Supplemental Table 2. Power calculation. Study power for the replication cohort of 4,789 individuals (2,228 cases / 2,561 controls) as a function of disease allele frequency and genotype relative risk. The power was calculated in reference to a protective allele; the range of allelic frequencies and effects was based on the results of the original GWAS. Assumptions include: disease prevalence of 1%, log-additive model, no heterogeneity, and alpha = 0.01 (Bonferroni-adjusted considering five independent loci tested).

	Relative Risk (Additive Model)			
Disease Allele Frequency	**0.50**	**0.60**	**0.70**	**0.80**
0.10	100%	100%	98.9%	70.7%
0.20	100%	100%	100%	94.8%
0.30	100%	100%	100%	98.9%
0.40	100%	100%	100%	99.6%
0.50	100%	100%	100%	99.8%