Variant Report

DETOX

Gene & Variation	rsID #	Risk Allele	Your Alleles & Results	Notes
GPX3	rs81772	C	TC	-/+ Glutathione peroxidase 3 gene polymorphisms and risk of differentiated thyroid cancer.
GSTP I105V	rs1695	G	AG	-/+ Influences asthma risk; the (A) allele encodes the Ile, while the (G) allele encodes the Val. This SNP is also known as GSTP1Val105, or GSTP1 Ile105Val.
PON1 Q192R	rs662	C	TC	-/+ It codes for amino acid 192 of the paraoxonase (PON) protein. Variants of this SNP affect PON catalytic efficiency and are correlated with Heart disease and trait-anxiety scores.
IRF6	rs987525	A	AC	+/- A genome-wide association study involving 224 cases and 383 controls of Central European origin found that significant association between **rs987525** and risk for nonsyndromic cleft lip with or without cleft palate.
HLA	rs7775228	C	TC	-/+ Associated with increased risk for osteoarthritis among Japanese, but not Europeans, with an odds ratio of 1.34 (CI: 1.21-1.49, combined p = 2.43×10e?8).
FCER1A	rs2427837	A	AG	+/- Gene encoding the alpha chain of the high affinity receptor for IgE (FCER1A) on chromosome 1q23. High levels of serum IgE are associated with allergies, and are mediators of autoimmune diseases.

C3	rs366510	G	TG	-/+ Variants in the gene encoding C3 are associated with asthma and related phenotypes among African Caribbean families.
FCER1A / OR10J2P	rs2494262	A	AC	+/- FcepsilonRIalpha gene -18483A>C polymorphism affects transcriptional activity through YY1 binding .
FCGR2A	rs1801274	A	AG	+/- SNP in the Fc fragment of IgG, low affinity IIa, receptor (CD32) FCGR2A gene. **rs1801274**(C) encodes the arginine (R) allele, with the (T) allele encoding the variant histidine (H). The (H) isoform is considered high-binding to IgG2 and IgG3, while the (R) isoform is considered low-binding. This SNP is known in the literature by many names, including A519C and H131R.
TNFRSF13B	rs4792800	G	AG	-/+ Associated with IgG level in a healthy Chinese male population.
CYP4V2	rs13146272	C	AC	-/+ Gene variants associated with deep vein thrombosis.
ITGB3 T196C	rs5918	C	TC	-/+ implicated as increasing the risk of myocardial infarctions, heart disease, and resistance to blood-thinning benefits of aspirin.
NR1I2	rs1523127	C	AC	-/+ Polymorphisms in NFkB, PXR, LXR and risk of colorectal cancer in a prospective study of Danes. Gene variants associated with deep vein thrombosis.
F11	rs2289252	T	TC	+/- Genetic variants associated with deep vein thrombosis.
F10 113777509	rs3211719	G	AG	-/+ have been found to cause a rare bleeding disorder called factor X deficiency. This disorder commonly causes nosebleeds, easy bruising, bleeding under the skin, bleeding of the gums, blood in the urine (hematuria), and prolonged or excessive bleeding following surgery or trauma.

BHMT	rs16876512	T	TC	+/- Betaine-homocysteine methyltransferase: human liver genotype-phenotype correlation.
BHMT R239Q	rs3733890	A	AG	+/- Variant BHMT allele may increase risk for neural tube defects, apparently only in folate rich environments, and possibly in conjunction with rs1801133.
CBS A13637G	rs2851391	T	TC	+/- 118 SNPs of folate-related genes and risks of spina bifida and conotruncal heart defects.
CBS C19150T	rs4920037	A	AG	+/- New evidence for the role of cystathionine beta-synthase in non-syndromic cleft lip with or without cleft palate.
CBS C699T	rs234706	A	AG	+/- Being investigated in Ehlers-Danlos syndrome.
DAO	rs2070586	A	AG	+/- Sex-different association of DAO with schizophrenia in Koreans.
DAO	rs2111902	G	TG	-/+ The Association of Schizophrenia Risk D-Amino Acid Oxidase Polymorphisms With Sensorimotor Gating, Working Memory and Personality in Healthy Males.
GAD1	rs2241165	C	TC	-/+ Association between glutamic acid decarboxylase genes and anxiety disorders, major depression, and neuroticism
MAO A R297R	rs6323	T	TG	+/- Monoamine oxidase A degrades serotonin, dopamine, epinephrine, and norepinephrine. The G allele encodes for the higher activity form of the enzyme.
MTHFD1L	rs17349743	C	TC	-/+ Dementia revealed: novel chromosome 6 locus for late-onset Alzheimer disease provides genetic evidence for folate-pathway abnormalities.

MTHFD1L	rs803422	A	AG	+/- Dementia revealed: novel chromosome 6 locus for late-onset Alzheimer disease provides genetic evidence for folate-pathway abnormalities.
MTHFR C677T	rs1801133	A	AG	+/- regulatory enzyme in the metabolism of folate. It also refers to a specific gene that plays a major role in the body's methylation process.
MTHFS	rs6495446	C	TC	-/+ an intronic SNP in the MTHFS gene, is associated with increased risk for chronic kidney disease
MTRR A66G	rs1801394	G	AG	-/+ The protein encoded by an **rs1801394** allele has a lower affinity for MTR ([PMID 12416982]) and is inconsistently associated with homocysteine level, although it is a risk factor for neural tube defects ([PMID 10444342]) and Down syndrome ([PMID 10930360]) in conditions of higher homocysteine
MTRR	rs162049	G	AG	-/+ Genetic polymorphisms in folate and alcohol metabolism and breast cancer risk: a case-control study in Thai women.
MTRR	rs3776467	G	AG	-/+ Sex-specific association of sequence variants in CBS and MTRR with risk for promoter hypermethylation in the lung epithelium of smokers
NOS2	rs2297518	A	AG	+/- Gastric cancer is associated with NOS2 -954G/C polymorphism and environmental factors in a Brazilian population.
PEMT	rs4244593	T	TG	+/- Polymorphic variants of folate and choline metabolism genes and the risk of endometriosis-associated infertility.
SHMT1	rs9909104	C	TC	-/+ 829 Caucasian cases with primary epithelial ovarian cancer and 941 frequency-matched unaffected controls.

TCN1	rs526934	G	AG	-/+ Associated with lower serum Vitamin B12. "The TCN1 rs526934 G variant may reduce transport of cobalamin, resulting in lower plasma vitamin B12 levels
VDR Bsm	rs1544410	T	TC	+/- rs1544410, also known as the BsmI polymorphism, is a SNP in the Vitamin D receptor (VDR). Multiple studies examining bone mineral density (BMD) in women have associated the A allele with increased risk of low BMD
CTLA4	rs231775	G	AG	-/+ **rs231775**, also known as +49A/G, is a SNP in the CTLA4 gene. which is linked to Hashimoto thyroiditis. In a meta-analysis of CTLA4 gene SNPs, **rs231775** was most associated with vitiligo; however, the association seems to hold only in the subgroup of patients with other autoimmune diseases.
ATP5c1	rs12770829	T	TC	+/- Unavailable
NDUFS7	rs7254913	G	AG	-/+ Homozygous for NDUFS7 rs7254913 and significantly cause mitochondrial damage.
NDUFS7	rs1142530	T	TC	+/- Can significantly impact mitochondrial function.
NDUFS7	rs11666067	A	AC	+/- Defects in NDUFS7 are a cause of complex I mitochondrial respiratory chain deficiency.
NDUFS7	rs2074895	A	AC	+/- Cause mitochondrial damage.
NDUFS8	rs1104739	C	AC	-/+ Unavailable.
SULT2A1	rs296366	T	TC	+/- Unavailable.
SULT2A1	rs4149449	T	TC	+/- Unavailable.

SULT2A1	rs4149448	G	AG	-/+ Unavailable.