SUPPLEMENTAL MATERIAL
Diabetes Metabolic Syndrome and Obesity: Targets and Therapy

Associations of GWAS-supported non-MHC genes with autoimmune thyroiditis in patients with type 1 diabetes

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Supplementary Table 1 Information of the five selected SNPs

SNP	Chromosome	Position	Gene	Allele	MAF (CHS)	P^a
rs1111695	1	114243899	*PHTF1*	C/A	0.133	0.636
rs1217407	1	114393748	*PTPN22*	A/G	0.362	0.231
rs2153977	1	114080071	*MAGI3*	T/C	0.324	0.774
rs2358994	1	114429461	*BCL2L15*	A/G	0.357	0.452
rs7679475	4	122314040	*QRFPR*	A/G	0.352	0.263

SNP, single nucleotide polymorphism; MAF, minor allele frequency; CHS, Southern Han Chinese

[a] *P* value for Hardy-Weinberg equilibrium

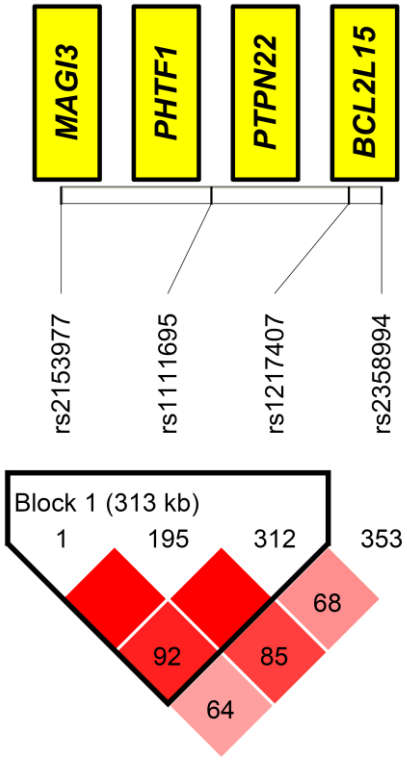
Supplementary Table 2 Haplotype frequencies of the chromosome 1p13 block in T1D patients with and without AITD

Haplotype[a]	Cases with AITD	Controls	OR (95%CI)	*P*[b]
rs1111695-rs1217407-rs2153977				
C-A-T	52.82%	56.12%	1	
C-G-C	21.12%	19.03%	1.07 (0.71 - 1.60)	0.761
A-G-C	14.41%	17.09%	0.82 (0.53 - 1.27)	0.380
C-G-T	6.87%	5.36%	1.08 (0.55 - 2.09)	0.833
C-A-C	3.47%	1.46%	2.69 (0.96 - 7.59)	0.062
A-G-T	1.32%	0.94%	0.53 (0.11 - 2.49)	0.421

T1D, type 1 diabetes; AITD, autoimmune thyroid diseases

[a] Haplotypes were reconstructed by the EM algorithm. Haplotypes with frequencies < 0.01 were excluded

[b] Adjusted for age, sex, BMI, proportion of late-onset T1D, fasting C-peptide, GADA positivity, LDL-C, and HDL-C



Supplementary Figure 1 Linkage disequilibrium(LD) plot among the five selected SNPs of non-MHC genes based on the 1000 Genome CHS (Southern Han Chinese) data. The depth of red color represents the magnitude of D'. Adapted from the Haploview program.