Supplemental Fig 1 MAF distribution of GWAS and imputed SNPs from the entire imputation region (+/- 200 kb flanking the gene sequence) for all six candidate genes. The poor representation of MAF values < 0.05 for the GWAS data was expected because the GWAS platform was designed to query MAF values of 0.05 or greater.

Supplemental Table 1. Number of tag SNPs from the original study that were either genotyped on the GWAS platform or imputed.

Gene	tSNPs	GWAS SNPs	HapMap imputed SNPs	"1000 Genomes" imputed SNPs
GLDC	76	29	35	45
AMT	2	0	2	2
DLD	12	3	8	9
GCSH	15	4	10	11
SHMT1	19	4	10	14
SHMT2	7	2	0	5
Total	131	42	65	86

Supplemental Table 2. MAF distributions for all SNPs within the six genes that were previously genotyped as a tag SNP and were either on the GWAS panel or were imputed.

MAF	GWAS	imputed HapMap	imputed "1000 Genomes"	tag SNPs
> 0.01 and <=0.05	0	1	3	3
> 0.05 and <=0.1	2	5	6	8
> 0.1 and <=0.25	16	18	26	42
> 0.25 and <=0.5	24	41	51	78
Total	42	65	86	131