

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

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

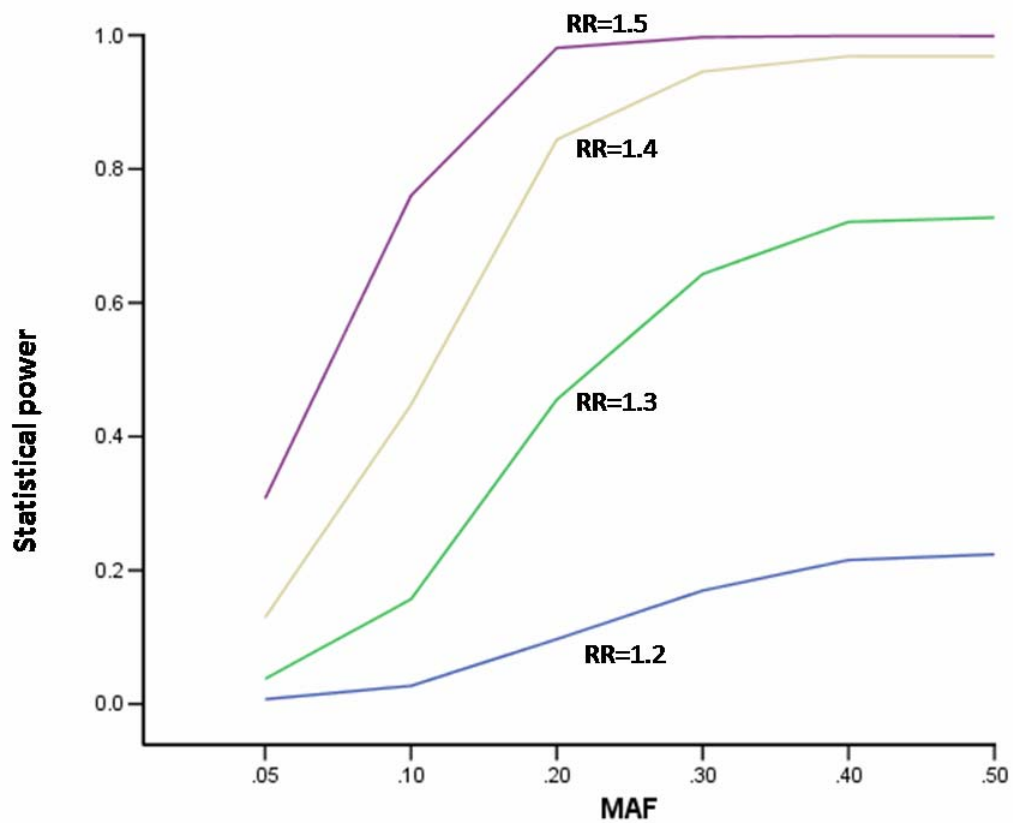
**Supplementary Table 3:** Age-of-onset comparisons of different genotypes of the three 12q13 SNPs

| Genotype   | N   | Median (25%, 75% quartile) | Kruskal-Wallis Test $\chi^2$ value (p value) |
|------------|-----|----------------------------|--|
| rs773107   |     |                            | 6.1 ( $\nu=2$ , $P=0.047$ )                  |
| 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 ( $\nu=2$ , $P=0.054$ )                  |
| 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 ( $\nu=2$ , $P=0.108$ )                  |
| 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)            |  |

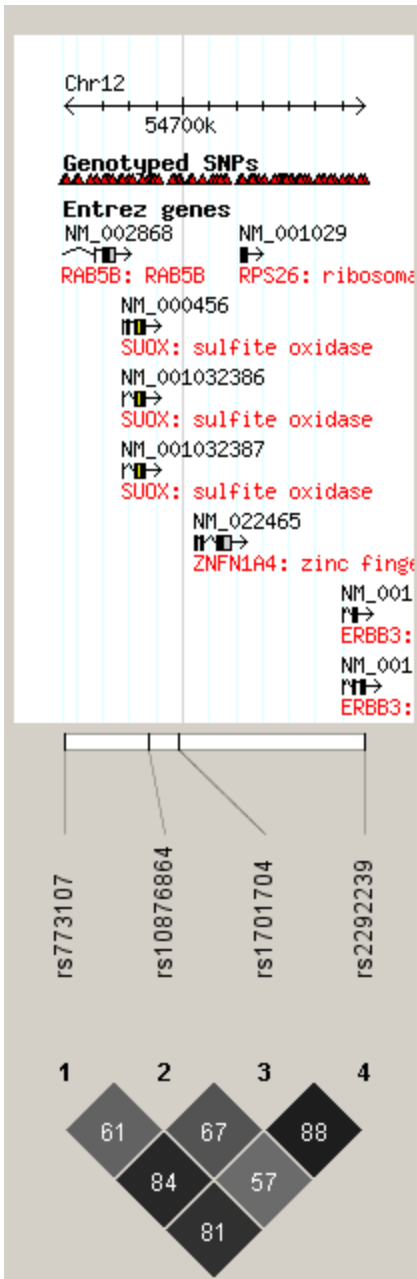
**Supplementary Table 4:** The combined analysis of our genotyping results and the imputed genotypes of WTCCC for the three 12q13 SNPs

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

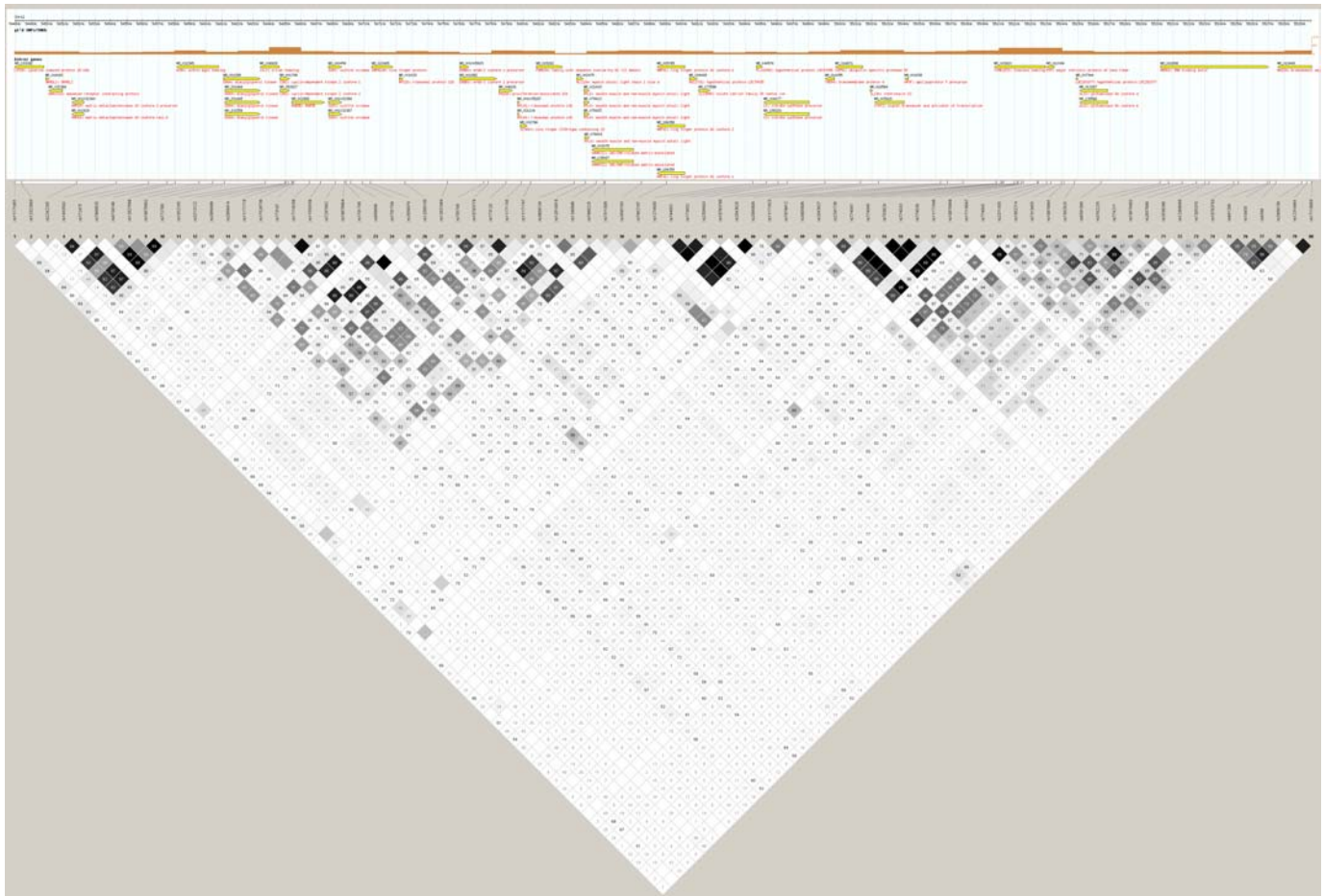
\* Based on the WTCCC imputation of the T1D case group and two control groups ([http://www.wtccc.org.uk/info/summary\\_stats.shtml](http://www.wtccc.org.uk/info/summary_stats.shtml)).



**Supplementary Fig.1:** The statistical power of our GWA to detect a range of effect sizes at  $\alpha=1 \times 10^{-4}$  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.