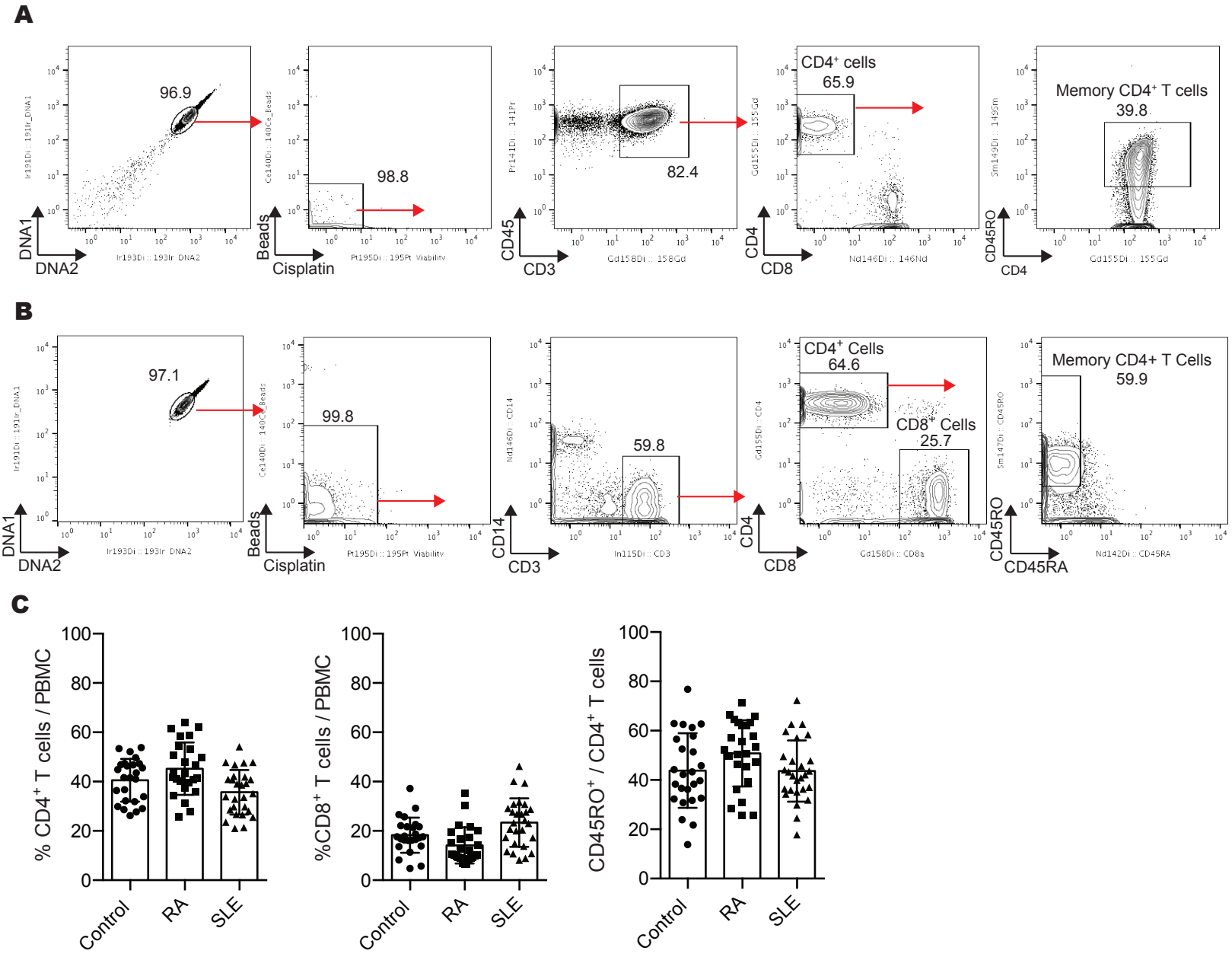
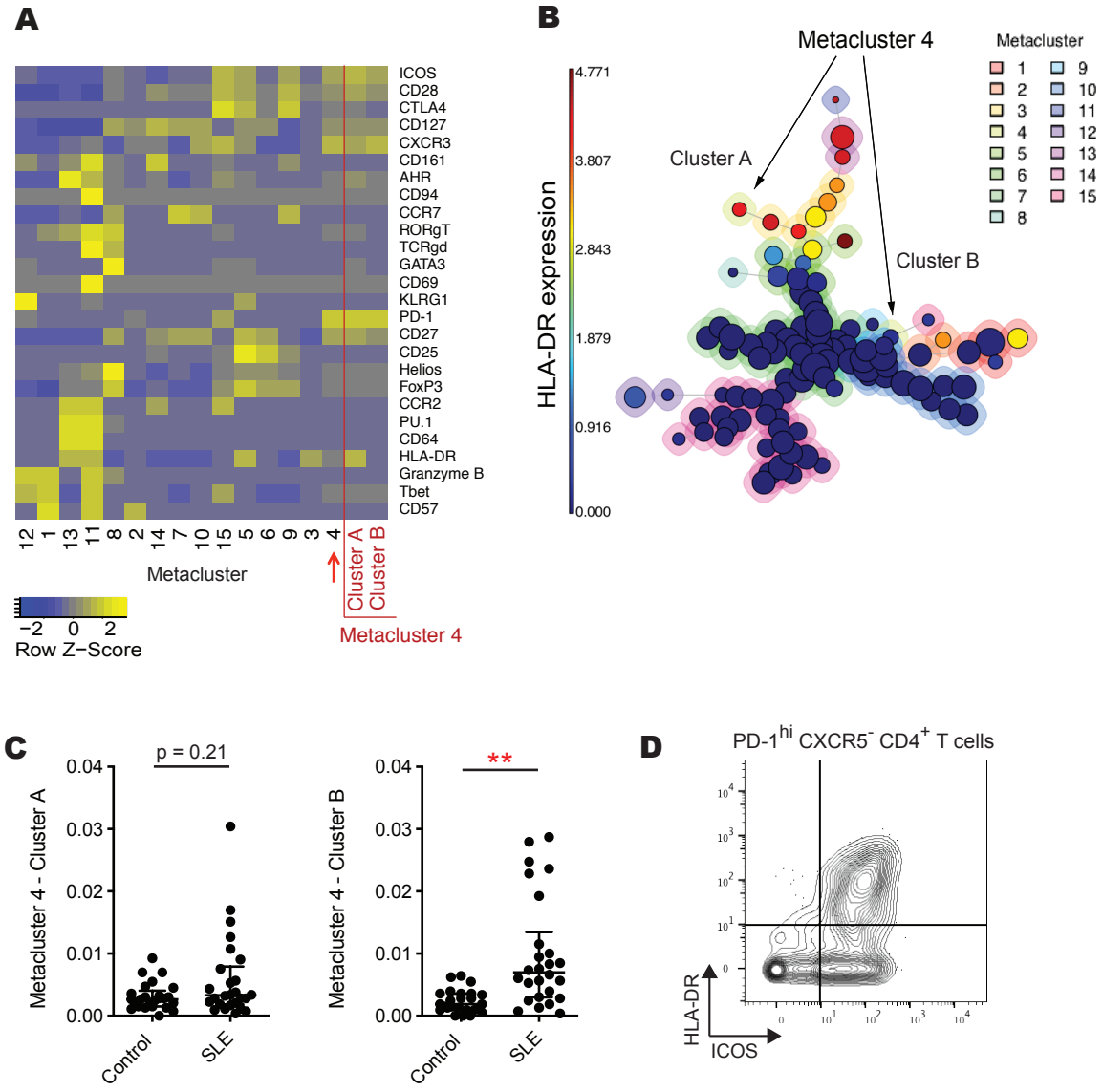
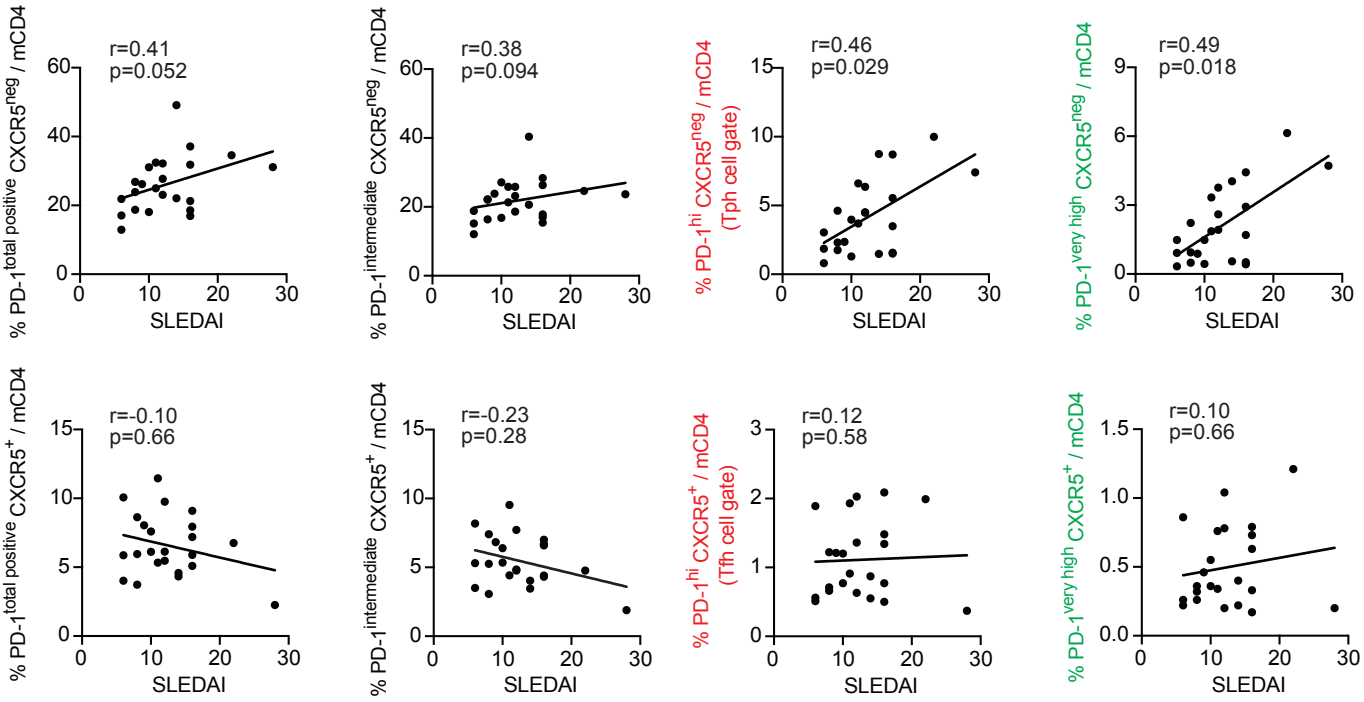


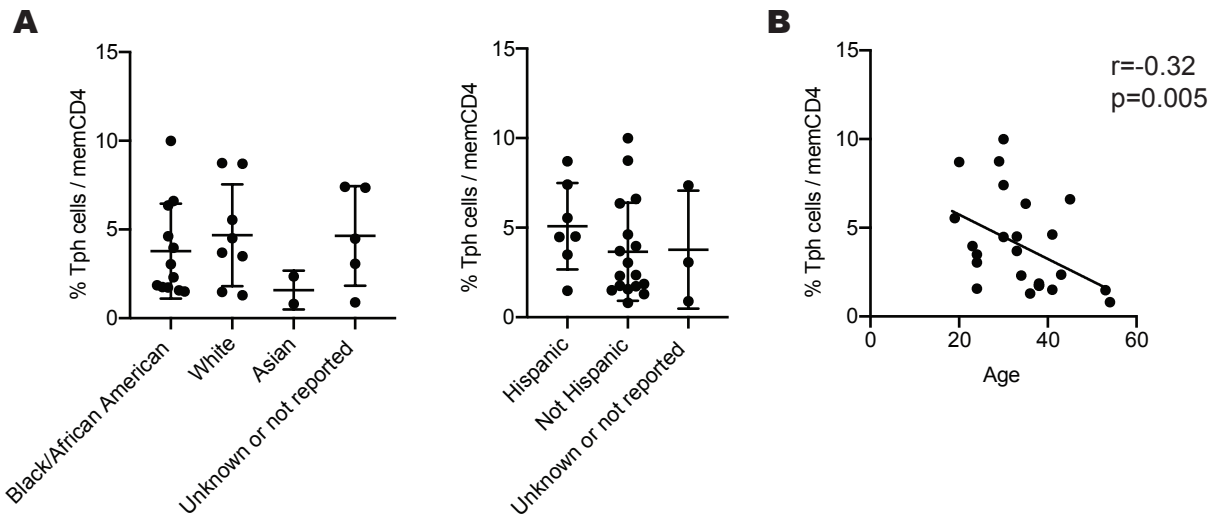

**Supplementary Figure 1: Identification of major T cell subsets in mass cytometry data.**
A) Example of biaxial gating for T cell populations in the AMP mass cytometry data. B) Example of biaxial gating for T cell populations in the BWH validation cohort mass cytometry data.
C) Quantification of $CD4^+$ T cells, $CD8^+$ T cells, and memory $CD4^+$ T cells in the AMP cohort. Error bars show median±interquartile range.



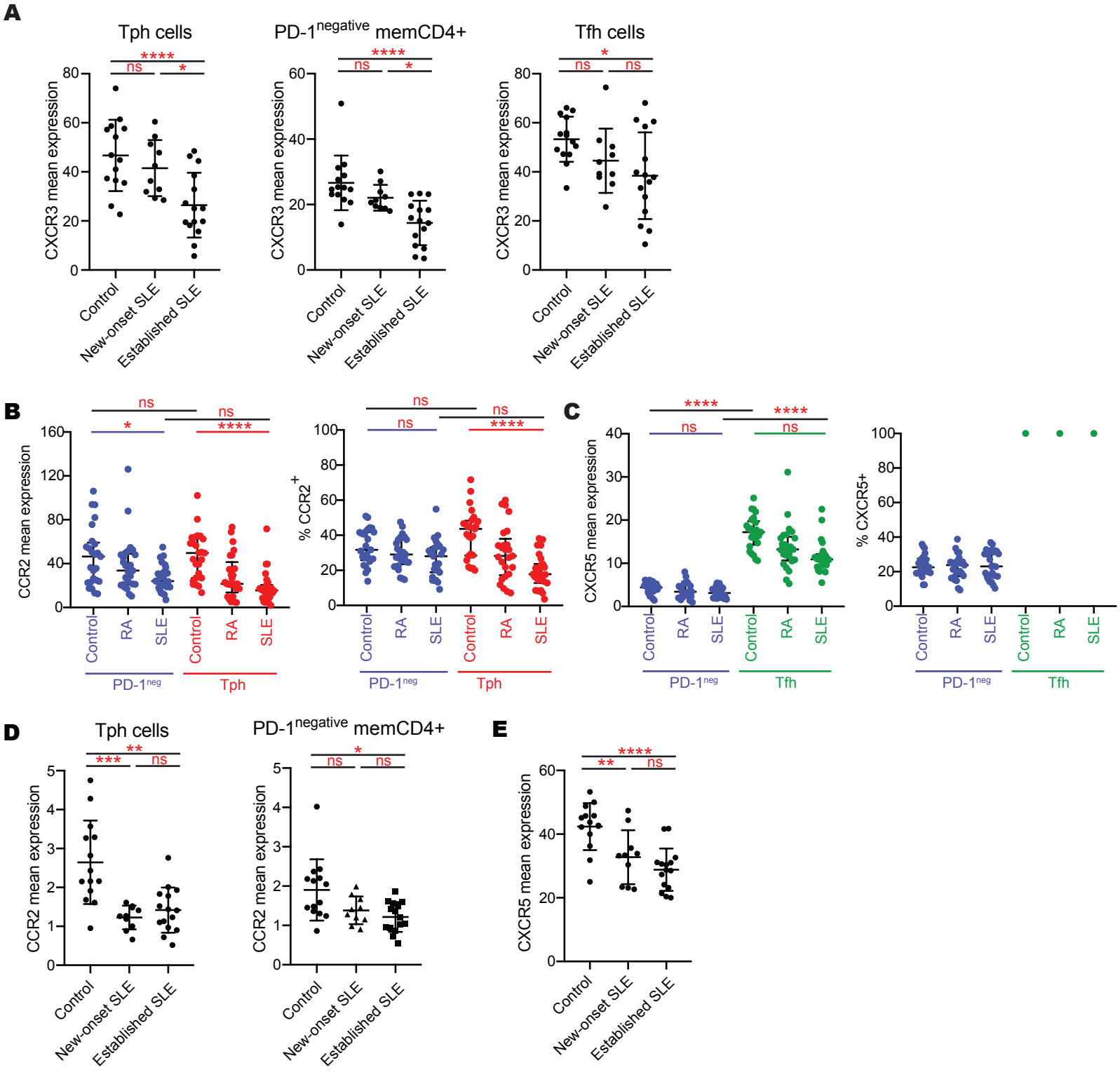

**Supplementary Figure 2: Phenotypic features of cells in metacluster 4.**
A) Heatmap of marker expression in FlowSOM metaclusters as in Figure 1D including the 2 clusters (cluster A, cluster B) that comprise metacluster 4. B) FlowSOM map demonstrating level of expression of HLA-DR in individual clusters. C) Abundance of the clusters that comprise metacluster 4, cluster A and cluster B, in SLE patients and controls as in Figure 1C. Error bars show median±interquartile range. **p<0.01 by Mann-Whitney test. D) Example contour plot of expression of HLA-DR and ICOS on gated PD-1$^{hi}$ CXCR5$^{-}$ CD4$^{+}$ T cells in mass cytometry data.



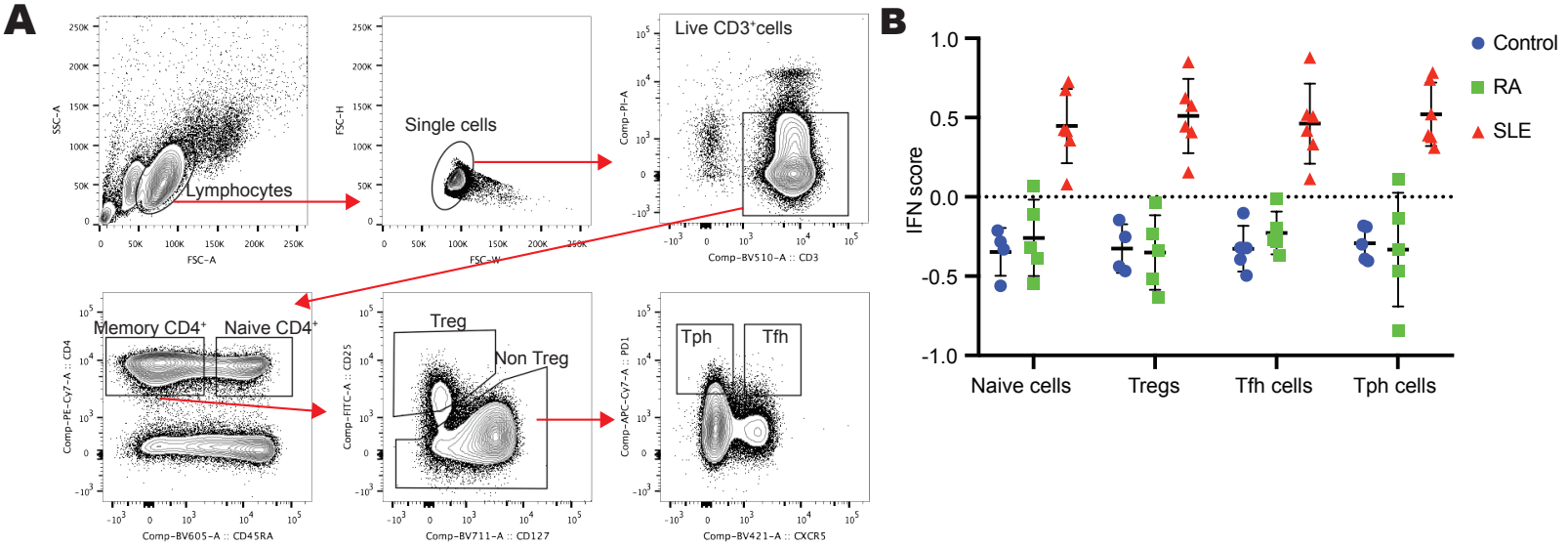

**Supplementary Figure 3: Correlation of PD-1⁺ T cell populations with lupus disease activity.** Correlation between lupus disease activity by SELENA-SLEDAI and the frequency of different CD4⁺ T cell populations defined based on expression of CXCR5 and level of expression of PD-1 (n=21 patients). Spearman correlation statistics shown.




**Supplementary Figure 4: Tph cell frequencies in SLE patients according to race, ethnicity, and age.** A) Tph cell frequency in SLE patients grouped by self-reported race or ethnicity. Error bars show mean±SD. B) Correlation between Tph cell frequency and age in SLE patients. Spearman correlation statistics shown.




**Supplementary Figure 5: Chemokine receptor expression on Tph cells in SLE.**
A) Mean expression of CXCR3 on Tph cells, Tfh cells, and PD-1neg memory CD4$^+$ T cells in mass cytometry analysis of samples from the BWH validation cohort. B) Mean expression of CCR2 and frequency of CCR2$^+$ cells in PD-1$^{neg}$ memory CD4$^+$ T cells and Tph cells from control (n=25), RA (n=25), and lupus nephritis (n=27) donors in the AMP cohort. C) Mean expression of CXCR5 and frequency of CXCR5$^+$ cells in PD-1$^{neg}$ memory CD4$^+$ T cells and Tfh cells as in (B). Tfh cells are CXCR5$^+$ by definition. D) Mean expression of CCR2 on Tph cells and PD-1$^{neg}$ memory CD4$^+$ T cells as in (A). E) Mean expression of CXCR5 on Tfh cells as in (A). Error bars show mean±SD. * p<0.05,** p<0.01, *** p<0.001, **** p<0.0001 by Kruskal–Wallis with Dunn's multiple comparisons test (A-E) statistics shown.




**Supplementary Figure 6: RNA-seq sorting and interferon scores in T cell populations.**
A) Example of gating for sorting T cell populations for RNA-seq. B) The interferon score was calculated for each T cell population from each donor using the RNA-seq transcriptomes. Plot shows the IFN score for controls (blue, n=4-5), RA patients (green, n=4-5), and SLE patients (red, n=6) for each T cell population. Error bars show mean±SD.

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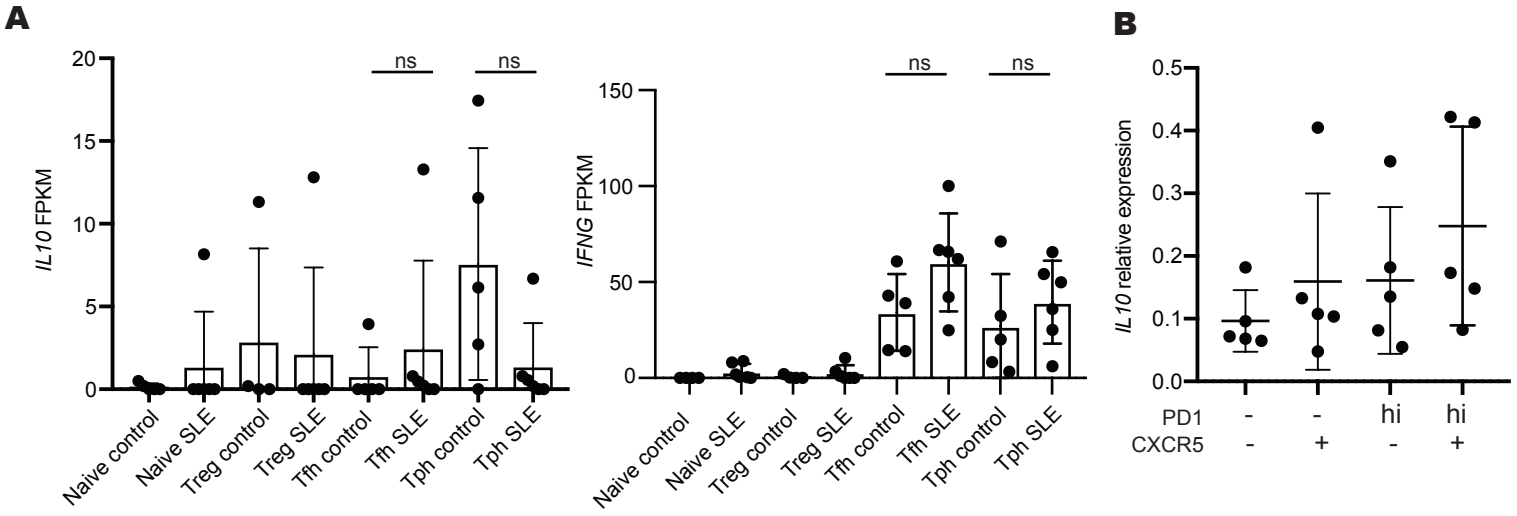
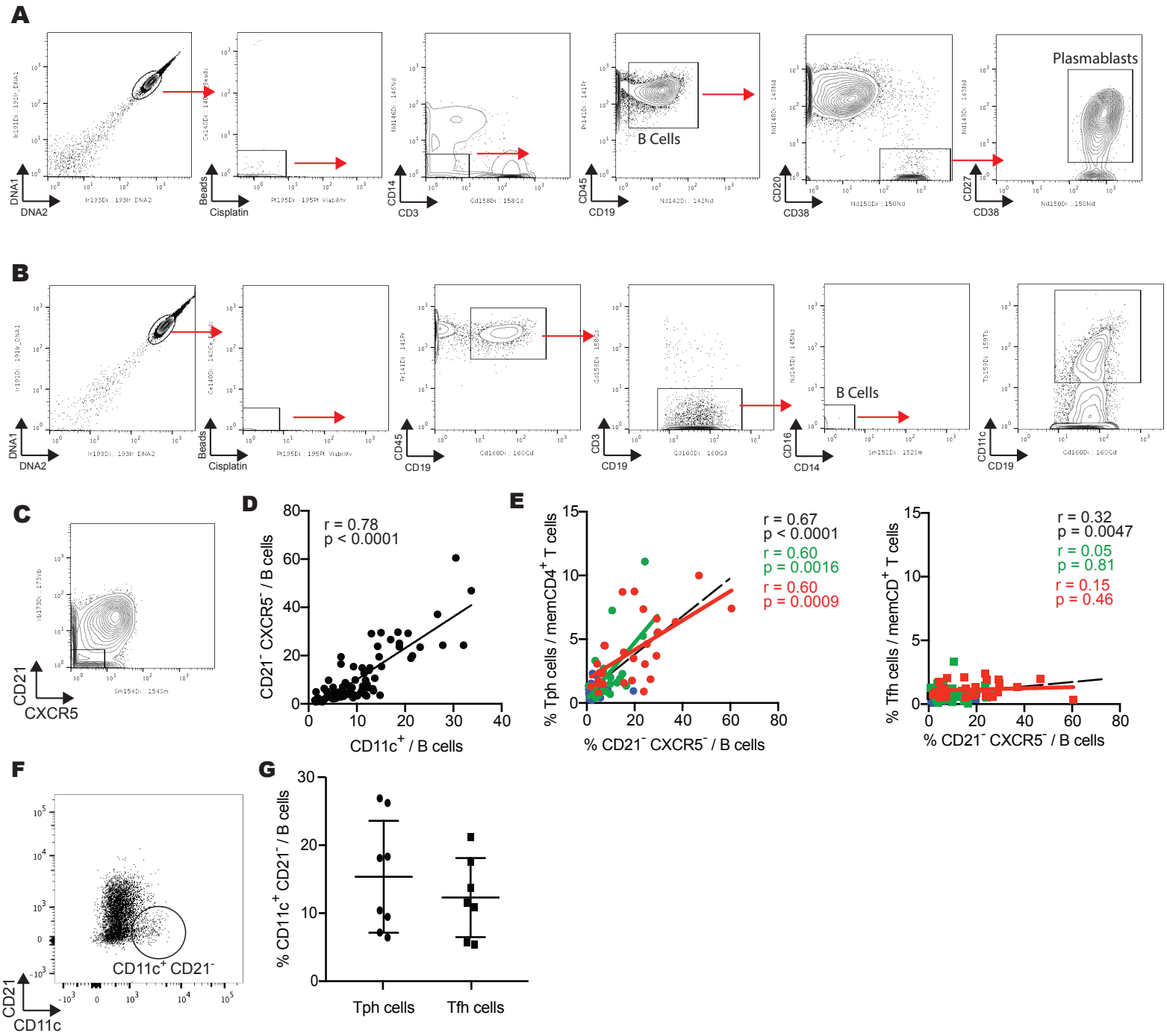
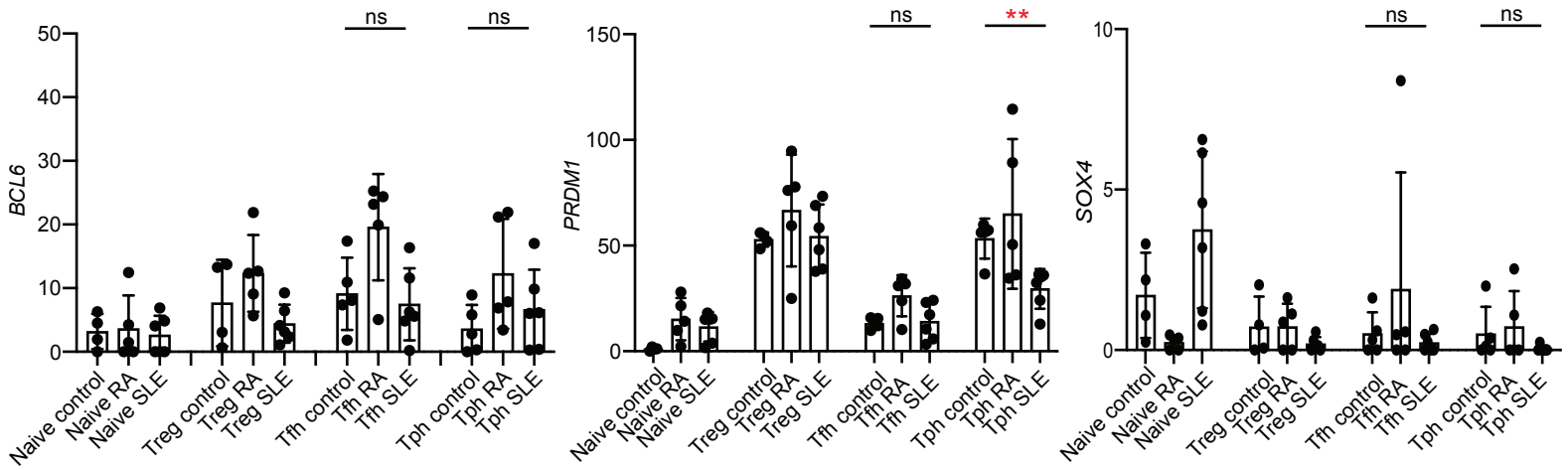



**Supplementary Figure 7: Expression of IL10 and IFNG in SLE Tph cells**
A) Expression of IL10 and IFNG in T cell subsets in RNA-seq data. B) IL10 expression by qPCR in PMA+ionomycin stimulated memory $CD4^+$ T cell subsets from SLE patients (n=4). Error bars show mean±SD (G). Mann Whitney test comparing Tph cells or Tfh cells from controls and SLE patients (A), or Kruskal–Wallis with Dunn's multiple comparisons test (B).




**Supplementary Figure 8: Tph cells correlate with CD11c+ B cells.**
A) Gating strategy for B cells and plasmablasts in the AMP mass cytometry data using the B cell panel. B) Gating strategy for $CD11c^+$ B cells in the AMP mass cytometry data using the myeloid panel. C) Example visualization of CD21 and CXCR5 on B cells gated as in (A) in the AMP mass cytometry data. D) Correlation between frequency of $CD11c^+$ B cells and $CD21^-$ $CXCR5^-$ B cells in all patients in the AMP cohort. E) Correlation between the frequency of Tph cells or Tfh cells and $CD21^-$ $CXCR5^-$ B cells in the AMP cohort (black = controls, green = RA patients, red = SLE patients). Spearman correlation statistics show (D,E). F) Example of detection of $CD11c^+$ $CD21^-$ B cells in co-cultures of memory B cells from controls co-cultured with indicated $CD4^+$ T cell subsets from SLE patients G) Quantification of $CD11c^+$ B cells among B cells (excluding plasmablasts) in co-cultures as in (F). Pooled data from 6 donors in 6 different experiments. Error bars show mean±SD.




**Supplementary Figure 9: Expression of BCL6, PRDM1, and SOX4 in circulating Tph and Tfh cells.** Expression of BCL6, PRDM1, and SOX4 in T cell subsets in RNA-seq data. Error bars show mean±SD. * p<0.05,** p<0.01, *** p<0.001, **** p<0.0001 by Mann-Whitney test comparing Tph cells or Tfh cells from controls and SLE patients.

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