GUIDELINE

A gene variant report is a graphical representation of genetic raw data, displayed as a color coded chart.Phenotypes are determined based on the presence or absence of variant alleles in your genotype. Alleles are considered variant if they are the minor allele i.e they occur with less frequency (GMAF) in the default global population. Having "no variant" alleles (green) is not necessarily "normal" or protective, and having a homozygous phenotype (red) is not always "abnormal". What is a normal or abnormal phenotype should NOT be determined solely based on this variant report. Please refer to the table below to explore this issue further.

The significance of your phenotypes should be assessed by reviewing related genome wide studies for context and in consultation with a qualified health practitioner or nutrigenetics specialist.

	By default, green means that there are no minor alleles or Hemizygous and therefore that there are no risk alleles. Sometimes, however a minor allele can be protective and in these cases it will also be marked as green.
	By default, yellow means that there is one minor allele. Sometimes, two major alleles (common alleles) are yellow if the major allele is the risk allele or Heterozygous.
	Red means that you need to pay attention to this SNP. By default, Red means that there are two minor (less common) alleles and therefore risk alleles or Homozygous. Sometimes, we change a color to Red if there is only one minor allele and one minor allele is associated with negative health outcomes.

Chemoprotection / Detox

Liver Detox Phase I & II

A lot of toxins – whether eaten, breathed, or created in our bodies – are broken down by the Cytochrome P450 family of enzymes in what is known as phase I of detoxification. Phase I break apart big toxins and makes them into polar molecules. Most of this takes place in the liver; Phase II detoxification involves taking the metabolites of phase I and changing them so that they can be excreted. Phase II binds with the metabolites from Phase I and makes them water-soluble so that they can be excreted. Sometimes the metabolites of phase I are carcinogenic or reactive, so having phase II detox in sync is very important. Understanding your own genes for detoxification can help you prioritize which toxicants are the most harmful to you and which drugs to avoid.

Yeast/ Alcohol metabolism

The alcohol dehydrogenases comprise a group of several isozymes that catalyse the oxidation of primary and secondary alcohols to aldehydes and ketones,respectively,Alcohol dehydrogenases (ADH) are a group of dehydrogenase enzymes that occur In humans and many other animals and facilitate the interconversion between alcohols and aldehydes or ketones with the reduction of nicotinamide adenine dinucleotide (NAD +) to NADH. Thus ADH serve to break down alcohols that otherwise are toxic, and they also participate in generation of useful aldehyde, ketone, or alcohol groups during biosynthesis of various metabolites. In yeast, plants, and many bacteria, some alcohol dehydrogenases catalyze the opposite reaction as part of fermentation to ensure a constant supply of NAD + .

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs2472304	CYP1A2*1F	**Liver Detox I**	Metabolizes caffeine, Converts estradiol to 2-OH-estradiol. Oxidizes steroids, fatty acids, and xenobiotics.	**AA**	**--**
rs762551	CYP1A2*1F C164A	**Liver Detox I**	Metabolizes caffeine, Converts estradiol to 2-OH-estradiol. Oxidizes steroids, fatty acids, and xenobiotics. AA= upregulation. CC, AC = downregulation	**CC**	**A**
rs1056836	CYP1B1 L432V	**Liver Detox I**	Hydroxylation of Estrogens	**CC**	**C**
rs1800440	CYP1B1 N453S	**Liver Detox I**	Estrogen Metabolism. Converts estradiol to 4-OH-estradiol	**TT**	**T**
rs9282671	CYP1B1 T241A	**Liver Detox I**	Hydroxylation of Estrogens	**AA**	**A**
rs1801272	CYP2A6*2 A1799T	**Liver Detox I**	Xenobiotics, nicotine, drugs metabolism. Works with CYP2B6	**TT**	**A**
rs12767583	CYP2C19 C5709T	**Liver Detox I**	Drugs metabolism	**TT**	**T**
rs4986894	CYP2C19 T98C	**Liver Detox I**	Drugs metabolism	**TT**	**T**
rs4986893	CYP2C19*3 G636A	**Liver Detox I**	Drugs metabolism	**AA**	**G**
rs41291556	CYP2C19*8 T358C	**Liver Detox I**	Drugs metabolism	**CC**	**T**
rs9332239	CYP2C9*12 1465C>T	**Liver Detox I**	Warfarin, ARBs, and NSAIDs metabolism	**TT**	**C**
rs1057910	CYP2C9*3	**Liver Detox I**	Warfarin, ARBs, and NSAIDs metabolism	**CC**	**A**
rs9332131	CYP2C9*6 818delA	**Liver Detox I**	Warfarin, ARBs, and NSAIDs metabolism	**DD**	**I**
rs28371706	CYP2D6*17 T107I	**Liver Detox I**	Drugs metabolism: Codeine, Morphine, Tramadol, Risk = lower activity	**AA**	**G**
rs2031920	CYP2E1_-1055C>T G1055T	**Liver Detox I**	Xenobiotics, drugs, carcinogens metabolism. Works with GST and other CYP genes.	**TT**	**C**
rs2740574	CYP3A4*1B A392G	**Liver Detox I**	Androgens, Xenobiotics, drugs metabolism, testosterone oxidation	**GG**	**T**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1799945	HFE	**Liver Detox I**	Human Hemochromatosis protein. Regulates iron absorption. This is lower impact gene	**GG**	**C**
rs1800562	HFE	**Liver Detox I**	Human Hemochromatosis protein. Regulates iron absorption. This is the key gene, increasing risk.	**AA**	**G**
rs662	PON1 Q192R	**Liver Detox I**	Organophosphates detox, Oxidation of LDL Cholersterol (CC being risk for LDL oxidation), Homocysteine to Homocysteine Thiolactone	**TT**	**T**
rs2472304	rs2472304	**Liver Detox I**	Metabolizes caffeine, Converts estradiol to 2-OH-estradiol. Oxidizes steroids, fatty acids, and xenobiotics.	**AA**	**--**
rs1049793	ABP1/DAO C1933G	**Liver Detox II**	Extracellular and GI Histamine deactivation, removal of Di-amino acids (associated with aging), NSAID sensitivity.	**GG**	**--**
rs3741049	ACAT1 G22670A	**Liver Detox II**	Dietary fat and protein breakdown	**AA**	**A**
rs73598374	ADA G22A	**Liver Detox II**	Adenosine to Inosine, Purine metabolism	**TT**	**--**
rs1042026	ADH1B	**Liver Detox II**	Alcohol and lipid peroxidation products metabolism. Converts alcohol to acetaldehyde. (Zn)	**CC**	**--**
rs6413413	ADH1B A178T	**Liver Detox II**	Alcohol and lipid peroxidation products metabolism. Converts alcohol to acetaldehyde. (Zn)	**AA**	**T**
rs2066702	ADH1B A396C	**Liver Detox II**	Alcohol and lipid peroxidation products metabolism. Converts alcohol to acetaldehyde. (Zn)	**AA**	**--**
rs737866	COMT/TXNRD2 A4251G	**Liver Detox II**	Adrenaline, Dopamine, Estrogen metabolism (Mg, SAMe) Mind the CYP1B1 upregulation, glucuronidation and sulfation.	**CC**	**T**
rs2020917	COMT/TXNRD2 C4622T	**Liver Detox II**	Adrenaline, Dopamine, Estrogen metabolism (Mg, SAMe) Mind the CYP1B1 upregulation, glucuronidation and sulfation.	**TT**	**--**
rs3741775	DAO	**Liver Detox II**	Extracellular and GI Histamine deactivation, removal of Di-amino acids (associated with aging), NSAID sensitivity.	**CC**	**--**
rs3918347	DAO	**Liver Detox II**	Extracellular and GI Histamine deactivation, removal of Di-amino acids (associated with aging), NSAID sensitivity.	**GG**	**A**
rs2273684	GSS	**Liver Detox II**	Glutathione Synthesis	**GG**	**T**
rs6060124	GSS	**Liver Detox II**	Glutathione Synthesis	**AA**	**A**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs6088659	GSS A5997G	**Liver Detox II**	Glutathione Synthesis	**TT**	**C**
rs1056806	GSTM1	**Liver Detox II**	Conjugation of Glutathione and toxins	**TT**	**--**
rs7483	GSTM3	**Liver Detox II**	GSTM3 encodes glutathione S-transferase that functions in the detoxification of carcinogens, drugs, toxins, and products of oxidative stress. Mutations of this gene can lead to various cancers. minor "T" allele = lower levels of GSTM3 protein.Reduced antioxidant defense causing oxidative stress in the body. Alzheimer's. Higher levels of pepsinogen, a precursor for pepsin which is used to digest proteins in the stomach.	**TT**	**T**
rs1138272	GSTP1	**Liver Detox II**	conjugation of Glutathione and toxins	**TT**	**C**
rs1695	GSTP1	**Liver Detox II**	conjugation of Glutathione and toxins.Persons having the alleles AA orAG had an increase ininflammatory interleukin-6 (IL-6)upon supplementingalpha-tocopherol (the mostcommon form of Vitamin E in aNorth American diet) while thosewith GG saw a decrease	**GG**	**A**
rs2073440	HDC	**Liver Detox II**	Histidine to Histamine	**GG**	**--**
rs901865	HRH1	**Liver Detox II**	Histamine Receptor	**TT**	**T**
rs11662595	HRH4	**Liver Detox II**	Histamine Receptor	**GG**	**A**
rs16940765	HRH4	**Liver Detox II**	Histamine Receptor	**CC**	**T**
rs4800573	HRH4	**Liver Detox II**	Histamine Receptor	**AA**	**G**
rs1041983	NAT2	**Liver Detox II**	Acethylation, xenobiotic metabolizing enzyme involved in the biotransformation of many aromatic amines and heterocyclicamines.	**TT**	**C**
rs1208	NAT2	**Liver Detox II**	Acethylation, xenobiotic metabolizing enzyme involved in the biotransformation of many aromatic amines and heterocyclicamines.	**GG**	**A**
rs1799929	NAT2	**Liver Detox II**	Acethylation, xenobiotic metabolizing enzyme involved in the biotransformation of many aromatic amines and heterocyclicamines.	**TT**	**C**
rs1799930	NAT2	**Liver Detox II**	Acethylation, xenobiotic metabolizing enzyme involved in the biotransformation of many aromatic amines and heterocyclicamines.	**AA**	**G**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1799931	NAT2	**Liver Detox II**	Acethylation, xenobiotic metabolizing enzyme involved in the biotransformation of many aromatic amines and heterocyclicamines.	**AA**	**G**
rs1801279	NAT2	**Liver Detox II**	Acethylation, xenobiotic metabolizing enzyme involved in the biotransformation of many aromatic amines and heterocyclicamines.	**AA**	**G**
rs10183914	NFE2L2 or Nrf2	**Liver Detox II**	Nuclear factor (erythroid-derived 2)-like 2, also known as NFE2L2 or Nrf2, is a protein (transcription factor). Nrf2 increases the expression of antioxidant proteins that protect against oxidative damage triggered by injury and inflammation. Substances that stimulate the Nrf2 pathway are being studied for the treatment of diseases that are caused by oxidative stress. It responds to injury and inflammation. http://www.ncbi.nlm.nih.gov/gene/4780 Transcription activator that binds to antioxidant response (ARE) elements in the promoter regions of target genes. Important for the coordinated up-regulation of genes in response to oxidative stress. May be involved in the transcriptional activation of genes of the beta-globin cluster by mediating enhancer activity of hypersensitive site 2 of the beta-globin locus control region. Alternative names: NF-E2-related factor 2 NFE2-related factor 2 Nuclear factor, erythroid derived 2, like 2 It's better to have this gene increased most of the time.	**CC**	**--**
rs1962142	NRF2	**Liver Detox II**	Promoter region, Stimulation of anti - oxidative enzymes	**AA**	**G**
rs35652124	NRF2	**Liver Detox II**	Promoter region, Stimulation of anti - oxidative enzymes	**TT**	**--**
rs6726395	NRF2	**Liver Detox II**	Promoter region, Stimulation of anti - oxidative enzymes	**AA**	**G**
rs2547231	SULT2A1	**Liver Detox II**	Sulfation, catalyses thesulfation of steroids in adrenal glands and bile acids in the liver.	**CC**	**A**
rs887829	UGT1A1	**Liver Detox II**	Glucuronidation, conversion of unconjugated bilirubin(toxic) to conjugated bilirubin. Xenobiotics metabolism/removal.	**TT**	**T**
rs6742078	UGT1A1 G179250T	**Liver Detox II**	Glucuronidation, conversion of unconjugated bilirubin(toxic) to conjugated bilirubin. Xenobiotics metabolism/removal.	**TT**	**T**
rs4148323	UGT1A1 G211A	**Liver Detox II**	Glucuronidation, conversion of unconjugated bilirubin(toxic) to conjugated bilirubin. Xenobiotics metabolism/removal.	**AA**	**G**
rs4244593	PEMT	**Membranes permeability**	phosphatidylethanolamine to phosphatidylcholine	**TT**	**T**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs7946	PEMT	**Membranes permeability**	phosphatidylethanolamine to phosphatidylcholine	**TT**	**T**
rs480575	CAT A12175G	**Oxidative Stress**	H202 reduction	**GG**	**A**
rs2300181	CAT C21068T	**Oxidative Stress**	H202 reduction	**TT**	**T**
rs4626565	COX6C	**Oxidative Stress**	Last enzyme in Electron Trabsport Chain. ROS scavenging.	**CC**	**T**
rs1050828	G6PD	**Oxidative Stress**	makes substrate for GSR, important for oxidised Glutathione reduction.	**TT**	**C**
rs1050829	G6PD	**Oxidative Stress**	makes substrate for GSR, important for oxidised Glutathione reduction.	**CC**	**T**
rs5030868	G6PD	**Oxidative Stress**	makes substrate for GSR, important for oxidised Glutathione reduction.	**AA**	**G**
rs8007267	GCH1 C36378991T	**Oxidative Stress**	GCH1 haplotype determines vascular and plasma biopterin availability in coronary artery disease effects on vascular superoxide production and endothelial function	**TT**	**C**
rs10483639	GCH1 G55306457C	**Oxidative Stress**	GCH1 haplotype determines vascular and plasma biopterin availability in coronary artery disease effects on vascular superoxide production and endothelial function.	**CC**	**G**
rs2551715	GSR	**Oxidative Stress**	Oxidised Glutathione reduction	**TT**	**T**
rs1799836	MAOB	**Oxidative Stress**	Oxidation (deactivation)Dopamine, Adrenaline, Noradrenaline (less Serotonin). T= upregulation.	**TT**	**T**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs10183914	NFE2L2 or Nrf2	**Oxidative Stress**	Nuclear factor (erythroid-derived 2)-like 2, also known as NFE2L2 or Nrf2, is a protein (transcription factor). Nrf2 increases the expression of antioxidant proteins that protect against oxidative damage triggered by injury and inflammation. Substances that stimulate the Nrf2 pathway are being studied for the treatment of diseases that are caused by oxidative stress. It responds to injury and inflammation. http://www.ncbi.nlm.nih.gov/gene/4780 Transcription activator that binds to antioxidant response (ARE) elements in the promoter regions of target genes. Important for the coordinated up-regulation of genes in response to oxidative stress. May be involved in the transcriptional activation of genes of the beta-globin cluster by mediating enhancer activity of hypersensitive site 2 of the beta-globin locus control region. Alternative names: NF-E2-related factor 2 NFE2-related factor 2 Nuclear factor, erythroid derived 2, like 2 It's better to have this gene increased most of the time.	**CC**	**--**
rs1800566	NQO1	**Oxidative Stress**	Breaks down superoxides and peroxides. Directly scavenges superoxide. Activates vitamin K.	**AA**	**A**
rs1962142	NRF2	**Oxidative Stress**	Promoter region, Stimulation of anti - oxidative enzymes	**AA**	**G**
rs35652124	NRF2	**Oxidative Stress**	Promoter region, Stimulation of anti - oxidative enzymes	**TT**	**--**
rs6726395	NRF2	**Oxidative Stress**	Promoter region, Stimulation of anti - oxidative enzymes	**AA**	**G**
rs854571	PON1	**Oxidative Stress**	Oxidised lipids removal	**TT**	**C**
rs662	PON1 Q192R	**Oxidative Stress**	Oxidised lipids removal	**TT**	**T**
rs4880	SOD2	**Oxidative Stress**	Superoxide Reduction (Mn, Zn, Cu)	**GG**	**A**
rs2273697	ABCC2	**Phase III Detox**	Intestial Toxic Conjugates Transport	**AA**	**A**
rs717620	ABCC2	**Phase III Detox**	Intestial Toxic Conjugates Transport	**TT**	**C**
rs8187710	ABCC2	**Phase III Detox**	Intestial Toxic Conjugates Transport	**AA**	**G**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs3741049	ACAT1 G22670A	**Phase III Detox**	Cholesterol synthesis to Bile production	**AA**	**A**
rs3733890	BHMT	**Phase III Detox**	Bile production, Methylation	**AA**	**G**
rs567754	BHMT-02	**Phase III Detox**	Bile production, Methylation	**TT**	**T**
rs1405655	LXR	**Phase III Detox**	LXR increases xenobiotic transport proteins, such as MDR1 (ABCB1) and MRP2 (ABCC2)	**TT**	**T**
rs17373080	LXR	**Phase III Detox**	LXR increases xenobiotic transport proteins, such as MDR1 (ABCB1) and MRP2 (ABCC2)	**GG**	**--**
rs2695121	LXR	**Phase III Detox**	LXR increases xenobiotic transport proteins, such as MDR1 (ABCB1) and MRP2 (ABCC2)	**TT**	**--**
rs4244593	PEMT	**Phase III Detox**	Hepatic PC utilisation, secretion of bile into the intestine.	**TT**	**T**
rs7946	PEMT	**Phase III Detox**	Hepatic PC utilisation, secretion of bile into the intestine.	**TT**	**T**
rs1544410	VDR Bsm1	**Phase III Detox**	Bile Production	**TT**	**C**
rs1042026	ADH1B	**Yeast/Alcohol Metabolism**	Members of the alcohol dehydrogenase family break down a wide variety of things, including alcohol, vitamin A/retinol, other aliphatic alcohols, hydroxysteroids, and lipid peroxidation products	**CC**	**--**
rs6413413	ADH1B A178T	**Yeast/Alcohol Metabolism**	Members of the alcohol dehydrogenase family break down a wide variety of things, including alcohol, vitamin A/retinol, other aliphatic alcohols, hydroxysteroids, and lipid peroxidation products. combinations of this SNP and others were shown to affect alcohol metabolism; most of these combinations are represented by the gs211 genoset.	**AA**	**T**
rs2066702	ADH1B A396C	**Yeast/Alcohol Metabolism**	Members of the alcohol dehydrogenase family break down a wide variety of things, including alcohol, vitamin A/retinol, other aliphatic alcohols, hydroxysteroids, and lipid peroxidation products	**AA**	**--**
rs2238151	ALDH2	**Yeast/Alcohol Metabolism**	Joint effects of alcohol consumption and polymorphisms in alcohol and oxidative stress metabolism genes on risk of head and neck cancer	**TT**	**C**
rs671	ALDH2	**Yeast/Alcohol Metabolism**	A allele significant contributor to alcohol flush and increased hangover effects. A allele is most common in Asian populations.	**AA**	**G**

Chemoprotection / Detox

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs72547566	ALDH3A2	**Yeast/Alcohol Metabolism**	.	**TT**	**--**
rs769214	CAT				**--**
rs769217	CAT C14185T				**T**

Diet & Nutrition

Diet & Nutrition

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs4148211	ABCG8	**Cholesterol Status**	The G (minor) allele is associated with: Increased total cholesterol levels Increased levels of LDL cholesterol but Decreased risk of developing type 2 diabetesThe A (major) allele is associated with: Increased levels of triglycerides (AA).Low levels of LDL cholesterol (AA).but Increased risk of developing type 2 diabetes (AA).	**GG**	**A**
rs3213445	CPT1A	**Cholesterol Status**	The Minor "C" allele is associated with:Carriers of the rare allele had significantly higher glutamyl transpeptidase (GGT), glutamic oxaloacetic transaminase (GOT) and glutamic pyruvate transaminase (GPT) activities.A higher fatty liver index.Triglycerides and fasting glucose were significantly higher in C allele carriers.Insulin sensitivity was lower in C allele carriers.Total cholesterol and LDL-cholesterol tended to be higher in C allele carriers.	**CC**	**T**
rs482548	FADS2	**Cholesterol Status**	(TT) Lower than common level of FADS enzyme activity	**TT**	**C**
rs4846914	GALNT2	**Cholesterol Status**	The A (minor) allele is associated with increased levels of HDL cholesterol (good cholesterol) but also is associated with higher risk of hypertriglyceridemia.	**GG**	**A**
rs1800961	HNF4A	**Cholesterol Status**	The Minor "T" allele is associated with: Decreased HDL cholesterol levels due to lower HNF4A levels.	**TT**	**C**
rs1884614	HNF4A	**Cholesterol Status**	The C (major) allele is associated with increased HDL cholesterol levels.The Minor "T" allele is associated with lower levels of HFN4A protein (potentially lower HDL cholesterol)	**TT**	**T**
rs1137100	LEPR	**Cholesterol Status**	G = Higher total cholesterol, (highest in GG).The Major "A" allele is associated with decreased overall cholesterol.	**GG**	**--**
rs17700633	MC4R	**Cholesterol Status**	The Minor "A" allele is associated with decreased HDL cholesterol .The G (major) allele is associated with increased HDL cholesterol.	**AA**	**--**
rs2229616	MC4R	**Cholesterol Status**	The C (major) allele is associated with decreased HDL cholesterol levels.	**CC**	**--**
rs174537	MYRF (FADS1)	**Cholesterol Status**	The G (major) allele is associated with increased LDL cholesterol (bad cholesterol) levels.The T (minor) allele is associated with decreased LDL cholesterol (bad cholesterol) levels.	**GG**	**G**
rs7946	PEMT	**Cholesterol Status**	The T (minor) allele is associated with possible decreased levels of HDL cholesterol (good cholesterol).	**TT**	**T**
rs8192678	PGC-1a Gly482Ser	**Cholesterol Status**	The T (minor) allele is associated with increased percentage of small dense-LDL particles.	**TT**	**C**

Diet & Nutrition

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs2016520	PPARD	**Cholesterol Status**	The T (major) allele is associated with increased cholesterol levels.	**TT**	**T**
rs646776	PSRC1	**Cholesterol Status**	The C (minor) allele is associated with increased levels of LDL (bad cholesterol).	**CC**	**T**
rs659366	UCP2	**Cholesterol Status**	The "T" (minor) allele is associated with:More UCP2 production and higher levels of UCP2 protein Increased levels of HDL-Cholestrol and decreased levels of LDL-Cholestrol in a Chinese population.Reduced LDL particle size levels in a Chinese population.Increased energy expenditure.Decreased lipid oxidation Decreased high-sensitivity Cholesterol reactive protein (hs-CRP), a biomarker of inflammation. This decrease may indicate a lower level of inflammation in the body.More difficulty in losing weight under a very low-calorie program in Korean women.Higher fasting glucose levels in the blood.Higher risk of Diabetes (Type 2).Increased hardening of the arteries in women.Increased heart disease risk. Increased resting energy expenditure in obese children and increased 24-hour energy expenditure in Pima Indians.	**CC**	**C**
rs2073658	USF1	**Cholesterol Status**	The T (minor) allele is associated with increased LDL cholesterol.	**TT**	**C**
rs3733890	BHMT	**Choline Status**	GG (major) = higher chance to die of breast cancer. Choline may help reduce this risk.http: //www.ncbi.nlm.nih.gov/pubmed/19635752? dopt=Abstract	**GG**	**G**
rs2236225	MTHFD1	**Choline Status**	G = Decreased risk of choline deficiency.	**AA**	**A**
rs1805087	MTR	**Choline Status**	A = Less choline is needed by the body.	**GG**	**A**
rs738409	PNPLA3	**Choline Status**	T (minor) = higher risk of fatty liver - encourage more Choline.Whites with fatty liver - which may be due to low choline - were more likely to carry the T allele.	**TT**	**C**
rs738409	PNPLA3	**Choline Status**	C = Decreased need for choline in the body.	**GG**	**C**
rs11605924	CRY2	**High Fat Diet, Ketogenic Diet**	A (major) = Reduction in energy utilisation in a high fat diet.	**AA**	**A**
rs1800562	HFE	**Iron Status**	G (major) = Decreased levels of Iron in the blood. The A allele has an association with higher risk for hemochromatosis.	**AA**	**G**

Diet & Nutrition

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs3811647	TF	**Iron Status**	A = Increased Iron levels in the blood.	**AA**	**A**
rs855791	TMPRSS6	**Iron Status**	A = Increased iron levels in blood.	**AA**	**A**
rs182549	MCM6	**Lactose Tolerance**	MCM6 has influence on the lactase LCT gene, rs182549 and is one of two SNPs that is associated with the primary haplotype associated with hypolactasia, more commonly known as lactose intolerance in European Caucasian populations. The T (minor) allele is associated with increased ability to digest lactose.	**CC**	**C**
rs4988235	MCM6	**Lactose Tolerance**	MCM6 has influence on the lactase LCT gene, rs182549 and is one of two SNPs that is associated with the primary haplotype associated with hypolactasia, more commonly known as lactose intolerance in European Caucasian populations. AA = Can digest milk .AG = Likely to be able to digest milk as an adult.GG = Likely lactose intolerant	**GG**	**G**
rs17300539	ADIPOQ	**Monounsaturated Fat**	The G (major) allele is associated with:Worse response to monounsaturated fat intake.GG = Higher BMI with increased monounsaturated fat intake (avoid monounsaturated fats)	**GG**	**--**
rs174537	MYRF (FADS1)	**Omega fatty acids**	The G (major) allele is associated with:Possible decreased need for fish oil supplements to maintain healthy omega-3 fatty acid levelsIncreased levels of arachidonic acid in the body [R]. Arachidonic acid is an Omega-6 polyunsaturated fatty acid.TT = Possible increased need for fish oil supplements to maintain healthy omega-3 fatty acid levels.TT = Lower levels of arachidonic acid in the body. Arachidonic acid is an Omega-6 polyunsaturated fatty acid.	**TT**	**G**
rs9939609	FTO	**Response to Carbohydrates**	Each A= increases hunger and caloric intake, but not energy expenditure.Obesity.Less brown fat and more white fat.FTO correlates with galanin, an orexigenic peptide.	**AA**	**A**
rs2338104	KCTD10	**Response to Carbohydrates**	GG (major) = lower LDL (bad cholesterol) if high carb intake.	**CC**	**G**
rs894160	PLIN1	**Response to Carbohydrates**	CC (major) =does worse with a high complex carb diet with regard to weight.People with the "T" or minor allele do better with complex carbs and worse with saturated fat. The T allele helps protects from weight gain from a higher complex carb diet, but causes weight gain on a lower carb complex carb diet and insulin resistance on a higher saturated fat diet.	**CC**	**--**
rs1799986	LRP1	**Saturated Fat**	The C (major) does better with saturated fat (decreased weight gain)The AG genotype is associated with normal saturated fat levels.	**TT**	**C**

Diet & Nutrition

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs744166	STAT3	**Saturated Fat**	G (minor) does worse with saturated fat (increased risk of abdominal obesity).	**GG**	**A**
rs8069645	STAT3	**Saturated Fat**	AA does better with saturated fat (decreased risk of abdominal obesity)The G (minor) allele is associated with:Increased levels of STAT3 proteinIncreased risk of abdominal obesity	**GG**	**A**
rs7579	CCDC152	**Selenium Status**	TT = Higher levels of Selenium in subjects with a high BMI.	**TT**	**C**
rs2072560	APOA5	**Triglyceride Status**	C = Lower levels of triglycerides.T = Higher levels of triglycerides.	**TT**	**--**
rs2075291	APOA5	**Triglyceride Status**	CC = Decreased risk of high triglyceride levels.AA = Greater than 4x the risk for high triglyceride levels (n=Asian populations) AC = 4x higher risk for high triglyceride levels (n=Asian populations)	**AA**	**C**
rs2266788	APOA5	**Triglyceride Status**	A = Decreased triglyceride levels.	**GG**	**A**
rs3135506	APOA5	**Triglyceride Status**	GG = Decreased triglyceride levels.CC = 34% Increase in triglyceride concentration.	**CC**	**G**
rs651821	APOA5	**Triglyceride Status**	TT = Decreased triglyceride levels.CC = Higher triglycerides.	**CC**	**T**
rs662799	APOA5	**Triglyceride Status**	AA = Decreased triglyceride levelsEach G=higher triglycerides	**GG**	**A**
rs3213445	CPT1A	**Triglyceride Status**	T = Decreased triglyceride levels.Triglycerides and fasting glucose were significantly higher in C allele carriers.	**CC**	**T**
rs174570	FADS2	**Triglyceride Status**	CC = Normal levels of triglycerides.TT = Increased triglycerides.CT = Increased triglycerides.	**TT**	**C**
rs13223993	IGFBP3	**Triglyceride Status**	A = Increased triglyceride levelsG = Decreased triglycerides and increased HDL, lowering the risk of cardiovascular disease and obesity	**AA**	**A**
rs6420424	BCMO	**Vitamin A metabolism**	GG= reduced BCM01 activity by 59%, which may reduce the amount of retinol being made	**GG**	**G**
rs6564851	BCMO	**Vitamin A metabolism**	TT= reduced BCMO1 activity by 48%.T allele= lower levels of vitamin A.The G allele may affect health negatively by reducing the availability of vitamin A (retinol) but also positively by increasing the plasma concentration of powerful antioxidant molecules. A number of studies have shown that higher plasma concentrations of antioxidant carotenoids are associated in a protective manner against the development of chronic diseases and disability.	**TT**	**T**

Diet & Nutrition

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs4889294	BCMO1	**Vitamin A metabolism**	Carotene to retinol conversion	**CC**	**T**
rs7501331	BCMO1 A379V	**Vitamin A metabolism**	Females carrying the T variant had a 32% lower ability to convert Beta-carotene.rs7501331(T)+ rs12934922(T)= 69% lower conversion of Beta-carotene to retinyl esters... The BCMO1 gene (rs12934922and rs7501331) is known to influence the conversion of beta-carotene to vitamin A.TT= 57% reduced conversion activity of beta-carotene (In test tubes)	**TT**	**C**
rs492602	FUT2	**Vitamin B 12 Status**	GG (minor) = Normal absorption of vitamin B12. Women homozygous for the G allele had higher B (12) levels in the blood. This is thought to be caused by increased B12 absorption.TT = Possible malabsorption of vitamin B12 from the GI tract.Absorption of B12 requires the secretion of intrinsic factor (IF) from the gastric cells, binding of IF to vitamin B12 and a functional gastrointestinal absorption system.	**TT**	**A**
rs492602	FUT2 A12190G	**Vitamin B 12 Status**	GG (minor) = Normal absorption of vitamin B12. Women homozygous for the G allele had higher B (12) levels in the blood. This is thought to be caused by increased B12 absorption.TT = Possible malabsorption of vitamin B12 from the GI tract.Absorption of B12 requires the secretion of intrinsic factor (IF) from the gastric cells, binding of IF to vitamin B12 and a functional gastrointestinal absorption system.	**TT**	**A**

GI Health

GI Health

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs231775	CTLA4	**Celiac & Gluten Intolerance**	This gene encodes a protein which transmits an inhibitory signal to T cells. Mutations in this gene have been associated autoimmune diseases including: diabetes, Graves disease, thryoid problems, celiac disease, and lupus.	**GG**	**A**
rs2858331	HLA	**Celiac & Gluten Intolerance**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**GG**	**G**
rs2187668	HLA-DQA1	**Celiac & Gluten Intolerance**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**TT**	**C**
rs9275224	HLA-DQA2	**Celiac & Gluten Intolerance**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**AA**	**A**
rs3741049	ACAT1 G22670A	**Disbiosis**	possibly higher tendency for gut dysbiosis (particularly clostridia).	**AA**	**A**
rs602662	FUT2	**H Antigen**	Non-secretors have lower levels of bifidobacteria and would benefit from probiotics	**AA**	**G**
rs1049793	ABP1/DAO C1933G	**Histamine**	Extracellular and GI Histamine deactivation, removal of Di-amino acids (associated with aging), NSAID sensitivity.	**GG**	**--**
rs3741775	DAO	**Histamine**	Extracellular and GI Histamine deactivation, removal of Di-amino acids (associated with aging), NSAID sensitivity.	**CC**	**--**
rs3918347	DAO	**Histamine**	Extracellular and GI Histamine deactivation, removal of Di-amino acids (associated with aging), NSAID sensitivity.	**GG**	**A**
rs10156191	DAO C47T or AOC1	**Histamine**	Protein. Catalyses the degradation of compounds such as putrescine, histamine, spermine, and spermidine, substances involved in allergic and immune responses, cell proliferation, tissue differentiation, tumour formation, and possibly apoptosis. Placental DAO is thought to play a role in the regulation of the female reproductive function. Other names: Diamine oxidase Amiloride-binding protein 1 Amine oxidase copper domain-containing protein 1 Histaminase Kidney amine oxidase KAO	**TT**	**T**
rs1800871	IL10-819	**Inflammation**	A=decreased IL-10..susceptibility to IBD	**AA**	**G**
rs2243828	MPO	**Microbial defense**	MPOD Myeloperoxidase deficiency is a disorder characterized by decreasedmyeloperoxidase activity in neutrophils and monocytes that results in disseminated candidiasis.	**AA**	**A**
rs854571	PON1	**Microbial defense**	PON1 protects against bacterial infection by destroying the bacterial signalling molecules that cause gram negative bacteria to invade human tissue and form colonies, thus PON1 contributes to the bodies innate immunity. Also associated with IBD.	**TT**	**C**

GI Health

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs662	PON1 Q192R	**Microbial defense**	PON1 protects against bacterial infection by destroying the bacterial signalling molecules that cause gram negative bacteria to invade human tissue and form colonies, thus PON1 contributes to the bodies innate immunity. Also associated with IBD.	**TT**	**T**
rs5443	GNB3T (5HT2A)	**Stress Response**	The T allele is thought to increase second messenger signalling. There are benefits and negative effects to this.IBS. People with genes who produced more 5HT2A receptors were more likely to have IBS.	**TT**	**C**
rs6311	HTR2A	**Stress Response**	The T allele is associated with IBS	**TT**	**C**

Health Report

Celiac Disease/Gluten Intolerance

Celiac disease, sometimes called celiac sprue or gluten-sensitive enteropathy, is an immune reaction to eating gluten, a protein found in wheat, barley and rye. If you have celiac disease, eating gluten triggers an immune response in your small intestine. Over time, this reaction damages your small intestine's lining and prevents it from absorbing some nutrients (malabsorption). The intestinal damage often causes diarrhea, fatigue, weight loss, bloating and anemia, and can lead to serious complications.

Clotting Factors

Coagulation, also known as clotting, is the process by which blood changes from a liquid to a gel, forming a blood clot. It potentially results in hemostasis, the cessation of blood loss from a damaged vessel, followed by repair. The mechanism of coagulation involves activation, adhesion and aggregation of platelets, as well as deposition and maturation of fibrin.

Health Report

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs3741049	ACAT1 G22670A	**Blood Glucose**	ketone body metabolism	**AA**	**A**
rs266729	ADIPOQ	**Blood Glucose**	Adiponectin is released in the bloodstream from fat cells, where it is involved in the control of fat metabolism and regulating glucose levels .CG was associated with type 2 diabetes in the obese group only OR=2.45. P=0.02, and 59% risk of diabetes could be attributed to that.	**GG**	**--**
rs10885122	ADRA2A	**Blood Glucose**	T=lower fasting glucoseG=higher fasting glucose	**GG**	**G**
rs553668	ADRA2A	**Blood Glucose**	A=increased ADRA2 receptors, higher fasting glucose and diabetes, hypertension, reduced insulin secretion and perhaps obesity. Having a C allele may help in sustaining the endurance training regime to attain a high level of maximal aerobic power in elite endurance athletes	**AA**	**A**
rs1405655	LXR	**Blood Glucose**	LXR helps the secretion of insulin, which helps combat diabetes	**TT**	**T**
rs17373080	LXR	**Blood Glucose**	LXR helps the secretion of insulin, which helps combat diabetes	**GG**	**--**
rs2695121	LXR	**Blood Glucose**	LXR helps the secretion of insulin, which helps combat diabetes	**TT**	**--**
rs8192678	PGC-1a Gly482Ser	**Blood Glucose**	PGC-1 increases energy metabolism and weight loss. This protein may be also involved in controlling blood pressure, regulating cellular cholesterol homoeostasis, and the development of obesity. PGC-1a protects against neurodegenerative diseases. PGC-1 decreases inflammation and insulin resistance. T is the less common allele (codes for serine). This variant causes a lower level of PGC-1a protein including in muscles The T allele results a less efficient coactivator of transcription factors, including those that regulate the PPARGC1A gene itself	**TT**	**C**
rs2858331	HLA	**Celiac & Gluten Intolerance**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**GG**	**G**
rs2187668	HLA-DQA1	**Celiac & Gluten Intolerance**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**TT**	**C**
rs9275224	HLA-DQA2	**Celiac & Gluten Intolerance**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**AA**	**A**
rs4961	ADD1	**Clotting Factors**	The risk (T) allele responded better to diuretics and sodium-restricted diets, in that they tended to lower their blood pressure by ~10 mmHg points compared to rs4961(G;G) homozygotes similarly treated.	**TT**	**G**
rs1800775	CETP	**Clotting Factors**	CETP encodes a protein that is involved in the transfer of cholesteryl ester from high density lipoprotein (HDL) to other lipoproteins.	**CC**	**A**

Health Report

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs13146272	CYP4V2	**Clotting Factors**	A study of 453 VTE cases and 1,327 controls was able to replicate the "mild effects" of this SNP on risk for VTE, however they felt that stronger associations were found between increased VTE risk and either the Factor V Leiden mutation (rs6025)or having blood types O or A2	**CC**	**A**
rs3211719	F10	**Clotting Factors**	This gene encodes a protein called coagulation factor X that helps blood clot after an injury. Mutations can cause deficiency of the protein, which leads to excessive bleeding	**GG**	**A**
rs2289252	F11,F11-AS1	**Clotting Factors**	This gene encodes a protein called coagulation factor XI that helps blood clot after an injury. Mutations can cause deficiency of the protein, which leads to excessive bleeding	**TT**	**T**
rs2731672	F12	**Clotting Factors**	This gene encodes a protein called coagulation factor XII that helps blood clot after an injury. It is involved in the inflammatory response. Mutations can cause deficiency of the protein, which leads to excessive bleeding	**TT**	**C**
rs6025	F5	**Clotting Factors**	he F5 gene encodes a protein that is called coagulation factor V. They that form blood clots to stop bleeding and trigger blood vessel repair after an injury. Mutations can cause abnormal bleeding	**TT**	**C**
rs6048	F9	**Clotting Factors**	This gene encodes a protein called coagulation factor IX, which helps form blood clots. Mutations can cause blood clots to be unable to form and lead to excessive bleeding (hemophilia) or warfarin sensitivity, which can cause severe bleeding problems	**GG**	**A**
rs1613662	GP6 Pro219Ser	**Clotting Factors**	The gene encodes a protein that is a receptor for collagen and plays an important role in collagen- induced platelet aggregation and thrombus formation. Mutations of this gene can cause a bleeding disorder	**GG**	**A**
rs9898	HRG Pro204Ser	**Clotting Factors**		**TT**	**--**
rs5918	ITGB3	**Clotting Factors**	C=increased resistance to blood thinning side effect of aspirin	**CC**	**T**
rs1523127	NR1I2	**Clotting Factors**	This gene encodes a protein that is a receptor and has both a ligand-binding domain and a DNA- binding domain	**CC**	**A**
rs2227589	SERPINC1	**Clotting Factors**	Gene variants associated with deep vein thrombosis	**TT**	**C**
rs12273363	BDNF	**Cognitive**	Neurotrophins are chemicals that help to stimulate and control neurogenesis, BDNF being one of the most active. The C allele is associated with more with mood disorders than T.The minor C allele might increased activity in the amygdala (a region in brain). This might increase anxiety and emotional memory.	**CC**	**T**

Health Report

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs6994992	NRG1	**Cognitive**	Neuregulin 1 is important for synaptic plasticity, inhibiting the amygdala (to shut down anxiety), myelination (Schwann cell maturation, survival, and motility), heart function (cardiac growth factor) and tumor suppression.TT= Decreased activation of frontal and temporal lobe regions.TT= Increased risk of Psychosis. TT=reduced white matter density in the anterior limb of the internal capsule and evidence of reduced structural connectivity in the same region.	**TT**	**T**
rs3746544	SNAP25	**Cognitive**	Synaptosomal-associated protein 25 (SNAP-25) plays a crucial role in the release of neurotransmitters (from presynapse- excocytosis). SNP variants that produce less SNAP25 are associated with less activation in areas of the brain that are critical for the regulation of attention and inhibition (prefrontal cortex). T=presumably lower SNAP25.	**TT**	**T**
rs3738401	TSNAX-DISC1, DISC1	**Cognitive**	This gene encodes a protein that helps neurons grow and assist cortical development through its interaction with other proteins. Mutations are associated with higher risk for schizophrenia.	**AA**	**--**
rs823162	TSNAX-DISC1, DISC1	**Cognitive**	This gene encodes a protein that helps neurons grow and assist cortical development through its interaction with other proteins. Mutations are associated with higher risk for schizophrenia.	**CC**	**T**
rs7483	GSTM3	**GI Health**	GST-M3 activity is possibly involved in protection against mucosal atrophy caused by H. pylori as the levels of IgG titer and PGI are linked to mucosal status.	**TT**	**T**
rs4343	ACE G2328A	**Kidney Health**	Angiotensin I to Angiotensin II,ACE stimulates production of thehormone, aldosterone, which triggers the absorption of salt and water by thekidneys. G=deletion at ACE Del16 and increase of ACE enzyme activity.	**GG**	**A**
rs4343	ACE G2328A	**Stress Response**	Angiotensin I to Angiotensin II,ACE stimulates production of the hormone, aldosterone. Anxiety, decreased learning memory, low frustration threshold, higher anxiety. Made worse by MAO A mutation. I G=deletion at ACE Del16 and increase of ACE enzyme activity.	**GG**	**A**
rs10885122	ADRA2A	**Stress Response**	These receptors have a critical role in regulating neurotransmitter release from your fight or flight system (sympathetic nerves and adrenergic neurons) in the brain. When activated, these receptors induce low heart rate, low blood pressure and sedation	**TT**	**G**
rs553668	ADRA2A	**Stress Response**	The ADRA2A encodes the ADRA2A receptor. These receptors have a critical role in regulating neurotransmitter release from your fight or slight system (sympathetic nerves and adrenergic neurons) in the brain.A=increased ADRA2 receptors	**AA**	**A**
rs1360780	FKBP5	**Stress Response**	Binding of FKBP5 to the Cortisol Receptor reduces its cortisol-binding capacity which leads to impaired negative feedback of HPA axis and a prolonged stress response. TT (worst) and CT are associated with emotional reactivity. Childhood trauma=even more FKBP5 in response to HPA activation.	**TT**	**--**

Health Report

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs3800373	FKBP5	**Stress Response**	Binding of FKBP5 to the Cortisol Receptor reduces its cortisol-binding capacity which leads to impaired negative feedback of HPA axis and a prolonged stress response.GG (worst) and AG are associated with emotional reactivity	**GG**	**A**
rs9470080	FKBP5	**Stress Response**	Binding of FKBP5 to the Cortisol Receptor reduces its cortisol-binding capacity which leads to impaired negative feedback of HPA axis and a prolonged stress response.TT and CT are equally are associated with emotional reactivity	**TT**	**--**
rs1978340	GAD1	**Stress Response**	A=lower GAD1.AA=increased GABA levels.Since GAD1 levels are believed to be lower with the A allele, the study speculates that GABA production by the GAD1 gene is actually reduced in the A allele carriers and that a compensatory change such as excessive production by GAD2 or a decreased breakdown by GABA transaminase may be causing this unpredicted increase in GABA.	**AA**	**--**
rs3749034	GAD1	**Stress Response**	The G allele=reduced GAD1 production	**AA**	**G**
rs5443	GNB3T (5HT2A)	**Stress Response**	The T allele is thought to increase second messenger signalling. There are benefits and negative effects to this.	**TT**	**C**
rs6313	HTR2A	**Stress Response**	The A allele was associated with lower general health and social function scores. This SNP correlates perfectly with rs6311, as in the A allele here will result in the T allele by rs6311. In schizophrenia, GG tend to do worse on working memory tasks than do individuals with a A allele	**AA**	**G**
rs6314	HTR2A	**Stress Response**	AA had significantly greater mental fatigue scores than the AG, AG is associated with ADHD, better response to antidepressants, worse memory.	**AA**	**G**
rs1042778	OXTR	**Stress Response**	People with the G allele had higher oxytocin levels than T carriers	**TT**	**T**
rs13316193	OXTR	**Stress Response**	CC or CT has been associated with empathy, whereas TT (the risky version) has been linked to decreased expression of oxytocin receptors in the brain, depressive mood and greater risk for Autism	**TT**	**--**
rs2268491	OXTR	**Stress Response**	CT had the highest level of empathy (IRI=68.7), followed by TT (65.8) and then CC (60.7)	**TT**	**C**
rs2268494	OXTR	**Stress Response**	TT is the social version. The A allele, which is not common, was associated with risk for Autism, which suggests lower oxytocin or worse processing of it.	**AA**	**--**
rs53576	OXTR (MAIN)	**Stress Response**	GG promotes efficient functioning of the oxytocin system and enhances the effects of oxytocin supplementation. GG take social rejection worse than others	**AA**	**G**

Health Report

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1867277	FOXE1	**Thyroid**	The FOXE1 protein regulates the transcription of thyroglobulin (Tg) and thyroid peroxidase (TPO). AA= production of FOXE1 gene is increased (by forming a complex with USF1/USF2 transcription factors).The higher level of production of FOXE1 gene associated with development of thyroid cancer.	**AA**	**--**

Immune Factors & Inflamation

IgG, IgE and IgA

Immunoglobulin's, also known as antibodies, comprise a family of proteins that occur in five major forms, also termed classes or isotopes – IgM, IgD, IgG, IgE and IgA. Immunoglobulins are produced by vertebrate animals as part of the normal immune response to microbial, e.g., bacterial or viral, infection.

Immune Factors & Inflamation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs231775	CTLA4	**Autoimmunity**	This gene encodes a protein which transmits an inhibitory signal to T cells. Mutations in this gene have been associated autoimmune diseases including: diabetes, Graves disease, thryoid problems, celiac disease, and lupus	**GG**	**A**
rs2858331	HLA	**Autoimmunity**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**GG**	**G**
rs11575839	HLA-C	**Autoimmunity**	Increases risk for autoimmunity/inflammation to toxins or infections. AG, AA can increase C4 levels.	**AA**	**--**
rs10484554	HLA-C/MHCI	**Autoimmunity**	Increases risk for autoimmunity/inflammation to toxins or infections. Each T allele=very significant increase in autoimmune disease risk.	**TT**	**T**
rs2187668	HLA-DQA1	**Autoimmunity**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**TT**	**C**
rs9275224	HLA-DQA2	**Autoimmunity**	Helps to recognise foreign particles when they enter our body and fight them away in an immune response.	**AA**	**A**
rs3135391	HLA-DRB1	**Autoimmunity**	Increases risk for autoimmunity/inflammation to toxins or infections. Each A allele=very significant increase in autoimmune disease risk.	**AA**	**G**
rs3135388	HLA-DRB5/HLA-DRB1/HLA-DRA/HLA-DQB1/ HLA-DQA1	**Autoimmunity**	Increases risk for autoimmunity/inflammation to toxins or infections. Each A allele=very significant increase in autoimmune disease risk.D3 is protective	**AA**	**G**
rs10181656	STAT4	**Autoimmunity**	The STAT4 protein is activated by cytokines, which are part of the inflammatory response to fight infection. It tells immune cells to get rid of foreign invaders in the cell (R).Mutations of this gene can cause arthritis, lupus, and other autoimmune disorders.The G allele has 1.7x risk for lupus compared to the other allele.	**GG**	**--**
rs6677604	CFH	**IgA**	C3, a protein coding gene, is part of a system of proteins that fight against disease.	**AA**	**G**
rs9271366	HLA	**IgA**	Its main function is to express the receptors on cells, especially T-cells (fighter white blood cells) which helps them recognize foreign particles when they enter our body and fight them away in an immune response.This gene helps to express receptors that can identify the dangerous particle or germ (pathogen) in the body and alert our immune system.	**GG**	**A**
rs1883414	HLA-DPB2	**IgA**		**AA**	**A**
rs9275224	HLA-DQA2	**IgA**	This gene encodes a protein that helps with peptide binding	**AA**	**A**

Immune Factors & Inflamation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1990760	IFIH1	**IgA**	This gene encodes a protein that is involved with RNA translation initiation, splicing, and assembly. It is also involved in the formation of embryos and sperm and cellular growth and division	**TT**	**C**
rs2280714	IRF5	**IgA**	IFN-regulatory factor 5 gene increases IFN-alpha. Interferon alpha induces the kynurenine pathway and is associated with depression because of NMDA overactivity.The C (minor) allele is associated with:Possible increased risk of depression when paired with STAT4 T allele. Increased levels of IFN-alpha protein.	**CC**	**T**
rs9275596	MTC03P1	**IgA**		**CC**	**--**
rs9357155	PSMB8 / TAP1 / TAP2	**IgA**		**AA**	**G**
rs2229765	IGF1R	**IgA, Insulin Growth Factor**	IGF1R encodes for insulin growth factor receptors; overexpression can stop cell death by enhancing cell survival and is present in malignant tissues. AA= lower levels of IGF-1 protein. Increased longevity in males 15% of people have AA. Most people have AG.	**AA**	**G**
rs2814778	ACKR1	**IgE**	rs2814778 is within the DARC gene, which encodes the Duffy blood group antigen [PMID 7663520]. This SNP shows an almost perfectly fixed difference in frequency between Europeans and those with African ancestry. (One exception appears to be a certain population of Czech gypsies, and certain non-Ashkenazi Jewish populations.) Additionally the Namibian San samples of the CEPH-HGDP are, uncharacteristically for Africans, all AA homozygotes for this SNP. The rs2814778 (G) allele is associated with African populations, while rs2814778 (A) is associated with European populations and southwestern Native American populations.	**CC**	**T**
rs2251746	FCER1A	**IgE**	This gene encodes a protein that initiates the body's allergic response. High levels of serum IgE are associated with allergies, and are mediators of autoimmune diseases.	**CC**	**C**
rs1800925	IL13	**IgE**	This gene encodes a cytokine that inhibits the production of pro-inflammatory cytokines and chemokines.This SNP is in the promoter region of the IL-13 gene, Asthma related.	**TT**	**--**
rs2040704	RAD50	**IgE**		**GG**	**A**
rs2240032	RAD50	**IgE**		**TT**	**--**
rs33977706	SOCS-1 -820G>T	**IgE**		**AA**	**--**

Immune Factors & Inflamation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1801274	FCGR2A	**IgG**	This gene encodes a protein that plays an important role in the immune system response by fighting off pathogens. It is associated with higher susceptibility to arthritis, lupus, and malaria.	**GG**	**A**
rs7483	GSTM3	**IgG**	GST-M3 activity is possibly involved in protection against mucosal atrophy caused by H. pylori as the levels of IgG titer and PGI are linked to mucosal status.	**TT**	**T**
rs1800871	IL10-819	**Inflammation**	A=decreased IL-10..susceptibility to IBD	**AA**	**G**
rs20541	IL13	**Inflammation**	rs20541 is a C/T polymorphism on the interleukin 13 gene IL13 associated with IgE levels	**AA**	**G**
rs1143643	IL1B	**Inflammation**	CC=Higher IL-1B, Less responsiveness to emotional stimuli.	**CC**	**--**
rs16944	IL1B 511	**Inflammation**	Each G=higher LPS induced IL-1B, more cortisol resistance.	**GG**	**A**
rs1801275	IL4R	**Inflammation**	Anti-inflamatory cytokines	**GG**	**A**
rs2069812	IL5	**Inflammation**	Anti-inflamatory cytokines	**GG**	**G**
rs2069837	IL6	**Inflammation**	A= higher L-6	**AA**	**A**
rs2069840	IL6	**Inflammation**	G= higher L-6	**GG**	**--**
rs1800795	IL6-174	**Inflammation**	G=Common, higher IL-6 (R).	**GG**	**G**
rs7529229	IL6R	**Inflammation**	CC= higher L-6	**CC**	**--**
rs1405655	LXR	**Inflammation**	LXR plays an anti-microbial role and protects against Tuberculosis. LXR decreases inflammation by inhibiting Nf-kB. LXR represses a set of inflammatory genes after activation by bacterial components or cytokines. Loss of LXR function compromised innate immunity in an animal model, which shows the importance of LXR for a normal functioning immune system.	**TT**	**T**

Immune Factors & Inflamation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs17373080	LXR	**Inflammation**	LXR plays an anti-microbial role and protects against Tuberculosis. LXR decreases inflammation by inhibiting Nf-kB. LXR represses a set of inflammatory genes after activation by bacterial components or cytokines. Loss of LXR function compromised innate immunity in an animal model, which shows the importance of LXR for a normal functioning immune system.	**GG**	**--**
rs2695121	LXR	**Inflammation**	LXR plays an anti-microbial role and protects against Tuberculosis. LXR decreases inflammation by inhibiting Nf-kB. LXR represses a set of inflammatory genes after activation by bacterial components or cytokines. Loss of LXR function compromised innate immunity in an animal model, which shows the importance of LXR for a normal functioning immune system.	**TT**	**--**
rs6503691	STAT3	**Inflammation**	CC=more STAT3 production in people.C is the more common allele. About 33% of the alleles in a population are T.Can increase Th1 and possibly Th17	**CC**	**C**
rs4833095	TLR1	**Inflammation**	Toll Like Receptors get activated mainly by bacterial, viral and fungal products. Some of our junk protein can also activate TLRs. Once activated, they start a cascade that will produce cytokines and other inflammatory mediators to combat the infection.	**GG**	**C**
rs361525	TNF -238	**Inflammation**	Tumor Necrosis Factor	**AA**	**G**
rs1800629	TNF -308	**Inflammation**	Tumor Necrosis Factor	**AA**	**G**
rs3761847	TRAF1	**Inflammation**	rs3761847, a SNP located between two genes associated with chronic inflammation (TRAF1 and C5), is associated with increased risk of anti CCP- positive rheumatoid arthritis.	**GG**	**A**
rs7975232	VDR Apal	**Inflammation**	Vitamin D Receptor, CC presumably results in better vitamin D receptor function in some way, given the associations involved.	**AA**	**--**
rs731236	VDR Taq	**Inflammation**	No difference in calcitriol/1,25(OH)(2)D level. AA=increased VDR in stimulated immune cells.AA genotype is associated with increased VDR expression	**AA**	**A**
rs854571	PON1	**Microbial defense**	PON1 protects against bacterial infection by destroying the bacterial signalling molecules that cause gram negative bacteria to invade human tissue and form colonies, thus PON1 contributes to the bodies innate immunity	**TT**	**C**
rs662	PON1 Q192R	**Microbial defense**	PON1 protects against bacterial infection by destroying the bacterial signalling molecules that cause gram negative bacteria to invade human tissue and form colonies, thus PON1 contributes to the bodies innate immunity	**TT**	**T**

Immune Factors & Inflamation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs6822844	4q27 Region			**TT**	**G**
rs429358	APOE		One C = Bad version = Less APOE4.CT: >3x increased risk for Alzheimer's; 1.4x increased risk for heart disease	**CC**	**--**
rs10210302	ATG16L1		rs10210302 has been reported in a large study to be associated with Crohn's disease.	**TT**	**T**
rs7216389	GSDMB		associated with susceptibility to childhood asthma in a study of ~1,000 British patients. The variation appears to be linked to altered levels of the ORMDL3 mRNA, which was shown in a cohort study of ~5,000 British and German patients to be correlated to childhood asthma	**CC**	**T**
rs7412	APOE				**C**

Methylation

Methylation & methionine/homocysteine pathways

Homocysteine is a naturally occurring amino acid produced as part of the body's methylation process. The level of homocysteine in the plasma is increasingly being recognised as a risk factor for disease and seen as a predictor of potential health problems such as cardiovascular disease and Alzheimer's. The complex metabolism of homocysteine within the body is highly dependent on vitamin derived cofactors, and deficiencies in vitamin B12, folic acid and vitamin B6 are associated with raised homocysteine levels. Other factors thought to raise levels are poor diet, poor lifestyle - especially smoking and high coffee and alcohol intake, some prescription drugs (such as proton pump inhibitors), diabetes, rheumatoid arthritis and poor thyroid function. Homocysteine levels can, in many cases, be normalised through diet and vitamin supplementation. The most important nutrients that help lower homocysteine levels are folate, the vitamins B12, B6 and B2, zinc and trimethylglycine (TMG).

Methylation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs17851582	GAMT	**Arginine**	Arginine to Guanidoacetate to Creatine (SAMe)	**AA**	**A**
rs55776826	GAMT	**Arginine**	Arginine to Guanidoacetate to Creatine (SAMe)	**TT**	**--**
rs4244593	PEMT	**CDP-choline pathway**	phosphatidylethanolamine to phosphatidylcholine	**TT**	**T**
rs7946	PEMT	**CDP-choline pathway**	phosphatidylethanolamine to phosphatidylcholine	**TT**	**T**
rs492602	FUT2	**Cobalamin**	B12 absorption	**GG**	**A**
rs602662	FUT2	**Cobalamin**	B12 absorption	**AA**	**G**
rs492602	FUT2 A12190G	**Cobalamin**	B12 absorption	**GG**	**A**
rs1047781	FUT2 A12404T	**Cobalamin**	B12 absorption	**TT**	**A**
rs1532268	MTRR	**Cobalamin**	Cobalamin II to Methylcobalamin	**TT**	**T**
rs1802059	MTRR - 11 A664A	**Cobalamin**	Cobalamin II to Methylcobalamin	**AA**	**A**
rs1801394	MTRR A66G	**Cobalamin**	Cobalamin II to Methylcobalamin	**GG**	**A**
rs162036	MTRR K350A	**Cobalamin**	Cobalamin II to Methylcobalamin	**GG**	**A**
rs526934	TCN1	**Cobalamin**	B12 transport	**GG**	**A**
rs1801198	TCN2	**Cobalamin**	B12 transport	**GG**	**G**
rs9606756	TCN2	**Cobalamin**	B12 transport	**GG**	**A**
rs1643659	DHFR	**Folate**	FOLR2 to DHF, DHF to THF	**CC**	**--**

Methylation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1650697	DHFR	**Folate**	FOLR2 to DHF, DHF to THF	**AA**	**G**
rs1677693	DHFR	**Folate**	FOLR2 to DHF, DHF to THF	**TT**	**--**
rs2071010	FOLR1	**Folate**	Dietary folates to DHF	**AA**	**A**
rs651933	FOLR2	**Folate**	Dietary folates to DHF	**GG**	**A**
rs7925545	FOLR3	**Folate**	Dietary folates to DHF	**GG**	**A**
rs3780126	GGH	**Folate**	Metabolism of folic acid andin the pharmacology of many antifolate drugs.	**AA**	**A**
rs3780127	GGH	**Folate**	Metabolism of folic acid andin the pharmacology of many antifolate drugs.	**AA**	**G**
rs4617146	GGH	**Folate**	Metabolism of folic acid andin the pharmacology of many antifolate drugs.	**TT**	**C**
rs2236225	MTHFD1	**Folate**	THF to Purines (ATP & GTP) & 10-Formyl-THF to 5,10 Methenyl THF to 5,10 Methylene THF	**AA**	**A**
rs1801131	MTHFR A1298C	**Folate**	5,10 Methylene THF to 5-MTHF	**GG**	**T**
rs1801133	MTHFR C677T	**Folate**	5,10 Methylene THF to 5-MTHF	**AA**	**G**
rs2733103	MTHFS	**Folate**	Helps regulate carbon flow through the folate- dependent one-carbonmetabolic network that supplies carbon for the biosynthesis of purines, thymidine, and amino acids.	**TT**	**T**
rs6495446	ST20	**Folate**	Helps regulate carbon flow through the folate- dependent one-carbonmetabolic network that supplies carbon for the biosynthesis of purines, thymidine, and amino acids.	**TT**	**T**
rs6495446	ST20	**Folate**	Helps regulate carbon flow through the folate- dependent one-carbonmetabolic network that supplies carbon for the biosynthesis of purines, thymidine, and amino acids.	**TT**	**T**
rs10925235	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**TT**	**--**
rs10925257	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**GG**	**A**

Methylation

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs11799670	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**GG**	**A**
rs1805087	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**GG**	**A**
rs2275565	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**TT**	**T**
rs2275568	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**TT**	**C**
rs2789352	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**AA**	**A**
rs3820571	MTR	**Folate, Cobalamin, Methionine**	5-MTHF to THF, Homocysteine to Methionine, Methylcobalamin to Cobalamin I (Zn)	**GG**	**T**
rs3733890	BHMT	**Methionine**	Homocysteine to Methionine shortcut	**AA**	**G**
rs567754	BHMT-02	**Methionine**	Homocysteine to Methionine shortcut	**TT**	**T**
rs2851391	CBS	**Methionine**	Homocysteine to Cystathionine	**TT**	**T**
rs4920037	CBS	**Methionine**	Homocysteine to Cystathionine	**AA**	**G**
rs234706	CBS C699T	**Methionine**	Homocysteine to Cystathionine	**AA**	**G**

Mitochondrial Function

Mitochondrial Function

Mitochondrial DNA contains 37 genes, all of which are essential for normal mitochondrial function. Thirteen of these genes provide instructions for making enzymes involved in oxidative phosphorylation. Oxidative phosphorylation is a process that uses oxygen and simple sugars to create adenosine triphosphate (ATP), the cell's main energy source. The remaining genes provide instructions for making molecules called transfer RNA (tRNA) and ribosomal RNA (rRNA), which are chemical cousins of DNA. These types of RNA help assemble protein building blocks (amino acids) into functioning proteins. The following conditions are associated with changes in the structure of mitochondrial DNA. Age-related hearing loss, Cancers, Cyclic vomiting syndrome, Cytochrome c oxidase deficiency, Kearns-Sayre syndrome, Leber hereditary optic neuropathy, Leigh syndrome, Maternally inherited diabetes and deafness, Mitochondrial complex III deficiency, Mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes, Myoclonic epilepsy with ragged-red fibers, Neuropathy, ataxia, and retinitis pigmentosa, Nonsyndromic hearing loss, Pearson marrow-pancreas syndrome, Progressive external ophthalmoplegia.

Mitochondrial Function

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs7134594	MMAB	**Cobalamin**	Conversion of vitamin B-12 into adenosylcobalamin	**CC**	**T**
rs1532268	MTRR	**Cobalamin**	Contribution of B12 to Krebs Cycle	**TT**	**T**
rs1802059	MTRR -11 A664A	**Cobalamin**	Contribution of B12 to Krebs Cycle	**AA**	**A**
rs1801394	MTRR A66G	**Cobalamin**	Contribution of B12 to Krebs Cycle	**GG**	**A**
rs162036	MTRR K350A	**Cobalamin**	Contribution of B12 to Krebs Cycle	**GG**	**A**
rs4147730	NDUFS3	**Complex I**	Electron Transport Chain, ATP Production	**AA**	**--**
rs1142530	NDUFS7	**Complex I**	Electron Transport Chain, ATP Production	**TT**	**T**
rs809359	NDUFS7	**Complex I**	Electron Transport Chain, ATP Production	**GG**	**--**
rs2075626	NDUFS8	**Complex I**	Electron Transport Chain, ATP Production	**CC**	**T**
rs3741049	ACAT1 G22670A	**Krebs Cycle**	Converts 2-methyl-acetoacetyl-CoA into propionyl-CoA and acetyl-CoA.	**AA**	**A**
rs4244593	PEMT	**Membranes permeability**	phosphatidylethanolamine to phosphatidylcholine	**TT**	**T**
rs7946	PEMT	**Membranes permeability**	phosphatidylethanolamine to phosphatidylcholine	**TT**	**T**
rs2293054	NOS1		nNOS (Brain)	**AA**	**G**
rs7298903	NOS1		nNOS (Brain)	**CC**	**--**
rs2248814	NOS2		iNOS, a reactive free radical	**AA**	**--**
rs2274894	NOS2		iNOS, a reactive free radical	**TT**	**--**

Mitochondrial Function

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1800779	NOS3		eNOS	**GG**	**A**
rs1800783	NOS3		eNOS	**AA**	**--**
rs2970869	PGC-1a		PGC-1? makes new mitochondria and improves its function. PGC-1a increases fatty acid burning by increasing the carnitine genes CPT1A.	**TT**	**--**
rs2970869	PGC-1a		PGC-1? makes new mitochondria and improves its function. PGC-1? makes new mitochondria and improves its function. PGC-1a increases fatty acid burning by increasing the carnitine genes CPT1A. Carriers of the T allele had significantly more DNA damage than CC	**TT**	**--**
rs3774923	PGC-1a		PGC-1? makes new mitochondria and improves its function. PGC-1a increases fatty acid burning by increasing the carnitine genes CPT1A.	**TT**	**C**
rs8192678	PGC-1a Gly482Ser		PGC-1? makes new mitochondria and improves its function. PGC-1a increases fatty acid burning by increasing the carnitine genes CPT1A. T is the less common allele (codes for serine). This variant causes a lower level of PGC-1a protein including in muscles The T allele results a less efficient coactivator of transcription factors, including those that regulate the PPARGC1A gene itself	**TT**	**C**

Neurotransmitters

Neurotransmitter Pathway: Serotonin & Dopamine

Dopamine and serotonin are both neurotransmitters. They are chemicals that are released from the nerve cells and serve to transfer impulses from nerve cells to other body tissues like other nerve cells, muscles, and organs. These chemicals are very important in sensory perceptions and motoric action-reaction mechanisms.

Dopamine plays an important role in controlling motor behavior, the emotional reward, and behavior motivation mechanisms. It regulates emotional responses, hormone secretion, and motoric actions related to reward sensations.

Serotonin regulates the functioning of the cardiovascular and endocrine systems and has an important role in regulating appetite, sleep, memory, mood, body temperature, and muscle contraction. Genetic variants can influence transporter function by various mechanisms, including substrate affinities, transport velocity, transporter expression levels (density), extracellular membrane expression, trafficking and turnover, and neurotransmitter release.

Neurotransmitters

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1643659	DHFR	Biopterin	Biopterin Recycling	CC	--
rs1650697	DHFR	Biopterin	Biopterin Recycling	AA	G
rs1677693	DHFR	Biopterin	Biopterin Recycling	TT	--
rs3783637	GCH1	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	TT	C
rs3783641	GCH1	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	AA	T
rs3783642	GCH1	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	CC	T
rs4411417	GCH1	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	CC	--
rs752688	GCH1	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	TT	--
rs8007267	GCH1 C36378991T	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	TT	C
rs10483639	GCH1 G55306457C	Biopterin	Tetrahydrobiopterin (BH4) biosynthesis.	CC	G
rs2293054	NOS1	Biopterin	Biopterin Recycling	AA	G
rs7298903	NOS1	Biopterin	Biopterin Recycling	CC	--
rs2248814	NOS2	Biopterin	Biopterin Recycling	AA	--
rs2274894	NOS2	Biopterin	Biopterin Recycling	TT	--
rs1800779	NOS3	Biopterin	Biopterin Recycling	GG	A
rs1800783	NOS3	Biopterin	Biopterin Recycling	AA	--

Neurotransmitters

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs5030858	PAH	**Biopterin**	Phenylalanine to Tyrosine	**AA**	**G**
rs2070762	TH	**Biopterin**	Tyrosine to L-Dopa	**GG**	**G**
rs6356	TH	**Biopterin**	Tyrosine to L-Dopa	**TT**	**T**
rs11178997	TPH2	**Biopterin**	A=lower production of TPH2 and therefore less serotonin	**AA**	**--**
rs4565946	TPH2	**Biopterin**	Each copy of the common G allele was associated with a increase in the number of psychosomatic symptoms.GG=2.58X increased risk for early onset OCDNo association with risk for bipolar disorder or suicidal behavior or autism Association with ADHD	**GG**	**T**
rs4570625	TPH2 G-703T	**Biopterin**	Tryptophan to 5-HTP, GG=Lower serotonin, more anxiety.	**GG**	**G**
rs2238151	ALDH2	**Catecholamine aldehyde**	Stress Hormones metabolism (Noradrenaline), Serotonin & 5-HIA metabolism (NAD, B1)	**TT**	**C**
rs671	ALDH2	**Catecholamine aldehyde**	Stress Hormones metabolism (Noradrenaline), Serotonin & 5-HIA metabolism (NAD, B1)	**AA**	**G**
rs72547566	ALDH3A2	**Catecholamine aldehyde**	Adrenaline metabolism (NAD,B1)	**TT**	**--**
rs4633	COMT H62H	**Catecholamines**	Methylation (deactivation) of Dopamine, Adrenaline	**TT**	**C**
rs4680	COMT V158M	**Catecholamines**	Methylation (deactivation) of Dopamine, Adrenaline	**AA**	**G**
rs1108580	DBH	**Catecholamines**	GG = Increased levels of DBH proteinGG = Lower Dopamine, higher norepinephrine.GG= Increased risk of having Parkinsons DiseaseGG = Increased risk of alcoholism GG = Methamphetamine psychosis, with more than a 2x greater chance of relapsing after going through complete remission. GG = Faster dependence on alcoholAA = Decreased levels of DBH proteinAA = Higher Dopamine, lower norepinephrine.AA = Slightly increased the risk of Schizophrenia.AA = Hyperactive and oppositional characteristic traits. AA = More accurate and speedier decision making when incorrect advice is given.AA = some association with ADHD in males.	**GG**	**A**

Neurotransmitters

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1611115	DBH	**Catecholamines**	Decreased levels of Dopamine-beta-Hydroxylase (T).Normal levels of Dopamine-beta-Hydroxylase (C).The Minor "T" allele is associated with:Higher dopamine and lower norepinephrine because of lower DBH (Dopamine-beta-hydroxylase), which converts dopamine to norepinephrine (T) .More neuroticism (TT).More novelty seeking (TT).More impulsivity (TT) .More aggression (TT) Increased risk of adult ADHD (TT) Lower conscientiousness (TT)	**TT**	**T**
rs1799836	MAOB	**Catecholamines**	Oxidation (deactivation)Dopamine, Adrenaline, Noradrenaline (less Serotonin). T= upregulation.	**TT**	**T**
rs10994336	ANK3	**Dopamine**	Density of the DRD2 receptor.	**TT**	**C**
rs9804190	ANK3	**Dopamine**	Density of the DRD2 receptor.	**TT**	**C**
rs265981	DRD1	**Dopamine**	Dopamine Receptor	**AA**	**A**
rs4532	DRD1	**Dopamine**	Dopamine Receptor	**CC**	**C**
rs686	DRD1	**Dopamine**	Dopamine Receptor	**GG**	**G**
rs1079596	DRD2	**Dopamine**	Dopamine Receptor	**TT**	**C**
rs1079597	DRD2	**Dopamine**	Dopamine Receptor	**TT**	**C**
rs1079727	DRD2	**Dopamine**	Dopamine Receptor	**CC**	**--**
rs1125394	DRD2	**Dopamine**	Dopamine Receptor	**CC**	**--**
rs2283265	DRD2	**Dopamine**	Dopamine Receptor	**AA**	**--**
rs4436578	DRD2	**Dopamine**	Dopamine Receptor	**CC**	**--**
rs4648317	DRD2	**Dopamine**	Dopamine Receptor	**AA**	**G**

Neurotransmitters

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1800497	DRD2 (MAIN)	**Dopamine**	AA = Less dopamine D2 receptors = lower functioning of dopamine [R].A = decreased level of dopamine D2 receptors = lower level of dopamine [R]G = normal dopamine D2 receptor density = normal level of dopamine	**AA**	**G**
rs6277	DRD2 (MAIN)	**Dopamine**	Dopamine Receptor. AA=decreased dopamine signaling.	**AA**	**--**
rs1799978	DRD2 A4651G	**Dopamine**	Dopamine Receptor	**CC**	**T**
rs2242592	DRD2 C71572T	**Dopamine**	Dopamine Receptor	**GG**	**G**
rs12364283	DRD2 T4047C	**Dopamine**	Dopamine Receptor	**GG**	**A**
rs167771	DRD3	**Dopamine**	Dopamine Receptor	**GG**	**A**
rs6280	DRD3	**Dopamine**	Dopamine Receptor	**CC**	**T**
rs1018381	DTNBP1	**Dopamine**	Synaptic vesicle trafficking, neurotransmitter release.Role in regulation of cell surface exposure of Dopamine Receptor 2	**AA**	**--**
rs27072	SLC6A3 G56022A	**Dopamine**	Dopamine Transport, Dopamine Reuptake via DAT is the primary mechanismthrough which dopamine is cleared from synapses.	**CC**	**T**
rs279836	GABRA2	**GABA**	GABA receptor. AA=Higher stress response	**AA**	**A**
rs3219151	GABRA6	**GABA**	GABA receptor. TT=higher cortisol, CT=Intermediate	**TT**	**T**
rs2241165	GAD1	**Glutamate, GABA**	Conversion of excitatory Glutamate to calming GABA.	**CC**	**T**
rs3749034	GAD1	**Glutamate, GABA**	Conversion of excitatory Glutamate to calming GABA.	**AA**	**G**
rs3791878	GAD1	**Glutamate, GABA**	Conversion of excitatory Glutamate to calming GABA.	**TT**	**--**
rs3828275	GAD1	**Glutamate, GABA**	Conversion of excitatory Glutamate to calming GABA.	**TT**	**T**
rs6994992	NRG1	**Glutamate, GABA**	Neuregulin 1 is important for synaptic plasticity, GABAergic function within the amygdala (to shut down anxiety). TT= Increased risk of Psychosis	**TT**	**T**

Neurotransmitters

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs1049793	ABP1/DAO C1933G	**Histamine, Serine, Dopamine**	D-serine neuromodulator in the brain, contribution to dopamine synthesis (via D-dopa)	**GG**	**--**
rs3741775	DAO	**Histamine, Serine, Dopamine**	D-serine neuromodulator in the brain, contribution to dopamine synthesis (via D-dopa)	**CC**	**--**
rs3918347	DAO	**Histamine, Serine, Dopamine**	D-serine neuromodulator in the brain, contribution to dopamine synthesis (via D-dopa)	**GG**	**A**
rs4244593	PEMT	**Methylation**	SAMe (cofactor also for COMT, PNMT) needed here first for cell membrane integrity.	**TT**	**T**
rs7946	PEMT	**Methylation**	SAMe (cofactor also for COMT, PNMT) needed here first for cell membrane integrity.	**TT**	**T**
rs3785143	SLC6A2	**Noradrenaline**	Noradrenaline Transporter, reuptake of noradrenaline	**TT**	**--**
rs3785152	SLC6A2	**Noradrenaline**	Noradrenaline Transporter, reuptake of noradrenaline	**TT**	**C**
rs40147	SLC6A2	**Noradrenaline**	Noradrenaline Transporter, reuptake of noradrenaline	**AA**	**A**
rs2242446	SLC6A2 C5884T	**Noradrenaline**	Noradrenaline Transporter, reuptake of noradrenaline	**CC**	**T**
rs11077820	AANAT	**Serotonin**	Serotonin to Melatonin (B5)	**CC**	**T**
rs1451375	DDC	**Serotonin**	Serotonin Synthesis	**AA**	**A**
rs2167364	DDC	**Serotonin**	Serotonin Synthesis	**CC**	**T**
rs7997012	HTR2A	**Serotonin**	Post-synaptic Serotonin receptor	**AA**	**A**
rs6323	MAO A R297R	**Serotonin**	Oxidation (deactivation) Serotonin, Dopamine, Adrenaline, Noradrenaline.	**GG**	**T**
rs1137070	MAOA	**Serotonin**	Oxidation (deactivation) Serotonin, Dopamine, Adrenaline, Noradrenaline.	**TT**	**C**
rs216013	CACNA1C		Mediate the entry of calcium ions intoexcitable cells and are also involved in a variety of calcium-dependent processes.	**GG**	**A**

Neurotransmitters

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs2302729	CACNA1C		Mediate the entry of calcium ions intoexcitable cells and are also involved in a variety of calcium-dependent processes.	**TT**	**T**
rs1006737	CACNA1C or SLC36A3		Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved in a variety of calcium-dependent processes, including muscle contraction, hormone or neurotransmitter release, gene expression, cell motility, cell division and cell death. The isoform alpha-1C gives rise to L-type calcium currents. Long-lasting (L-type) calcium channels belong to the 'high-voltage activated' (HVA) group. They are blocked by dihydropyridines (DHP), phenylalkylamines, benzothiazepines, and by omega-agatoxin-IIIA (omega-Aga-IIIA). They are however insensitive to omega-conotoxin-GVIA (omega-CTx-GVIA) and omega-agatoxin-IVA (omega-Aga-IVA). Calcium channels containing the alpha-1C subunit play an important role in excitation-contraction coupling in the heart. The various isoforms display marked differences in the sensitivity to DHP compounds. Binding of calmodulin or CABP1 at the same regulatory sites results in an opposit effects on the channel function.	**AA**	**A**
rs2007044	CACNA1C				**A**

Trans-sulfuration

Trans-sulfuration pathway

The trans-sulfuration pathway is a metabolic pathway where transfer of sulfur from homocysteine to cysteine occurs. The pathway leads to the generation of several sulfur metabolites, which include cysteine, GSH and the gaseous signaling molecule hydrogen sulfide (H 2 S). Precise control of this pathway is critical for maintenance of optimal cellular function and, therefore, the key enzymes of the pathway, cystathionine β-synthase and cystathionine γ-lyase, are regulated at multiple levels. Disruption of the trans-sulfuration pathway contributes to the pathology of several conditions such as vascular dysfunction, Huntington's disease.

Trans-sulfuration

SNP RSID	GENE & VARIANT	PATHWAY	VARIANT MEANING	RISK ALLELE	GENOTYPE
rs2851391	CBS		It is responsible for using vitamin B6 to convert amino acids called homocysteine and serine to a molecule called cytathionine. Another enzyme converts cystathionine to cysteine, which is used to build proteins or is broken down and excreted in urine	**TT**	**T**
rs4920037	CBS		It is responsible for using vitamin B6 to convert amino acids called homocysteine and serine to a molecule called cytathionine. Another enzyme converts cystathionine to cysteine, which is used to build proteins or is broken down and excreted in urine.	**AA**	**G**
rs234706	CBS C699T		AA=Increased responsiveness to homocysteine- lowering effects of folic acid. Limits homocysteine into downstream path. People with CBS mutations will need to be careful with sulfur containing supplements. Increased risk for ammonia detoxification issues.	**AA**	**G**

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This report is intended to translate your results into an easier to understand form. It is not intended to diagnose or treat. For diagnosis or treatment, please present this to your doctor Additionally, genetic mutations are flags that something could be wrong and not a guarantee that you are having all or any of the associated issues. Other factors like environment, ethnic background, diet, age, personal history, etc all have a factor in whether a mutation starts to present itself or not and when.