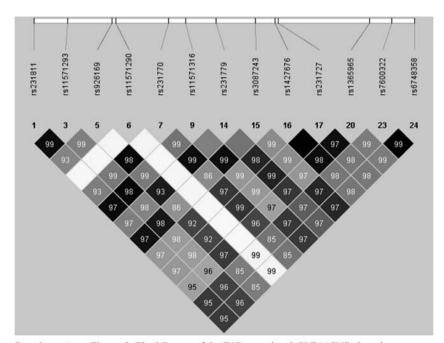


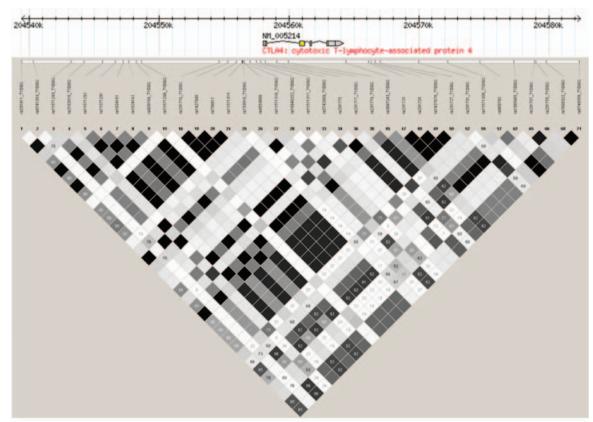
Supplementary Figure 1 The T1D association of the 24 SNPs in the *CTLA4* locus. Both genotyping methods have consistent T1D association results. The peak of T1D association is from rs1427676 and rs231727.



Supplementary Figure 2 The LD map of the T1D-associated *CLTA4* SNPs based on the *Illumina* genotyping data from the T1DGC. The two SNPs with highest T1D association, rs1427676 and rs231727, are in tight LD. Except rs11571290, all the other T1D-associated SNPs have high LD rs1427676 with $r^2 \ge 0.299$. The haplotype map is made by the Haploview v4.0 software. D' values (%) are shown in the boxes, and the empty boxes have D'=1. The grey scale represents the r^2 values.



Supplementary Figure 3 The LD map of SNPs at the CTLA4-ICOS locus based on the HapMap CEU data (www.hapmap.org). The LD plot is made by the Haploview v4.0 software (www.broad.mit.edu/personal/jcbarret/haploview). The red colour depth represents the D' values.



Supplementary Figure 4 The LD map of the CLTA4 SNPs based on the HapMap data. Among the 36 HapMap SNPs with MAF>0.01, 24 SNPs were genotyped by the T1DGC (the SNP IDs with "_T1DGC"). The haplotype map is made by the Haploview v4.0 software. D' values (%) are shown in the boxes, and the empty boxes have D'=1. The grey scale represents the r² values. The black boxes have r2=1, and the white boxes have r2=0.