

Supplementary Figures:

Rheumatoid arthritis synovial fibroblasts modulate T cell activation

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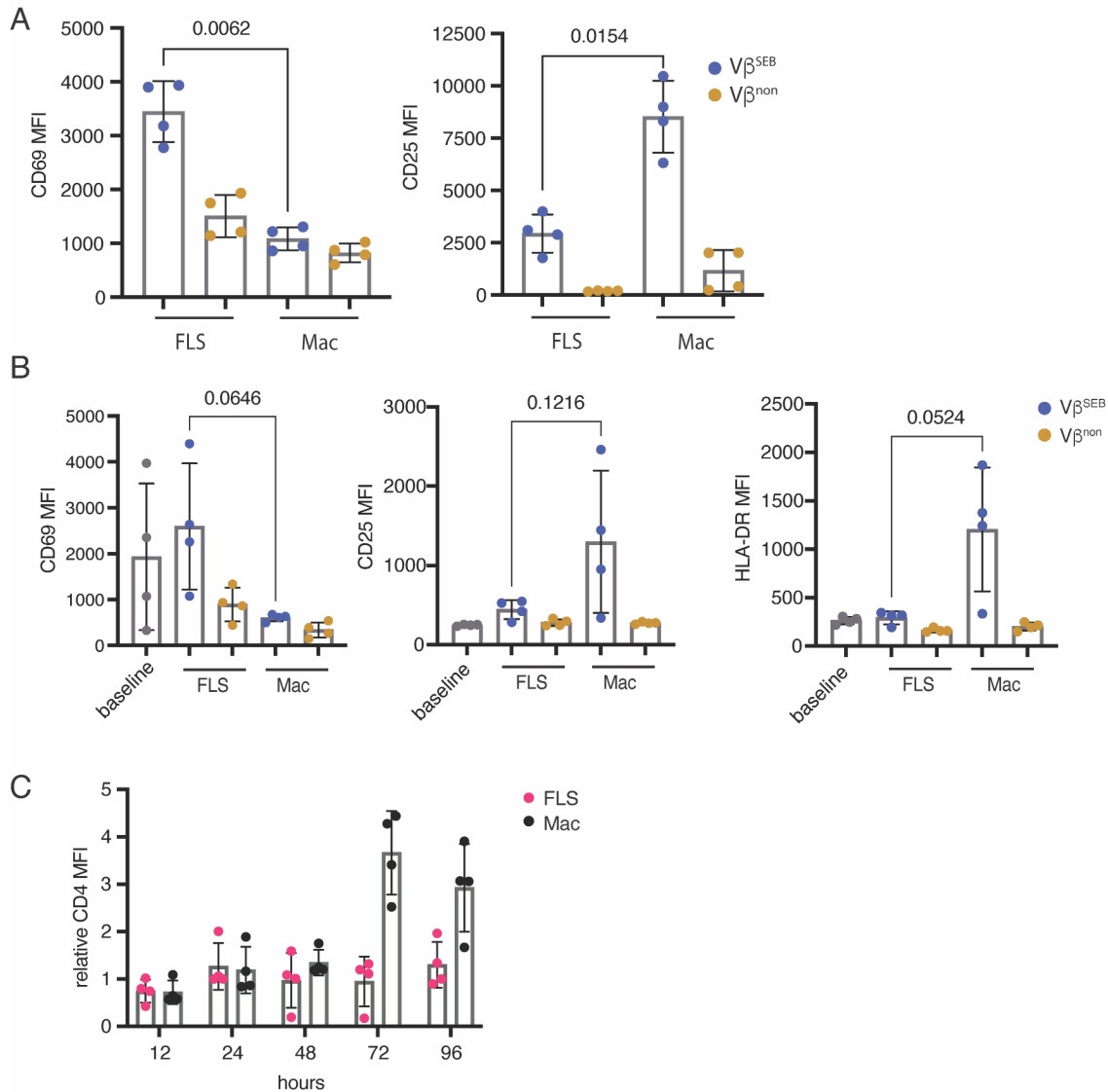
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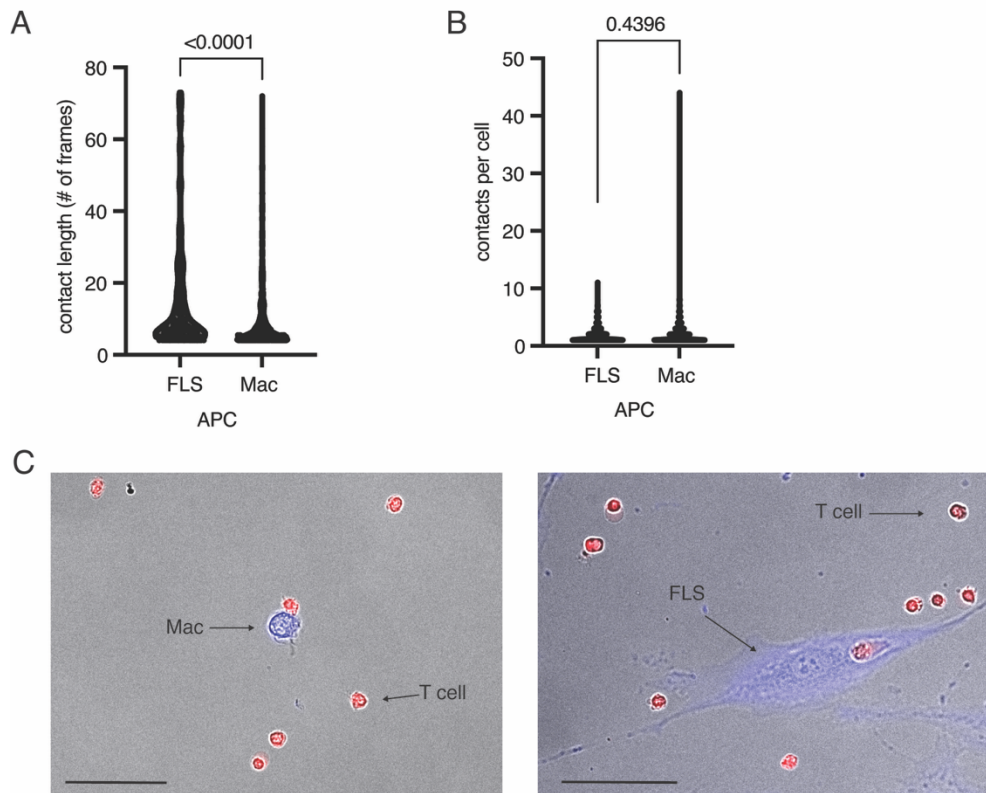
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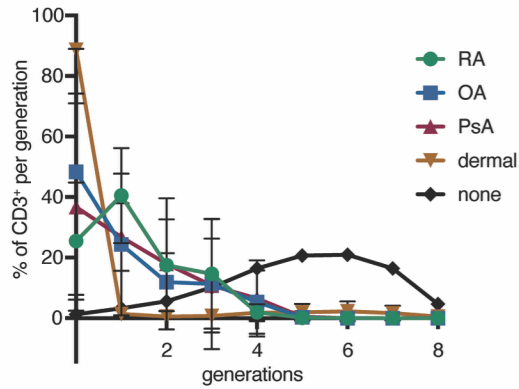


Supplementary Figure 2: FLS effects on T cell activation are the same when compared to autologous synovium-derived T cells and macrophages. (A) CD69, CD25 and HLA-DR expression (MFI) on CD3⁺ with SEB stimulated co-cultures in which both CD14⁺ macrophages and CD3⁺ T cells isolated from the RA synovium are used along with autologous FLS. Baseline indicates marker expression prior to co-culture and 72 hour SEB addition. N=4. (B) CD69 and CD25 expression (MFI) on CD3⁺ T cells sorted from RA synovial tissue with a high synovial lymphocytic infiltrate on histologic scoring, cultured with either autologous blood-derived M-CSF differentiated macrophages or FLS, and stimulated with SEB for 72 hours. N = 4. (C) Intracellular CD4 expression (MFI) by CD3⁺ $V\beta^{SEB}$ T cells with FLS or macrophages as APCs relative to no APCs. Magenta: T cells with FLS as APCs; black: T cells with macrophages as APC. N=4. Mean +/- standard deviation is shown. Statistical comparisons were made using paired two-tailed t-tests.

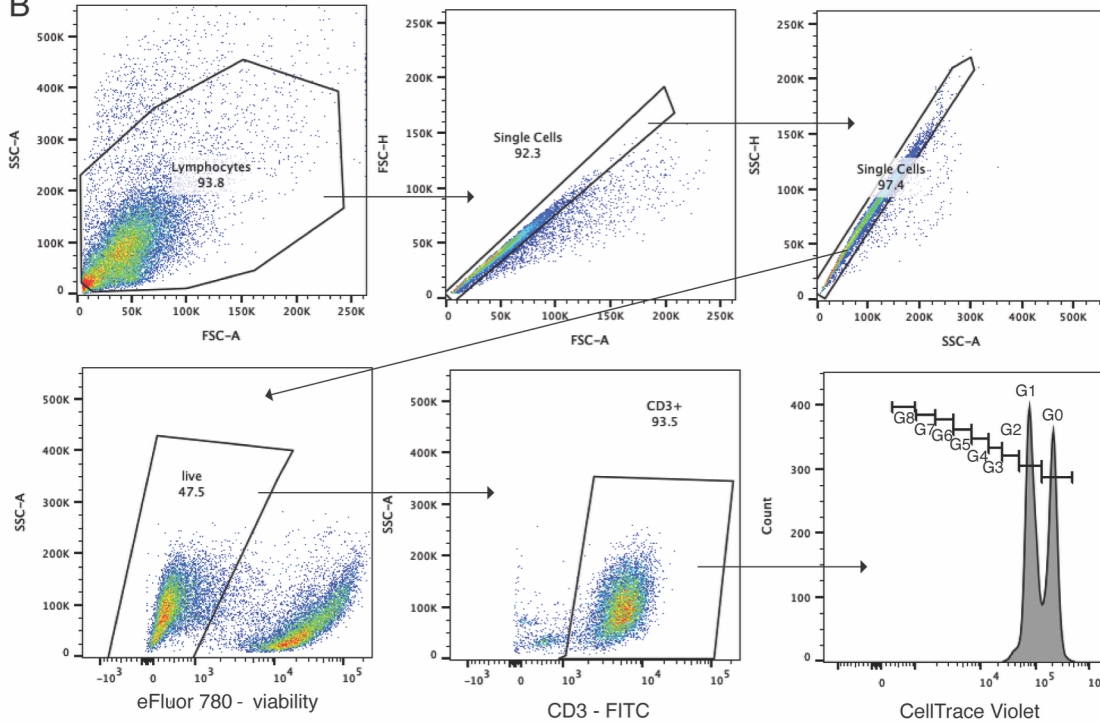


Supplementary Figure 3. FLS make prolonged contact with T cells. Using fluorescently labeled APCs (either FLS or macrophages) and T cells (CellTrace dyes) stimulated with SEB, live cells were imaged over 12 hours. Tracked APCs: 1691 FLS (with 215 T cell contacts) and 3713 macrophages (with 735 contacts). **(A)** Contact duration (non-zero, number of frames) between interacting T cells and APCs were measured using a cell area-based analysis with a 10 μ m distance cut off. **(B)** Number of distinct contacts per APC. For **A** and **B**, statistical comparisons were performed using a two-tailed Mann-Whitney U Test. **(C)** Representative images of macrophages (left) or FLS (right) (both APCs: blue) interacting with T cells (red). Scale bar = 40 μ m.

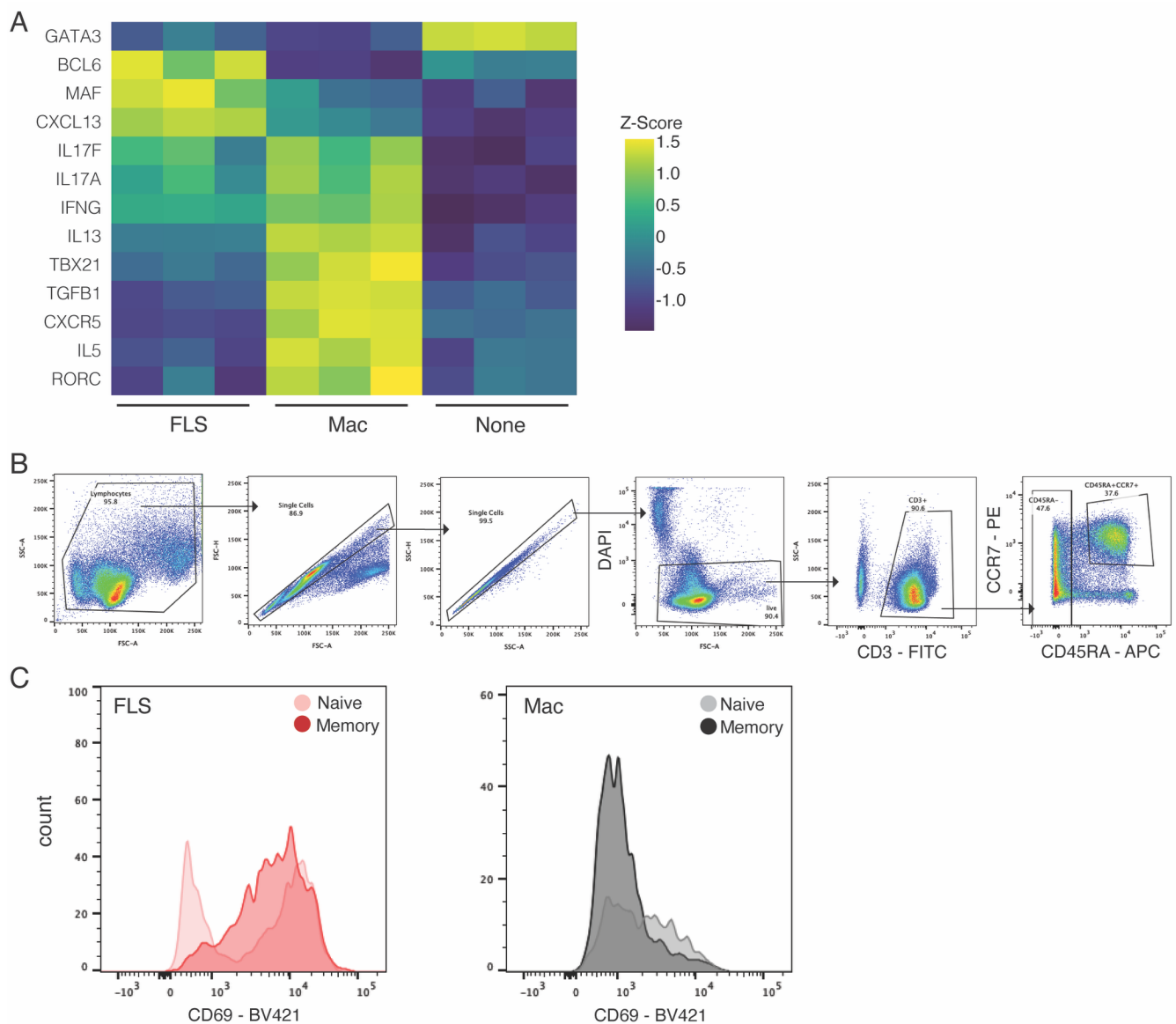
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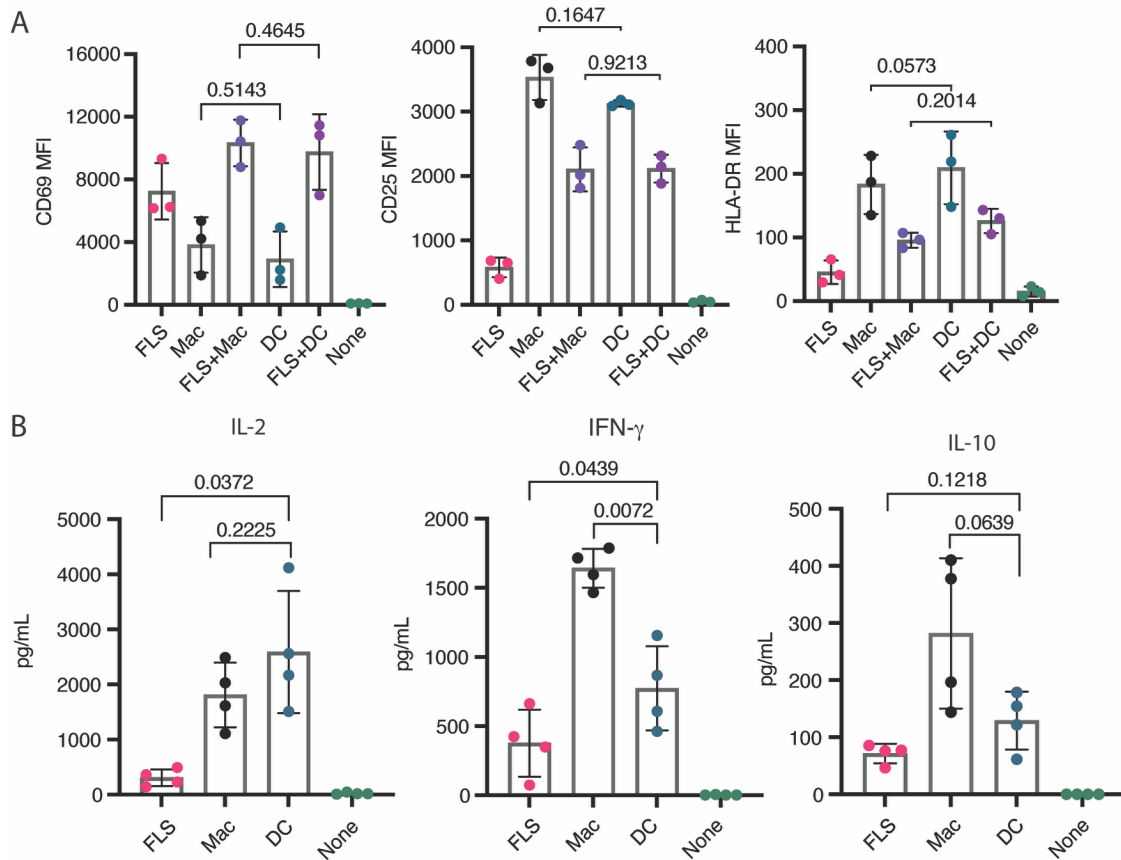
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Supplementary Figure 4. FLS from multiple diseases suppress T cell proliferation. (A) Proliferation of CD3⁺ T cells after 6 days of anti-CD3/CD28 bead stimulation with fibroblasts as in Figure 2, in addition to a no fibroblast control (none). Percent of CD3⁺ T cells in each of 8 observed generations (divisions). **(B)** Gating strategy shown for T cells after bead stimulation in the presence of one of the RA primary FLS donors. Generations labeled G0-G8.

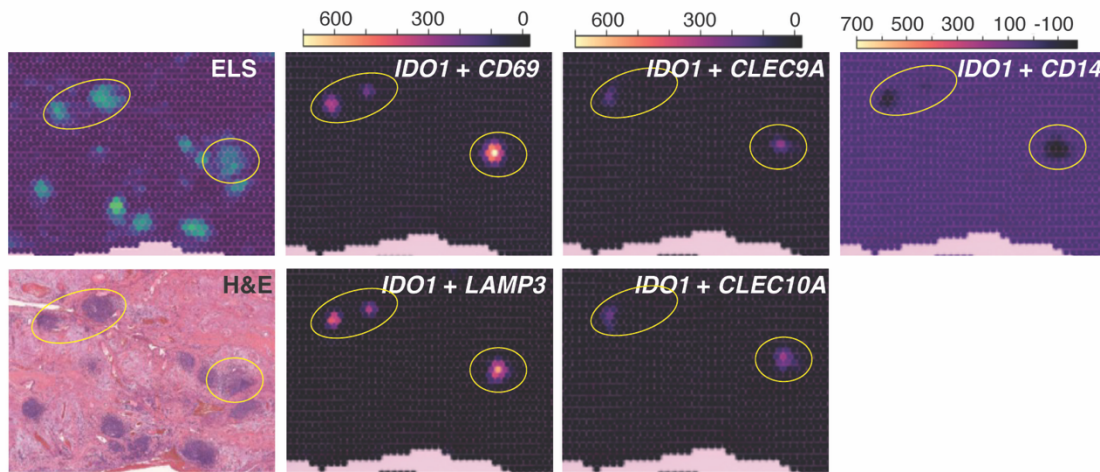


Supplementary Figure 5. APC effect on the expression of T cell expression differentiation factors and memory versus naïve T cells. (A) Heatmap of predominantly T cell-expressed genes related to T cell differentiation across conditions (FLS, macrophages, none). N=3 T cell donors for each condition. **(B)** Gating strategy for sorting naïve (CD45RA⁺CCR7⁺) and memory (CD45RA⁻) CD3⁺ T cells from healthy donor PBMCs. Population percentages shown with gate names are the percent of the parent population. **(C)** Representative histograms from flow cytometric expression of CD69 on CD3⁺Vβ^{SEB}CD69⁺ cells after 72 hours of SEB stimulation for FLS (left) and Mac (right) as APC from experiment quantified in Figure 4A.



Supplementary Figure 6. Dendritic cell activation of T cells is similar to that of macrophages. (A)

Surface expression (MFI) of activation markers CD69, CD25 and HLA-DR measured on CD3⁺V β ^{SEB} T cells via flow cytometry after 72 hours of SEB activation. The APC identity is shown on the x axis. Dendritic cells (DC) were differentiated using GM-CSF and IL-4 from blood-derived CD14⁺. N=3. **(B)** Cytokine concentrations measured by Luminex assay in the supernatant of APC-T cell co-cultures stimulated with SEB for 48 hours. APC identity indicated on the x axis. N=4. Mean +/- standard deviation is shown. Statistical comparisons were made using paired two-tailed t-tests with corrections for multiple comparisons within each outcome to maintain an overall Type I error rate of 0.05 as described in the methods section.



Supplementary Figure 7. Spatial colocalization of *IDO1* with *CD69* and macrophage/DC markers. Expression colocalization across RNA capture spots via local Lee's L statistic. Yellow ovals indicate regions of interest across panels.