SUPPLEMENTARY MATERIAL (*CD70* methylation in lupus: MILES Program)

Figure S1. Region of *CD70* assessed by pyrosequencing, with primers and CpG sites of interest noted
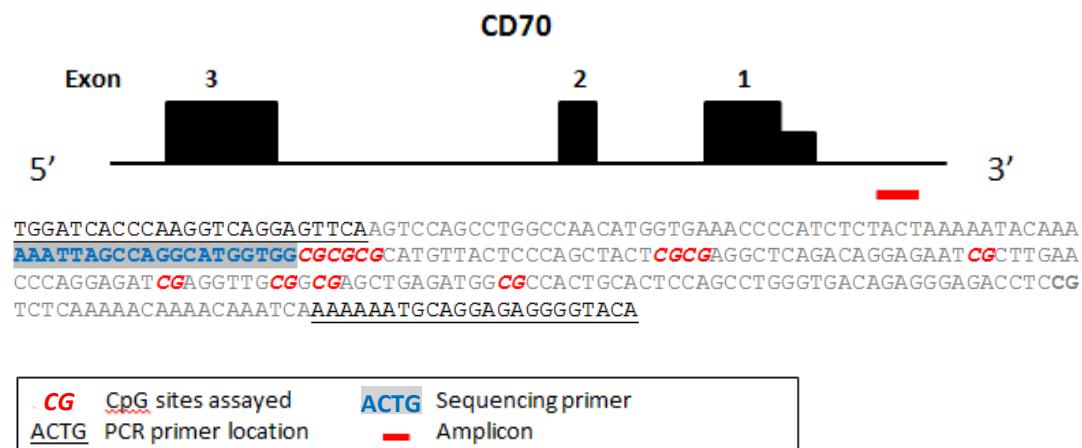
This figure displays the region of CD70 amplified and the CpG sites of interest in the pyrosequencing assay. Genomic sequence prior to bisulfite conversion is displayed, though primers are designed to amplify the bisulfite converted sequence.

Table S1. Pyrosequencing assay information for *CD70*

Sequence information										
Forward primer (5' to 3')	TGGATTATTTAAGGTTAGGAGTTTA									
Reverse primer (5' to 3')	Biotin-TATACCCCTCTCCTACATTTTTT									
Sequencing primer (5' to 3')	AAATTAGTTAGGTATGGTGG									
Sequence to analyze in PyroMark^	YGYGYGTATGTTATTTTTAGTTATTYGYGAGGTTTAGATAGGAGAATYGTT TGAATTTAGGAGATYGAGGTTGYGGYGAGTTGAGATGGYGTTATT									

CpG site information										
CpG site	1	2	3	4	5	6	7	8	9	10
CpG site location on Chr19*	6591663	6591661	6591659	6591638	6591636	6591616	6591598	6591590	6591587	6591574
Base pair distance**	-512	-510	-508	-487	-485	-465	-447	-439	-436	-423

^Y is target CpG site (PyroMark dispenses C and T)
*Chromosomal location is from Genome Reference Consortium Human Build 38 (GRCh38)
**Base pair distance relative to transcription start site (TSS=0). The sequenced region spanned 89 base pairs.

Figure S2a-b. Bee swarm boxplot comparing CD4+ *CD70* DNA methylation levels between controls and SLE cases, based on pyrosequencing. Each dot represents the intra-person mean methylation for the 10 CpG sites. Overall, *CD70* is significantly hypermethylated in SLE cases compared to controls. Solid markers (•) designate persons with complete methylation data (all 10 CpG sites); hollow markers (▫) designate individuals with missing values for one or more of the 10 CpG sites.
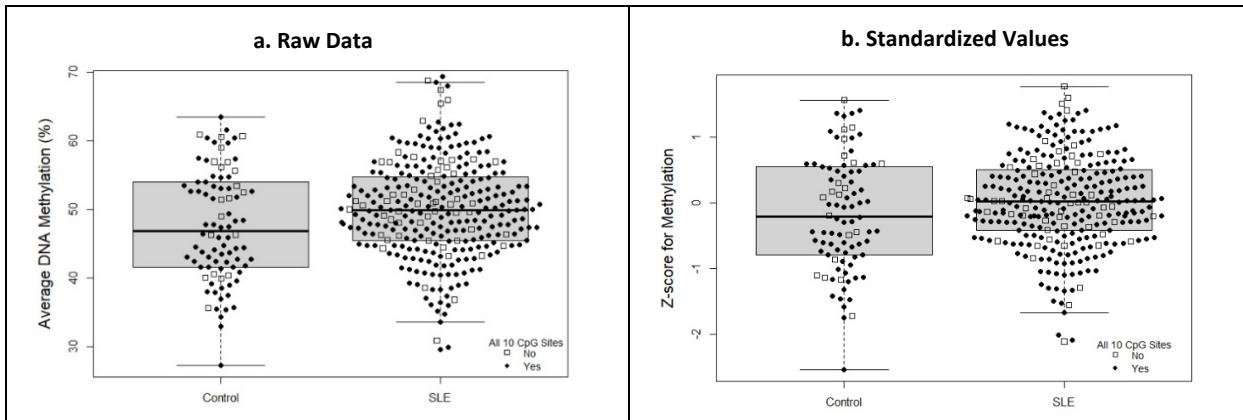
Raw data: p=0.01 (overall); p=0.007 (subset with all sites complete)
Standardized data: p=0.06 (overall); p=0.04 (subset with all sites complete)

Boxplots: lower and upper hinges of box represent 25th & 75th percentiles; horizontal line within box represents median; markers outside the whiskers represent outliers (outer 2.5 percentiles).

Table S2. Regression results for the associations between SLE-Control status and age with DNA Methylation Levels at 18 *CD70* CpG Sites Included on the MethylationEPIC Array, in CD4+ and CD8+ T cells

			CD4+ T Cells				CD8+ T cells			
			SLE vs Control		Age		SLE vs Control		Age	
Probe ID	Location^	Region Relative to Gene	Estimate (SE)	p-value	Estimate (SE)	p-value	Estimate (SE)	p-value	Estimate (SE)	p-value
cg04312604	chr19:6594232	promoter/upstream	-0.83 (0.58)	0.153	0.0176 (0.0198)	0.374	-0.45 (1.64)	0.782	-0.1584 (0.0434)	**<0.001**
cg03316332	chr19:6594222	promoter/upstream	-1.69 (0.59)	**0.005**	0.0326 (0.0201)	0.106	0.05 (1.79)	0.976	-0.0767 (0.0473)	0.107
cg11904429	chr19:6592543	1500 bp upstream of TSS	-7.08 (1.65)	**<0.001**	-0.0353 (0.056)	0.529	-8.26 (3.74)	**0.028**	-0.3703 (0.0989)	**<0.001**
cg22633597	chr19:6591663	1500 bp upstream of TSS	-0.47 (1.19)	0.692	0.0983 (0.0404)	**0.015**	3.83 (2.55)	0.135	0.2984 (0.0675)	**<0.001**
cg22431965	chr19:6591489	1500 bp upstream of TSS	-0.27 (0.22)	0.232	0.0121 (0.0075)	0.108	-1.41 (0.61)	**0.021**	0.0621 (0.016)	**<0.001**
cg04120164	chr19:6591276	200 bp upstream of TSS	-0.02 (0.06)	0.744	-0.0011 (0.0022)	0.607	-0.08 (0.13)	0.563	-0.0077 (0.0035)	**0.032**
cg13119122	chr19:6591214	200 bp upstream of TSS	-0.07 (0.06)	0.294	-0.0025 (0.0021)	0.240	-0.14 (0.1)	0.177	-0.0023 (0.0027)	0.389
cg23263923	chr19:6591193	200 bp upstream of TSS	-0.15 (0.07)	**0.039**	-0.009 (0.0024)	**<0.001**	0.11 (0.14)	0.427	-0.0086 (0.0037)	**0.022**
cg21779443	chr19:6591160	200 bp upstream of TSS	-0.2 (0.08)	**0.013**	-0.0027 (0.0027)	0.322	-0.16 (0.17)	0.336	-0.0048 (0.0044)	0.272
cg24778383	chr19:6590884	in gene	0.04 (0.06)	0.489	0.0024 (0.0019)	0.207	0.01 (0.12)	0.937	-0.0051 (0.0031)	0.101
cg14870229	chr19:6590790	in gene	0.5 (0.26)	0.058	0.0458 (0.0089)	**<0.001**	0.61 (0.71)	0.389	0.0674 (0.0187)	**<0.001**
cg25949886	chr19:6590505	in gene	-0.02 (0.03)	0.487	0.0002 (0.0009)	0.845	0.02 (0.05)	0.719	-0.0019 (0.0014)	0.196
cg18475039	chr19:6590095	in gene	0.2 (0.22)	0.365	0.0212 (0.0075)	**0.005**	0.75 (0.99)	0.451	0.0958 (0.0263)	**<0.001**
cg27335924	chr19:6588887	in gene	2.26 (0.94)	**0.016**	0.094 (0.0318)	**0.003**	4.82 (3.02)	0.112	0.3681 (0.0798)	**<0.001**
cg17136649	chr19:6588885	in gene	2.9 (0.98)	**0.003**	0.0763 (0.0332)	**0.022**	4.61 (2.96)	0.121	0.3132 (0.0785)	**<0.001**
cg15679532	chr19:6588827	in gene	0.34 (0.25)	0.171	0.0056 (0.0084)	0.505	0.87 (0.97)	0.369	0.065 (0.0256)	**0.012**
cg15267702	chr19:6588798	in gene	0.66 (0.28)	**0.018**	0.0144 (0.0095)	0.130	2.2 (1.17)	0.060	0.1097 (0.0308)	**<0.001**
cg10807045	chr19:6588142	in gene	2.28 (0.64)	**<0.001**	0.0411 (0.0217)	0.059	5.32 (1.46)	**<0.001**	0.1204 (0.0386)	**0.002**

Estimates are from linear regression models of each CpG site, adjusting for race (Black, White, other/unknown), sex, age, and case/control status.

Estimates are shown for variables of interest - SLE cases compared to controls and age (in years). Estimates represent the % increase or decrease in DNA methylation at the CpG site.

p-value <0.05 in bold

^Genomic location from GRCh38/hg38 build

Table S3. Regression Results for Models of DNA Methylation Levels at 18 *CD70* CpG Sites Included on the MethylationEPIC Array in CD4+ and CD8+ T cells: Assessing Interactions between SLE-Control Status and Age

Probe ID	Location^	CD4+ T Cells						CD8+ T cells					
		SLE vs Control		Age		Case*Age		SLE vs Control		Age		Case*Age	
		Estimate (SE)	p-value	Estimate (SE)	p-value	Estimate (SE)	p-value	Estimate (SE)	p-value	Estimate (SE)	p-value	Estimate (SE)	p-value
cg04312604	chr19:6594232	3.61 (2.58)	0.163	0.08 (0.04)	**0.049**	-0.08 (0.05)	0.078	-0.18 (6.66)	0.979	-0.15 (0.11)	0.158	-0.01 (0.12)	0.966
cg03316332	chr19:6594222	2.93 (2.63)	0.266	0.1 (0.04)	**0.018**	-0.08 (0.05)	0.072	2.93 (7.25)	0.687	-0.03 (0.12)	0.785	-0.05 (0.13)	0.683
cg11904429	chr19:6592543	-5.24 (7.35)	0.477	-0.01 (0.11)	0.927	-0.03 (0.13)	0.797	-6.53 (15.18)	0.667	-0.34 (0.25)	0.167	-0.03 (0.27)	0.907
cg22633597	chr19:6591663	-6.98 (5.29)	0.188	0.01 (0.08)	0.904	0.12 (0.09)	0.207	-7.46 (10.32)	0.471	0.12 (0.17)	0.463	0.21 (0.18)	0.260
cg22431965	chr19:6591489	-1.62 (0.98)	0.101	-0.01 (0.02)	0.678	0.02 (0.02)	0.160	-2.01 (2.46)	0.414	0.05 (0.04)	0.189	0.01 (0.04)	0.801
cg04120164	chr19:6591276	-0.37 (0.28)	0.195	-0.01 (0)	0.179	0.01 (0)	0.209	0.41 (0.54)	0.449	0 (0.01)	0.988	-0.01 (0.01)	0.354
cg13119122	chr19:6591214	-0.59 (0.28)	**0.032**	-0.01 (0)	**0.023**	0.01 (0)	0.051	-0.58 (0.41)	0.156	-0.01 (0.01)	0.171	0.01 (0.01)	0.263
cg23263923	chr19:6591193	0.21 (0.31)	0.514	0 (0)	0.387	-0.01 (0.01)	0.252	-0.2 (0.57)	0.720	-0.01 (0.01)	0.149	0.01 (0.01)	0.567
cg21779443	chr19:6591160	0 (0.36)	0.994	0 (0.01)	0.989	0 (0.01)	0.558	0.55 (0.67)	0.409	0.01 (0.01)	0.572	-0.01 (0.01)	0.273
cg24778383	chr19:6590884	-0.28 (0.25)	0.267	0 (0)	0.621	0.01 (0)	0.194	0.4 (0.47)	0.396	0 (0.01)	0.899	-0.01 (0.01)	0.392
cg14870229	chr19:6590790	-0.65 (1.16)	0.577	0.03 (0.02)	0.089	0.02 (0.02)	0.312	-1.82 (2.86)	0.526	0.03 (0.05)	0.524	0.04 (0.05)	0.382
cg25949886	chr19:6590505	0.04 (0.11)	0.723	0 (0)	0.581	0 (0)	0.600	0.19 (0.22)	0.385	0 (0)	0.825	0 (0)	0.420
cg18475039	chr19:6590095	-0.6 (0.98)	0.542	0.01 (0.02)	0.491	0.01 (0.02)	0.404	3.93 (4.02)	0.330	0.14 (0.07)	**0.029**	-0.06 (0.07)	0.416
cg27335924	chr19:6588887	-1.91 (4.17)	0.646	0.04 (0.06)	0.560	0.08 (0.07)	0.305	5.26 (12.24)	0.668	0.37 (0.2)	0.062	-0.01 (0.22)	0.970
cg17136649	chr19:6588885	-0.98 (4.35)	0.822	0.02 (0.07)	0.724	0.07 (0.08)	0.360	4.36 (12.04)	0.718	0.31 (0.2)	0.117	0 (0.21)	0.983
cg15679532	chr19:6588827	-2.66 (1.09)	**0.015**	-0.04 (0.02)	**0.036**	0.05 (0.02)	**0.005**	1.76 (3.93)	0.654	0.08 (0.06)	0.221	-0.02 (0.07)	0.816
cg15267702	chr19:6588798	0.6 (1.24)	0.628	0.01 (0.02)	0.476	0 (0.02)	0.960	2.71 (4.73)	0.568	0.12 (0.08)	0.130	-0.01 (0.08)	0.913
cg10807045	chr19:6588142	4.01 (2.84)	0.159	0.06 (0.04)	0.137	-0.03 (0.05)	0.531	3.51 (5.92)	0.554	0.09 (0.1)	0.340	0.03 (0.1)	0.753

Estimates are from linear regression models of each CpG site, adjusting for race (Black, White, other/unknown), sex, age, and case/control status.

Estimates are shown for variables of interest - SLE cases compared to controls, age (in years), and interaction between SLE disease status and age. Estimates represent the % increase or decrease in DNA methylation at the CpG site.

p-value <0.05 in bold

^Genomic location from GRCh38/hg38 build