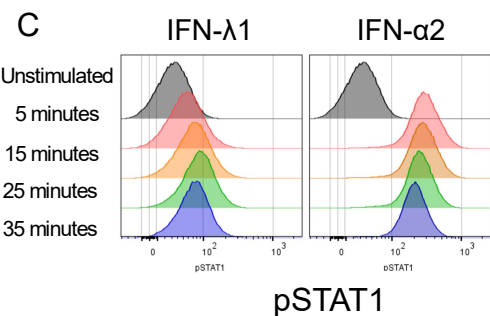
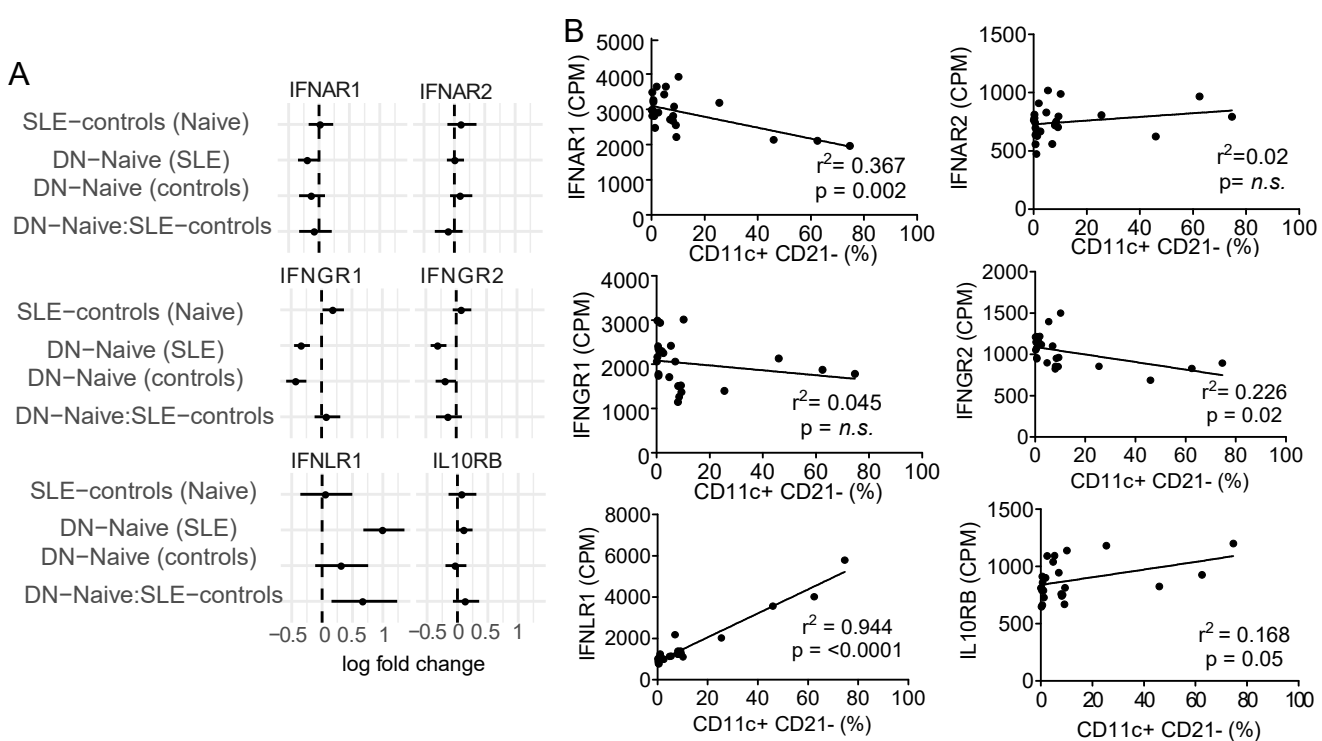


SLE:												
Demographics			% CD11c+ CD21-		Lupus-Associated Antibodies (ever +)						Lupus Activity	Rx
Age	Race	Sex	DN	Naive	ANA	R o	L a	S m	R N P	ds DNA	SLEDAI	
64	NH, AA	F	46.0	1.3	640 H	-	-	-	-	+	0	P2
35	NH, AA	F	74.7	5.4	640 S	+	+	+	+	+	12 (arthritis, proteinuria, low complements, anti-dsDNA)	H, A
34	NH, AA	F	15.5*	1.9	640 S	+	-	-	+	-	2 (new rash)	H
61	NH, C	F	9.2	0.3	80 H	-	-	-	-	+	2 (anti-dsDNA)	H, A
24	NH, AA	M	7.0	1.0	2560 S	-	-	+	+	+	4 (low complements anti-dsDNA)	H
50	NH, AA	F	25.5	2.5	>2560 S	+	+	+	+	+	2 (anti-dsDNA)	H
50	NH, AA	F	62.5	10.2	640 H	+	-	-	+	+	0	H, M, P1
69	NH, C	F	4.8	0.37	160 S	-	-	-	-	+	8 (low complements, proteinuria, & anti-ds DNA)	H
HD:												
58	NH, C	F	8.0	0.1								
49	NH, AA	M	3.6*	0.8								
39	NH, C	F	8.5	0.7								
36	H, C	M	9.4	0.7								
37	NH, C	F	8.1	0.6								

Supplemental Table 1: Demographic data for transcriptomic analysis cohort. Peripheral blood from this cohort was flow sorted into monocytes, double negative B cells (DN), and naïve B cells. For the double negative B cell samples, one SLE and one healthy donor had to be excluded due to poor RNA quality (*). Abbreviations: Race (H = Hispanic ethnicity, NH = non-Hispanic ethnicity, AA = African American, C = Caucasian). Sex (F = female, M = male). ANA = antinuclear antibody titer (H = homogeneous pattern, S = speckled pattern). Rx = lupus medications at the time of blood draw (H = hydroxychloroquine, A = azathioprine, M = mycophenolic acid, P1 = prednisone 1mg daily, P2 prednisone 2mg daily).



Supplemental Figure 1. Gene set enrichment analysis for SLE upregulated genes in naïve B, monocyte, and DN B cells utilizing A) msigdb, B) GO, and C) KEGG databases. Color represents adjusted p-value. Size of dot represents gene ratio.



Supplemental Figure 2: A) IFN Receptor Gene Transcripts.

Coefficients and 95% credible intervals for regressions with subject-level random effect and fixed effects for disease status, B cell subset and its interaction. B) Linear regression for Type I, Type II, and Type III IFN receptor transcripts from bulk RNA-seq (normalized CPM) with CD11c+ CD21- (% cells) frequency in each sample. Naïve and DN from both HD and SLE are displayed for each graph. Goodness of fit (r^2) and p-value (F test) shown. C) Peripheral blood mononuclear cells stimulated with IFN- α 2 or IFN- λ 1 for 0-35 minutes for detection of phosphorylated STAT1 protein by flow cytometry. Histograms shown for CD19+ CD20+ B cells.