**Supplementary Table 1 Analysis of the novel SNPs identified from resequencing in type 1 diabetes**

| SNP | MAF in controls | Cases *N* | Controls *N* | OR (95% c.i.) | *P* (1-d.f. test) | $r^2$ with rs763361 | D' with rs763361 |
|---|---|---|---|---|---|---|---|
| ss102661466 (Ala279Leu) | 0.065 | 7,583 | 7,185 | 1.15 (1.05-1.26) | $2.08 \times 10^{-3}$ | 0.07 | 0.95 |
| ss102661465 (Gln282Gln) | 0.078 | 7,176 | 6,759 | 0.90 (0.82-0.99) | 0.0298 | 0.07 | 0.99 |

A multiplicative allelic effects model was assumed (see methods), as it was not significantly different from the full genotype model. OR is reported for the minor allele. MAF = minor allele frequency, *P* = *P* value, *N* = number, OR = odds ratio, 95% c.i. = 95% confidence interval, $r^2$ = correlation coefficient, D' = Lewontin's D'[28]

**Supplementary Table 2 Analysis of *CD226* tag SNPs in type 1 diabetes (restricted to individuals with genotype information available for all single nucleotide polymorphisms)**

| rs number | MAF in controls | *P* (1-d.f. test) | OR (95% c.i.) | *N* (cases) | *N* (controls) |
|---|---|---|---|---|---|
| rs763361 | 0.46 | $8.67 \times 10^{-8}$ | 1.19 (1.12 - 1.28) | 3,606 | 4,092 |
| rs1009847 | 0.28 | $8.48 \times 10^{-3}$ | 1.10 (1.02 - 1.18) | 3,606 | 4,092 |
| rs1124980 | 0.38 | $2.06 \times 10^{-5}$ | 1.15 (1.08 - 1.23) | 3,606 | 4,092 |
| rs11661553 | 0.44 | $9.36 \times 10^{-7}$ | 0.85 (0.79 - 0.91) | 3,606 | 4,092 |
| rs12604328 | 0.26 | $1.40 \times 10^{-4}$ | 1.15 (1.07 - 1.24) | 3,606 | 4,092 |
| rs17208329 | 0.24 | 0.033 | 1.09 (1.01 - 1.17) | 3,606 | 4,092 |
| rs17842596 | 0.38 | $6.38 \times 10^{-5}$ | 1.14 (1.07 - 1.22) | 3,606 | 4,092 |
| rs1788114 | 0.42 | $4.04 \times 10^{-4}$ | 1.13 (1.05 - 1.20) | 3,606 | 4,092 |
| rs1788234 | 0.39 | $2.75 \times 10^{-3}$ | 1.11 (1.04 - 1.18) | 3,606 | 4,092 |
| rs4891781 | 0.40 | $7.97 \times 10^{-4}$ | 1.12 (1.05 - 1.20) | 3,606 | 4,092 |

A multiplicative allelic effects model was assumed (see materials and methods), as it was not significantly different from the full genotype model. OR is reported for the minor allele
MAF = minor allele frequency, OR = odds ratio, 95% c.i. = 95% confidence interval,
rs17208112, a SNP only tagging itself, failed quality control checks and was therefore excluded in the analysis

**Supplementary Table 3 Analysis of *CD226* tag SNPs in multiple sclerosis (restricted to individuals with genotype information available for all single nucleotide polymorphisms)**

| | Cases and controls | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | USA | | | | | UK | | | | |
| **rs number** | **MAF in controls** | ***P* (1-d.f. test)** | **OR (95% c.i.)** | ***N* (cases)** | ***N* (controls)** | **MAF in controls** | ***P* (1-d.f. test)** | **OR (95% c.i.)** | ***N* (cases)** | ***N* (controls)** |
| rs763361 | 0.46 | 0.033 | 1.17 (1.01 – 1.35) | 1,143 | 545 | 0.46 | 0.011 | 1.14 (1.03 – 1.26) | 933 | 3,606 |
| rs1009847 | 0.25 | 0.014 | 1.23 (1.04 - 1.44) | 1,143 | 545 | 0.28 | 0.20 | 1.08 (0.96 - 1.20) | 933 | 3,606 |
| rs1124980 | 0.38 | 0.025 | 1.18 (1.02 - 1.37) | 1,143 | 545 | 0.38 | 0.046 | 1.11 (1.00 - 1.23) | 933 | 3,606 |
| rs11661553 | 0.42 | 0.18 | 0.91 (0.78 - 1.05) | 1,143 | 545 | 0.44 | 0.10 | 0.92 (0.83 - 1.02) | 933 | 3,606 |
| rs12604328 | 0.26 | 0.11 | 1.14 (0.97 - 1.35) | 1,143 | 545 | 0.26 | 0.14 | 1.09 (0.97 - 1.22) | 933 | 3,606 |
| rs17208329 | 0.20 | 0.11 | 1.15 (0.97 - 1.38) | 1,143 | 545 | 0.24 | 0.48 | 1.04 (0.93 - 1.18) | 933 | 3,606 |
| rs17842596 | 0.38 | 0.098 | 1.13 (0.98 - 1.31) | 1,143 | 545 | 0.38 | 0.33 | 1.05 (0.95 - 1.17) | 933 | 3,606 |
| rs1788114 | 0.44 | 0.22 | 1.09 (0.95 - 1.26) | 1,143 | 545 | 0.42 | 0.13 | 1.08 (0.98 - 1.20) | 933 | 3,606 |
| rs1788234 | 0.38 | 0.032 | 1.18 (1.01 - 1.36) | 1,143 | 545 | 0.39 | 0.10 | 1.09 (0.98 - 1.21) | 933 | 3,606 |
| rs4891781 | 0.38 | 0.027 | 1.18 (1.02 - 1.37) | 1,143 | 545 | 0.40 | 0.18 | 1.07 (0.97 - 1.19) | 933 | 3,606 |

A multiplicative allelic effects model was assumed (see methods), as it was not significantly different from the full genotype model. OR is reported for the minor allele
MAF = minor allele frequency, *P* = *P* value, OR = odds ratio, 95% c.i. = 95% confidence interval, *N* = number

**Supplementary Table 4 Separate analysis of Gly307Ser in autoimmune thyroid disease subgroups: Graves' disease and Hashimoto's disease**

| Disease | Cohort | MAF in controls | *P* (1-d.f. test) | OR (95% c.i.) | *P* combined | *N* (trios) | *N* (cases) | *N* (controls) |
|---|---|---|---|---|---|---|---|---|
| Graves' disease[I] | UK (case/control) | 0.47 | 0.0182 | 1.10 (1.02-1.20) | - | | 2,137 | 3,511 |
| Graves' disease[II] | UK (case/control) | 0.47 | 0.0382 | 1.08 (1.00-1.16) | - | | 2,295 | 5,431 |
| Hashimoto's disease[III] | UK (case/control) | 0.47 | 0.367 | 1.05 (0.94-1.19) | - | | 663 | 5,431 |

A multiplicative allelic effects model was assumed (see methods), as it was not significantly different from the full genotype model. OR is reported for the minor allele
MAF = minor allele frequency, *P* = *P* value, OR = odds ratio, 95% c.i. = 95% confidence interval, *N* = number

[I]Original Graves' disease samples reported in Nature Genetics[17]
[II]Additional 158 Graves' disease cases and 1,920 controls
[III]Hashimoto's disease samples