Variant Report

DETOX

Gene & Variation	rsID #	Risk Allele	Your Alleles & Results	Notes
NAT2 T341C (I114T)	rs1801280	C	CC	+/+ N-acetylation polymorphism is determined by a low or high NAT activity in liver, it has been implicated in the action and toxicity of amine-containing drugs, and in the susceptibility to bladder cancer and systemic lupus erythematosus.
TRAF1	rs3761847	G	GG	+/+ **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.
CETP	rs1800775	C	CC	+/+ Associated with increased risk, and**rs1800775**(A) with reduced risk of recurrent venous thromboembolism.
KNG I598T	rs2731672	T	TT	+/+ KNG1 Ile581Thr and susceptibility to venous thrombosis.
F12	rs1801020	A	AA	+/+ Affects heart disease risk for both men and women.
FOLR2	rs651933	A	AA	+/+ Unavailable.

FUT2	rs492602	G	GG	+/+ Between **rs492602** in theFUT2 gene and plasma vitamin B(12) levels in a genome-wide scan (n = 1,658) and an independent replication sample (n = 1,059) from the Nurses' Health Study. Women homozygous for the **rs492602**(C) allele (in dbSNP orientation) had higher B(12) levels.
FUT2	rs602662	A	AA	+/+ Genome-wide significant predictors of metabolites in the one-carbon metabolism pathway.
PEMT	rs7946	C	CC	+/+ Caucasians with nonalcoholic fatty liver are more likely to carry the **rs7946** (A), with the effect being most pronounced for rs7946(A;A) genotypes.
SLC19A1	rs1888530	T	TT	+/+ Association of folate receptor (folr1, folr2, folr3) and reduced folate carrier (slc19a1) genes with meningomyelocele.
SLC19A1	rs3788200	A	AA	+/+ Association of folate receptor (folr1, folr2, folr3) and reduced folate carrier (slc19a1) genes with meningomyelocele.
GSDMB	rs7216389	T	TT	+/+ 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.
IL5	rs2069812	A	AA	+/+ Identification of a haplotype block in the 5q31 cytokine gene cluster associated with the susceptibility to severe malaria.