Supplemental Table 1: Association between Non-HLA T1D Candidate SNPs and Development of IA, Progression from IA to T1D, and Development of T1D Unadjusted for HLA-DR3/4,DQB1*0302 and First Degree Relative with T1D.

	Development of IA (n = 1619)		Progression from IA to T1D (n = 132)		Development of T1D (n = 1619)	
SNP	HR and 95% CI	*P* Value	HR and 95% CI[a]	*P* Value	HR and 95% CI	*P* Value
C1QTNF6 (rs229541)	**1.55 (1.18, 2.02)[b]**	**0.001**	1.25 (0.86, 1.83)[b]	0.25	**1.94 (1.33, 2.84)[b]**	**0.001**
C6orf173 (rs9388489)	1.16 (0.88, 1.52)[b]	0.29	0.93 (0.68, 1.27)[b]	0.66	1.05 (0.70, 1.56)[b]	0.83
C14orf181 (rs1465788)	1.00 (0.77, 1.31)[b]	0.98	1.04 (0.59, 1.84)[c]	0.89	0.79 (0.46, 1.39)[c]	0.42
IL2 (rs2069762)	1.06 (0.80, 1.40)[b]	0.69	1.33 (0.88, 2.00)[b]	0.18	1.19 (0.78, 1.81)[b]	0.42
IL2 (rs4505848)	1.02 (0.79, 1.32)[b]	0.88	0.93 (0.66, 1.30)[b]	0.66	1.16 (0.80, 1.68)[b]	0.43
IL2RA (rs12722563)	0.83 (0.53, 1.30)[c]	0.41	0.63 (0.23, 1.72)[c]	0.37	**0.37 (0.15, 0.92)[c]**	**0.03**
IL2RA (rs2104286)	0.82 (0.60, 1.10)[b]	0.19	1.04 (0.59, 1.83)[c]	0.90	0.66 (0.37, 1.19)[c]	0.17
IL7R (rs6897932)	0.93 (0.68, 1.29)[b]	0.67	0.88 (0.51, 1.51)[c]	0.64	0.84 (0.48, 1.49)[c]	0.55
PRKCQ (rs947474)	1.11 (0.74, 1.65)[c]	0.62	0.64 (0.36, 1.12)[c]	0.12	0.75 (0.40, 1.42)[c]	0.38
SKAP2 (rs7804356)	0.90 (0.66, 1.22)[b]	0.49	1.32 (0.78, 2.24)[c]	0.31	0.96 (0.54, 1.69)[c]	0.88
SMARCE1 (rs7221109)	0.94 (0.71, 1.23)[b]	0.63	0.88 (0.51, 1.51)[b]	0.63	0.69 (0.41, 1.16)[b]	0.16
TLR8 (rs5979785)[d]	0.84 (0.64, 1.09)[b]	0.18	0.90 (0.65, 1.26)[b]	0.54	0.92 (0.63, 1.34)[b]	0.66
UBASH3A (rs3788013)	1.22 (0.92, 1.63)[b]	0.17	1.28 (0.88, 1.87)[b]	0.20	**1.76 (1.15, 2.69)[b]**	**0.01**
rs10517086	*	*	1.60 (0.89, 2.87)[c]	0.12	**1.90 (1.28, 2.83)[b]**	**0.002**

Abbreviations: CI, confidence interval; DAISY, Diabetes Autoimmunity Study in the Young; HLA, human leukocyte antigen; HR, hazard ratio; IA, islet autoimmunity; MAF, minor allele frequency; T1D, type 1 diabetes.

[a]Adjusted for age at first autoantibody positive visit.

[b]SNP analyzed additively with HR representing increase in risk for each additional minor allele.

[c]SNP analyzed dichotomously with HR representing increase in risk for at least one minor allele.

[d]*TLR8* (rs5979785) is adjusted for sex because it is on the X chromosome.

*SNP rs10517086 did not meet the assumptions of proportional hazards in the development of IA analysis.