

Supplemental Table 1. Selected SNPs associated with SLE with  $p < 1 \times 10^{-5}$  for the current study

Chr	SNP	Gene	Ref.	Chr	SNP	Gene	Ref.	Chr	SNP	Gene	Ref.	Chr	SNP	Gene	Ref.
1	rs16840639	CFHR3-1Δ	(11)	5	rs3212227	IL12B	(1)	7	rs4728142	IRF5	(3, 7)	12	rs3184504	SH2B3	(4, 1)
1	rs6677604	CFHR3-1Δ	(11)	5	rs11951576	POLS	(2, 1)	7	rs1167796	Intergenic	(2)	12	rs10847697	SLC15A4	(3)
1	rs1801274	FCGR2A	(2, 4)	5	rs2431099	PTTG1	(2)	7	rs10239340	TNPO3	(4)	12	rs1385374	SLC15A4	(3, 7)
1	rs1874791	IL12RB2	(2)	5	rs2431697	PTTG1	(8)	8	rs2248932	BLK	(3, 4)	12	rs428073	TAOK3	(2, 1)
1	rs9782955	LYST	(2)	5	rs10036748	TNIP1	(3, 7)	8	rs2254546	BLK	(7)	12	rs497273	UNQ1887	(1)
1	rs10911363	NCF2	(2, 1)	6	rs548234	ATG5	(3, 7)	8	rs2618476	BLK	(8)	13	rs7329174	ELF1	(7)
1	rs2022013	NMNAT2	(2, 4, 1)	6	rs573775	ATG5	(4)	8	rs2618479	BLK	(3)	16	rs7197475	Intergenic	(7)
1	rs2476601	PTPN22	(2, 4)	6	rs6568431	ATG5	(2, 4)	8	rs2736340	BLK	(2, 7)	16	rs11648084	IRF8	(6)
1	rs1234315	TNFSF4	(3, 10)	6	rs641153	CFB	(2, 1)	8	rs7812879	BLK	(3)	16	rs2280381	IRF8	(1)
1	rs2205960	TNFSF4	(3, 7)	6	rs3131379	HLA	(4)	8	rs7836059	C8orf12	(4)	16	rs11574637	ITGAM	(5)
1	rs10798269	RPL26P11	(4)	6	rs9501626	HLA	(7)	8	rs2667978	LYN	(4)	16	rs11860650	ITGAM	(2)
2	rs1990760	IFIH1	(2, 4, 1)	6	rs3135394	HLA-DRB1	(2)	8	rs7829816	LYN	(2,	16	rs9888739	ITGAM	(4)

										4)					
2	rs13385731	RASGRP3	(3, 7)	6	rs9271366	HLA-DRB1	(2, 7)	8	rs11783247	XKR6	(4)	16	rs9937837	ITGAM	(5)
2	rs10168266	STAT4	(7)	6	rs2230926	TNFAIP3	(3, 7)	8	rs4240671	XKR6	(4)	17	rs8076347	IKZF3	(6)
2	rs7574865	STAT4	(3, 4, 7)	6	rs5029937	TNFAIP3	(2)	8	rs6984496	XKR6	(4)	17	rs8079075	IKZF3	(6)
2	rs7601754	STAT4	(4)	6	rs5029939	TNFAIP3	(2)	8	rs6985109	XKR6	(4)	17	rs9913957	IKZF3	(6)
3	rs6438700	CD86	(2, 1)	6	rs6920220	TNFAIP3	(2)	8	rs6601327	Intergenic	(4)	17	rs1453560	ZPBP2	(6)
3	rs485499	IL12A	(6)		rs1861525	CYCS	(2, 1)	10	rs1913517	WDFY4	(7)	19	rs280519	TYK2	(2, 4, 1)
3	rs669003	IL12A	(6)	7	rs6964720	HIP1	(7)	10	rs7922169	WDFY4	(7)	22	rs2071725	SCUBE1	(2, 4)
3	rs2176082	PXK	(2)	7	rs10156091	ICA1	(2, 4, 1)	10	rs877819	WDFY4	(7)	22	rs131654	UBE2L3	(2)
3	rs6445975	PXK	(4, 7, 1)	7	rs4917014	IKZF1	(3, 7)	11	rs6590330	ETS1	(7)	22	rs463426	UBE2L3	(2, 7)
3	rs1132200	TMEM39A	(6)	7	rs10488631	IRF5	(8)	11	rs4639966	Intergenic	(7)	22	rs5754217	UBE2L3	(2, 4)
4	rs340630	AFF1	(7)	7	rs12537284	IRF5	(4)	11	rs4963128	KIAA1542	(4, 7)	23	rs2269368	IRAK1-MECP2	(2)
4	rs10516487	BANK1	(2, 8, 7, 1)	7	rs2070197	IRF5	(2)	12	rs17696736	SH2B3	(2)	23	rs3853839	TLR7	(9)

Chr, chromosome; SLE, systemic lupus erythematosus; SNP, single nucleotide polymorphism; Ref, reference

Supplemental Table 2 Gene–gene interactions among identified IgAN loci according to SNP combinations

Interaction	PXK* HLA-DRA number (cases/controls %)	CFH* HLA-DRB1	HLA-DRA* HLA-DRB1
SNP*SNP	rs6445961* rs9501626	rs6677604* rs9271366	rs9501626* rs9271366
<i>Additive interaction</i>			
0-0 (Ref.)	72(6.04)/18(2.00)	851(71.27)/525(58.27)	853(71.44)/532(59.05)
0-1	15(1.26)/18(2.00) 0.21(0.09–0.49)	247(20.69)/253(28.08) 0.60(0.49–0.74)	90(7.54)/101(11.21) 0.56(0.41–0.75)
1-0	870(72.92)/615(68.18) 0.35(0.21–0.60)	80(6.70)/67(7.44) 0.74(0.52–1.04)	78(6.53)/60(6.66) 0.81(0.57–1.16)
1-1	236(19.78)/250(27.72) 0.24(0.14–0.41)	16(1.34)/56(6.21) 0.18(0.10–0.31)	173(14.49)/208(23.08) 0.52(0.41–0.65)
AP	2.86(0.55–5.16)	–0.92(–2.85–1.01)	0.29(–0.36–0.95)
RERI	0.67(0.45–0.90)	–0.16(–0.47–0.14)	0.15(–0.19–0.49)
Synergy Index	0.53(0.47–0.60)	1.25(0.78–1.97)	0.76(0.43–1.32)
p for interaction	<b>1.51×10<sup>-2</sup></b>	0.35	0.38
<i>Multiplicative interaction</i>			

p for interaction	$6.70 \times 10^{-2}$	$1.77 \times 10^{-2}$	$3.23 \times 10^{-2}$
-------------------	-----------------------	-----------------------	-----------------------

0-0 indicates no protective allele combination; 0-1 and 1-0 indicate one with a protective allele but not with the other one; 1-1 indicates both with the protective allele.

These measures are defined as follows:

$$RERI = RR_{11} - RR_{10} - RR_{01} + 1,$$

$$AP = RERI / RR_{11},$$

$$SI = [RR_{11} - 1] / [(RR_{10} - 1) + (RR_{01} - 1)]$$

RERI, relative excess risk due to interaction; AP, attributable proportion due to interaction; and SI, the synergy index

Referent group = group with G(-) and G(-), G(-)with no protective allele.

RR<sub>11</sub> = Risk of disease in G(+)/G(+) group/Risk in reference group

RR<sub>10</sub> = Risk of disease in G(+)/G(-) group/Risk in reference group

RR<sub>01</sub> = Risk of disease in G(-)/G(+) group/Risk in reference group

If there is no biological interaction, RERI and AP = 0 and SI = 1.

Sup. Table 3 Differential gene-expression analyses of genes linked with identified novel IgAN loci.

Candidate gene	Samples								
	Renal biopsies						Whole blood		
	<u>Experiment E-GEOD-37460</u>			<u>Experiment E-GEOD-35489</u>			<u>Experiment E-GEOD-14795</u>		
IgAN (n=27)	Controls (n=27)	p	IgAN (n=25)	Controls (n=6)	p	IgAN (n=12)	Controls (n=8)	p	
<i>ADM</i>	11.38±0.61	10.98±0.55	<b>1.37×10<sup>-2</sup></b>	8.17±0.62	9.25±0.72	<b>1.12×10<sup>-2</sup></b>	1201.27±659.99	1125.89±233.29	0.72
<i>BARD</i>	5.52±0.30	5.41±0.33	0.25	5.11±0.20	5.04±0.19	0.50	171.54±89.96	200.15±124.92	0.56
<i>BCL2</i>	6.29±0.17	6.56±0.42	<b>3.12×10<sup>-3</sup></b>	5.97±0.13	5.94±0.04	0.54	59.13±52.51	102.51±100.64	0.22
<i>BCR</i>	7.75±0.36	7.81±0.30	0.45	7.42±0.24	7.34±0.21	0.43	877.31±245.42	768.40±129.32	0.27
<i>BRCA</i>	4.14±0.12	4.24±0.32	0.17	3.84±0.08	3.88±0.09	0.25	57.50±70.43	62.38±53.80	0.87
<i>C3</i>	9.18±1.64	7.90±0.66	<b>6.11×10<sup>-4</sup></b>	8.69±1.42	7.39±0.22	<b>1.54×10<sup>-4</sup></b>	153.79±144.84	68.25±42.59	0.13
<i>CBL</i>	6.13±0.20	6.20±0.25	0.32	5.14±0.17	5.25±0.18	0.19	214.39±171.89	84.91±39.13	<b>2.63×10<sup>-2</sup></b>
<i>CD1D</i>	4.91±0.44	4.71±0.37	0.08	4.20±0.11	4.18±0.11	0.70	751.28±205.60	721.90±185.35	0.74
<i>CD38</i>	6.76±0.33	6.60±0.33	0.10	6.34±0.23	6.31±0.11	0.80	301.85±243.29	304.39±136.90	0.98
<i>CD63</i>	13.12±0.22	12.92±0.21	<b>1.40×10<sup>-3</sup></b>	11.59±0.24	11.38±0.08	<b>1.07×10<sup>-3</sup></b>	5830.54±999.47	5154.65±983.69	0.15
<i>CD74</i>	11.38±0.21	11.14±0.77	0.13	10.09±0.57	9.31±0.25	<b>6.69×10<sup>-5</sup></b>	13744.27±3366.53	14337.47±2729.72	0.68
<i>CD79A</i>	6.15±0.28	6.24±0.34	0.29	5.71±0.17	5.78±0.16	0.40	1463.41±460.23	1581.10±584.93	0.62
<i>CD79B</i>	6.85±0.41	6.52±0.36	<b>3.42×10<sup>-3</sup></b>	5.26±0.15	5.26±0.15	0.95	876.31±260.02	717.94±181.27	0.15
<i>CRP</i>	4.63±0.09	4.76±0.27	<b>2.39×10<sup>-2</sup></b>	4.42±0.10	4.48±0.05	0.22	61.40±53.58	31.40±9.75	0.08
<i>CTAG1B</i>							68.15±52.89	46.99±16.15	0.22
<i>DMP1</i>	4.07±0.08	4.17±0.26	0.06	3.72±0.07	3.79±0.08	<b>3.67×10<sup>-2</sup></b>	16.44±52.89	14.06±6.48	0.75
<i>E2F4</i>	9.13±0.18	9.25±0.25	0.06	8.56±0.12	8.64±0.13	0.14	1772.88±238.87	1769.45±390.65	0.98
<i>EGFR</i>	7.16±0.16	7.41±0.28	<b>2.14×10<sup>-4</sup></b>	6.88±0.13	6.95±0.21	0.27	47.52±59.34	77.06±70.79	0.33
<i>ERBB2</i>	6.95±0.26	7.13±0.33	<b>3.02×10<sup>-2</sup></b>	7.43±0.17	7.36±0.12	0.38	46.25±27.77	69.28±84.47	0.39
<i>FCGR2A</i>							6647.87±2323.91	6323.33±1951.18	0.75

<i>FCGR2B</i>	5.92±0.79	5.42±0.36	<b><math>4.14 \times 10^{-3}</math></b>	5.27±0.38	5.17±0.18	0.52	497.32±330.72	574.34±262.31	0.89
<i>HLA-DMA</i>	10.83±0.25	10.30±0.44	<b><math>2.37 \times 10^{-6}</math></b>	8.45±0.64	7.84±0.14	<b><math>1.56 \times 10^{-4}</math></b>	2984.39±700.02	2617.08±410.23	0.20
<i>HLA-DMB</i>	10.78±0.40	10.15±0.44	<b><math>1.62 \times 10^{-6}</math></b>	8.05±0.52	7.65±0.13	<b><math>1.79 \times 10^{-3}</math></b>	3308.06±514.76	2713.27±972.99	0.15
<i>HLA-DRB3</i>							16548.89±4833.56	15362.38±4639.16	0.60
<i>HLA-DRB5</i>							380.64±246.37	455.47±118.39	0.44
<i>CFI</i>	9.78±0.84	9.94±0.51	0.41	10.52±0.24	10.15±0.10	<b><math>1.11 \times 10^{-3}</math></b>	72.60±48.33	62.37±37.08	0.62
<i>ITGAM</i>	7.21±0.80	6.42±0.66	<b><math>2.15 \times 10^{-4}</math></b>	4.73±0.24	4.67±0.15	0.59	275.50±134.79	222.10±143.77	0.41
<i>CD82</i>	7.77±0.23	7.77±0.18	1.00	7.05±0.17	7.06±0.11	0.95	804.37±319.90	829.77±282.34	0.86
<i>SMAD4</i>	7.94±0.42	8.21±0.46	<b><math>2.54 \times 10^{-2}</math></b>	6.44±0.31	6.34±0.11	0.43	130.18±76.89	64.09±50.85	<b><math>4.72 \times 10^{-2}</math></b>
<i>SMAD7</i>	8.83±0.36	8.45±0.38	<b><math>3.65 \times 10^{-4}</math></b>	6.65±0.30	7.22±0.16	<b><math>1.17 \times 10^{-4}</math></b>	269.09±111.03	299.50±146.37	0.60
<i>MAX</i>	7.65±0.13	7.63±0.25	0.68	7.52±0.08	7.49±0.09	0.53	537.63±303.02	506.51±142.20	0.79
<i>MBP</i>	6.72±0.17	6.81±0.14	<b><math>4.12 \times 10^{-2}</math></b>	5.96±0.20	6.10±0.24	0.13	699.51±282.94	759.65±264.70	0.64
<i>MYC</i>	7.25±0.64	7.43±0.89	0.38	7.49±0.61	8.29±0.37	<b><math>4.68 \times 10^{-3}</math></b>	789.59±336.65	1062.07±273.45	0.07
<i>NEDD4</i>	7.96±0.35	7.72±0.38	<b><math>2.23 \times 10^{-2}</math></b>	7.00±0.27	6.88±0.11	0.31	156.95±149.66	150.86±96.96	0.92
<i>PARK2</i>	5.26±0.11	5.61±0.47	<b><math>1.17 \times 10^{-3}</math></b>	5.87±0.18	5.94±0.06	0.38	125.53±106.04	107.97±69.02	0.69
<i>PLCG2</i>	11.03±1.03	11.25±1.12	0.47	9.47±0.32	9.45±0.28	0.90	2650.25±308.66	2650.90±446.61	1.00
<i>PTEN</i>	7.20±0.35	6.87±0.28	<b><math>3.90 \times 10^{-4}</math></b>	6.62±0.18	6.45±0.05	<b><math>2.57 \times 10^{-4}</math></b>	1499.32±473.55	1879.45±288.41	<b><math>3.89 \times 10^{-2}</math></b>
<i>PARC</i>	4.78±0.50	4.52±0.30	<b><math>2.31 \times 10^{-2}</math></b>	4.20±0.15	4.13±0.06	0.30	174.82±84.23	162.63±74.85	0.75
<i>SELL</i>	7.49±0.91	7.26±0.97	0.35	5.44±0.29	5.58±0.19	0.27	19529.63±4906.52	21071.23±6755.84	0.56
<i>AURKA</i>	6.32±0.52	5.95±0.29	<b><math>2.04 \times 10^{-3}</math></b>	4.91±0.18	4.74±0.07	<b><math>3.08 \times 10^{-2}</math></b>	103.36±59.43	84.17±56.00	0.48
<i>TAFI</i>	6.21±0.18	6.51±0.43	<b><math>2.09 \times 10^{-3}</math></b>	6.94±0.22	7.04±0.27	0.32	381.02±99.49	378.81±110.97	0.96
<i>TRA</i>							4280.94±1262.13	4182.18±1334.01	0.87
<i>TRB</i>							10608.57±2815.05	10375.70±3128.35	0.86
<i>THBS1</i>	8.17±0.30	8.45±0.35	<b><math>3.08 \times 10^{-3}</math></b>	8.00±0.27	8.06±0.27	0.57	37.76±18.98	30.66±10.08	0.35
<i>UBA1</i>	10.55±0.36	10.80±0.60	0.07	9.56±0.20	9.40±0.19	0.08	2648.89±644.43	2582.77±481.57	0.81
<i>UBE3A</i>	8.12±0.15	8.22±0.17	<b><math>2.43 \times 10^{-2}</math></b>	6.56±0.10	6.58±0.09	0.69	549.28±178.33	686.08±231.56	0.15

<i>ZAP70</i>	5.44±0.21	5.28±0.18	<b><u>2.92×10<sup>-3</sup></u></b>	4.59±0.21	4.51±0.18	0.41	1009.06±257.97	1041.08±314.32	0.81
<i>EIF4E2</i>	9.06±0.32	8.55±0.29	<b><u>1.01×10<sup>-7</sup></u></b>	7.58±0.26	7.50±0.22	0.51	572.30±229.39	572.36±132.99	1.00
<i>PDIA4</i>	9.08±0.19	8.73±0.20	<b><u>2.16×10<sup>-8</sup></u></b>	7.15±0.19	6.64±0.19	<b>3.59×10<sup>-4</sup></b>	549.55±139.67	560.36±153.08	0.88
<i>CTR9</i>	8.94±0.31	9.04±0.32	0.31	7.60±0.25	7.54±0.24	0.57	330.76±192.87	465.83±214.25	0.16
<i>RNF144A</i>	8.80±0.33	8.44±0.31	<b><u>1.30×10<sup>-4</sup></u></b>	6.20±0.19	6.18±0.09	0.77	221.17±143.05	289.51±138.67	0.30
<i>BCAS2</i>	9.38±0.24	9.50±0.30	0.11	8.53±0.20	8.64±0.19	0.22	611.30±152.41	634.24±105.79	0.72
<i>ARIH2</i>	7.46±0.13	7.49±0.10	0.30	6.46±0.07	6.52±0.11	0.13	232.06±138.98	183.63±125.90	0.44
<i>UBOX5</i>	7.61±0.20	7.90±0.36	<b><u>6.61×10<sup>-4</sup></u></b>	7.32±0.17	7.36±0.10	0.61	472.66±114.33	534.15±212.27	0.41
<i>NEDD4L</i>	8.25±0.30	8.58±0.27	<b><u>7.56×10<sup>-5</sup></u></b>	8.43±0.17	8.37±0.24	0.44	318.12±166.71	305.49±86.61	0.85
<i>ARIH1</i>	7.65±0.27	7.56±0.29	0.23	6.46±0.07	6.52±0.11	0.16	254.49±137.86	231.43±119.06	0.70
<i>RNF19A</i>	6.83±0.25	6.80±0.40	0.74	5.14±0.24	5.12±0.19	0.79	286.60±194.32	194.21±125.35	0.25
<i>RNF216</i>	6.75±0.15	6.75±0.20	0.94	5.53±0.08	5.54±0.09	0.89	566.23±134.98	547.68±155.88	0.78
<i>CCNB1IP1</i>	8.77±0.36	9.08±0.25	<b><u>6.68×10<sup>-4</sup></u></b>	8.79±0.32	8.94±0.16	0.28	286.19±98.22	280.42±113.80	0.91
<i>SMURF2</i>	7.85±0.30	7.67±0.34	<b><u>4.83×10<sup>-2</sup></u></b>	7.34±0.24	7.49±0.33	0.21	546.83±212.93	502.74±163.63	0.63

Only genes that could be retrieved in the database are shown.

p<0.05 are marked in bold, and those still significant after multiple corrections using Benjamini and Hochberg false discovery rate methods underlined.

Data are the mean ± SD.

## References:

1. Cunninghame, GD, Morris, DL, Bhangale, TR, Criswell, LA, Syvanen, AC, Ronnblom, L, Behrens, TW, Graham, RR & Vyse, TJ: Association of NCF2, IKZF1, IRF8, IFIH1, and TYK2 with systemic lupus erythematosus. *PLoS Genet*, 7: e1002341, 2011.
2. Gateva, V, Sandling, JK, Hom, G, Taylor, KE, Chung, SA, Sun, X, Ortmann, W, Kosoy, R, Ferreira, RC, Nordmark, G, Gunnarsson, I, Svenungsson, E, Padyukov, L, Sturfelt, G, Jonsen, A, Bengtsson, AA, Rantapaa-Dahlqvist, S, Baechler, EC, Brown, EE, Alarcon, GS, Edberg, JC, Ramsey-Goldman, R, McGwin, GJ, Reveille, JD, Vila, LM, Kimberly, RP, Manzi, S, Petri, MA, Lee, A, Gregersen, PK, Seldin, MF, Ronnblom, L, Criswell, LA, Syvanen, AC, Behrens, TW & Graham, RR: A large-scale

replication study identifies TNIP1, PRDM1, JAZF1, UHRF1BP1 and IL10 as risk loci for systemic lupus erythematosus. *Nat Genet*, 41: 1228-33, 2009.

3. Han, JW, Zheng, HF, Cui, Y, Sun, LD, Ye, DQ, Hu, Z, Xu, JH, Cai, ZM, Huang, W, Zhao, GP, Xie, HF, Fang, H, Lu, QJ, Xu, JH, Li, XP, Pan, YF, Deng, DQ, Zeng, FQ, Ye, ZZ, Zhang, XY, Wang, QW, Hao, F, Ma, L, Zuo, XB, Zhou, FS, Du WH, Cheng, YL, Yang, JQ, Shen, SK, Li, J, Sheng, YJ, Zuo, XX, Zhu, WF, Gao, F, Zhang, PL, Guo, Q, Li, B, Gao, M, Xiao, FL, Quan, C, Zhang, C, Zhang, Z, Zhu, KJ, Li, Y, Hu, DY, Lu, WS, Huang, JL, Liu, SX, Li, H, Ren, YQ, Wang, ZX, Yang, CJ, Wang, PG, Zhou, WM, Lv, YM, Zhang, AP, Zhang, SQ, Lin, D, Li, Y, Low, HQ, Shen, M, Zhai, ZF, Wang, Y, Zhang, FY, Yang, S, Liu, JJ & Zhang, XJ: Genome-wide association study in a Chinese Han population identifies nine new susceptibility loci for systemic lupus erythematosus. *Nat Genet*, 41: 1234-7, 2009.

4. Harley, JB, Alarcon-Riquelme, ME, Criswell, LA, Jacob, CO, Kimberly, RP, Moser, KL, Tsao, BP, Vyse, TJ, Langefeld, CD, Nath, SK, Guthridge, JM, Cobb, BL, Mirel, DB, Marion, MC, Williams, AH, Divers, J, Wang, W, Frank, SG, Namjou, B, Gabriel, SB, Lee, AT, Gregersen, PK, Behrens, TW, Taylor, KE, Fernando, M, Zidovetzki, R, Gaffney, PM, Edberg, JC, Rioux, JD, Ojwang, JO, James, JA, Merrill, JT, Gilkeson, GS, Seldin, MF, Yin, H, Baechler, EC, Li, QZ, Wakeland, EK, Bruner, GR, Kaufman, KM & Kelly, JA: Genome-wide association scan in women with systemic lupus erythematosus identifies susceptibility variants in ITGAM, PXX, KIAA1542 and other loci. *Nat Genet*, 40: 204-10, 2008.

5. Hom, G, Graham, RR, Modrek, B, Taylor, KE, Ortmann, W, Garnier, S, Lee, AT, Chung, SA, Ferreira, RC, Pant, PV, Ballinger, DG, Kosoy, R, Demirci, FY, Kamboh, MI, Kao, AH, Tian, C, Gunnarsson, I, Bengtsson, AA, Rantapaa-Dahlqvist, S, Petri, M, Manzi, S, Seldin, MF, Ronnblom, L, Syvanen, AC, Criswell, LA, Gregersen, PK & Behrens, TW: Association of systemic lupus erythematosus with C8orf13-BLK and ITGAM-ITGAX. *N Engl J Med*, 358: 900-9, 2008.

6. Lessard, CJ, Adrianto, I, Ice, JA, Wiley, GB, Kelly, JA, Glenn, SB, Adler, AJ, Li, H, Rasmussen, A, Williams, AH, Ziegler, J, Comeau, ME, Marion, M, Wakeland, BE, Liang, C, Ramos, PS, Grundahl, KM, Gallant, CJ, Alarcon-Riquelme, ME, Alarcon, GS, Anaya, JM, Bae, SC, Boackle, SA, Brown, EE, Chang, DM, Cho, SK, Criswell, LA, Edberg, JC, Freedman, BI, Gilkeson, GS, Jacob, CO, James, JA, Kamen, DL, Kimberly, RP, Kim, JH, Martin, J, Merrill, JT, Niewold, TB, Park, SY, Petri, MA, Pons-Estel, BA, Ramsey-Goldman, R, Reveille, JD, Scofield, RH, Song, YW, Stevens, AM, Tsao, BP, Vila, LM, Vyse, TJ, Yu, CY, Guthridge, JM, Kaufman, KM, Harley, JB, Wakeland, EK, Langefeld, CD, Gaffney, PM, Montgomery, CG & Moser, KL: Identification of IRF8, TMEM39A, and IKZF3-ZPBP2 as susceptibility loci for systemic lupus erythematosus in a large-scale multiracial replication study. *Am J Hum Genet*, 90: 648-60, 2012.

7. Okada, Y, Shimane, K, Kochi, Y, Tahira, T, Suzuki, A, Higasa, K, Takahashi, A, Horita, T, Atsumi, T, Ishii, T, Okamoto, A, Fujio, K, Hirakata, M, Amano, H, Kondo, Y, Ito, S, Takada, K, Mimori, A, Saito, K, Kamachi, M, Kawaguchi, Y, Ikari, K, Mohammed, OW, Matsuda, K, Terao, C, Ohmura, K, Myouzen, K, Hosono, N, Tsunoda, T, Nishimoto, N, Mimori, T, Matsuda, F, Tanaka, Y, Sumida, T, Yamanaka, H, Takasaki, Y, Koike, T, Horiuchi, T, Hayashi, K, Kubo, M, Kamatani, N, Yamada, R, Nakamura, Y & Yamamoto, K: A genome-wide association study identified AFF1 as a susceptibility locus for systemic lupus erythematosus in Japanese. *PLoS Genet*, 8: e1002455, 2012.

8. Ramos, PS, Criswell, LA, Moser, KL, Comeau, ME, Williams, AH, Pajewski, NM, Chung, SA, Graham, RR, Zidovetzki, R, Kelly, JA, Kaufman, KM, Jacob, CO, Vyse,



TJ, Tsao, BP, Kimberly, RP, Gaffney, PM, Alarcon-Riquelme, ME, Harley, JB & Langefeld, CD: A comprehensive analysis of shared loci between systemic lupus erythematosus (SLE) and sixteen autoimmune diseases reveals limited genetic overlap. *PLoS Genet*, 7: e1002406, 2011.

9. Shen, N, Fu, Q, Deng, Y, Qian, X, Zhao, J, Kaufman, KM, Wu, YL, Yu, CY, Tang, Y, Chen, JY, Yang, W, Wong, M, Kawasaki, A, Tsuchiya, N, Sumida, T, Kawaguchi, Y, Howe, HS, Mok, MY, Bang, SY, Liu, FL, Chang, DM, Takasaki, Y, Hashimoto, H, Harley, JB, Guthridge, JM, Grossman, JM, Cantor, RM, Song, YW, Bae, SC, Chen, S, Hahn, BH, Lau, YL & Tsao, BP: Sex-specific association of X-linked Toll-like receptor 7 (TLR7) with male systemic lupus erythematosus. *Proc Natl Acad Sci U S A*, 107: 15838-43, 2010.

10. Yang, W, Shen, N, Ye, DQ, Liu, Q, Zhang, Y, Qian, XX, Hiranakarn, N, Ying, D, Pan, HF, Mok, CC, Chan, TM, Wong, RW, Lee, KW, Mok, MY, Wong, SN, Leung, AM, Li, XP, Avihingsanon, Y, Wong, CM, Lee, TL, Ho, MH, Lee, PP, Chang, YK, Li, PH, Li, RJ, Zhang, L, Wong, WH, Ng, IO, Lau, CS, Sham, PC & Lau, YL: Genome-wide association study in Asian populations identifies variants in ETS1 and WDFY4 associated with systemic lupus erythematosus. *PLoS Genet*, 6: e1000841, 2010.

11. Zhao, J, Wu, H, Khosravi, M, Cui, H, Qian, X, Kelly, JA, Kaufman, KM, Langefeld, CD, Williams, AH, Comeau, ME, Ziegler, JT, Marion, MC, Adler, A, Glenn, SB, Alarcon-Riquelme, ME, Pons-Estel, BA, Harley, JB, Bae, SC, Bang, SY, Cho, SK, Jacob, CO, Vyse, TJ, Niewold, TB, Gaffney, PM, Moser, KL, Kimberly, RP, Edberg, JC, Brown, EE, Alarcon, GS, Petri, MA, Ramsey-Goldman, R, Vila, LM, Reveille, JD, James, JA, Gilkeson, GS, Kamen, DL, Freedman, BI, Anaya, JM, Merrill, JT, Criswell, LA, Scofield, RH, Stevens, AM, Guthridge, JM, Chang, DM, Song, YW, Park, JA, Lee, EY, Boackle, SA, Grossman, JM, Hahn, BH, Goodship, TH, Cantor, RM, Yu, CY, Shen, N & Tsao, BP: Association of genetic variants in complement factor H and factor H-related genes with systemic lupus erythematosus susceptibility. *PLoS Genet*, 7: e1002079, 2011.