The American Journal of Human Genetics, Volume *92*

Supplemental Data

Meta-Analysis Followed by Replication Identifies Loci in or near *CDKN1B*, *TET3*, *CD80*, *DRAM1*, and *ARID5B* as Associated with Systemic Lupus Erythematosus in Asians

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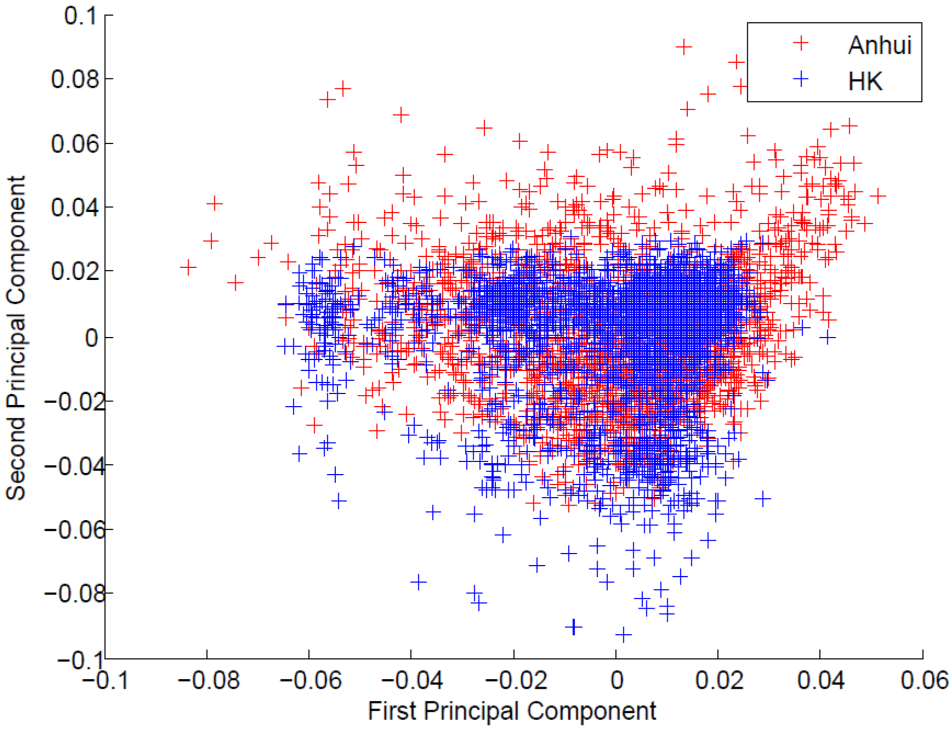


Figure S1. Population Substructure Analysis on the Samples from Hong Kong and Anhui in the GWAS Stage by Principal Component Analysis Using Eigenstrat

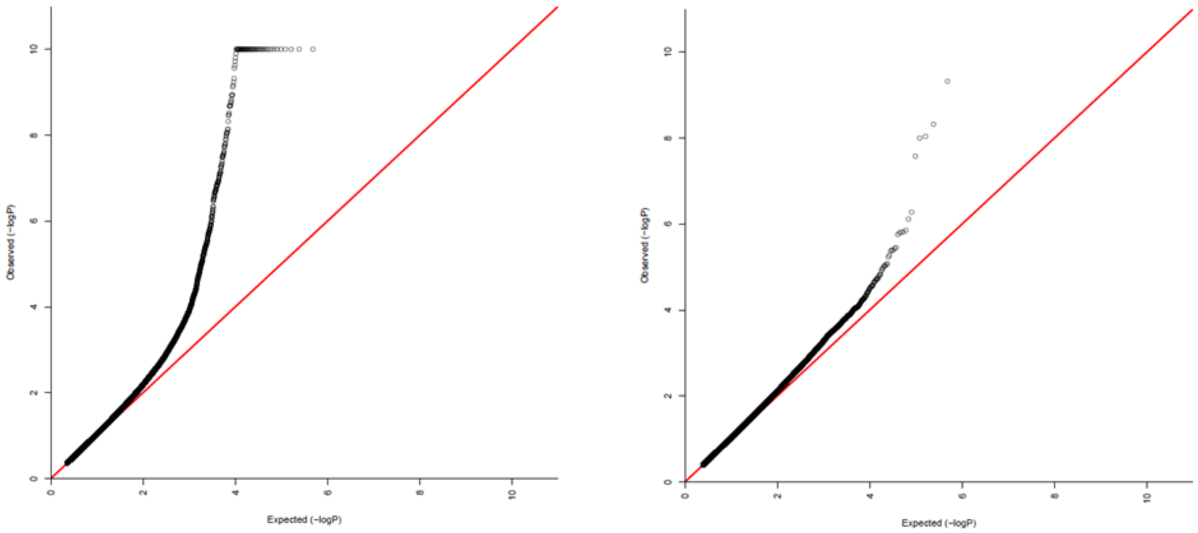
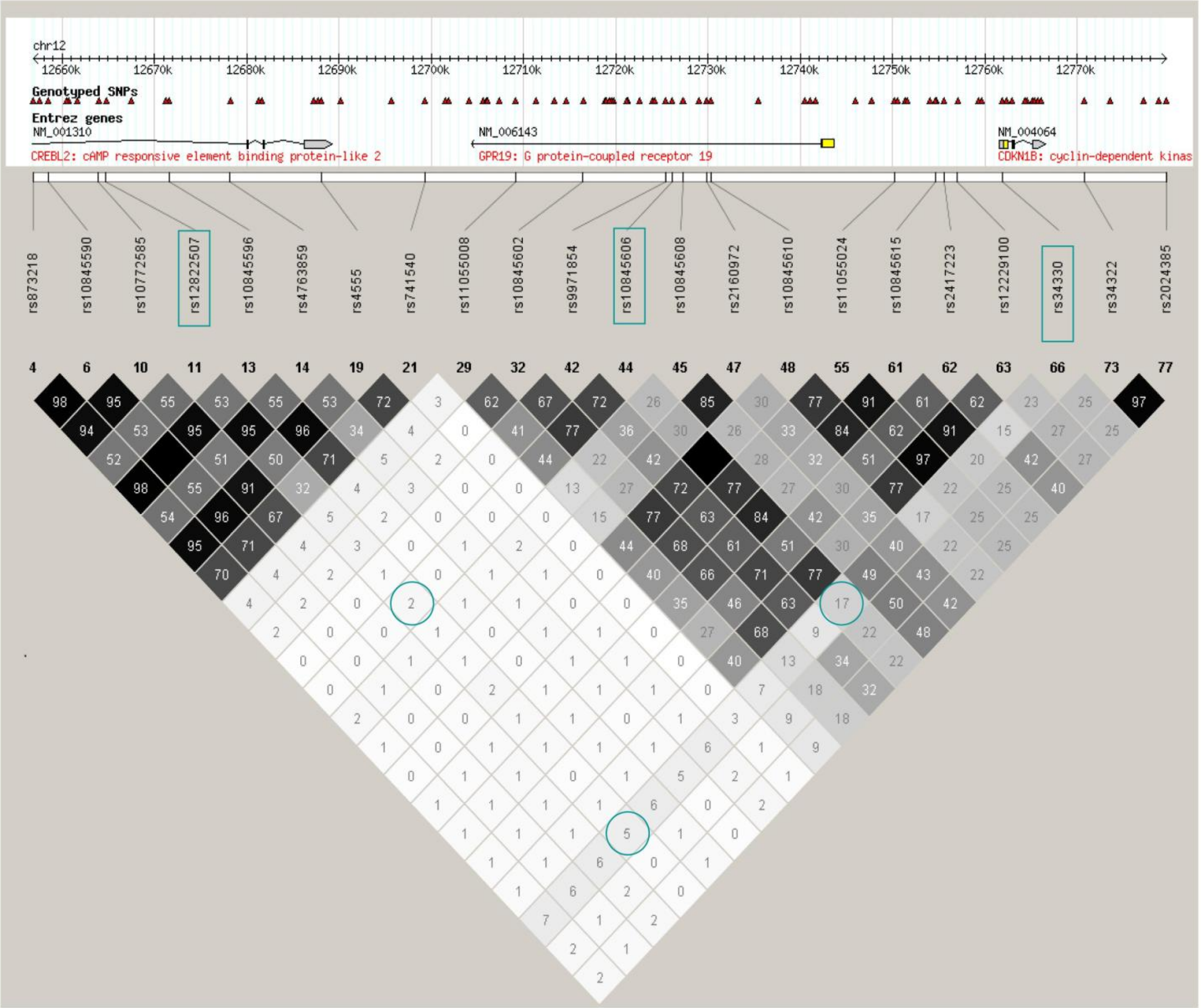


Figure S2. Q-Q Plot of the Meta-analysis Results

Left panel: Q-Q plot based on all the SNPs from GWAS that passed QC.

Right panel, Q-Q plot on the remaining SNPs after the removal of SNPs in the established susceptibility gene and within 100 Kb up- and down-stream of those genes. These genes include *ATG5*, *BANK1*, *BLK*, *ELF1*, *ETS1*, *HIC2*, *IKZF1*, *IRF5*, *LRRC18*, *PRDM1*, *RASGRP3*, *SLC15A4*, *STAT4*, *TNFAIP3*, *TNFSF4*, *TNIP1*, *UBE2L3*, *WDFY4* and the *HLA* region.

A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Genotyped SNPs
Entrez genes
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NM_006143
NM_004064
CREBL2: cAMP responsive element binding protein-like 2
GPR19: G protein-coupled receptor 19
CDKN1B: cyclin-dependent kinas
rs873218
rs10845590
rs10772585
rs12822507
rs10845596
rs4763859
rs4555
rs741540
rs11055008
rs10845602
rs9971854
rs10845606
rs10845608
rs2160972
rs10845610
rs11055024
rs10845615
rs2417223
rs12229100
rs34330
rs34322
rs2024385
4 6 10 11 13 14 19 21 29 32 42 44 45 47 48 55 61 62 63 66 73 77
98 95 55 53 55 53 72 3 62 67 72 26 85 30 77 91 61 62 23 25 97
94 53 95 95 96 34 4 0 41 77 36 30 26 33 84 62 91 15 27 25
52 51 50 71 5 2 0 44 22 42 28 32 51 97 20 42 27
98 55 91 32 4 3 0 0 13 27 72 77 27 30 77 22 25 40
54 96 67 5 2 0 0 0 15 77 63 84 42 35 17 25 25
95 71 4 3 0 1 2 0 44 68 61 51 30 40 22 25
70 4 2 1 0 1 1 0 40 66 71 77 49 43 22
4 2 0 2 1 1 0 0 35 46 63 17 50 42
2 0 0 1 0 1 1 0 27 68 9 22 48
0 0 1 1 0 1 1 0 40 13 34 22
0 1 0 2 1 1 1 0 7 18 32
2 0 0 1 1 0 1 3 9 18
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1 1 6 0 1
1 6 2 0
7 1 2
2 1
2

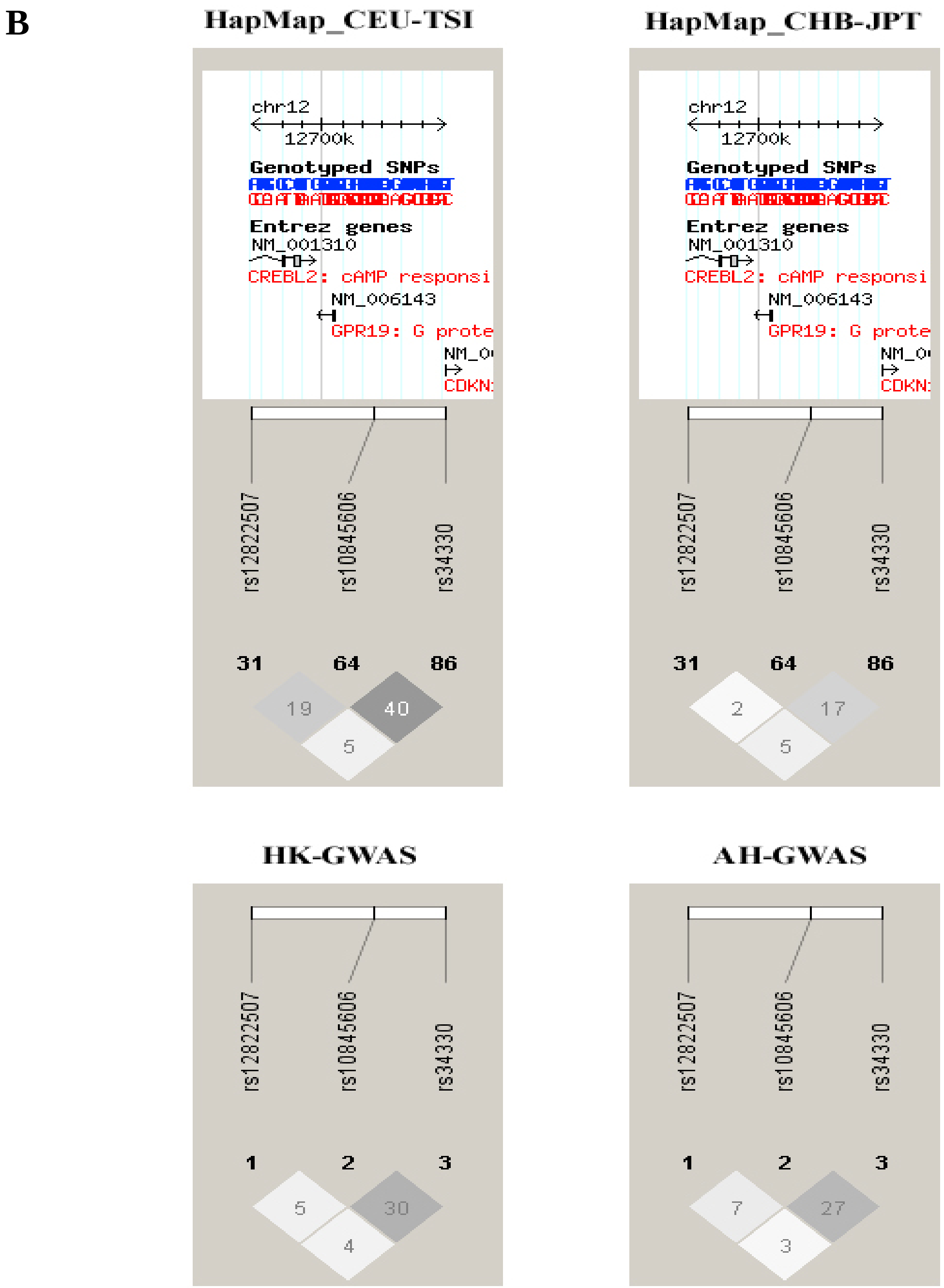

Figure S3. Lack of High LD among the Three SNPs in the 12p13 Locus Found to be Associated with SLE in This Study

(A) LD for 12p13 region based on data from HapMap CHB and JPT. All the numbers in the figure are pair-wise r^2 values. The three SNPs validated in this study were bracketed and the LD among them are circled. It seems that a recombination hotspot exists between rs12822507 and the other two SNPs, res10845606 and rs34330. The r^2 value between the latter two SNPs is 0.17 in Asians.

(B) LD (r^2) between the three identified SNPs in the 12p13 region based on HapMap and GWAS data.

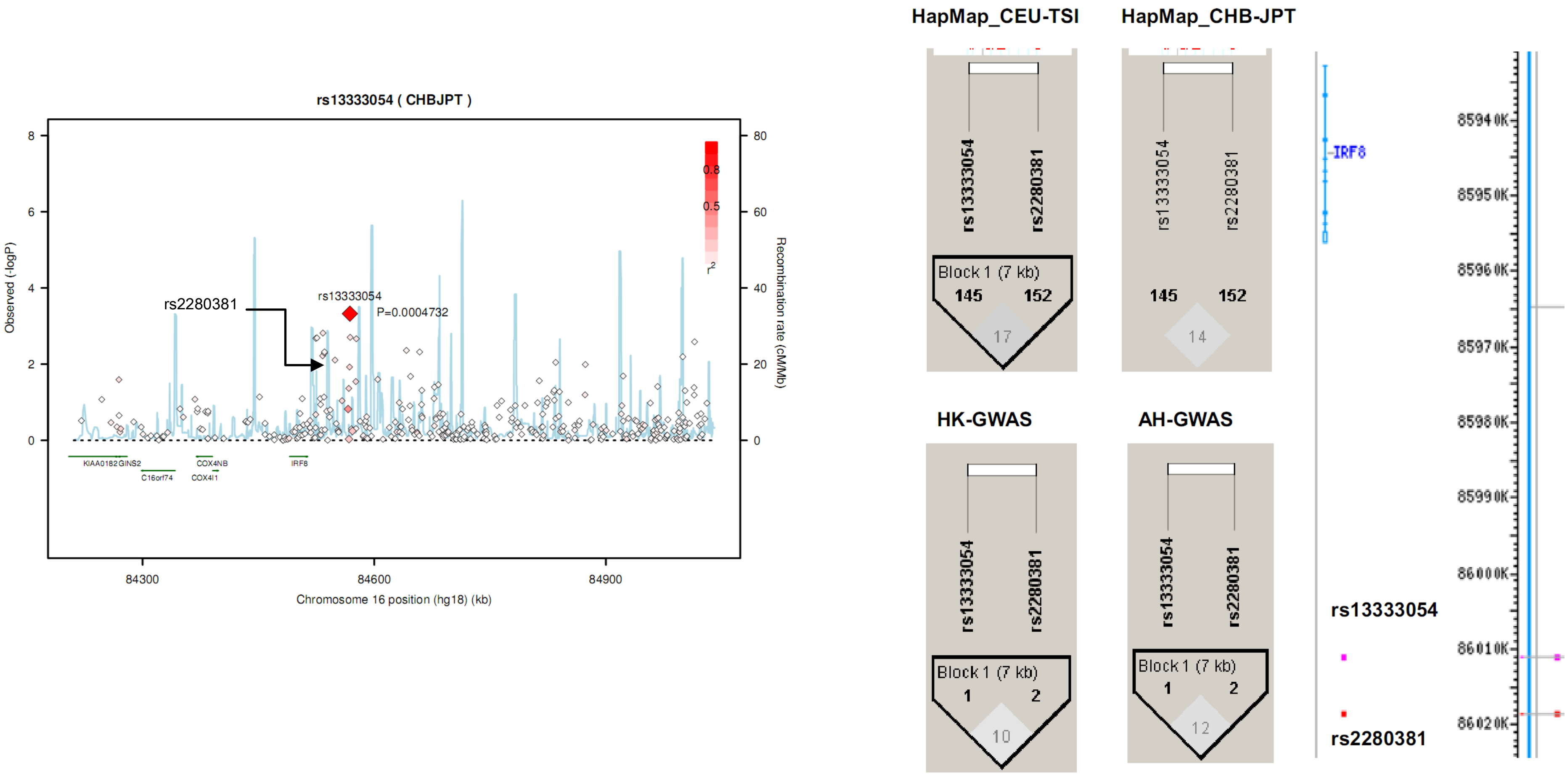

Figure S4. LD between rs13333054 Identified in This Study and rs2280381 Reported in a European Study on SLE in the *IRF8* Locus

(Left panel) Regional association plots show association from meta-analysis ($-\log_{10}(p_{meta})$) versus chromosomal position (Kb) for all the SNPs in a 500 kb region centered on rs13333054. p_{meta} values are plotted for all SNPs shaded white to red by the degree of LD (r^2; see insets) with rs13333054. Local recombination rates estimated from HapMap CHB-JPT (cM/Mb, blue lines) are plotted against the secondary y axis, showing recombination hotspots across the region and haplotype blocks in between.

(Right panel) LD between rs13333054 and rs2280381 in different cohorts and the relative positions of the two SNPs and their position relative to gene *IRF8* shown in MapViewer. There is minimal LD between the two SNPs in both Europeans and Asians. Association from rs2280381 is likely dependent on that of rs13333054 in Asian populations.

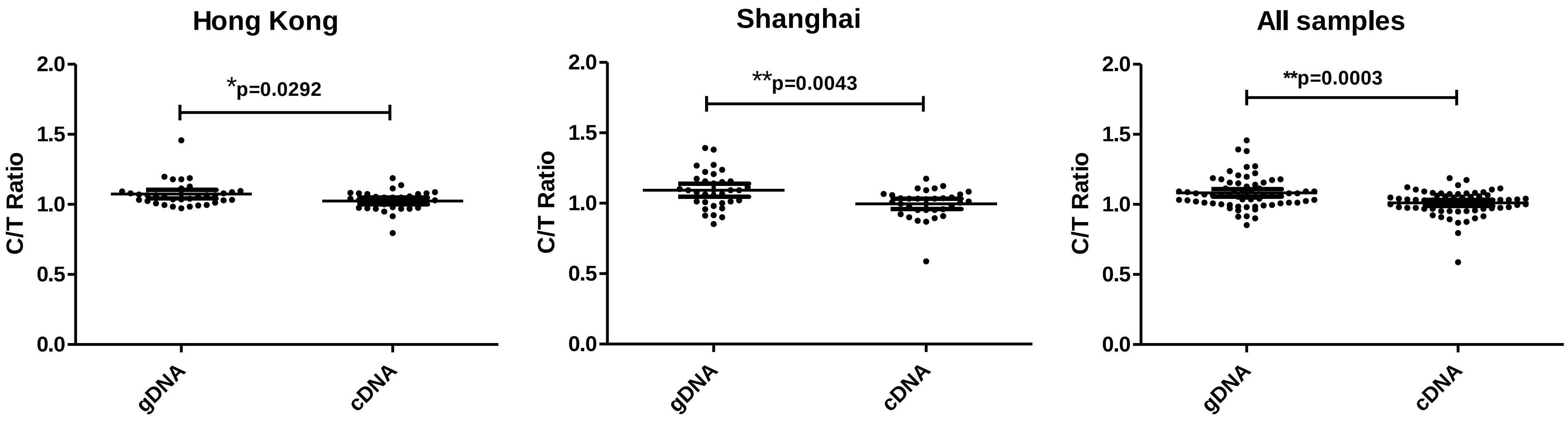

Figure S5. Allelic Expression of *CDKN1B* for SNP rs34330 in PBMC of Healthy Controls

PBMC cDNA from 67 healthy individuals heterozygous on rs34330 were used for allelic expression comparison of *CDKN1B* by pyrosequencing. The ratio of C/T allelic expression was detected using both DNA and cDNA for each sample.

Two cohorts were used in this assay. The first cohort contains 34 Hong Kong healthy controls and the experiment was conducted in Hong Kong (left panel). The median C/T ratio for DNA was measured at 1.060 (95% CI: 1.042–1.105) and the median C/T ratio for cDNA was 1.028 (95% CI: 1.000–1.049). A small but significant difference was observed (P = 0.0292) when comparing the two ratios using paired student's *t* test.

(Central panel) A second cohort (n=33), also samples of healthy individuals from Hong Kong, was sent for testing in Shanghai (Joint Molecular Rheumatology Laboratory of the Institute of Health Sciences and Shanghai Renji Hospital, Chinese Academy of Sciences and Shanghai Jiaotong University, Shanghai, China). The median C/T ratio for DNA was measured at 1.092 (95% CI: 1.046–1.139) and the median C/T ratio for cDNA expression was 1.012 (95% CI: 0.9587–1.033), and P = 0.0043 by paired student's *t* test.

If all the healthy individuals heterozygous on rs34330 (n = 67) were pooled together (right panel), the median C/T ratio for DNA was 1.066 (95% CI: 1.055–1.110) and the median C/T ratio for cDNA was 1.028 (95% CI: 0.9887–1.032) and P = 0.0003 by paired student's t test. It seems that the risk allele C is corresponding to a relatively lower expression of *CDKN1B* in PBMC of the healthy controls.

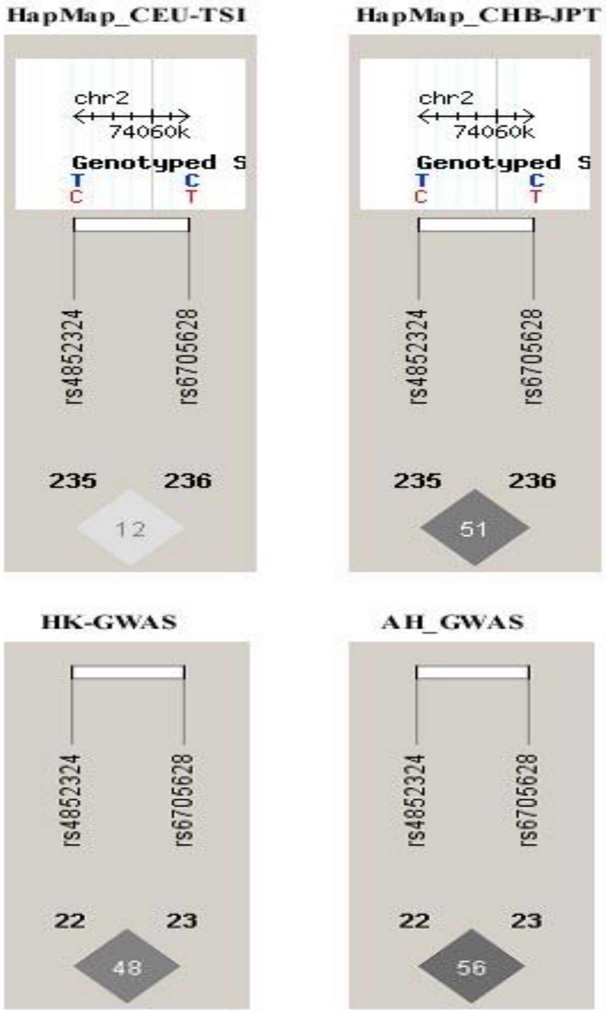

Figure S6. **LD between rs4852324 and rs6705628 in the *DGUOK/TET3* Region**

Table S1. Meta-analysis Results on Reported Susceptibility Loci (p_{meta} < 1E-4)

SNP	Genes	A1/A2	Hong Kong GWAS Results				Anhui GWAS Results				Meta-analysis
			Cases	Controls	OR	p	Cases	Controls	OR	p	p_{meta}
rs4522865*	*BANK1*	G/A	0.39	0.46	0.74	6.2E-06	0.35	0.39	0.87	2.6E-02	5.0E-06
rs4276281		C/A	0.53	0.47	1.25	4.7E-04	0.43	0.40	1.14	2.9E-02	1.1E-04
rs10516487***		T/C	0.15	0.19	0.74	6.1E-04	0.11	0.14	0.82	2.6E-02	1.2E-04
rs10516486		G/A	0.53	0.47	1.25	6.0E-04	0.43	0.40	1.14	3.3E-02	1.6E-04
rs13129744		C/T	0.16	0.20	0.75	7.5E-04	0.12	0.14	0.84	5.4E-02	3.2E-04
rs2254546	*BLK*	A/G	0.20	0.27	0.67	6.5E-07	0.17	0.25	0.65	7.6E-09	1.5E-13
rs7812879		T/C	0.20	0.27	0.69	2.3E-06	0.17	0.25	0.65	5.0E-09	3.4E-13
rs1564267		T/C	0.20	0.27	0.69	2.5E-06	0.18	0.25	0.65	4.5E-09	3.5E-13
rs13277113*		G/A	0.23	0.30	0.69	6.6E-07	0.22	0.29	0.69	6.9E-08	1.1E-12
rs2736340***		C/T	0.22	0.29	0.69	7.6E-07	0.20	0.27	0.69	1.9E-07	3.3E-12
rs9270984	*HLA-DRB1*	T/G	0.28	0.18	1.73	1.3E-13	0.25	0.16	1.73	1.9E-13	4.6E-24
rs9271055		G/T	0.28	0.18	1.73	1.6E-13	0.25	0.16	1.73	2.5E-13	7.4E-24
rs9271100		T/C	0.29	0.19	1.69	7.9E-13	0.27	0.18	1.68	8.5E-13	1.0E-22
rs9271366***		G/A	0.21	0.14	1.67	4.3E-10	0.21	0.14	1.67	8.1E-11	2.4E-18
rs660895		G/A	0.19	0.26	0.68	9.4E-07	0.15	0.22	0.63	4.4E-09	1.3E-13
rs10276619	*IKZF1*[a]	A/G	0.33	0.37	0.85	1.7E-02	0.33	0.39	0.77	3.3E-05	5.9E-06
rs4917014**		G/T	0.26	0.29	0.86	3.7E-02	0.26	0.32	0.75	1.0E-05	6.7E-06
rs11761913		T/C	0.07	0.10	0.66	7.3E-04	0.09	0.11	0.74	2.8E-03	1.4E-05
rs12669163		A/C	0.32	0.35	0.88	6.5E-02	0.28	0.34	0.78	1.8E-04	1.0E-04

rs1456893		A/G	0.32	0.35	0.88	7.2E-02	0.28	0.34	0.78	1.5E-04	1.1E-04
rs960633	*IRF5*	T/G	0.14	0.12	1.22	4.0E-02	0.13	0.11	1.24	1.8E-02	2.3E-03
rs729302		C/A	0.26	0.34	0.68	1.6E-07	0.29	0.34	0.79	2.3E-04	1.2E-09
rs4728142***		A/G	0.18	0.13	1.51	1.9E-06	0.18	0.14	1.38	9.0E-05	3.0E-09
rs2231241	*NCF2* [b]	T/C	0.12	0.09	1.42	4.7E-04	0.07	0.06	1.32	2.3E-02	8.8E-05
rs11811536		A/C	0.12	0.09	1.42	5.0E-04	0.07	0.06	1.31	2.7E-02	1.1E-04
rs2296164		G/A	0.41	0.39	1.06	4.1E-01	0.42	0.38	1.20	2.4E-03	6.9E-03
rs2274064		A/G	0.39	0.38	1.03	6.4E-01	0.42	0.37	1.21	1.5E-03	1.1E-02
rs3845466		A/G	0.27	0.26	1.08	3.0E-01	0.25	0.22	1.16	3.3E-02	2.8E-02
rs742108	*PRDM1-ATG5* [c]	T/C	0.39	0.34	1.24	1.1E-03	0.36	0.32	1.24	5.6E-04	4.0E-06
rs548234**		C/T	0.33	0.29	1.22	4.3E-03	0.32	0.27	1.28	1.7E-04	5.2E-06
rs6568431		A/C	0.41	0.36	1.24	1.2E-03	0.38	0.33	1.23	8.5E-04	6.6E-06
rs1040411		G/A	0.45	0.39	1.27	3.2E-04	0.41	0.38	1.15	2.2E-02	6.1E-05
rs633724		T/C	0.48	0.45	1.11	1.2E-01	0.47	0.42	1.24	4.5E-04	4.4E-04
rs7574865*	*STAT4*	T/G	0.46	0.34	1.63	8.4E-14	0.42	0.33	1.50	7.7E-11	1.3E-21
rs10168266		T/C	0.46	0.34	1.64	4.3E-14	0.42	0.34	1.45	2.1E-09	2.3E-20
rs7601754*		G/A	0.10	0.15	0.62	4.0E-06	0.10	0.14	0.66	1.1E-05	6.8E-10
rs16833239		A/G	0.07	0.11	0.57	5.4E-06	0.07	0.10	0.62	1.5E-05	1.2E-09
rs7594501		A/G	0.07	0.11	0.57	4.9E-06	0.07	0.10	0.63	2.2E-05	1.6E-09
rs2230926***	*TNFAIP3*	G/T	0.06	0.02	2.71	6.9E-11	0.08	0.04	1.74	1.4E-05	1.4E-13
rs3757173		C/T	0.07	0.03	2.00	5.6E-07	0.09	0.06	1.48	4.8E-04	7.2E-09
rs670369		C/T	0.11	0.08	1.45	4.6E-04	0.14	0.11	1.37	4.7E-04	1.6E-06

rs619796		T/C	0.10	0.08	1.37	3.8E-03	0.14	0.10	1.39	3.8E-04	9.4E-06
rs774628		A/G	0.11	0.09	1.30	1.2E-02	0.14	0.11	1.37	5.8E-04	4.2E-05
rs2205960***		T/G	0.32	0.25	1.36	1.6E-05	0.34	0.26	1.46	6.6E-09	3.2E-12
rs10489265		G/T	0.32	0.26	1.36	1.5E-05	0.34	0.26	1.44	2.0E-08	7.6E-12
rs1012507	*TNFSF4*	T/G	0.35	0.29	1.31	8.8E-05	0.37	0.29	1.41	8.2E-08	1.6E-10
rs704840		G/T	0.48	0.42	1.28	1.7E-04	0.48	0.40	1.39	4.6E-08	1.9E-10
rs844648*		G/A	0.46	0.51	0.84	6.9E-03	0.46	0.54	0.74	4.3E-07	7.9E-08
rs10036748**		C/T	0.22	0.26	0.80	3.5E-03	0.21	0.25	0.76	1.2E-04	3.2E-06
rs13168551		T/C	0.22	0.26	0.79	2.0E-03	0.20	0.25	0.77	3.1E-04	4.0E-06
rs4958894	*TNIP1* [d]	T/C	0.34	0.40	0.79	6.1E-04	0.32	0.37	0.81	1.1E-03	4.6E-06
rs4958893		T/C	0.28	0.32	0.80	1.8E-03	0.28	0.33	0.80	7.9E-04	8.9E-06
rs868641		A/G	0.28	0.32	0.81	2.4E-03	0.28	0.33	0.80	8.4E-04	1.2E-05
rs5754217***		G/T	0.41	0.44	0.89	8.7E-02	0.46	0.53	0.75	1.2E-06	4.9E-06
rs4821112		G/A	0.42	0.45	0.88	5.0E-02	0.45	0.52	0.76	5.3E-06	6.0E-06
rs463426**	*UBE2L3*	C/T	0.42	0.45	0.89	8.4E-02	0.46	0.53	0.78	4.2E-05	5.2E-05
rs465500		G/A	0.42	0.45	0.90	9.4E-02	0.47	0.53	0.78	3.4E-05	5.2E-05
rs131654**		G/T	0.38	0.40	0.93	2.5E-01	0.48	0.41	1.29	2.1E-05	1.5E-04
rs3734266		G/A	0.19	0.13	1.56	2.0E-07	0.18	0.12	1.54	2.3E-07	1.2E-12
rs205284		A/G	0.18	0.12	1.63	2.6E-08	0.16	0.11	1.51	3.2E-06	2.8E-12
rs3734261	*UHRF1BP1* [e]	T/C	0.18	0.12	1.60	6.6E-08	0.16	0.11	1.50	3.2E-06	6.2E-12
rs7764921		A/C	0.18	0.12	1.61	4.6E-08	0.17	0.12	1.47	6.0E-06	8.7E-12
rs13205210*		C/T	0.19	0.13	1.57	1.8E-07	0.17	0.12	1.49	2.7E-06	1.2E-11

rs12599402**		G/A	0.37	0.44	0.78	1.3E-04	0.36	0.42	0.81	4.9E-04	5.4E-07
rs2903692		G/A	0.31	0.35	0.84	1.5E-02	0.30	0.34	0.83	3.7E-03	9.0E-05
rs17673553	*CLEC16A*	G/A	0.32	0.37	0.83	5.6E-03	0.32	0.36	0.85	1.2E-02	1.7E-04
rs9933507		A/G	0.19	0.23	0.82	1.5E-02	0.21	0.25	0.79	1.2E-03	2.4E-04
rs12103174		G/A	0.05	0.08	0.67	4.2E-03	0.08	0.10	0.75	8.4E-03	3.1E-04
rs1143678*		T/C	0.03	0.02	1.84	1.9E-03	0.01	0.00	3.09	1.3E-02	8.7E-05
rs1143683		T/C	0.03	0.02	1.84	1.9E-03	0.01	0.00	3.09	1.3E-02	8.6E-05
rs7193268	*ITGAM*	T/C	0.03	0.02	1.84	1.9E-03	0.01	0.00	3.09	1.3E-02	8.7E-05
rs9888739		T/C	0.03	0.02	1.84	2.1E-03	0.01	0.00	3.48	1.0E-02	7.3E-05
rs9937837		G/T	0.04	0.02	1.86	6.8E-04	0.01	0.00	3.67	3.0E-03	7.4E-06

* SNP reported previously in studies based on Hong Kong GWAS [1-5]

** SNP reported previously in studies based on Anhui GWAS [6,7]

*** SNP reported previously in studies based on Caucasian GWAS [8,9]

a. The Caucasian study reported SNP rs2366293, which has no LD with SNPs listed here based on either HapMap Release22 CEU data or HapMap Release22 CHB&JPT data [8]

b. The Caucasian study reported SNP rs10911363, which has intermediate LD with rs2274064 (r^2=0.449) based on HapMap Release22 CEU data, r^2=0.386 based on HapMap Release22 CHB&JPT data [8]

c. The Caucasian study reported SNP rs2245214, which has r^2 = 0.934 with rs633724 based on HapMap Release22 CEU data, r^2=0.837 based on HapMap Release22 CHB&JPT data [9]

d. The Caucasian study reported SNP rs7708392, which has r^2=0.906 with rs10036748 based on HapMap Release22 CEU data, r^2=0.835 based on HapMap Release22 CHB&JPT data[9]

e. The Caucasian study reported SNP rs11755393, which has intermediate LD with rs3734266 (r^2=0.374) based on HapMap Release22 CEU data, and r^2=0.220 based on HapMap Release22 CHB&JPT data [5,9]

Table S2. Meta-analysis Results on Reported Susceptibility Genes (1E-4 < p_{meta} < 0.01)

SNP	Genes	A1/A2	Hong Kong GWAS Results				Anhui GWAS Results				Meta-analysis
			Cases	Controls	OR	p	Cases	Controls	OR	p	p_{meta}
rs4657039	*FCGR2A*	G/A	0.31	0.27	1.20	1.1E-02	0.30	0.28	1.12	8.4E-02	3.6E-03
rs6696854		C/T	0.33	0.30	1.18	1.6E-02	0.32	0.30	1.09	1.7E-01	9.8E-03
rs10800309		G/A	0.33	0.30	1.17	2.0E-02	0.32	0.30	1.10	1.4E-01	9.5E-03
rs1801274***		C/T	0.36	0.33	1.18	1.7E-02	0.36	0.34	1.10	1.4E-01	8.6E-03
rs2431097	*PTTG1*	*A/G*	0.26	0.24	1.11	1.7E-01	0.26	0.21	1.32	9.0E-05	2.2E-04
rs17057846		*A/G*	0.22	0.20	1.15	7.4E-02	0.24	0.20	1.26	1.2E-03	5.1E-04
rs2431099***		*T/C*	0.31	0.34	0.85	2.1E-02	0.36	0.40	0.85	1.0E-02	8.0E-04
rs4921283		*G/A*	0.34	0.37	0.85	1.6E-02	0.40	0.43	0.89	4.5E-02	2.6E-03
rs1862390		*G/A*	0.35	0.38	0.90	1.2E-01	0.36	0.39	0.85	1.0E-02	4.4E-03
rs896126	*Lyn*	*C/T*	0.28	0.32	0.83	7.5E-03	0.28	0.31	0.86	2.0E-02	7.1E-04
rs765158		*T/C*	0.26	0.30	0.82	7.5E-03	0.26	0.29	0.86	2.7E-02	9.2E-04
rs6997351		*G/A*	0.29	0.33	0.84	1.1E-02	0.27	0.31	0.86	1.9E-02	1.0E-03
rs11986856		*C/T*	0.29	0.33	0.84	1.1E-02	0.27	0.31	0.86	1.9E-02	1.0E-03
rs7829816***		*G/A*	0.01	0.02	0.69	2.2E-01	0.03	0.02	1.02	9.3E-01	4.6E-01
rs2732547	*PDHX-CD44*	*A/G*	0.21	0.23	0.88	1.1E-01	0.22	0.26	0.80	1.4E-03	8.2E-04
rs497476		*A/G*	0.45	0.50	0.84	9.3E-03	0.47	0.51	0.87	2.5E-02	8.7E-04
rs2732520		*C/T*	0.45	0.49	0.84	6.7E-03	0.48	0.51	0.88	3.5E-02	9.2E-04
rs2785160		*G/A*	0.45	0.49	0.85	9.5E-03	0.48	0.51	0.88	3.1E-02	1.1E-03
rs2785157		*T/C*	0.51	0.47	1.14	4.9E-02	0.48	0.44	1.18	6.2E-03	1.1E-03

rs2785197***		*T/C*	0.21	0.23	0.88	1.0E-01	0.22	0.26	0.80	1.3E-03	7.7E-04
rs305059	*IRF8*	*G/A*	0.18	0.21	0.82	1.7E-02	0.20	0.22	0.86	4.0E-02	2.1E-03
rs10521318		*A/G*	0.06	0.08	0.75	3.0E-02	0.07	0.09	0.80	3.7E-02	2.7E-03
rs2934498		*G/A*	0.32	0.30	1.11	1.5E-01	0.38	0.34	1.20	4.2E-03	2.8E-03
rs419030		*T/C*	0.33	0.30	1.12	9.6E-02	0.38	0.34	1.18	9.2E-03	2.9E-03
rs2280381***		*G/A*	0.11	0.13	0.83	7.1E-02	0.11	0.13	0.90	2.3E-01	3.4E-02
rs13333054		*T/C*	0.52	0.47	1.18	9.4E-03	0.47	0.44	1.15	1.8E-02	6.9E-04

* SNP reported previously in studies based on Hong Kong GWAS [1-5]

** SNP reported previously in studies based on Anhui GWAS [6,7]

*** SNP reported previously in studies based on GWAS on European populations [8-10]

Table S3. Meta-analysis Results on Reported Susceptibility Genes with p_{meta} > 0.01 Based on the SNPs Interrogated in Illumina 610 Quad 200Kb Upstream and Downstream of the Reported SNP

SNP	Gene Symbol	A1/A2	Hong Kong GWAS Results				Anhui GWAS Results				Meta-analysis	Previous Report			
			Cases	Controls	OR	p	Cases	Controls	OR	p	p_{meta}	Risk Allele/Freq	OR^b	p	REF
rs2052401	*IFIH1*	T/C	0.30	0.31	0.95	0.44	0.30	0.33	0.90	0.09	0.09				
rs2241242		G/A	0.31	0.32	0.95	0.43	0.32	0.35	0.89	0.06	0.06				
rs2075302		C/T	0.17	0.15	1.15	0.10	0.16	0.15	1.09	0.31	0.07				
rs3788964		G/A	0.31	0.34	0.87	0.04	0.33	0.35	0.91	0.15	0.02				
rs1990760***		T/C	0.21	0.19	1.16	0.07	0.21	0.20	1.03	0.72	0.14	T/0.61	0.87	1.6E-08	8
rs6598025	*PHRF1*	A/G	0.41	0.43	0.92	0.20	0.44	0.47	0.89	0.05	0.02				
rs4074794		C/T	0.42	0.44	0.92	0.20	0.43	0.45	0.92	0.16	0.06				
rs3758650		A/G	0.09	0.10	0.84	0.12	0.11	0.12	0.92	0.35	0.09				
rs936466		A/G	0.09	0.09	0.89	0.32	0.13	0.14	0.88	0.16	0.10				
rs4963128***		A/G	0.07	0.08	0.91	0.47	0.05	0.06	0.91	0.47	0.32	C/0.67	0.83	4.9E-09	9
rs13434020	*PXK* [a]	G/T	0.25	0.24	1.08	0.31	0.24	0.22	1.13	0.09	0.06				
rs1127745		C/T	0.25	0.24	1.08	0.32	0.24	0.22	1.13	0.09	0.06				
rs9853873		C/T	0.24	0.22	1.13	0.12	0.24	0.22	1.08	0.27	0.07				
rs4681690		G/T	0.26	0.25	1.05	0.47	0.25	0.24	1.10	0.19	0.16				
rs6445975*/***		G/T	0.17	0.17	0.99	0.93	0.22	0.21	1.05	0.47	0.65	G/0.28	1.25	7.1E-09	9
rs6693578	*IL10*	C/T	0.45	0.41	1.17	0.02	0.50	0.48	1.07	0.26	0.02				
rs4844540		G/A	0.47	0.43	1.17	0.02	0.51	0.49	1.07	0.26	0.02				

rs94872		G/A	0.49	0.44	1.22	0.00	0.37	0.36	1.02	0.76	0.02				
rs2000056		G/A	0.40	0.35	1.27	0.00	0.28	0.29	0.98	0.74	0.03				
rs3024505***		T/C	0.02	0.03	0.66	0.07	0.04	0.05	0.85	0.26	0.05	A/0.16	1.19	4.0E-08	9
rs849142***	*JAZF1*	monomorphic in HapMap CHB									NA#	T/0.49	1.19	1.5E-09	8
rs2158622		T/C	0.09	0.10	0.92	0.49	0.11	0.14	0.79	0.01	0.02				
rs122362		C/A	0.10	0.12	0.82	0.07	0.11	0.12	0.88	0.19	0.03				
rs10951190		C/T	0.17	0.17	1.00	0.99	0.21	0.24	0.83	0.01	0.07				
rs7456467		A/G	0.46	0.44	1.08	0.23	0.42	0.40	1.09	0.16	0.07				
rs2476601***	*PTPN22*	A/G A allele with very low frequency									NA#	A/0.10	1.26	3.1E-12	
rs7545038		A/G	0.18	0.16	1.12	0.19	0.13	0.12	1.08	0.37	0.12				
rs2040041		T/C	0.04	0.05	0.78	0.12	0.04	0.04	0.96	0.78	0.20				
rs2476599		A/G	0.04	0.05	0.80	0.15	0.04	0.04	0.96	0.79	0.23				
rs1217394		G/A	0.16	0.15	1.08	0.38	0.13	0.12	1.07	0.48	0.27				
rs2304240	*TYK2*	A/G	0.13	0.14	0.92	0.38	0.13	0.16	0.82	0.02	0.02				
rs35193259		G/A	0.20	0.22	0.90	0.17	0.25	0.27	0.88	0.06	0.02				
rs12462703		C/T	0.20	0.22	0.90	0.17	0.25	0.27	0.88	0.06	0.02				
rs280519***		A/G	0.35	0.36	0.96	0.59	0.45	0.45	0.99	0.91	0.66	A/0.47	NA	3.9E-08	8
rs2053769	AFF1	T/C	0.42	0.46	0.87	3.2E-02	0.41	0.42	0.94	0.33	0.04				
rs340639		A/G	0.44	0.48	0.87	3.4E-02	0.42	0.42	0.97	0.57	0.07				
rs340637		G/A	0.44	0.47	0.87	4.0E-02	0.41	0.42	0.97	0.57	0.08				
rs340630***		G/A	0.43	0.47	0.88	4.6E-02	0.42	0.43	0.96	0.53	0.08	A/0.56	0.7937	8.3E-09	12

* SNP reported previously in studies based on Hong Kong GWAS [1-5,11]

** SNP reported previously in studies based on Anhui GWAS [6,7]

*** SNP reported previously in studies based on another GWAS [8,9,12]

#NA : Not available

a. rs2176082 which proved to be associated with SLE in Caucasians, has absolute LD with rs6445975 based on HapMap Release22 CEU data [2], r2=0.962 in HapMap CHB+JPT data

b. ORs were converted to the notion used for our results. OR<1 indicates that the risk allele is major allele and OR>1 indicates that the risk allele is minor allele.

Table S4. Susceptibility SNPs Only Detected in Studies on Asian Populations as of Aug. 2012

SNP	Gene Symbol	A1/A2	Hong Kong GWAS Results				Anhui GWAS Results				Meta-analysis
			Cases	Controls	OR	p	Cases	Controls	OR	p	p_{meta}
rs1913517*	*WDFY4*	A/G	0.33	0.27	1.38	5.7E-04	0.33	0.29	1.28	1.3E-03	3.1E-06
rs877819*	*WDFY4*	A/G	0.24	0.18	1.46	1.1E-06	0.20	0.16	1.32	3.3E-04	8.1E-09
rs4639966**	*DDX6*	G/A	0.45	0.42	1.12	1.9E-01	0.34	0.28	1.39	2.4E-05	4.8E-05
rs6590330**	*ETS1*	A/G	0.44	0.35	1.51	2.7E-06	0.41	0.34	1.37	1.3E-05	3.1E-08
rs10893872*	*ETS1*	A/G	0.48	0.43	1.23	1.5E-03	0.47	0.41	1.26	1.6E-04	1.8E-06
rs10847697**	*SLC15A4*	A/G	0.23	0.17	1.41	1.3E-03	0.26	0.21	1.31	1.2E-03	1.1E-07
rs1385374**	*SLC15A4*	A/G	0.23	0.17	1.41	1.1E-03	0.26	0.21	1.32	9.2E-04	7.5E-08
rs7329174*	*ELF1*	G/A	0.28	0.21	1.45	4.0E-07	0.23	0.21	1.13	1.0E-01	6.2E-06
rs7197475**	*ZNF689/PRR14*	A/G	0.13	0.13	1.03	8.4E-01	0.10	0.07	1.58	6.5E-04	1.6E-03
rs13385731**	*RASGRP3*	G/A	0.13	0.17	0.72	8.6E-03	0.11	0.15	0.64	2.8E-05	4.4E-06
rs1167796**	*HIP1*	A/G	0.29	0.30	0.92	4.0E-01	0.23	0.28	0.80	4.7E-03	8.8E-05
rs704853*	*CD247*	A/C	0.17	0.22	0.72	8.7E-05	0.16	0.18	0.88	1.05E-01	1.79E-04
rs858543*		C/T	0.52	0.47	1.24	8.4E-04	0.47	0.44	1.12	6.09E-02	4.00E-04

* previously published in studies based on Hong Kong GWAS data [3]

** previously published in studies based on Anhui GWAS data [6]

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Table S5. Detailed Association Information for SNPs Listed in Table 1

Discovery Panel

SNP	A1/A2	Hong Kong GWAS Results 612 Cases; 2,193 Controls				Anhui GWAS Results 1,044 Cases; 1,201 Controls			
		Cases	Controls	OR	p	Cases	Controls	OR	p
rs4852324	C/T	0.13	0.19	0.63	4.4E-07	0.21	0.25	0.78	3.9E-04
rs6705628	T/C	0.10	0.16	0.62	2.5E-06	0.18	0.22	0.77	5.5E-04
rs6804441	G/A	0.31	0.36	0.82	3.8E-03	0.30	0.34	0.80	6.5E-04
rs4948496	T/C	0.32	0.38	0.78	3.8E-04	0.34	0.37	0.89	6.2E-02
rs12822507	G/A	0.39	0.44	0.84	9.9E-03	0.37	0.41	0.84	3.4E-03
rs10845606	A/C	0.27	0.32	0.77	2.7E-04	0.24	0.28	0.83	4.9E-03
rs34330	T/C	0.43	0.50	0.77	8.2E-05	0.45	0.47	0.91	1.3E-01
rs4622329	G/A	0.34	0.39	0.82	3.2E-03	0.40	0.44	0.85	6.0E-03
rs10911390	T/C	0.12	0.09	1.39	1.3E-03	0.07	0.06	1.29	3.7E-02
rs1393820	A/G	0.09	0.13	0.67	2.4E-04	0.16	0.18	0.85	4.9E-02
rs515983	C/T	0.36	0.41	0.79	6.9E-04	0.43	0.46	0.88	2.8E-02
rs11717455	C/T	0.04	0.06	0.56	4.3E-04	0.06	0.08	0.73	8.4E-03
rs2023532	T/C	0.12	0.16	0.73	1.2E-03	0.13	0.15	0.82	2.0E-02
rs2367894	A/G	0.26	0.29	0.85	3.2E-02	0.23	0.28	0.79	7.2E-04
rs12529935	T/C	0.06	0.08	0.72	1.2E-02	0.09	0.11	0.74	3.3E-03
rs6957263	C/T	0.13	0.16	0.73	1.2E-03	0.13	0.15	0.82	1.9E-02
rs2252996	G/A	0.26	0.30	0.82	6.6E-03	0.29	0.32	0.87	2.9E-02
rs4910907	G/A	0.32	0.27	1.25	1.4E-03	0.27	0.23	1.29	2.2E-04
rs12917712	T/C	0.43	0.38	1.24	1.1E-03	0.31	0.27	1.20	6.4E-03
rs12461589	T/C	0.20	0.23	0.85	4.4E-02	0.22	0.27	0.76	1.0E-04

rs2303745	A/C	0.45	0.41	1.20	6.5E-03	0.43	0.38	1.21	2.1E-03
rs13333054	T/C	0.52	0.47	1.18	9.4E-03	0.47	0.44	1.15	1.8E-02
rs2785197	T/C	0.21	0.23	0.88	1.0E-01	0.22	0.26	0.80	1.3E-03

Replication Panel

		Hong Kong Replication			Anhui Replication 1			Thailand Replication			Anhui Replication 2		
SNP	A1/A2	793 Cases; 1,063 Controls			1,359 Cases; 1,358 Controls			453 Cases, 963 Controls			1,104 Cases; 3,246 Controls		
		Cases	Controls	OR	Cases	Controls	OR	Cases	Controls	OR	Cases	Controls	OR
rs4852324	C/T	0.18	0.19	0.92	0.21	0.26	0.75	0.13	0.16	0.83	0.21	0.24	0.84
rs6705628	T/C	0.13	0.16	0.82	0.18	0.23	0.77	0.10	0.12	0.81	0.18	0.22	0.76
rs6804441	G/A	0.31	0.35	0.85	0.30	0.34	0.87	0.28	0.32	0.85	0.29	0.39	0.64
rs4948496	T/C	0.33	0.37	0.85	0.35	0.38	0.88	0.31	0.40	0.69	0.34	0.37	0.88
rs12822507	G/A	0.40	0.42	0.90	0.37	0.39	0.90	0.41	0.41	0.99	0.38	0.43	0.82
rs10845606	A/C	0.29	0.31	0.91	0.24	0.30	0.73	0.31	0.35	0.85	0.24	0.29	0.75
rs34330	T/C	0.43	0.48	0.82	0.44	0.48	0.84	0.41	0.45	0.83	0.43	0.48	0.85
rs4622329	G/A	0.38	0.39	0.97	0.39	0.45	0.76	0.27	0.35	0.70	0.41	0.44	0.89
rs10911390	T/C	0.11	0.09	1.18	0.07	0.07	1.15	0.15	0.13	1.13	0.07	0.06	1.22
rs1393820	A/G	0.12	0.13	0.89	0.16	0.17	0.89	0.10	0.12	0.80	0.16	0.17	0.97
rs515983	C/T	0.38	0.41	0.87	0.44	0.47	0.90	0.36	0.38	0.91	0.47	0.46	1.02
rs11717455	C/T	0.06	0.07	0.73	0.07	0.07	0.98	0.07	0.09	0.83	0.06	0.07	0.82
rs2023532	T/C	0.13	0.14	0.90	0.12	0.14	0.81	0.15	0.17	0.87	0.13	0.14	0.96
rs2367894	A/G	0.26	0.27	0.95	0.24	0.27	0.84	0.26	0.27	0.96	0.25	0.26	0.97
rs12529935	T/C	0.07	0.08	0.97	0.08	0.10	0.80	0.07	0.09	0.84	0.08	0.09	0.86
rs6957263	C/T	0.14	0.18	0.77	0.14	0.15	0.88	0.21	0.19	1.15	0.14	0.15	0.88

rs2252996	G/A	0.26	0.28	0.87	0.29	0.30	0.95	0.31	0.30	1.01	0.28	0.32	0.83
rs4910907	G/A	0.28	0.29	0.94	0.26	0.25	1.09	0.27	0.24	1.12	0.25	0.24	1.06
rs12917712	T/C	0.39	0.36	1.16	0.29	0.26	1.15	0.36	0.36	1.04	0.29	0.29	1.01
rs12461589	T/C	0.20	0.23	0.87	0.25	0.25	1.03	0.16	0.19	0.80	0.24	0.26	0.93
rs2303745	A/C	0.46	0.43	1.16	0.45	0.42	1.11	0.54	0.51	1.17	0.40	0.39	1.05
rs13333054	T/C	0.53	0.47	1.27	0.47	0.45	1.09	0.42	0.45	0.88	NA	NA	NA
rs2785197	T/C	0.21	0.22	0.97	0.21	0.24	0.82	0.24	0.24	1.00	0.22	0.26	0.81

Table S6. Independent Test Results on the Three SNPs in the 12p13 Locus Using Logistic Regression Conditional on the Other Two SNPs

A. Results Based on Six Cohorts Used in Both the GWAS and Replication Stages

CHR	SNP	A1	TEST	NMISS	OR	STAT	**p**
12	rs34330	T	ADD	13016	0.92	-2.72	**6.5E-03**
12	rs34330	T	rs12822507	13016	0.90	-4.36	**1.3E-05**
12	rs34330	T	rs10845606	13016	0.84	-4.98	**6.3E-07**

p = 6.5E-03 for rs34330 when conditioning on the effect of the other two SNPs, rs12822507 and rs10845606.

p = 1.3E-05 for rs12800507 when conditioning on the effect of the other two SNPs.

p = 6.3E-07 for rs10845606 when conditioning on the effect of the other two SNPs.

B. Results on Conditional Logistic Regression When Grouping the Samples into Cohorts According to Their Geographical Regions: Hong Kong, Anhui, and Thailand

CHR	SNP	A1	TEST	NMISS	OR	STAT	**p**
12	rs34330	T	ADD	13016	0.92	-2.05	**4.0E-02**
12	rs34330	T	rs12822507	13016	0.90	-5.03	**5.0E-07**
12	rs34330	T	rs10845606	13016	0.84	-7.36	**1.9E-13**

NMISS: Number of nonmissing individuals included in analysis

STAT: Coefficient t-statistic

Table S7. Independent Test Results on the Two SNPs in the *TET3/DGUOK* Region Using Logistic Regression When Conditioning on the Effect of the Other SNP

A. Based on the Six Cohorts Used in GWAS and Replication

CHR	SNP	A1	TEST	NMISS	OR	STAT	p
2	rs6705628	T	ADD	14985	0.85	-2.32	**2.0E-02**
2	rs6705628	T	rs4852324	14985	0.92	-1.62	**1.1E-01**

B. Based on Hong Kong, Anhui, and Thai Groups

CHR	SNP	A1	TEST	NMISS	OR	STAT	p
2	rs6705628	T	ADD	14985	0.85	-6.33	**2.5E-10**
2	rs6705628	T	rs4852324	14985	0.92	-4.87	**1.1E-06**

NMISS: Number of nonmissing individuals included in analysis

STAT: Coefficient t-statistic

Table S8. Gene Expression Differences between SLE Patients and Controls on the Genes Identified in This Study

A. Expression Profile of Genes Harboring SNPs Reaching Genome-wide Significance

Gene Symbol	CD4 T Cells			CD19 B Cells			Neutrophils/Myeloid Cells		
	GEO Accession	Fold Change	p Value	GEO Accession	Fold Change	p Value	GEO Accession	Fold Change	p Value
TET3	GSE4588	2.32	0.0952	GSE4588	1.32	0.4652	GSE27427	N/A	N/A
	GSE10325	-1.14	0.6275	GSE10325	1.08	0.7407	GSE10325	1.38	0.2275
CD80	GSE4588	1.43	0.2839	GSE4588	-1.84	0.2876	GSE27427	-2.70	**0.0022**
	GSE10325	1.07	0.6504	GSE10325	-1.17	0.1901	GSE10325	-1.01	0.9611
ARID5B	GSE4588	1.86	0.4113	GSE4588	1.12	0.8079	GSE27427	2.46	**0.0027**
	GSE10325	1.28	**0.0019**	GSE10325	-1.14	0.1458	GSE10325	1.10	0.8537
CDKN1B	GSE4588	-1.38	**0.0099**	GSE4588	-1.01	0.9278	GSE27427	1.05	0.5871
	GSE10325	-1.11	0.1272	GSE10325	1.02	0.8231	GSE10325	1.26	0.2716
DRAM1	GSE4588	1.10	0.6021	GSE4588	1.21	0.1202	GSE27427	N/A	N/A
	GSE10325	1.05	0.7226	GSE10325	1.02	0.8769	GSE10325	1.57	**0.0410**
CREBL2	GSE4588	-1.22	0.0840	GSE4588	-1.22	0.0575	GSE27427	1.30	**0.0382**
	GSE10325	-1.24	**0.0027**	GSE10325	-1.15	0.1279	GSE10325	1.36	0.0838
GPR19	GSE4588	1.03	0.9364	GSE4588	2.14	0.1983	GSE27427	-2.66	**0.0054**
	GSE10325	1.54	**0.0154**	GSE10325	1.39	0.3622	GSE10325	-1.30	0.1150

p values < 0.05 were bolded and underlined

B. Expression Profile of Genes Harboring SNPs with Suggestive Association

Gene Symbol	CD4 T Cells			CD19 B Cells			Neutrophils/Myeloid Cells		
	GEO Accession	Fold Change	p Value	GEO Accession	Fold Change	p Value	GEO Accession	Fold Change	p Value
RGL1	GSE4588	-1.09	0.4426	GSE4588	-1.27	0.2528	GSE27427	1.35	**0.0309**
	GSE10325	-1.25	0.0846	GSE10325	0.89	0.4042	GSE10325	3.31	**0.0300**
C1D	GSE4588	1.07	0.5047	GSE4588	-1.01	0.9254	GSE27427	5.99	**0.0045**
	GSE10325	1.01	0.8837	GSE10325	1.26	0.0900	GSE10325	1.51	0.1067
TMEM163	GSE4588	1.29	0.6192	GSE4588	1.39	0.1973	GSE27427	N/A	N/A
	GSE10325	N/A	N/A	GSE10325	N/A	N/A	GSE10325	N/A	N/A
SCN10A	GSE4588	1.16	0.6797	GSE4588	1.37	0.2591	GSE27427	-1.32	0.6403
	GSE10325	1.39	0.0606	GSE10325	-1.06	0.7946	GSE10325	-1.15	0.4728
SCN11A	GSE4588	1.19	0.5781	GSE4588	1.03	0.9474	GSE27427	1.43	0.7325
	GSE10325	1.21	0.4921	GSE10325	-1.66	0.0536	GSE10325	-1.93	**0.0284**
UBE2D3	GSE4588	1.05	0.2253	GSE4588	-1.19	**0.0085**	GSE27427	-2.02	**0.0024**
	GSE10325	1.04	0.5056	GSE10325	1.21	0.0510	GSE10325	1.51	**0.0119**
FYB	GSE4588	1.19	0.0551	GSE4588	1.19	0.4853	GSE27427	-1.10	0.5974
	GSE10325	-1.41	0.1194	GSE10325	-1.10	0.8714	GSE10325	2.16	**0.0114**
BACH2	GSE4588	-1.16	0.3827	GSE4588	-1.00	0.9741	GSE27427	2.02	**0.0158**
	GSE10325	-1.44	**0.0037**	GSE10325	-1.51	**0.0069**	GSE10325	-3.93	0.2794
PUS7	GSE4588	1.22	0.2010	GSE4588	1.06	0.7372	GSE27427	-2.78	0.1361
	GSE10325	1.24	**0.0450**	GSE10325	1.02	0.7893	GSE10325	-1.25	0.4085
SLC29A3	GSE4588	1.24	0.4273	GSE4588	1.10	0.6004	GSE27427	-4.52	0.1410
	GSE10325	1.01	0.9628	GSE10325	-1.24	0.4106	GSE10325	-1.18	0.4112
RRM1	GSE4588	-1.35	**0.0350**	GSE4588	1.02	0.8902	GSE27427	1.06	0.7506
	GSE10325	-1.12	0.3879	GSE10325	1.51	**0.0315**	GSE10325	1.28	0.3987

SEZ6L2	GSE4588	1.64	0.4670	GSE4588	1.27	0.6976	GSE27427	-3.78	0.0684
	GSE10325	1.01	0.9836	GSE10325	1.07	0.8180	GSE10325	-1.25	0.3946
PDCD5	GSE4588	1.39	**0.0151**	GSE4588	-1.30	0.2060	GSE27427	1.22	0.4191
	GSE10325	1.01	0.8569	GSE10325	1.18	0.1395	GSE10325	1.14	0.4282
DDA1	GSE4588	1.15	0.2072	GSE4588	1.05	0.7640	GSE27427	1.14	0.1551
	GSE10325	-1.04	0.7928	GSE10325	1.18	0.3715	GSE10325	1.72	**0.0019**
IRF8	GSE4588	1.13	0.6715	GSE4588	-1.02	0.7927	GSE27427	2.36	**0.0419**
	GSE10325	-1.04	0.7692	GSE10325	-1.28	0.1083	GSE10325	1.05	0.8012
PDHX	GSE4588	1.10	0.2323	GSE4588	-1.13	0.2232	GSE27427	1.13	0.6211
	GSE10325	1.01	0.9047	GSE10325	1.26	0.0720	GSE10325	1.44	0.1315
CD44	GSE4588	-1.24	0.1473	GSE4588	1.46	0.1403	GSE27427	-2.20	0.0632
	GSE10325	-1.24	0.1535	GSE10325	1.04	0.7433	GSE10325	1.24	0.2232

p values < 0.05 were **bolded** and underlined