Supplementary Table 1: The combined *P*-values of T1D association of the other SNPs in the Sequenom panel

SNP	CHR	Position	WGA Case-Control cohort *P*-value	WGA Family cohort *P*-value	Combined GWA *P*-value	Replication *P*-value*
rs4659853	1	233,641,596	3.39×10^{-6}	2.48×10^{-2}	1.45×10^{-6}	0.7653
rs938095	2	111,665,279	8.35×10^{-5}	3.68×10^{-2}	4.21×10^{-5}	0.7318
rs11123410	2	111,673,543	2.50×10^{-5}	1.54×10^{-2}	6.06×10^{-6}	0.6841
rs4849163	2	113,651,498	1.47×10^{-3}	2.25×10^{-4}	5.26×10^{-6}	0.7620
rs12612676	2	185,027,690	7.34×10^{-3}	7.49×10^{-4}	7.21×10^{-5}	0.4070
rs7622560	3	109,226,712	1.93×10^{-4}	2.76×10^{-2}	6.98×10^{-5}	0.8653
rs9842994	3	141,933,344	9.86×10^{-3}	4.64×10^{-4}	6.08×10^{-5}	0.7371
rs10856836	4	38,102,715	2.26×10^{-4}	1.86×10^{-2}	5.62×10^{-5}	0.3402
rs12186776	5	81,085,295	2.41×10^{-4}	1.33×10^{-2}	4.38×10^{-5}	0.1366
rs17553805	5	168,163,497	7.25×10^{-5}	7.53×10^{-5}	7.16×10^{-5}	0.9176
rs16928839	9	9,051,233	1.17×10^{-3}	5.50×10^{-3}	8.31×10^{-5}	0.9576
rs2011091	9	15,001,914	2.45×10^{-5}	1.45×10^{-2}	5.64×10^{-6}	0.1058
rs12684746	9	128,514,921	1.80×10^{-2}	2.74×10^{-5}	7.66×10^{-6}	0.0220
rs1189309	10	52,785,383	1.71×10^{-3}	1.11×10^{-3}	2.68×10^{-5}	0.4117
rs4918487	10	111,974,745	3.32×10^{-4}	1.11×10^{-2}	4.98×10^{-5}	0.7832
rs7917093	10	112,018,620	4.33×10^{-4}	1.08×10^{-2}	6.19×10^{-5}	0.6654
rs10901815	10	126,425,587	4.11×10^{-4}	1.06×10^{-3}	6.80×10^{-6}	0.6258
rs486111	11	133,401,746	1.64×10^{-2}	2.56×10^{-4}	5.60×10^{-5}	0.6678
rs3923616	12	3,088,160	1.75×10^{-3}	1.15×10^{-3}	2.84×10^{-5}	1.0000
rs773107	12	54,655,773	2.89×10^{-5}	7.81×10^{-3}	3.68×10^{-6}	2.48×10^{-8}
rs10876864	12	54,687,352	8.39×10^{-5}	2.97×10^{-4}	4.61×10^{-7}	2.47×10^{-9}
rs1701704	12	54,698,754	9.89×10^{-6}	1.62×10^{-3}	3.03×10^{-7}	9.13×10^{-10}
rs11840556	13	102,641,528	1.26×10^{-4}	4.95×10^{-2}	8.07×10^{-5}	0.7576
rs11622517	14	75,835,499	2.39×10^{-3}	1.34×10^{-3}	4.38×10^{-5}	0.6021
rs1835499	18	38,589,879	1.45×10^{-4}	1.70×10^{-2}	3.43×10^{-5}	0.9510
rs8119653	20	3,997,803	1.41×10^{-4}	1.28×10^{-2}	2.55×10^{-5}	0.7574
rs4814154	20	12,652,803	1.52×10^{-7}	4.88×10^{-2}	1.46×10^{-7}	0.1845

* The combined *P*-value in the Stage 2 cohorts, i.e. the T1DGC cohort and the Canadian cohort.

Supplementary Table 2: Genotypic association of the three 12q13 SNPs

	Frequency	Informative family number*	S†	E(S)‡	Var(S)§	Z value	*P*
rs773107							
A/A	0.448	847	400	450	247	-3.17	0.00153
A/G	0.431	1022	661	653	326	0.43	0.66444
G/G	0.122	465	246	204	125	3.76	0.00017
rs10876864							
A/A	0.317	832	356	409	234	-3.47	0.00053
A/G	0.491	1106	707	704	351	0.17	0.86923
G/G	0.192	653	344	294	177	3.76	0.00017
rs1701704							
A/A	0.417	879	409	464	256	-3.43	0.00061
A/C	0.455	1063	691	678	339	0.70	0.48549
C/C	0.128	493	257	215	132	3.65	0.00026

*Number of nuclear families informative for (with a non-zero contribution to) FBAT analysis; †Observed genotype number in the affected offspring; ‡Expected genotype number in the affected offspring; §Variance of genotype distribution among the affected offspring.

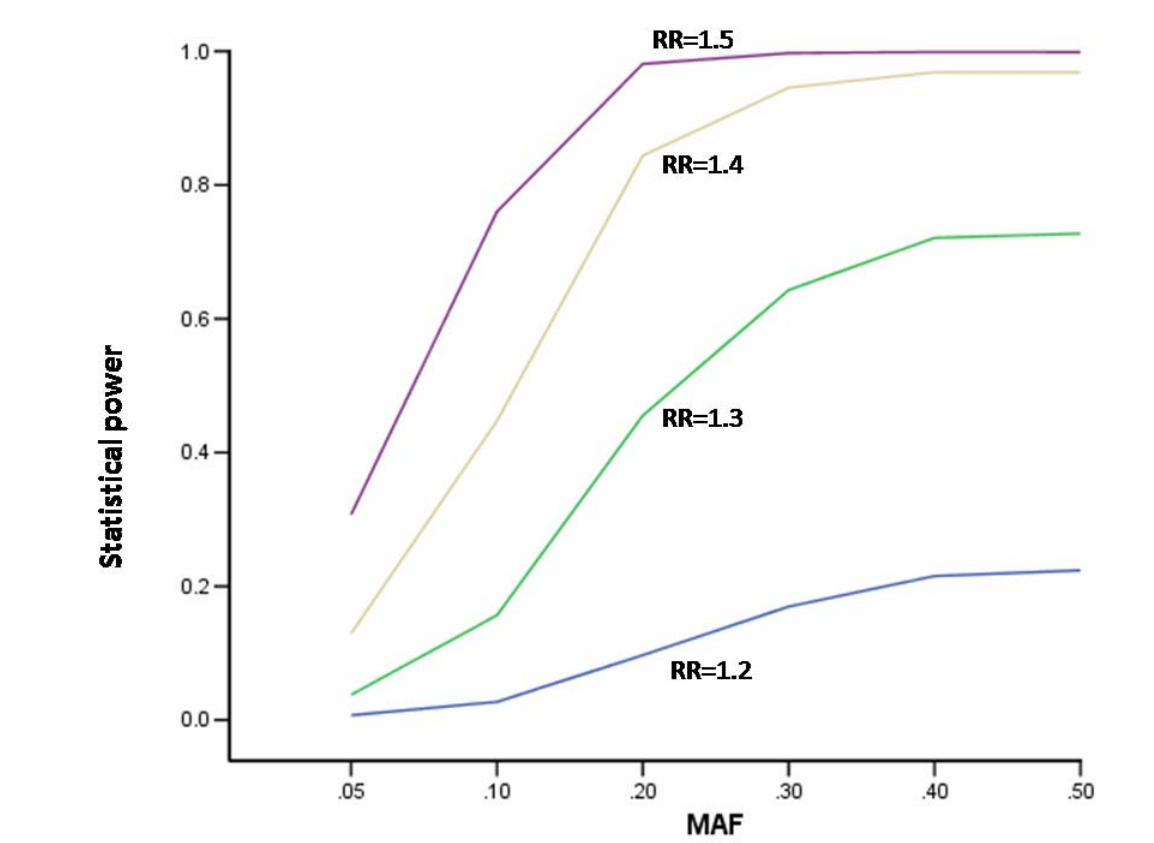
Supplementary Table 3: Age-of-onset comparisons of different genotypes of the three 12q13 SNPs

Genotype	N	**Median (25%, 75% quatile)**	Kruskal-Wallis Test χ^2 value (p value)
rs773107			6.1 (v=2, P=0.047)
A/A	760	9.0 (5.0, 13.0)	
A/G	827	8.6 (4.8, 13.0)	
G/G	238	8.0 (4.0, 11.3)	
rs10876864			5.9 (v=2, P=0.054)
A/A	524	9.0 (5.0, 13.0)	
A/G	923	8.5 (4.6, 13.0)	
G/G	379	8.0 (4.4, 12.0)	
rs1701704			4.5 (v=2, P=0.108)
A/A	709	9.0 (5.0, 13.0)	
A/C	860	8.5 (5.0, 12.9)	
C/C	256	8.0 (4.0, 11.7)	

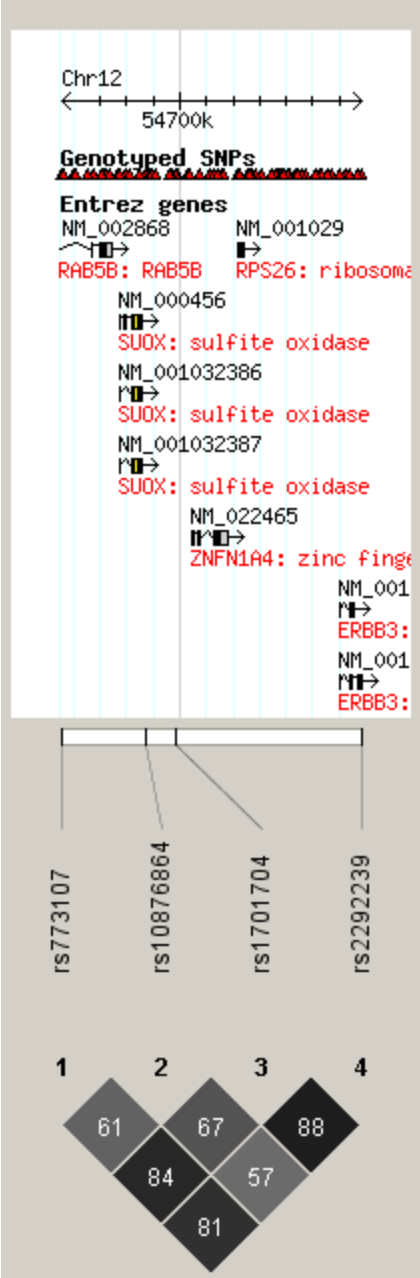
Supplementary Table 4: The combined analysis of our genotyping results and the imputed genotypes of WTCCC for the three 12q13 SNPs

	p value		
SNP	Our dataset	WTCCC imputation*	Combined
rs773107	2.48×10^{-8}	8.51×10^{-7}	6.85×10^{-13}
rs10876864	2.47×10^{-9}	2.04×10^{-9}	2.05×10^{-16}
rs1701704	9.13×10^{-10}	5.91×10^{-9}	2.20×10^{-16}

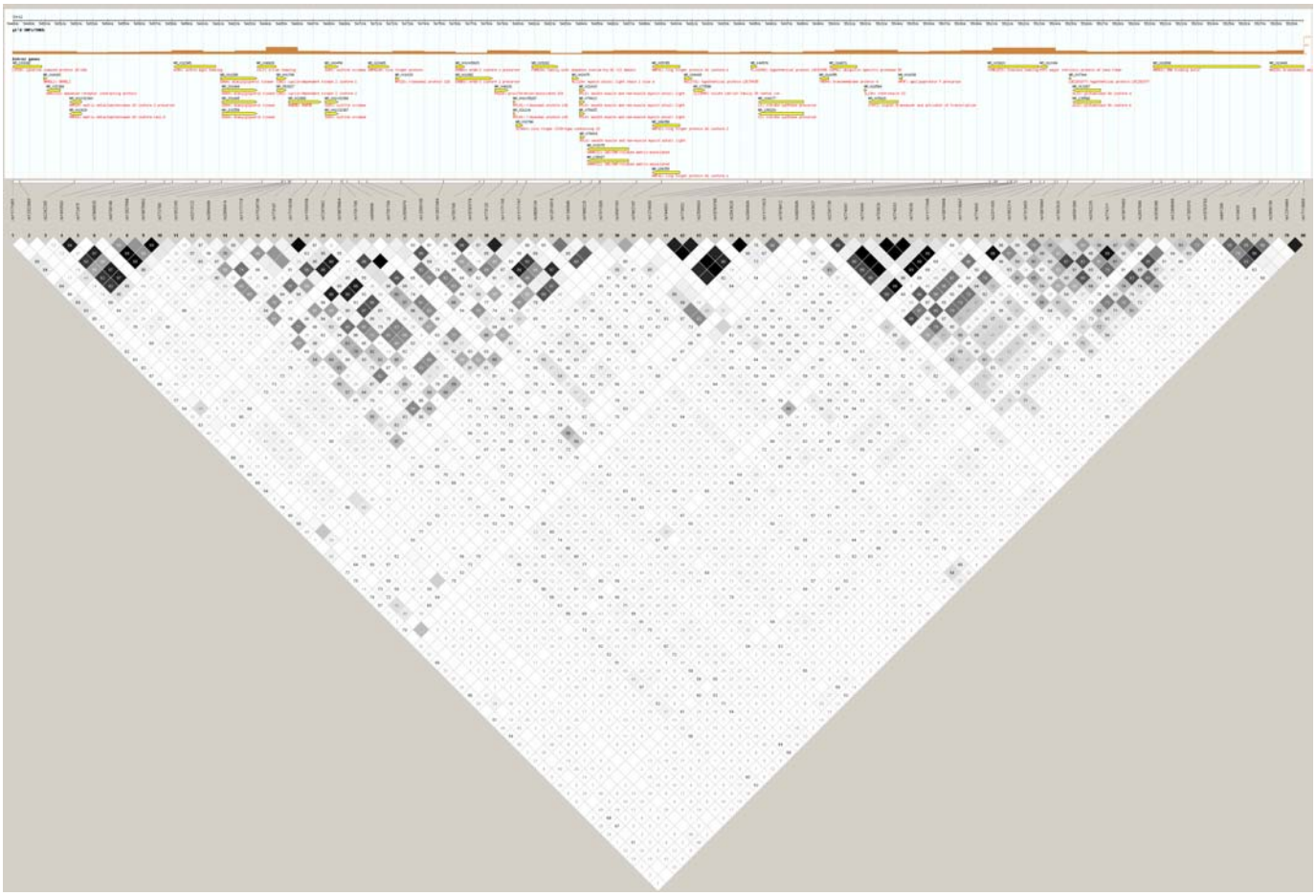
* Based on the WTCCC imputation of the T1D case group and two control groups (http://www.wtccc.org.uk/info/summary_stats.shtml).



Supplementary Fig.1: The statistical power of our GWA to detect a range of effect sizes at $\alpha=1x10^{-4}$ level.



Supplementary Fig.2: The LD map of the T1D-associated SNPs based on the HapMap data. The haplotype map is made by Haploview v3.2 software. r^2 values (%) are shown in the boxes, and represented by the grey scale. The first three SNPs are the SNPs found of T1D association in our study. The fourth SNP is reported to be T1D-associated by Todd et al[1].



Supplementary Fig. 3. The extended LD diagram around the novel T1D locus based on our genotyping data of the family cohort. The haplotype map is made by Haploview v3.2 software. D' values (%) are shown in the boxes. The grey scale represents the r^2 values.

Reference:

1. Todd JA, Walker NM, Cooper JD, Smyth DJ, Downes K, Plagnol V, Bailey R, Nejentsev S, Field SF, Payne F *et al*: **Robust associations of four new chromosome regions from genome-wide analyses of type 1 diabetes**. *Nat Genet* 2007, **39**(7):857-864.