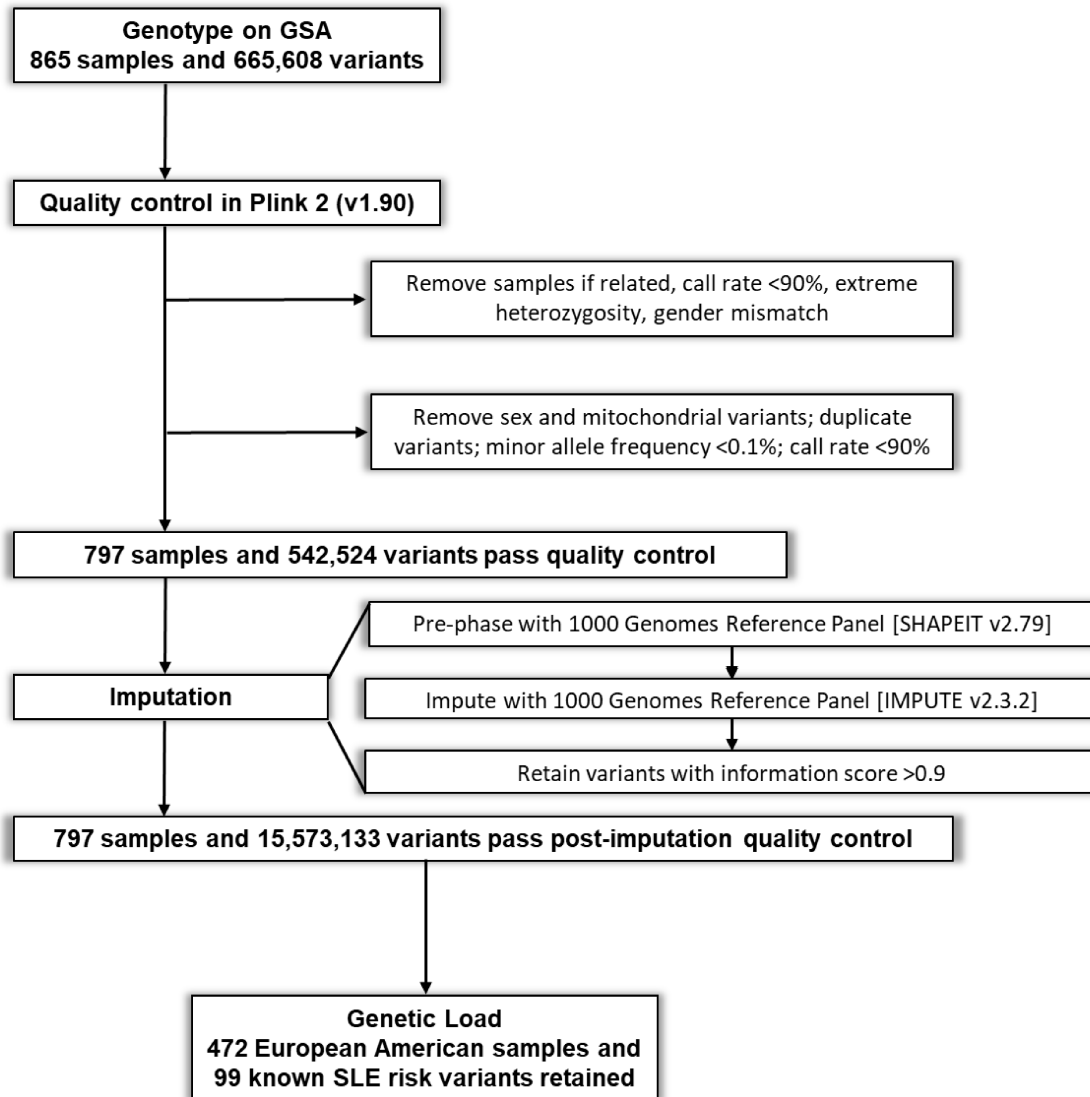
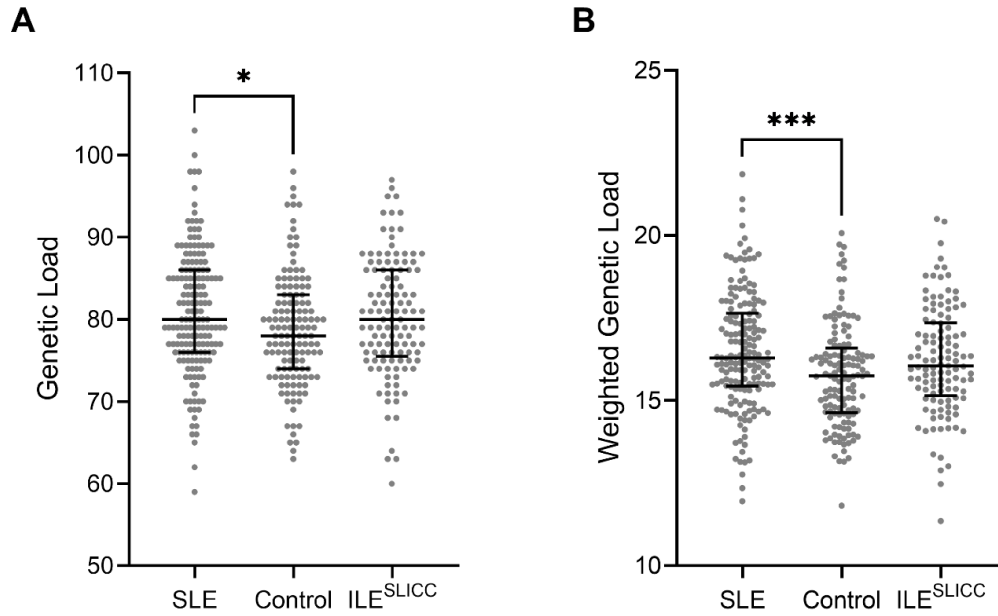


## Supplementary Material



**Supplementary Figure 1. Genotyping and quality control pipeline.** 865 study participants were genotyped on the Illumina Global Screening Array (GSA) for genetic load calculations. Following a series of quality control steps, 472 European American (EA) patients were included for genetic load calculations.



**Supplementary Figure 2. Incomplete lupus erythematosus (ILE) patients who do not meet SLICC criteria (ILE<sup>SLICC</sup>) have a trend towards increased genetic load of systemic lupus erythematosus (SLE) risk alleles, comparable to SLE patients. (A) Unweighted and (B) weighted SLE-risk allele genetic loads in European American SLE patients (n=170), ILE<sup>SLICC</sup> patients (n=117), and healthy controls (n=133). Graphs show the median and interquartile range. Statistical significance was determined using Kruskal Wallis with Dunn's posttest. \*p<0.05, \*\*\*p< 0.001.**

**Supplementary Table 1.** Systemic lupus erythematosus (SLE)-associated single nucleotide polymorphisms (SNPs) used to calculate genetic load, derived from Langefeld *et al.*[11]

SNP	Chr.	Gene Region	Risk Allele	P-value	OR (95% CI)
rs1237290	1p13	PTPN22	T	1.37x10 <sup>-6</sup>	0.86 (0.81-0.91)
rs116660017	1q23	FCGR2A	A	1.00x10 <sup>-3</sup>	0.80 (0.70-0.91)
rs10800309	1q23	FCGR2A	T	1.18x10 <sup>-7</sup>	0.88 (0.84-0.92)
rs10753074	1q25	TNFSF4-LOC100506023	C	9.54x10 <sup>-13</sup>	0.84 (0.81-0.88)
rs41263646	1q25	NMNAT2	A	1.54x10 <sup>-8</sup>	0.78 (0.71-0.85)
rs2111485	2q24	IFIH1	A	1.54x10 <sup>-9</sup>	0.87 (0.83-0.91)
rs1990760	2q24	IFIH1	C	1.69x10 <sup>-8</sup>	0.88 (0.84-0.92)
rs6715106	2q32	STAT4	G	8.33x10 <sup>-15</sup>	0.67 (0.60-0.74)
rs1132200	3q13	TMEM39A-TIMMDC1	A	1.37x10 <sup>-7</sup>	0.83 (0.77-0.89)
rs1131265	3q13	TMEM39A-TIMMDC1	C	1.42x10 <sup>-9</sup>	0.81 (0.76-0.87)
rs564976	3q25	IL12A	T	2.20x10 <sup>-10</sup>	0.87 (0.83-0.91)
rs3733345	4p16	DGKQ	G	5.84x10 <sup>-8</sup>	0.89 (0.85-0.93)
rs10516487	4q24	BANK1	T	3.58x10 <sup>-11</sup>	0.85 (0.81-0.89)
rs4426778	4q24	BANK1	T	1.03x10 <sup>-12</sup>	0.79 (0.74-0.84)
rs13126505	4q24	BANK1	A	1.69x10 <sup>-7</sup>	0.78 (0.71-0.86)
rs12526490	6q21	ATG5	C	1.48x10 <sup>-6</sup>	0.86 (0.81-0.91)
rs17779870	6q23	OLIG3-LOC100130476	C	5.35x10 <sup>-7</sup>	0.85 (0.80-0.91)
rs4917014	7p12	C7orf72-IKZF1	G	3.17x10 <sup>-9</sup>	0.87 (0.83-0.91)
rs73137125	7q11	GTF2IRD1-GTF2I	G	3.27x10 <sup>-3</sup>	0.92 (0.88-0.97)
rs7808907	7q32	IRF5-TNPO3	T	1.44x10 <sup>-31</sup>	0.77 (0.74-0.80)
rs7812879	8p23	BLK	T	1.42x10 <sup>-5</sup>	0.86 (0.80-0.92)
rs2663054	10q11	WDFY4	A	1.49x10 <sup>-8</sup>	0.83 (0.78-0.88)
rs1913517	10q11	WDFY4	C	1.19x10 <sup>-6</sup>	0.85 (0.79-0.91)
rs496312	11p15	IRF7	T	1.89x10 <sup>-15</sup>	0.83 (0.79-0.87)
rs112006329	11p15	IRF7	A	1.06x10 <sup>-16</sup>	0.81 (0.77-0.85)
rs11246217	11p15	IRF7	C	1.11x10 <sup>-16</sup>	0.81 (0.77-0.85)
rs73029013	11q24	ETS1	C	1.09x10 <sup>-5</sup>	0.70 (0.59-0.82)
rs9652601	16p13	CLEC16A	T	6.26x10 <sup>-13</sup>	0.84 (0.80-0.88)
rs12599402	16p13	CLEC16A	C	5.55x10 <sup>-11</sup>	0.86 (0.82-0.90)
rs243323	16p13	CLEC16A	C	5.51x10 <sup>-4</sup>	0.90 (0.84-0.95)
rs11117431	16q24	IRF8	G	6.25x10 <sup>-11</sup>	0.82 (0.78-0.87)
rs930297	17q25	GRB2	G	1.43x10 <sup>-7</sup>	0.83 (0.77-0.89)
rs74908652	19p13	TYK2	G	2.28x10 <sup>-9</sup>	0.83 (0.78-0.88)
rs34536443	19p13	TYK2	G	1.24x10 <sup>-21</sup>	0.52 (0.45-0.59)
rs34725611	19p13	TYK2	G	4.93x10 <sup>-23</sup>	0.78 (0.74-0.82)
rs6679677	1p13	PTPN22	A	2.02x10 <sup>-23</sup>	1.41 (1.32-1.51)
rs2476601	1p13	PTPN22	A	2.02x10 <sup>-23</sup>	1.41 (1.32-1.51)
rs1801274	1q23	FCGR2A	C	2.10x10 <sup>-8</sup>	1.13 (1.08-1.18)
rs2227203	1q24	TNFSF4-LOC100506023	T	5.90x10 <sup>-7</sup>	1.12 (1.07-1.17)
rs2205960	1q25	TNFSF4-LOC100506023	A	3.84x10 <sup>-23</sup>	1.29 (1.23-1.36)
rs3122605	1q32	IL10	G	1.22x10 <sup>-11</sup>	1.23 (1.16-1.30)
rs13023380	2q24	IFIH1	T	1.23x10 <sup>-6</sup>	1.11 (1.07-1.16)
rs7568275	2q32	STAT4	C	4.51x10 <sup>-68</sup>	1.55 (1.48-1.63)
rs7582694	2q32	STAT4	C	4.30x10 <sup>-69</sup>	1.56 (1.48-1.64)
rs6445975	3p14	PXK	C	6.27x10 <sup>-8</sup>	1.14 (1.09-1.19)
rs11130633	3p14	PXK	A	5.35x10 <sup>-8</sup>	1.14 (1.08-1.19)

rs1534154	3q13	TMEM39A-TIMMDC1	G	2.60x10 <sup>-4</sup>	1.11 (1.05-1.18)
rs78481160 <sup>d</sup>	3q25	IL12A	A	8.35x10 <sup>-6</sup>	1.44 (1.23-1.69)
rs4690229 <sup>i</sup>	4p16	DGKQ	T	1.62x10 <sup>-8</sup>	1.13 (1.09-1.19)
rs7708392 <sup>i,P</sup>	5q33	TNIP1	C	2.00x10 <sup>-24</sup>	1.29 (1.23-1.35)
rs6889239	5q33	TNIP1	C	6.73x10 <sup>-25</sup>	1.29 (1.23-1.35)
rs57095329 <sup>i,P</sup>	5q33	PTTG1-MIR146A	G	1.43x10 <sup>-3</sup>	1.25 (1.09-1.43)
rs888656	5q34	PTTG1-MIR146A	C	5.60x10 <sup>-3</sup>	1.07 (1.02-1.12)
rs10498722 <sup>d</sup>	6p22	LRRC16A	A	2.87x10 <sup>-10</sup>	1.30 (1.20-1.41)
rs35789010 <sup>i</sup>	6p22	LRRC16A	A	4.59x10 <sup>-19</sup>	1.46 (1.35-1.59)
rs4712969	6p22	SLC17A4	T	1.83x10 <sup>-22</sup>	1.42 (1.32-1.52)
rs36014129 <sup>i</sup>	6p22	SLC17A4	A	1.21x10 <sup>-24</sup>	1.50 (1.39-1.62)
rs9462027	6p21	UHRF1BP1-DEF6	T	1.88x10 <sup>-8</sup>	1.15 (1.09-1.20)
rs11755393 <sup>P</sup>	6p21	UHRF1BP1-DEF6	G	2.64x10 <sup>-6</sup>	1.11 (1.07-1.17)
rs13205210 <sup>P</sup>	6p21	UHRF1BP1-DEF6	C	1.06x10 <sup>-4</sup>	1.14 (1.07-1.22)
rs6938946 <sup>d</sup>	6p21	UHRF1BP1-DEF6	C	1.29x10 <sup>-3</sup>	1.12 (1.04-1.20)
rs6923608	6q21	ATG5	T	6.13x10 <sup>-9</sup>	1.20 (1.13-1.28)
rs548234 <sup>P</sup>	6q21	ATG5	C	5.85x10 <sup>-9</sup>	1.14 (1.09-1.20)
rs9373839	6q21	ATG5	G	3.84x10 <sup>-14</sup>	1.22 (1.16-1.29)
rs2299864 <sup>i</sup>	6q21	ATG5	T	5.77x10 <sup>-15</sup>	1.24 (1.17-1.30)
rs2327832	6q23	OLIG3-LOC100130476	C	1.76x10 <sup>-13</sup>	1.22 (1.15-1.28)
rs5029939	6q23	TNFAIP3	C	2.39x10 <sup>-29</sup>	1.81 (1.63-2.01)
rs2230926 <sup>P</sup>	6q23	TNFAIP3	C	2.79x10 <sup>-29</sup>	1.81 (1.63-2.01)
rs77000060 <sup>i</sup>	6q23	TNFAIP3	T	1.84x10 <sup>-29</sup>	1.89 (1.69-2.11)
rs10245867 <sup>i</sup>	7p15	JAZF1	T	4.31x10 <sup>-8</sup>	1.14 (1.09-1.19)
rs702814	7p15	JAZF1	C	4.67x10 <sup>-8</sup>	1.13 (1.08-1.18)
rs849142 <sup>P</sup>	7p15	JAZF1	A	1.82x10 <sup>-7</sup>	1.12 (1.08-1.17)
rs3807307	7q32	IRF5-TNPO3	C	3.75x10 <sup>-62</sup>	1.46 (1.39-1.52)
rs12706861 <sup>i</sup>	7q32	IRF5-TNPO3	T	3.85x10 <sup>-71</sup>	1.76 (1.65-1.87)
rs2955587	8p23	FAM86B3P	C	7.91x10 <sup>-10</sup>	1.15 (1.10-1.20)
rs2980512 <sup>i</sup>	8p23	FAM86B3P	C	3.54x10 <sup>-10</sup>	1.15 (1.10-1.20)
rs7831557	8p23	MSRA	G	1.22x10 <sup>-9</sup>	1.14 (1.10-1.20)
rs7819602 <sup>i</sup>	8p23	MSRA	C	9.54x10 <sup>-10</sup>	1.15 (1.10-1.20)
rs6985109 <sup>P</sup>	8p23	BLK	G	1.50x10 <sup>-8</sup>	1.13 (1.09-1.19)
rs2736336 <sup>i</sup>	8p23	BLK	T	6.46x10 <sup>-32</sup>	1.34 (1.28-1.41)
rs13277113	8p23	BLK	T	2.19x10 <sup>-31</sup>	1.34 (1.27-1.40)
rs1966115	8q21	PKIA-ZC2HC1A	A	1.43x10 <sup>-7</sup>	1.14 (1.09-1.20)
rs12114284	8q21	PKIA-ZC2HC1A	A	2.75x10 <sup>-5</sup>	1.11 (1.06-1.17)
rs2928403	10q11	WDFY4	C	7.18x10 <sup>-7</sup>	1.17 (1.10-1.25)
rs6598011	11p15	IRF7	A	1.12x10 <sup>-9</sup>	1.15 (1.10-1.21)
rs12575600	11q24	ETS1	G	5.96x10 <sup>-10</sup>	1.24 (1.16-1.33)
rs4936059	11q24	ETS1	C	2.10x10 <sup>-5</sup>	1.10 (1.05-1.16)
rs11059927	12q24	SLC15A4	C	2.44x10 <sup>-8</sup>	1.21 (1.13-1.30)
rs1385374 <sup>P</sup>	12q24	SLC15A4	T	4.35x10 <sup>-8</sup>	1.21 (1.13-1.29)
rs78318981 <sup>d</sup>	16p13	CLEC16A	A	2.91x10 <sup>-5</sup>	1.43 (1.21-1.69)
rs72799341	16p11	ITGAM	A	1.99x10 <sup>-3</sup>	1.08 (1.03-1.14)
rs34572943	16p11	ITGAM	A	2.63x10 <sup>-58</sup>	1.67 (1.57-1.78)
rs4252665 <sup>d</sup>	17q12	ERBB2-IKZF3	A	6.23x10 <sup>-11</sup>	1.43 (1.28-1.59)
rs8079075 <sup>d,P</sup>	17q12	ERBB2-IKZF3	C	3.02x10 <sup>-9</sup>	1.41 (1.26-1.57)
rs1453560 <sup>d,P</sup>	17q12	ERBB2-IKZF3	C	5.14x10 <sup>-9</sup>	1.40 (1.25-1.56)
rs1463485 <sup>d</sup>	17q25	GRB2	G	7.34x10 <sup>-5</sup>	1.14 (1.07-1.21)
rs280519 <sup>P</sup>	19p13	TYK2	T	2.14x10 <sup>-12</sup>	1.17 (1.12-1.22)

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rs131658 <sup>i</sup>	22q11	UBE2L3	G	1.03x10 <sup>-16</sup>	1.25 (1.19-1.32)
rs11089629	22q11	UBE2L3	G	1.11x10 <sup>-16</sup>	1.25 (1.18-1.31)

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Chr, chromosome, OR, odds ratio. All SNPs, p-values, and ORs were reported in Langefeld *et al.*[11] All SNPs reported tier 1 statistical significance ( $P > 5 \times 10^{-8}$ ) in a European population.

**Supplementary Table 2.** Demographic characteristics of incomplete lupus erythematosus (ILE) and systemic lupus erythematosus (SLE) patients and healthy controls used in genetic load calculations.

	<b>ILE</b> (n=169)	<b>SLE</b> (n=170)	<b>Control</b> (n=133)
<b>Age, mean (SD)</b>	47.3 (13.7)	43.6 (13.7)	46.6 (14.8)
<b>Female, n (%)</b>	151 (89)	147 (87)	115 (86)

**Supplementary Table 3.** Clinical characteristics of incomplete lupus erythematosus (ILE) and systemic lupus erythematosus (SLE) used in genetic load calculations.

	<b>ILE</b> (n=169)	<b>SLE</b> (n=170)	<b>p-value</b>
<b>Childhood-onset (<math>\leq 18</math>), n (%)<sup>a</sup></b>	6/85 (7.1)	4/61 (3.7)	>0.9999
<b>No. of ACR criteria, mean (SD)<sup>b</sup></b>	5.7 (1.5)	3 (0)	<b>&lt;0.0001</b>
<b>ACR criteria categories, n (%)<sup>a</sup></b>			
<b>Malar rash</b>	109 (64)	26 (15.4)	<b>&lt;0.0001</b>
<b>Discoid rash</b>	19 (11.2)	8 (4.7)	<b>0.0432</b>
<b>Photosensitivity</b>	105 (61.8)	47 (27.8)	<b>&lt;0.0001</b>
<b>Oral or nasal ulcers</b>	113 (66.5)	19 (11.2)	<b>&lt;0.0001</b>
<b>Arthritis</b>	149 (87.6)	81 (47.9)	<b>&lt;0.0001</b>
<b>Serositis</b>	69 (40.6)	7 (4.1)	<b>&lt;0.0001</b>
<b>Renal disorder</b>	37 (21.8)	5 (3)	<b>&lt;0.0001</b>
<b>Neurologic</b>	18 (10.6)	2 (1.2)	<b>0.0003</b>
<b>Hematologic</b>	86 (50.6)	46 (27.2)	<b>&lt;0.0001</b>
<b>Immunologic</b>	112 (65.9)	100 (59.2)	0.2181
<b>Antinuclear antibodies</b>	161 (94.7)	166 (98.2)	0.1388

ACR, American College of Rheumatology. <sup>a</sup>Statistical significance determined using Fisher's Exact Test. <sup>b</sup>Statistical significance determined using a Mann-Whitney test. Bold text indicates p-values less than 0.05.

**Supplementary Table 4.** Unweighted and weighted genetic load comparisons between incomplete lupus erythematosus (ILE) patients (n=169), systemic lupus erythematosus (SLE) patients (n=170), and controls (n=133).

	Median (IQR)	95% CI	p-value (vs. control)	p-value (vs. SLE)
<b>Unweighted</b>				
SLE	80 (10)	79, 82	0.0208	1
Control	78 (9)	77, 80	1	0.0208
ILE	81 (10)	79, 82	0.0144	>0.9999
<b>Weighted</b>				
SLE	16.29 (2.2)	16.08, 16.77	0.0006	1
Control	15.76 (1.95)	15.3, 16.1	1	0.0006
ILE	16.3 (2.41)	15.95, 16.66	0.0015	>0.9999

IQR, interquartile range; CI, confidence interval. Statistical significance was determined using Kruskal Wallis with Dunn's posttest.

**Supplementary Table 5.** Unweighted and weighted genetic load comparisons between incomplete lupus erythematosus (ILE) patients who do not meet SLICC criteria (ILE<sup>SLICC</sup>; n=117), systemic lupus erythematosus (SLE) patients (n=170), and controls (n=133).

	Median (IQR)	95% CI	p-value (vs. control)	p-value (vs. SLE)
<b>Unweighted</b>				
SLE	80 (10)	79, 82	0.0216	1
Control	78 (9)	77, 80	1	0.0216
ILE <sup>SLICC</sup>	80 (10.5)	78, 82	0.1371	>0.9999
<b>Weighted</b>				
SLE	16.29 (2.2)	16.08, 16.77	0.0006	1
Control	15.76 (1.95)	15.3, 16.1	1	0.0006
ILE <sup>SLICC</sup>	16.05 (2.21)	15.77, 16.42	0.0708	0.6719

IQR, interquartile range; CI, confidence interval. Statistical significance was determined using Kruskal Wallis with Dunn's posttest.