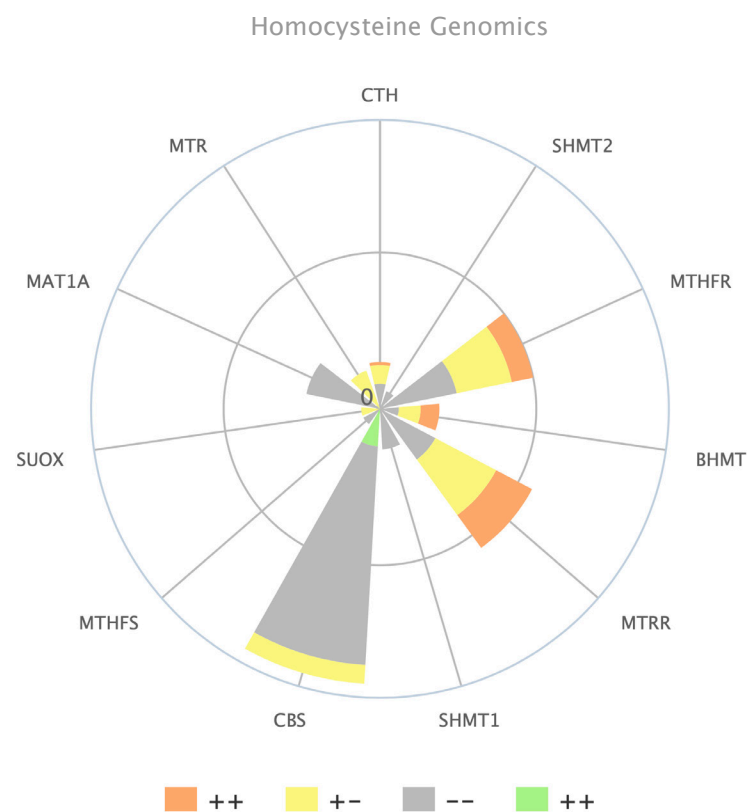
When it comes to a particular disease or syndrome, most SNPs have rather small ORs. This does not mean that they are unworthy of attention, but rather that the findings must be interpreted as part of an integrated whole, including: other SNP results that also support the conclusion; lifestyle factors; family history, and environmental exposures. Further, a positive test result does not guarantee an occurrence of disease since the SNP variants in most genes are not 100% penetrant (even genes with several risk SNPs will very likely function to some degree). Rather, pathogenic variants may predispose a person to a higher or lower risk of disease. The results of genomic testing must be interpreted in the context of your clinical history. Genetic counseling is recommended for the individual and for other at-risk family members.

## **And now, the usual indemnification statement:**

The data provided by Opus23 Explorer is for informational purposes only and is not designed or intended to suggest the treatment or diagnosis of any disease or condition. Opus23 Explorer and Datapunk Bioinformatics, LLC, take no responsibility for any harm arising from incorrect data being uploaded to our server or incorrect data interpretation, errors, or omissions by the software. By agreeing to access this Opus 23 Pro report you hereby agree to indemnify Opus23 Explorer and Datapunk Bioinformatics, LLC from any consequences resulting from the use or misuse of this information. The statements made on this page have not been evaluated by the FDA (U.S. Food & Drug Administration). This material is presented for informational and education purposes only and is not intended to diagnose, cure or prevent any disease.

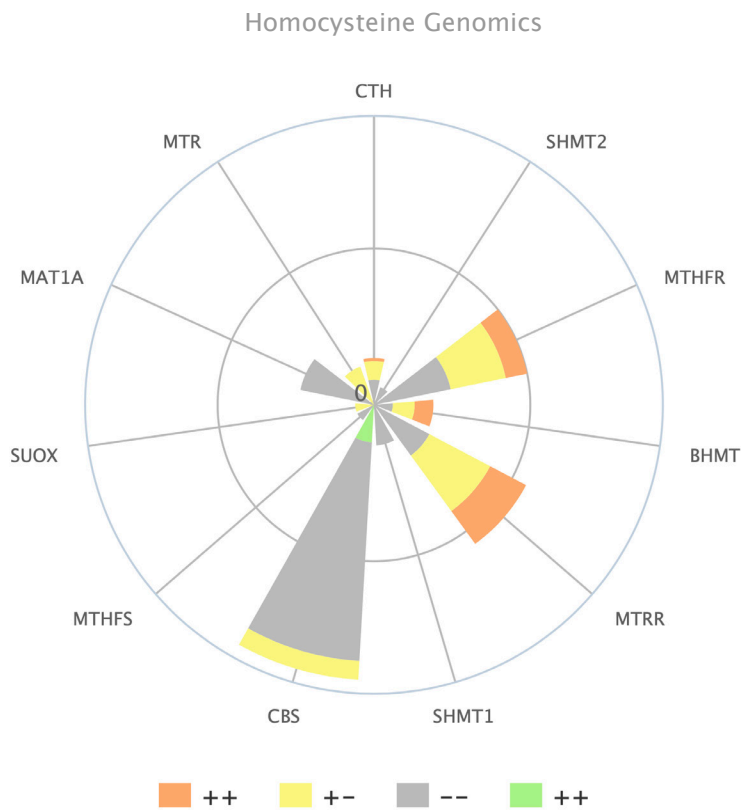
## Templates

Templates are collections of gene SNPs that are organized around a central function that they share or contribute to, such as detoxification, methylation, metabolism, etc.



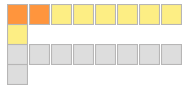
## Homocysteine Genomics

Homocysteine is a non-proteinogenic  $\alpha$ -amino acid. It is a homologue of the amino acid cysteine, differing by an additional methylene bridge (-CH<sub>2</sub>-). It is biosynthesized from methionine by the removal of its terminal C $\epsilon$  methyl group. Homocysteine can be recycled into methionine or converted into cysteine with the aid of certain B-vitamins. A high level of homocysteine in the blood (hyperhomocysteinemia) makes a person more prone to endothelial cell injury, which leads to inflammation in the blood vessels, which in turn may lead to atherogenesis, which can result in ischemic injury. Hyperhomocysteinemia is therefore a possible risk factor for coronary artery disease. Coronary artery disease occurs when an atherosclerotic plaque blocks blood flow to the coronary arteries, which supply the heart with oxygenated blood. Homocysteine is not obtained from the diet. Instead, it is biosynthesized from methionine via a multi-step process. First, methionine receives an adenosine group from ATP, a reaction catalyzed by S-adenosyl-methionine synthetase, to give S-adenosyl methionine (SAM). SAM then transfers the methyl group



to an acceptor molecule, (e.g., norepinephrine as an acceptor during epinephrine synthesis, DNA methyltransferase as an intermediate acceptor in the process of DNA methylation). The adenosine is then hydrolyzed to yield L-homocysteine. L-Homocysteine has two primary fates: conversion via tetrahydrofolate (THF) back into L-methionine or conversion to L-cysteine. Hyperhomocysteinemia has been correlated with the occurrence of blood clots, heart attacks and strokes, though it is unclear whether hyperhomocysteinemia is an independent risk factor for these conditions. Hyperhomocysteinemia has also been associated with early pregnancy loss and with neural tube defects.


# CTH



## *cystathionase (cystathionine gamma-lyase)*

The CTH gene provides instructions to make an enzyme that converts one amino acid into another: cystathionine (which comes from the amino acid methionine) is converted to cysteine by cystathionine gamma-lyase. Glutathione is an antioxidant that prevents damage from free radicals, and the liver needs cysteine to make glutathione. Mutations in the CTH gene can cause cystathionine to be found in the urine (cystathioninuria), high levels of the inflammatory protein homocysteine and low levels of glutathione.

SNP outcomes in CTH relevant to Venus deMilo:

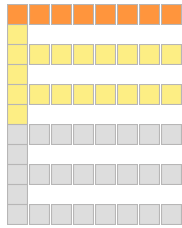
SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs1021737	T	R	TG	+-		CLEFT PALATE WITH HOMOZYGOUS RISK ALLELE, HIGHER HOMOCYSTEINE, AGING

### *New concepts:*



- The *gene* is the fundamental physical and functional unit of heredity. A gene is an ordered sequence of nucleotides located in a particular position on a particular chromosome that encodes a specific product (i.e., a protein).
- *Proteins* are large molecules composed of one or more chains of amino acids. Proteins are required for the structure, function, and regulation of the body's cells, tissues, and organs, and each protein has unique functions. Examples are hormones, enzymes, and antibodies.
- *Amino acid* are small molecules that are the components of proteins. There are 20 different kinds of amino acids in living things. Proteins are composed of different combinations of amino acids assembled in chain-like molecules.

# MTHFR



## *methylenetetrahydrofolate reductase (NAD(P)H)*

Perhaps the most studied SNP-containing gene of all, Methylene tetrahydrofolate reductase (MTHFR) allows conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, needed for conversion of homocysteine (HCy) to the protein-building amino acid methionine via methylation, in the rate-limiting step of the methyl cycle. MTHFR is a highly polymorphic gene, and genetic variation influences susceptibility to occlusive vascular disease, neural tube defects, colon cancer and acute leukemia, and mutations in this gene are associated with methylenetetrahydrofolate reductase deficiency. Lower MTHFR enzyme activity results in lower levels of methylated folate, leading to elevated homocysteine (HCy). Natural variation in this gene is common in healthy people. Although some variants have been reported to influence susceptibility to occlusive vascular disease, neural tube defects, Alzheimer's disease and other forms of dementia, colon cancer, and acute leukemia, findings from small early studies have not been consistently reproduced. Two of the most investigated are C677T (rs1801133) and A1298C (rs1801131) single nucleotide polymorphisms (SNPs).

- Individuals with two copies of 677C (677CC) have the most common genotype. 677TT individuals (homozygous) have lower MTHFR activity than CC or CT (heterozygous) individuals.
- 1298AA is the "normal" homozygous, 1298AC the heterozygous, and 1298CC the homozygous for the "variant". The C mutation does not appear to affect the MTHFR protein. It does not result in thermolabile MTHFR and does not appear to affect homocysteine levels. It does, however, affect the conversion of MTHF to BH4 (tetrahydrobiopterin), an important cofactor in the production of neurotransmitters, production of nitric oxide, and detoxification of ammonia.

SNP outcomes in MTHFR relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs17367504	G	R	<b>AG</b>	<b>--</b>		HYPERTENSION, ORTHOSTATIC HYPERTENSION, RESPONSE TO BETA BLOCKERS
rs1999594	A	R	<b>AA</b>	<b>++</b>		FOLATE TRANSPORTER, LOW SERUM FOLATE, HIGH HOMOCYSTEINE
rs1801131	G	R	<b>GT</b>	<b>+-</b>		NEUROTRANSMITTER SYNTHESIS

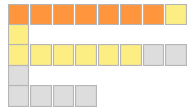


*New concepts:*



- The *genotype* is the genetic makeup of an individual. Genotype can refer to a person's entire genetic makeup or the alleles at a particular locus
- A *nucleotide* is subunit of DNA or RNA consisting of a nitrogenous base (adenine, guanine, thymine, or cytosine), a phosphate molecule, and a sugar molecule. Thousands of nucleotides are linked to form a DNA or RNA molecule.
- A *mutation* is an alteration of genetic material such that a new variation is produced.
- A *homozygous* genotype has the same allele at the same locus (location) on both chromosomes. Homozygous also refers to a genotype consisting of two identical alleles of a gene for a particular trait.
- A *heterozygous* genotype consists of two different alleles of a gene for a particular trait. Individuals who are heterozygous for a trait are referred to as heterozygotes.
- The *rate limiting step* is the slowest step in a metabolic pathway or series of chemical reactions, which determines the overall rate of the other reactions in the pathway.
- A *polymorphism* is a difference in DNA sequence among individuals.
- *Methylation* is the addition of a single carbon and three hydrogen atoms (called a methyl group) to another molecule. The removal of a methyl group is called demethylation. Methylation is a key mechanism behind the regulation of gene expression.

# BHMT



## *betaine--homocysteine S-methyltransferase*

The BHMT gene (not BHMT2) provides instructions for making a protein that converts betaine (trimethylglycine) and homocysteine (a byproduct of the amino acid methionine, and toxic at high levels) to dimethylglycine and methionine, respectively. BHMT2 converts homocysteine to methionine, and the cofactor for this conversion is zinc. BHMT2 is inhibited by high levels of methionine, and does not use S-adenosylmethionine (S-AdoMet) as a methyl donor. Defects in the BHMT gene could lead to elevated blood homocysteine levels. The product of this gene is central to the 'short cut' through the methylation cycle in helping to convert homocysteine to methionine. BHMT may therefore play a critical role in homocysteine homeostasis, or balance, when the manufacture of methionine, a folate-dependent process, is compromised by dietary or genetic influences.

The activity of the BHMT gene product can be affected by stress, by cortisol levels, and may play a role in ADD/ADHD through its affect on norepinephrine (adrenaline) levels. Phosphatidylcholine may be indicated.

SNP outcomes in BHMT relevant to Venus deMilo:

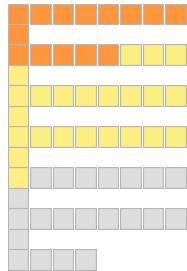
SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs6875201	G	R	<b>AG</b>	--+		LIVER, METHYLATION,
rs567754	T	R	<b>TT</b>	++		FOLATE METABOLISM, FOLATES, HOMOCYSTEINURIA

### *New concepts:*



- *Homeostasis* is the tendency of a system, especially the physiological system of higher animals, to maintain internal stability, owing to the coordinated response of its parts to any situation or stimulus that would tend to disturb its normal condition or function.

## MTRR



### 5-methyltetrahydrofolate-homocysteine methyltransferase reductase

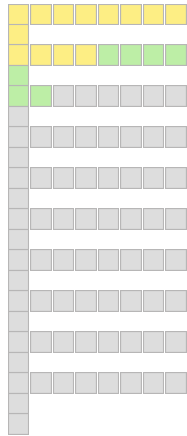
Methionine synthase reductase (MTRR) is an enzyme that is encoded by the MTRR gene. Methionine is an essential amino acid required for protein synthesis and one-carbon metabolism (methylation of the B-vitamin folate), converting homocysteine into methionine. If MTRR function is compromised due to genetic variation, toxic homocysteine levels can build up because homocysteine is not being converted into methionine. Having the MTRR 66G variant can be a part of this effect. The function of methionine synthase reductase is also inhibited by lead, arsenic, mercury and aluminum toxicity.

Medications that deplete vitamin B12 can affect MTRR function. These include: antacids and acid blockers, corticosteroids, metformin, oral contraceptives, gout medications and some cholesterol-lowering drugs.

SNP outcomes in MTRR relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs7703033	A	R	<b>AG</b>	+-	■■■■■■■■■■	HOMOCYSTEINE ASSOCIATION, B12 UTILIZATION
rs2303080	T	R	<b>TT</b>	++	■■■■■■■■	CLEFT LIP AND PALATE
rs1802059	A	R	<b>AG</b>	+-	■■■■■■■■	
rs1801394	G	R	<b>GG</b>	++	■■■■■■■■	NEURAL TUBE DEFECT, MENINGIOMA, LOW SERUM FOLATE, REDUCED RISK PSA ELEVATION
rs1532268	T	R	<b>CT</b>	-+	■■■■■■■■	FOLATE METABOLISM, CANCER

# CBS



## *cystathionine-beta-synthase*

Cystathionine β-synthase, or the CBS enzyme that begins the transsulfuration pathway to provide sulfur groups needed for detoxification, neuroprotection by making glutathione and hydrogen sulfide, as well as for neurotransmitter and hormone modification. Sulfation can be blocked by non-steroidal anti-inflammatory drugs (e.g. aspirin), tartrazine (yellow food dye) and molybdenum deficiency.

CBS enzyme activation needs pyridoxal-5' phosphate, the active form of vitamin B6. S-adenosyl methionine regulates enzyme activity. The downstream pathway from CBS is the sulfite oxidase enzyme, made by the SUOX gene, requires molybdenum produces sulfates from toxic sulfites. SUOX can be inactivated by tungsten toxicity.

CBS may be upregulated to produce hydrogen sulfide if persists can counter the neuroprotective effects of hydrogen sulfide and deplete cofactors needed to make glutathione. Elevated homocysteine or cysteine may contribute to brain fog. Some CBS SNPs are associated with midline defects.

Issues in the methionine and folate cycle may contribute to depletion of sulfur production in the transsulfation pathway. Other subunits of transsulfation and the sulfation pathways may be involved in neurotoxicity, or neurotransmitter dysregulation.

SNP outcomes in CBS relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs234709	T	R	CT	--+		METABOLISM, ARSENIC METABOLISM, LUNG CANCER
rs1801181	A	B	AA	++		TRANSSULFATION NO REDUCTION OF ACTIVITY
rs234706	A	B	AG	+ -		NO REDUCTION OF ACTIVITY, B-6 RESPONSIVE, RESPONSIVE TO HCY LOWERING EFFECTS OF FOLIC ACID


# SUOX



## *sulfite oxidase*

Downstream from the cystathionine beta synthase enzyme (CBS) is the sulfite oxidase enzyme, made by the SUOX gene. This requires molybdenum to produce sulfates from toxic sulfites. SUOX can be inactivated by tungsten toxicity. Sulfite sensitivity to sulfite-containing dried fruits and wines can be caused by SUOX mutations or from the bottleneck effect of up regulated transsulfation (CBS pathway) due to hyperglycemia (high blood sugar), infection and other conditions of oxidative stress.

SNP outcomes in SUOX relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs7297662	A	R	AG	+ -		LEUKEMIAS IN TUNGSTEN AND ARSENIC TOXICITY

### *New concepts:*



- *Oxidative stress* reflects an imbalance between the levels of reactive oxygen species and the body's ability to readily detoxify the reactive intermediates or to repair the resulting damage.

## Multi SNP macros

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Macros (algorithms) are perhaps the most significant and flexible aspect of your Opus 23 data. They are usually the easiest result for the non-medical person to understand, because their conclusions are usually simplified statements in everyday language.

Many correlations between SNPs and various traits exist as 'haplotypes,' clusters of SNPs, often on different genes, that must be evaluated as 'true' or 'false' based on their total outcome values. Some algorithms may identify risks for certain problems, while others identify special strengths or benefits you might possess. It's helpful to think of an Opus 23 algorithm as a tiny flowchart, that depending on which way the result branches, generates a 'true or false' result.

For example, a simple macro to determine if you should get out of bed might be:

- If you hear the alarm clock, open your eyes.
- If it's dark outside, go back to bed.
- If it's light outside, check the time.
- If it's earlier than 7AM, go back to bed.
- If it's later than 7AM, get up, check calendar
- If it's Saturday, go back to bed.

As can be seen, there are a lot of ways you can go back to bed with this algorithm! And this is also true as well for the Opus 23 Pro algorithms: In order for an algorithm to be true, it must fulfill all of several conditions. *If even one condition fails, the whole algorithm will be false.*

Each macro algorithm is displayed in its own box, and contain information about the genes and SNPs used in its creation. The title of the algorithm is generally its conclusion. Typically, your report contains only true algorithms, although your clinical team may choose to include false algorithms as well, especially if it would be helpful to make you aware of something you're likely to not be prone to. Thus:

- An algorithm that returns a **true** will have a 'check' icon in the bottom left-hand box. The conclusions of these algorithms **pertain** to you based on your genomic data results.
- An algorithm that returns a **false** will have a 'cross' icon in the bottom left-hand box. The conclusions of these algorithms **do not pertain** to you based on your genomic data, other than perhaps the added knowledge that this is one less thing in life to worry about.

## Drug interactions

This section documents potential drug interactions or complications you may be genetically susceptible to.

DRUG	SNP	GENE	RISK ALLELE	YOUR GENOTYPE	SIDE EFFECT
Acitretin	rs7412	APOE	C	<b>CC</b>	Psoriasis
Amitriptyline	rs4244285	CYP2C19	A	<b>AG</b>	Those with the AA or AG genotype are poor metabolizers of amitriptyline
Azathioprine	rs1800460	TPMT	T	<b>CT</b>	Hepatotoxicity
Azathioprine	rs1142345	TPMT	C	<b>CT</b>	Hepatotoxicity
Azathioprine	rs1142345	TPMT	C	<b>CT</b>	Patients with CC or CT genotype have decreased inactivation of thiopurines and increased risk of toxicity
Carbamazepine	rs3909184	FLOT1	G	<b>GG</b>	Patients with the CG or GG genotype (in Asian patients) were at a higher risk of Steven-Johnson Syndrome compared to those with the CC genotype (non-carriers of HLA-b*1502)
Cisplatin	rs1695	GSTP1	A	<b>AG</b>	Tinnitus, hearing impairment, Raynaud syndrome
Clobazam	rs4244285	CYP2C19	G	<b>AG</b>	Clobazem is metabolized into N-desmethylclobazem (NCLB) mostly by CYP3A4. NCLB is primarily metabolized by 2C19. Those with one 2C19*2 allele mutation (1*/2*) are intermediate metabolizers of NCLB. Those with two (2*/2*) mutations will metabolize NCLB poorly in comparison to extensive metabolizers (1*/1*). Levels of NCLB can be five times higher in poor metabolizers, and two times higher in intermediate metabolizers as compared to individuals who are extensive metabolizers. The safety and efficacy of clobazem may be affected by polymorphic expression of CYP2C19*2.

Cyclosporine	rs231775	CTLA4	A	<b>AG</b>	Gingival overgrowth, periodontal disease
Fluorouracil	rs1695	GSTP1	A	<b>AG</b>	Hematological toxicity, gastrointestinal toxicity
Gefitinib	rs2231142	ABCG2	T	<b>GT</b>	Diarrhea
Gefitinib	rs2231142	ABCG2	T	<b>GT</b>	In non-small lung cancer patients, those that are heterozygous (ABCG2 421C>A) have a higher risk of diarrhea.
Irinotecan	rs4149056	SLCO1B1	C	<b>CT</b>	Diarrhea, leucopenia, neutropenia
Isoniazid	rs6413419	CYP2E1	GG	<b>GG</b>	Hepatotoxicity
Mercaptopurine	rs1800460	TPMT	T	<b>CT</b>	Hepatotoxicity
Mercaptopurine	rs1142345	TPMT	C	<b>CT</b>	Hepatotoxicity
Venlafaxine	rs5030655	CYP2D6	I	<b>II</b>	Nausea, vomiting diarrhea
Almotriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Citalopram	rs1954787	GRIK4	C	<b>CC</b>	Improved response to antidepressant medication
Clopidogrel	rs4244285	CYP2C19	A	<b>AG</b>	Patients are poor metabolizers of clopidogrel. More likely to experience poor cardiovascular outcomes.
Clopidogrel	rs4244285	CYP2C19	A	<b>AG</b>	Patients are poor metabolizers of clopidogrel. More likely to experience poor cardiovascular outcomes.
Codeine	rs5030655	CYP2D6	I	<b>II</b>	Poor drug metabolizer, lower dose requirements
Dextromethorphan	rs5030655	CYP2D6	II	<b>II</b>	Poor drug metabolizer, lower dose requirements
Eletriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Frovatriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Infliximab	rs1801274	FCGR3A	GG	<b>GG</b>	Better ACR20 response
Modafinil	rs4680	COMT	GG	<b>GG</b>	Those with the GG genotype respond better to drug therapy (improved vigor and well being). Those with the AA genotype do not respond well to drug therapy



Morphine	rs1799971	OPRM1	A	<b>AA</b>	Better response to pain relief drugs
Naratriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Rizatriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Rosuvastatin	rs2231142	ABCG2	T	<b>GT</b>	Greater response to drug therapy
Sildenafil	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Sumatriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment
Trastuzumab	rs351855	FGFR4	G	<b>AG</b>	Reduced response to herceptin
Venlafaxine	rs5030655	CYP2D6	I	<b>II</b>	Poor drug metabolizer, lower dose requirements, nausea, vomiting and diarrhea
Venlafaxine	rs5030655	CYP2D6	I	<b>II</b>	Poor drug metabolizer, lower dose requirements, nausea, vomiting and diarrhea
Zolmitriptan	rs5443	GNB3	T	<b>CT</b>	Better response to drug treatment

## Natural products

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This section documents potential drug interactions or complications you may be genetically susceptible to.

**PLEASE NOTE - THIS IS A SAMPLE REPORT ONLY.**

This section will include actual recommendations in a report that apply specifically to the patient being tested.