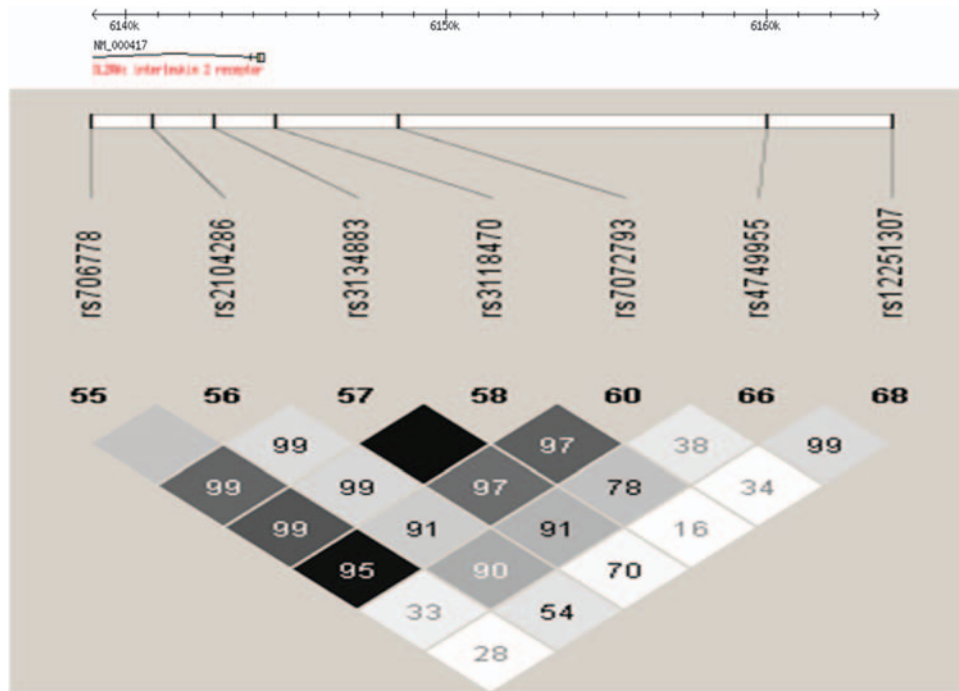


**Supplementary Figure 1** The LD map of the *IL2RA* SNPs based on the HapMap CEU data (Public Release #21a in Jan 2007, [www.hapmap.org](http://www.hapmap.org)). 69 SNPs were genotyped by the T1DGC (the SNP IDs with “\_T1DGC”). The T1DGC SNPs captured 93.7% HapMap SNPs with  $MAF \geq 0.05$  at  $r^2 > 0.8$  in this region, and 45% HapMap SNPs with  $0.001 \leq MAF < 0.05$ . The haplotype map is made by the Haploview v4.0 software ([www.broad.mit.edu/personal/jcbarret/haploview](http://www.broad.mit.edu/personal/jcbarret/haploview)).  $D'$  values (%) are shown in the boxes, and the empty boxes have  $D'=1$ . The grey scale represents the  $r^2$  values.

**Supplementary Table 1** The T1D association assay of 69 *IL2RAS* SNPs

Marker	Physical Position	ILMN call rate	ILMN HWE p	SQNM call rate	SQNM HWE p	Consistency of ILMN vs. SQNM	MA	MAF	ILMN T1D association Z	ILMN T1D association P	SQNM T1D association Z	SQNM T1D association P
rs6602363	6,076,150	0.998	0.927	0.984	0.005	0.987	A	0.319	0.563	0.574	0.164	0.870
rs7898880	6,077,559	0.999	0.297	0.993	0.160	0.998	T	0.225	-0.002	0.998	-0.276	0.782
rs7911500	6,077,732	0.999	0.573	0.995	0.181	0.999	A	0.127	2.168	0.030	1.737	0.082
rs17147986	6,078,484	--	--	0.983	0.331	--	A	0.167	--	--	-0.915	0.360
rs6602364	6,078,859	1.000	0.502	0.997	0.254	0.998	G	0.440	-1.243	0.214	-0.831	0.406
rs1323653	6,079,064	0.984	0.460	0.989	0.481	1.000	G	0.095	-0.583	0.560	-0.250	0.802
rs7477011	6,080,600	0.999	0.236	0.983	0.069	0.978	A	0.495	0.719	0.472	0.454	0.650
rs10795731	6,082,040	0.999	0.382	0.996	1.000	1.000	C	0.050	-0.800	0.424	-0.798	0.425
rs17322780	6,082,478	0.999	1.000	0.988	0.973	1.000	G	0.104	0.226	0.821	-0.113	0.910
rs10795733	6,083,484	0.995	0.412	0.980	0.110	0.983	C	0.498	-0.768	0.443	0.292	0.770
rs764851	6,087,950	1.000	0.552	0.986	0.303	0.999	A	0.161	-0.400	0.689	-1.294	0.196
rs10795737	6,089,350	0.987	0.091	0.997	0.704	1.000	A	0.262	0.913	0.361	0.656	0.512
rs12359875	6,091,113	0.999	0.287	0.989	0.362	1.000	T	0.230	-0.022	0.983	-0.186	0.853
rs12722608	6,092,847	1.000	0.591	0.995	0.338	1.000	T	0.039	0.481	0.630	-0.087	0.931
rs12722605	6,093,169	0.999	0.582	0.976	0.722	1.000	A	0.161	1.598	0.110	0.318	0.751
rs12244380	6,093,380	0.998	1.000	0.997	0.904	1.000	C	0.428	-1.825	0.068	-1.469	0.142
rs12722598	6,095,156	0.996	1.000	0.995	0.000	0.998	G	0.013	0.152	0.880	0.076	0.940
rs9663421	6,095,610	0.998	0.171	0.993	0.338	1.000	A	0.268	0.032	0.974	-0.474	0.635
rs12722596	6,096,300	1.000	0.871	0.987	0.916	1.000	G	0.098	-0.469	0.639	0.299	0.765
rs2386841	6,097,738	0.999	0.866	0.971	0.306	0.979	T	0.167	1.867	0.062	0.794	0.427
rs7899538	6,099,904	0.999	0.304	0.955	0.001	0.998	A	0.129	2.275	0.023	0.383	0.701
rs12722588	6,100,439	1.000	0.831	0.995	0.849	1.000	A	0.193	0.234	0.815	-0.331	0.741
rs2274037	6,102,114	0.999	1.000	0.993	1.000	1.000	A	0.040	0.412	0.681	-0.117	0.907
rs2076846	6,103,259	0.999	0.300	0.989	0.011	0.990	G	0.340	-0.852	0.394	-0.962	0.336
rs7093069	6,103,325	1.000	0.831	0.989	0.464	0.999	A	0.193	0.188	0.851	-0.351	0.726
rs11596355	6,104,187	0.999	0.793	0.991	0.990	1.000	C	0.099	0.161	0.872	0.526	0.599
rs12722574	6,106,468	0.999	0.467	0.990	0.504	0.999	T	0.229	1.227	0.220	0.499	0.618
rs2031229	6,106,574	0.978	0.094	--	--	--	A	0.238	1.306	0.192	--	--
rs2025345	6,107,694	0.999	0.532	0.995	0.660	0.999	C	0.359	0.024	0.980	-0.290	0.772
rs12722561	6,109,899	0.999	0.286	0.985	0.548	0.986	A	0.158	-0.537	0.591	-2.248	0.025
rs7910961	6,117,802	0.998	0.877	0.996	0.571	1.000	A	0.330	0.687	0.492	0.362	0.718
rs6602391	6,118,038	0.999	0.211	0.995	0.095	1.000	T	0.072	0.111	0.912	0.463	0.643
rs12722521	6,118,802	0.999	0.721	--	--	--	T	0.044	1.230	0.219	--	--
rs11256448	6,119,485	--	--	0.987	1.000	--	G	0.272	--	--	1.588	0.112
rs7072398	6,119,852	0.999	0.209	0.982	0.490	1.000	A	0.482	2.387	0.017	1.314	0.189
rs12722518	6,120,643	0.999	1.000	0.985	0.958	0.995	G	0.044	1.201	0.230	0.207	0.836
rs11256456	6,120,718	0.989	0.492	0.992	0.993	0.995	G	0.227	1.129	0.259	1.077	0.281
rs12722516	6,121,223	1.000	0.199	0.986	0.000	0.993	C	0.031	0.028	0.978	-2.304	0.021
rs4749924	6,122,402	0.998	0.189	0.978	0.825	0.966	G	0.304	0.534	0.593	-0.495	0.620
rs6602398	6,122,959	0.997	0.187	0.994	0.149	0.999	A	0.303	0.480	0.631	0.263	0.793
rs4749926	6,125,318	0.968	0.072	0.995	0.571	0.994	T	0.372	-0.353	0.724	0.262	0.793
rs10905656	6,126,099	0.999	0.967	0.979	0.147	0.991	A	0.410	1.180	0.238	1.479	0.139
rs942201	6,126,298	0.987	0.417	0.994	0.647	1.000	T	0.239	0.857	0.392	1.301	0.193
rs706780	6,127,032	0.992	0.491	0.996	0.529	0.999	T	0.052	1.086	0.278	1.743	0.081
rs1107345	6,127,301	0.998	0.885	0.994	0.673	0.999	T	0.238	1.087	0.277	1.096	0.273
rs11256497	6,127,800	0.992	0.160	0.995	0.345	0.999	A	0.380	2.390	0.017	1.661	0.097
rs791587	6,128,705	0.998	0.971	0.988	0.878	1.000	A	0.486	1.852	0.064	1.397	0.162
rs791589	6,129,577	0.943	0.797	--	--	--	G	0.142	-1.707	0.088	--	--
rs791590	6,130,328	1.000	0.434	0.983	0.350	0.999	T	0.159	-1.056	0.291	-1.873	0.061
rs10905669	6,132,099	1.000	0.238	0.959	0.011	0.948	T	0.246	0.989	0.322	-1.669	0.095
*												
rs1323658	6,134,360	0.998	0.588	0.989	0.541	1.000	G	0.056	-0.512	0.609	-0.324	0.746
rs2476491	6,135,416	0.999	0.816	0.989	0.862	0.999	A	0.299	1.400	0.161	0.527	0.598
rs2256774	6,137,171	0.999	0.504	0.964	0.000	0.963	C	0.359	1.162	0.245	0.083	0.934
rs706779	6,138,830	0.998	0.882	0.985	0.377	0.988	C	0.448	-1.680	0.093	-2.166	0.030
rs706778	6,138,955	0.999	0.073	0.967	0.431	0.991	T	0.439	1.996	0.046	1.987	0.047
rs2104286	6,139,051	0.998	0.852	--	--	--	C	0.231	-3.407	6.56 x 10 <sup>-3</sup>	--	--
rs3134883	6,140,731	0.998	1.000	0.997	0.884	1.000	A	0.322	2.458	0.014	2.549	0.011
rs3118470	6,141,719	0.998	0.601	0.994	0.846	0.999	C	0.342	2.846	4.43 x 10 <sup>-3</sup>	3.156	1.60 x 10 <sup>-3</sup>
rs12722486	6,143,768	1.000	0.384	0.984	0.000	0.731	T	0.053	-0.978	0.328	-0.532	0.595
*												
rs7072793	6,146,272	1.000	0.081	0.996	0.213	1.000	C	0.443	2.019	0.043	2.246	0.025
rs7073236	6,146,558	0.963	0.374	0.991	0.289	0.999	C	0.444	1.489	0.136	2.287	0.022
rs4147359	6,148,445	--	--	0.995	0.143	--	A	0.372	--	--	2.093	0.036
rs7089861	6,150,332	0.999	0.318	0.989	0.330	1.000	G	0.276	-0.995	0.320	-1.302	0.193
rs7090512	6,150,835	0.999	0.201	0.992	0.308	1.000	G	0.311	0.425	0.671	-0.202	0.840
rs1887027	6,153,788	0.995	0.405	0.997	0.462	1.000	T	0.210	-1.250	0.211	-1.424	0.154
rs4749955	6,158,972	0.997	0.373	0.994	0.281	0.999	C	0.426	-3.262	1.10 x 10 <sup>-3</sup>	-2.699	6.96 x 10 <sup>-3</sup>
rs11594656	6,162,015	0.999	0.364	0.986	0.260	0.964	A	0.252	0.482	0.629	-0.623	0.534
rs12251307	6,163,501	0.999	0.858	0.998	0.824	1.000	A	0.099	-3.148	1.64 x 10 <sup>-3</sup>	-2.211	0.027
rs7100400	6,164,086	0.999	0.502	0.993	0.908	1.000	C	0.047	0.433	0.665	1.345	0.179

T1D association was tested by the Family Based Association Test (FBAT) (<http://www.biostat.harvard.edu/~fbat/fbat.htm>).<sup>14</sup> Considering that most of the T1DGC families have multiple siblings, the option of the empirical variance was used in the FBAT statistics to permit a robust but unbiased test of genetic association. \* Low Consistency rate of the genotyping methods and, therefore, not used for analysis.



**Supplementary Figure 2** The LD map of the T1D-associated *IL2RA* SNPs based on the Illumina genotyping data from the T1DGC. The haplotype map is made by the Haploview v4.0 software ([www.broad.mit.edu/personal/jcbarret/haploview](http://www.broad.mit.edu/personal/jcbarret/haploview)).  $D'$  values (%) are shown in the boxes, and the empty boxes have  $D'=1$ . The grey scale represents the  $r^2$  values.