Client Report

Venus deMilo

Opus23 Explorer

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 to 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.

REPORT FOCUS

STRUCTURAL

Welcome to your owner's manual

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 remeber 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

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

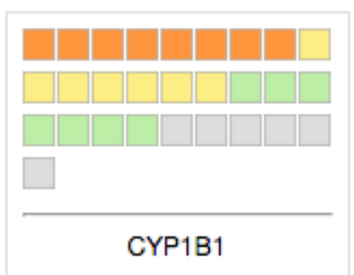
When it comes to a particular disease or syndrome, most SNPs have rather small ORs. This does not mean that they are unworthy of attention, but rather that the findings must be interpreted as part of an integrated whole, including: other SNP results that also support the conclusion; lifestyle factors; 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:

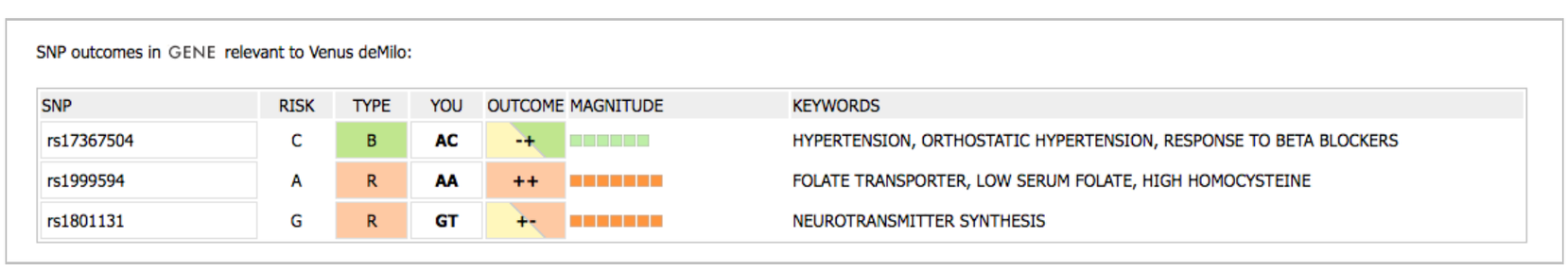
The data provided by Opus23 Explorer is for informational purposes only and is not designed or intended to suggest the treatment or diagnosis of any disease or condition. Opus23 Explorer and Datapunk Bioinformatics, LLC, take no responsibility for any harm arising from incorrect data being uploaded to 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 indemify Opus23 Explorer and Datapunk Bioinformatics, LLC from any consequences resulting fro 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.

Understanding the report

Each gene is depicted as a grid showing the result of its SNPs:



- The sum of the significant SNPs in the gene that indicate a higher (homozygous) risk are the orange squares
- The sum of the significant SNPs in the gene that indicate a lower (heterozygous) risk are the yellow squares
- The sum of the significant SNPs that are working just fine (no problem polymorphisms) risk are the gray squares
- You might even find that for some genes you may have a polymorphism that conveys some benefit. These are the green squares



SNP outcomes in GENE relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs17367504	C	B	**AC**	-+		HYPERTENSION, ORTHOSTATIC HYPERTENSION, RESPONSE TO BETA BLOCKERS
rs1999594	A	R	**AA**	++		FOLATE TRANSPORTER, LOW SERUM FOLATE, HIGH HOMOCYSTEINE
rs1801131	G	R	**GT**	+-		NEUROTRANSMITTER SYNTHESIS

Multi SNP macros

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.

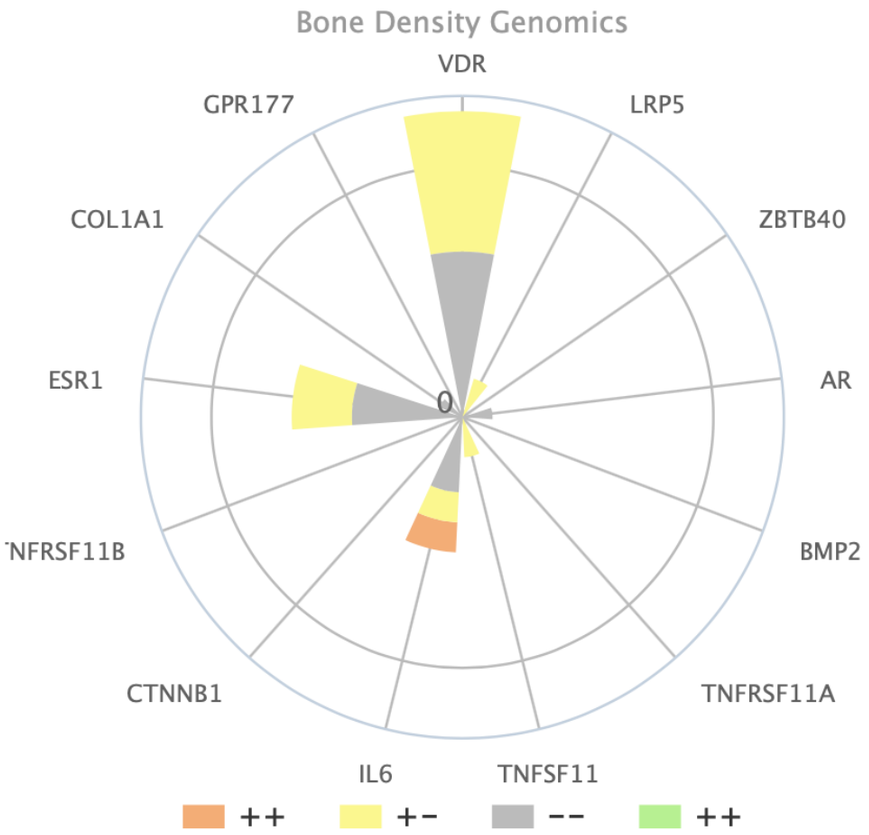
For example, a simple macro to determine if you should get out of bed might be:

- 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 fufill 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 algoriths, 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.

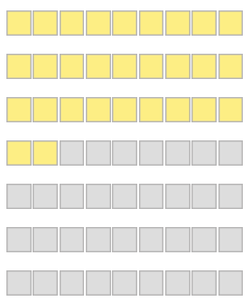


STRUCTURAL

Bone Density Genomics

It is believed that there are strong genetic determinants associated with peak bone mass, bone turnover, and bone loss. It is well recognized that estrogen action is favorably associated with the maintenance of BMD following menopause and in the subsequent prevention of fractures. The androgen receptor genotypes were strongly associated with the quintiles of BMD. Androgen receptors are present in low density on osteoblasts, although a direct influence on osteoclasts has not been demonstrated. Osteocalcin is the most abundant noncollagenous protein component of bone. Furthermore, osteocalcin is believed to regulate 1,25-dihydroxyvitamin D activity. LRP5, low-density-lipoprotein-receptor-related protein 5, is a determinant for bone mineral density, showed a significant association with BMD. Vitamin D receptor (VDR) polymorphisms have been strongly associated with bone mineral density (BMD) in some studies but not in others. Bone morphogenetic protein 2 (BMP-2) plays a role in osteoblast differentiation. BMP-2 gene variation has previously been associated with osteoporosis in various small populations, but has not been reliably confirmed in larger studies. Thus it is important to view genetic risk factors for bone mineral density issues as part of a a total picture that includes lifestyle and diet.

VDR



vitamin D (1,25- dihydroxyvitamin D3) receptor

The VDR gene provides instructions for making a protein called vitamin D receptor (VDR), which allows the body to respond appropriately to vitamin D. This vitamin can be acquired from foods in the diet or made in the body with help from sunlight. Vitamin D is involved in maintaining the proper balance of several minerals in the body, including calcium and phosphate, which are essential for the normal formation of bones and teeth. One of vitamin D's major roles is to control the absorption of calcium and phosphate from the intestines into the bloodstream. Vitamin D is also involved in several process unrelated to bone formation.

VDR attaches (binds) to the active form of vitamin D, known as calcitriol. This interaction allows VDR to partner with another protein called retinoid X receptor (RXR). The resulting complex of proteins then binds to particular regions of DNA, known as vitamin D response elements, and regulates the activity of vitamin D-responsive genes. By turning these genes on or off, VDR helps control calcium and phosphate absorption and other processes.

A VDR variant FokI is involved with Blood sugar regulation. Certain VDR mutations oppose COMT mutations in the regulation of dopamine levels. A VDR TaqI++ mutation means that a person is less sensitive to mood swings when taking methyl group supplement levels. A VDR Taq1 mutation can result in behaviors opposite to certain COMT mutations.

The vitamin D receptor plays an important role in regulating the hair cycle. Loss of VDR is associated with hair loss in experimental animals. Glucocorticoids are known to decrease expression of VDR, which is expressed in most tissues of the body and regulate intestinal transport of calcium, iron and other minerals. The VDR BsmI variant has been associated with low bone mineral density and osteoporosis.

Mutations in the VDR gene cause vitamin D-dependent rickets type 2 (VDDR2), also known as hereditary vitamin D-resistant rickets (HVDRR). This disorder of bone development is characterized by low levels of calcium (hypocalcemia) and phosphate (hypophosphatemia) in the blood, which lead to soft, weak bones (rickets) that are prone to fracture. A common feature of this condition is bowed legs.

The VDR gene mutations that cause this condition prevent the VDR protein from functioning properly. Some changes in the VDR gene lead to an abnormally short version of the VDR protein; others result in the production of an abnormal receptor that cannot bind to calcitriol, to RXR, or to DNA. Despite plenty of calcitriol in the body, the altered VDR cannot stimulate gene activity important for mineral absorption. The lack of calcium and phosphate absorption in the intestines slows deposition of these minerals into developing bone (bone mineralization), which leads to soft, weak bones and other features of VDDR2. Hypocalcemia also causes muscle weakness and seizures in some affected individuals. Most VDR gene mutations impair hair growth, leading to alopecia; however, mutations that block VDR's ability to interact with calcitriol do not cause alopecia, indicating that calcitriol is not necessary for the receptor's role in hair development.

SNP outcomes in VDR relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs3847987	A	R	**CC**	**--**	■■■■■■	COPD, PULMONARY, LUNG, VITAMIN D, T1D, TYPE 1 DIABETES, DIABETES, DEFICIENCY, CHRONIC OBSTRUCTIVE PULMONARY DISEASE
rs731236	G	R	**AG**	**-+**	■■■■■■■	TAQ1 DOPAMINE SYNTHESIS, BREAST CANCER SUSCEPTIBILITY
rs1540339	T	R	**CC**	**--**	■■■■■■	INCREASED CYP1A2 ACTIVITY
rs2238135	G	R	**CC**	**--**	■■■■■■	CANCER
rs1544410	T	R	**CT**	**-+**	■■■■■■■	BONE DENSITY RESPONSE TO ESTROGENS AND ALENDRONATE, HASHIMOTOS THYROIDITIS, INFERTILITY
rs7139166	G	R	**CG**	**-+**	■■■■■■	
rs4516035	T	R	**CT**	**-+**	■■■■■■	MELANOMA
rs2107301	A	R	**GG**	**--**	■■■■■■	CANCER

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).
- A *receptor* is a molecule in a cell membrane, that responds specifically to a particular neurotransmitter, hormone, antigen, or other substance.
- A *mutation* is an alteration of genetic material such that a new variation is produced.
- A *methyl group* is one of the commonest structural units of organic compounds, consisting of three hydrogen atoms bonded to a carbon atom, which is linked to the remainder of the molecule.
- *Proteins* are large molecules composed of one or more chains of amino acids. Proteins are required for the structure, function, and regulation of the bodys cells, tissues, and organs, and each protein has unique functions. Examples are hormones, enzymes, and antibodies.

IL6

interleukin 6 (interferon, beta 2)

IL6 is a cell signalling protein activated in response to various inflammatory triggers. A mutated SNP causes a fixed response with or without inflammatory triggers. Normally IL6 is a signalling protein secreted by T cells and macrophages to stimulate immune response, e.g. during infection and after trauma, especially burns or other tissue damage leading to inflammation, either an acute and chronic inflammation response. A mutated gene will induce chronicity.

IL6 encodes a cytokine that functions in inflammation and the maturation of B lymphocyte cells. In addition, the protein encoded by IL6 has been shown to be an endogenous pyrogen capable of inducing fever in people with autoimmune diseases or infections. The protein is primarily produced at sites of acute and chronic inflammation, where it is secreted into the serum and induces a transcriptional inflammatory response through interleukin 6 receptor, alpha. The functioning of this gene is implicated in a wide variety of inflammation-associated disease states, including suspectibility to diabetes mellitus and systemic juvenile rheumatoid arthritis.

Polymorphism (-174CC) predicts greater severity of common cold symtoms.

SNP outcomes in IL6 relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs2069837	G	R	**AA**	**--**		INFLAMMASOME CHRONIC HBV
rs2066992	T	R	**GT**	**-+**		INFLAMMASOME CHRONIC HBV
rs1800795	C	R	**GG**	**--**		HRV & RSV SEVERITY OF SYMPTOMS, ISCHEMIC STROKE, FIBRINOGEN LEVELS, HETEROZYGOUS SHOWED LESS EXPRESSED HSP70, DIABETES, CANCER, HYPERTENSION, ALZHEIMER'S, PERIODONTITIS, SUDDEN INFANT DEATH, CELIAC DISEASE IN GIRLS
rs2069852	G	R	**GG**	**++**		INFLAMMASOME CHRONIC HBV

New concepts:

- *Interleukins* are one of a large group of proteins produced mainly by T lymphocyte cells. Interleukins participate in communication among leukocytes and are important in the inflammatory response.
- *Transcription* is the first step of gene expression, in which a particular segment of DNA is copied into RNA
- *Cytokines* are chemicals important in cell signaling. They are released by cells and affect the behavior of other cells. Cytokines include chemokines, interferons and interleukins. Cytokines are produced by a broad range of cells, including immune cells like macrophages, B lymphocytes and T lymphocytes.

ESR1

estrogen receptor 1

This gene encodes an estrogen receptor. Estrogen and its receptors are essential for sexual development and reproductive function, but also play a role in other tissues such as bone. Estrogen receptors are also involved in pathological processes including breast cancer, endometrial cancer, and osteoporosis. ESRs interact with COMT via methylation reactions.

- ESR function may be helped by the inclusion of sulforaphanes (a sulfur containing detoxifying compound) in the diet. Sulforaphane has been identified in broccoli sprouts, which, of the cruciferous vegetables, have the highest concentration. It is also found in Brussels sprouts, cabbage, cauliflower, bok choy, kale, collards, Chinese broccoli, broccoli raab, kohlrabi, mustard, turnip, radish, arugula, and watercress.
- Transcription factors, vitamin D and A support repression of cell proliferation.
- Upregulating COMT aids in the clearance of carcinogenic estrogen metabolites.

SNP outcomes in ESR1 relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs9340799	G	R	**AA**	--		ENDOMETRIOSIS, ENDOMETRIAL CANCER, COGNITIVE IMPAIRMENT, AGE
rs2144025	T	R	**TC**	+-		HYPOMANIA, SCHIZOPHRENIA
rs2228480	A	R	**GG**	--		PELVIC ORGAN PROLAPSE, SPERM CONCENTRATION
rs2077647	C	R	**TT**	--		PROSTATE CANCER, RESPONSE TO ISOFLAVONES, BREAST CANCER, COLON CANCER, HEPATITIS B VIRUS-RELATED LIVER CIRRHOSIS, RISK OF ALZHEIMERS DISEASE IN DOWN SYNDROME, ARTERIAL STIFFNESS, ANOGENITAL DISTANCE
rs3020314	T	R	**CT**	-+		BREAST CANCER
rs2234693	C	R	**TT**	--		BREAST CANCER CORONARY HEART DISEASE MIGRAINE BILIARY STONES, HEPATITIS B VIRUS-RELATED LIVER CIRRHOSIS

New concepts:

- *Transcription* is the synthesis of an RNA copy from a sequence of DNA (a gene); the first step in gene expression
- A *metabolite* is a product of metabolism; a substance essential to the metabolism of a particular organism or to a particular metabolic process.
- *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.

HSD11B1

hydroxysteroid (11-beta) dehydrogenase 1

HSD11B1 catalyzes the conversion of the stress hormone cortisol to the inactive metabolite cortisone. In addition, the encoded protein can catalyze the reverse reaction, the conversion of cortisone to cortisol. Too much cortisol can lead to central obesity, and a particular variation in this gene has been associated with obesity and insulin resistance in children.

SNP outcomes in HSD11B1 relevant to Venus deMilo:

SNP	RISK	TYPE	YOU	OUTCOME	MAGNITUDE	KEYWORDS
rs846906	T	R	**TC**	+-		

New concepts:

- To *Catalyze* is to cause or accelerate (a reaction) by acting as a catalyst.

STRUCTURAL

MULTI-SNP MACROS

Increased risk of developing osteoarthritis

Genes	COL6A4P1
Repute:	RISK
Magnitude:	2.3
Frequency:	30%

INTERPRETATION: You have a higher risk of developing osteoarthritis. rs7639618(T) is one of several variations in the COL6A4P1 collagen gene found to be associated with osteoarthritis based on a study of Japanese patients.

This algorithm is **true** and applies to you

Your results: rs7639618 (**CT**)

Structural macro algorithms returning as false:

- Bone mineral density

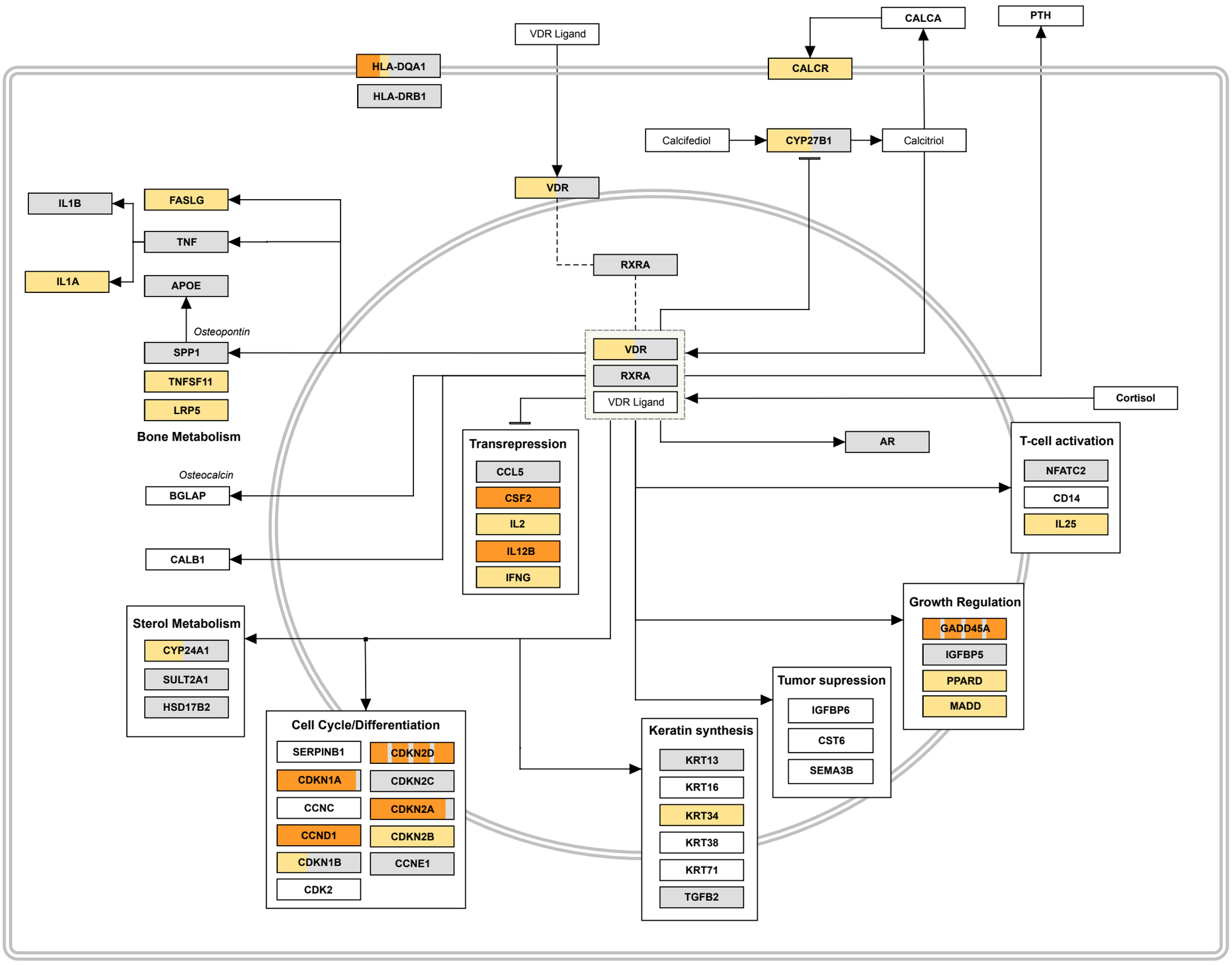
STRUCTURAL

NETWORK MAPS

Network maps allow you to visualize how certain gene pathways interact and contribute to health maintenance. These network maps allows you to visualize your genomic data directly in a number of hand-curated pathway maps. Boxes in the map generally depict genes, and the box color(s) are determined by the percentage of SNP values that are homozygous recessive for risk (orange), heterozygous for risk (yellow) and negative for risk (gray).

Vitamin D Mediated Expression

A number of studies have suggested that patients with chronic inflammatory diseases are deficient in 25-hydroxyvitamin-D (25-D) and that consuming greater quantities of vitamin D, which elevates 25-D levels, alleviates symptoms of disease. When active, the Vitamin D nuclear receptor (VDR) affects transcription of at least 913 genes and impacts processes ranging from calcium metabolism to expression of key antimicrobial peptides. Located in the nucleus of a variety of cells including immune cells, the VDR is a control system of sorts. When exposed to infection and damage, especially that which is caused by pathogens, the body begins to convert the inactive form 25-D into the active form, 1,25-D.



NATURAL PRODUCTS

This section lists the top 25 natural products that may be worthy of attention as potentially valuable therapeutic agents:

RANK	AGENT	INDICATION VALUE
1.	Curcumin	
2.	Krill oil, vitamin D3, and Lactobacillus reuteri mixture	
3.	Yerba Mate Tea	
4.	Dexamethasone	
5.	Resveratrol	
6.	Gossypol, gossypium spp.	
7.	Exercise	
8.	Silymarin	
9.	Genistein	
10.	Sulforaphane	
11.	Salvia miltiorrhiza (Danshen)	
12.	alpha Lipoic acid	
13.	Vitamin A (retinol)	
14.	Retinoic acid therapeutic levels	
15.	Lactobacillus plantarum	
16.	Migu capsule	
17.	Strengthening Spleen prescriptions	
18.	Magnesium	
19.	Vitamin D (calciferols)	
20.	Retinoic acid	
21.	Vitamin B-2 (riboflavin)	
22.	Butyric Acid (Butyrate)	
23.	Kaempferol	
24.	Pinitol	
25.	2,3,5,6-Tetramethylpyrazine (TMP)	

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	**CC**	Psoriasis
Amitriptyline	rs4244285	CYP2C19	A	**AG**	Those with the AA or AG genotype are poor metabolizers of amitriptyline
Azathioprine	rs1800460	TPMT	T	**CT**	Hepatotoxicity
Azathioprine	rs1142345	TPMT	C	**CT**	Hepatotoxicity
Azathioprine	rs1142345	TPMT	C	**CT**	Patients with CC or CT genotype have decreased inactivation of thiopurines and increased risk of toxicity
Carbamazepine	rs3909184	FLOT1	G	**GG**	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	**AG**	Tinnitus, hearing impairment, Raynaud syndrome
Clobazam	rs4244285	CYP2C19	G	**AG**	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 comparisone 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	**AG**	Gingival overgrowth, periodontal disease
Fluorouracil	rs1695	GSTP1	A	**AG**	Hematological toxicity, gastrointestinal toxicity
Gefitinib	rs2231142	ABCG2	T	**GT**	Diarrhea
Gefitinib	rs2231142	ABCG2	T	**GT**	In non-small lung cancer patients, those that are heterozygous (ABCG2 421C>A) have a higher risk of diarrhea.
Irinotecan	rs4149056	SLCO1B1	C	**CT**	Diarrhea, leucopenia, neutropenia
Isoniazid	rs6413419	CYP2E1	GG	**GG**	Hepatotoxicity
Mercaptopurine	rs1800460	TPMT	T	**CT**	Hepatotoxicity
Mercaptopurine	rs1142345	TPMT	C	**CT**	Hepatotoxicity
Venlafaxine	rs5030655	CYP2D6	I	**II**	Nausea, vomiting diarrhea
Almotriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment
Citalopram	rs1954787	GRIK4	C	**CC**	Improved response to antidepressant medication
Clopidogrel	rs4244285	CYP2C19	A	**AG**	Patients are poor metabolizers of clopidogrel. More likely to experience poor cardiovascular outcomes.
Clopidogrel	rs4244285	CYP2C19	A	**AG**	Patients are poor metabolizers of clopidogrel. More likely to experience poor cardiovascular outcomes.
Codeine	rs5030655	CYP2D6	I	**II**	Poor drug metabolizer, lower dose requirements
Dextromethorphan	rs5030655	CYP2D6	II	**II**	Poor drug metabolizer, lower dose requirements
Eletriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment
Frovatriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment
Infliximab	rs1801274	FCGR3A	GG	**GG**	Better ACR20 response
Modafinil	rs4680	COMT	GG	**GG**	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	**AA**	Better response to pain relief drugs
Naratriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment
Rizatriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment

Rosuvastatin	rs2231142	ABCG2	T	**GT**	Greater response to drug therapy
Sildenafil	rs5443	GNB3	T	**CT**	Better response to drug treatment
Sumatriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment
Trastuzumab	rs351855	FGFR4	G	**AG**	Reduced response to herceptin
Venlafaxine	rs5030655	CYP2D6	I	**II**	Poor drug metabolizer, lower dose requirements, nausea, vomiting and diarrhea
Venlafaxine	rs5030655	CYP2D6	I	**II**	Poor drug metabolizer, lower dose requirements, nausea, vomiting and diarrhea
Zolmitriptan	rs5443	GNB3	T	**CT**	Better response to drug treatment