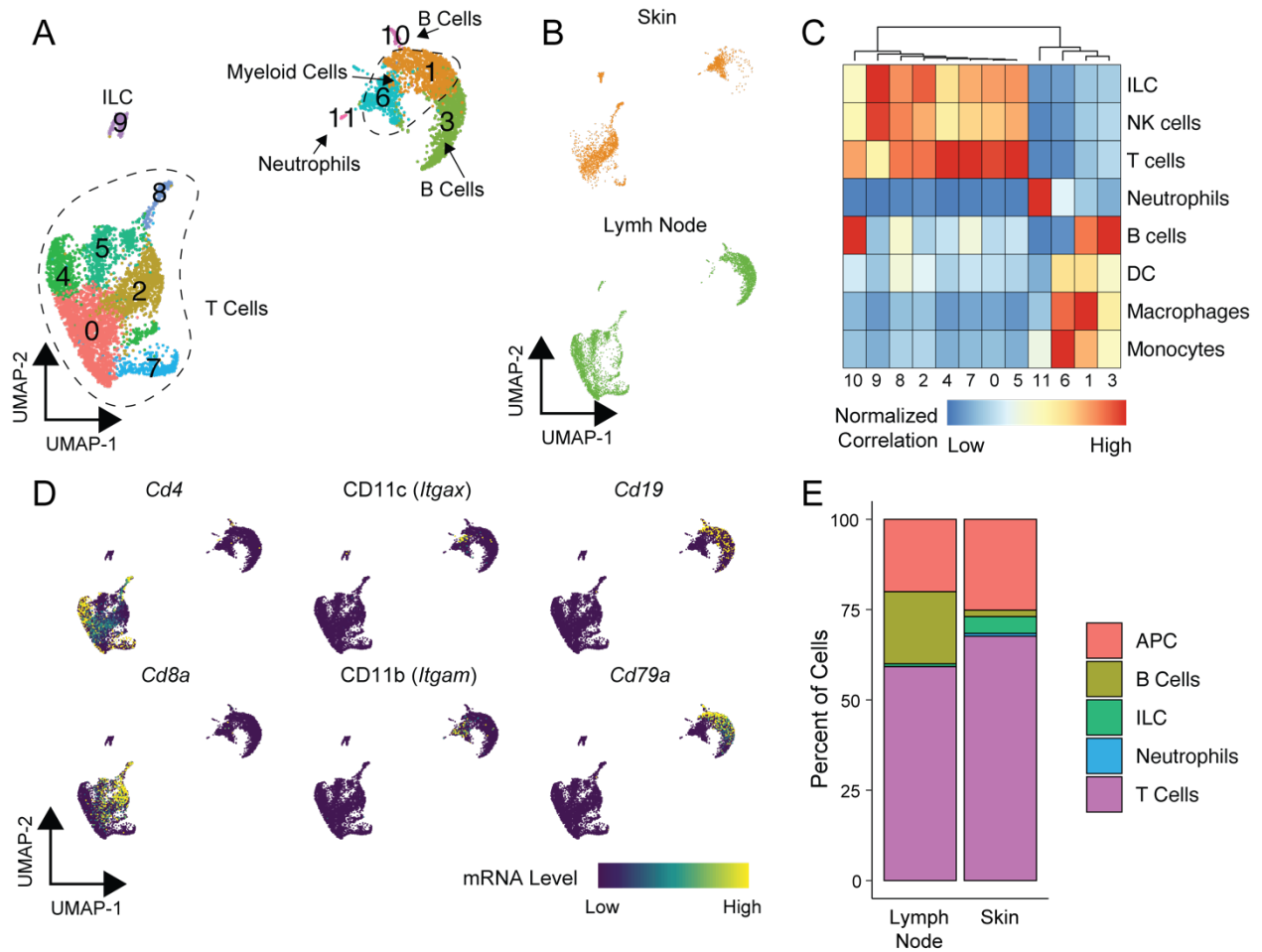


Supplemental Methods

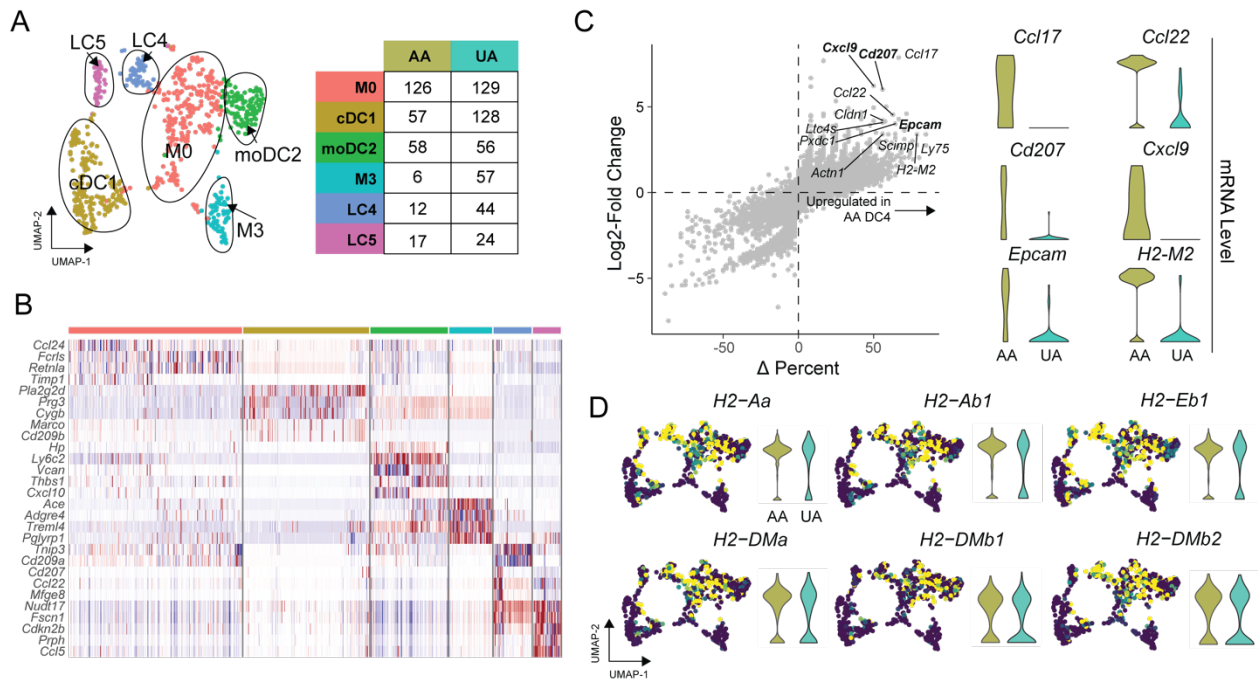
Secondary murine AA single-cell cohort.

Single immune cell suspensions from AA-affected C3H/HeJ mice were derived as described in the Methods section for both skin and lymph nodes. A total of 5,000 cells were targeted for sequencing by tissue type. Sequencing for 5' gene expression was performed using the Chromium (10x Genomics, Pleasanton, CA) and Illumina (San Diego, CA) sequencing technologies. Library preparation and alignment proceeded as described in the methods section. Across aligned AA immune skin cells, the mean number of reads per cell was 67,541, with an average of 94.7% of reads mapped, while AA lymph node cells had 33,741 and 95%, respectively. A total of 2,672 skin and 5,055 lymph nodes were then processed as described in the methods, with the exception of UMAP methods using a resolution of 0.3, to compensate for the reduction in total number of cells. Gene set enrichment analysis was performed using the *scone* (v1.0.0) R package with the top 50 genes markers from the *FindAllMarkers* function for the original T cells clusters as ranked by significance and log₂-fold change.

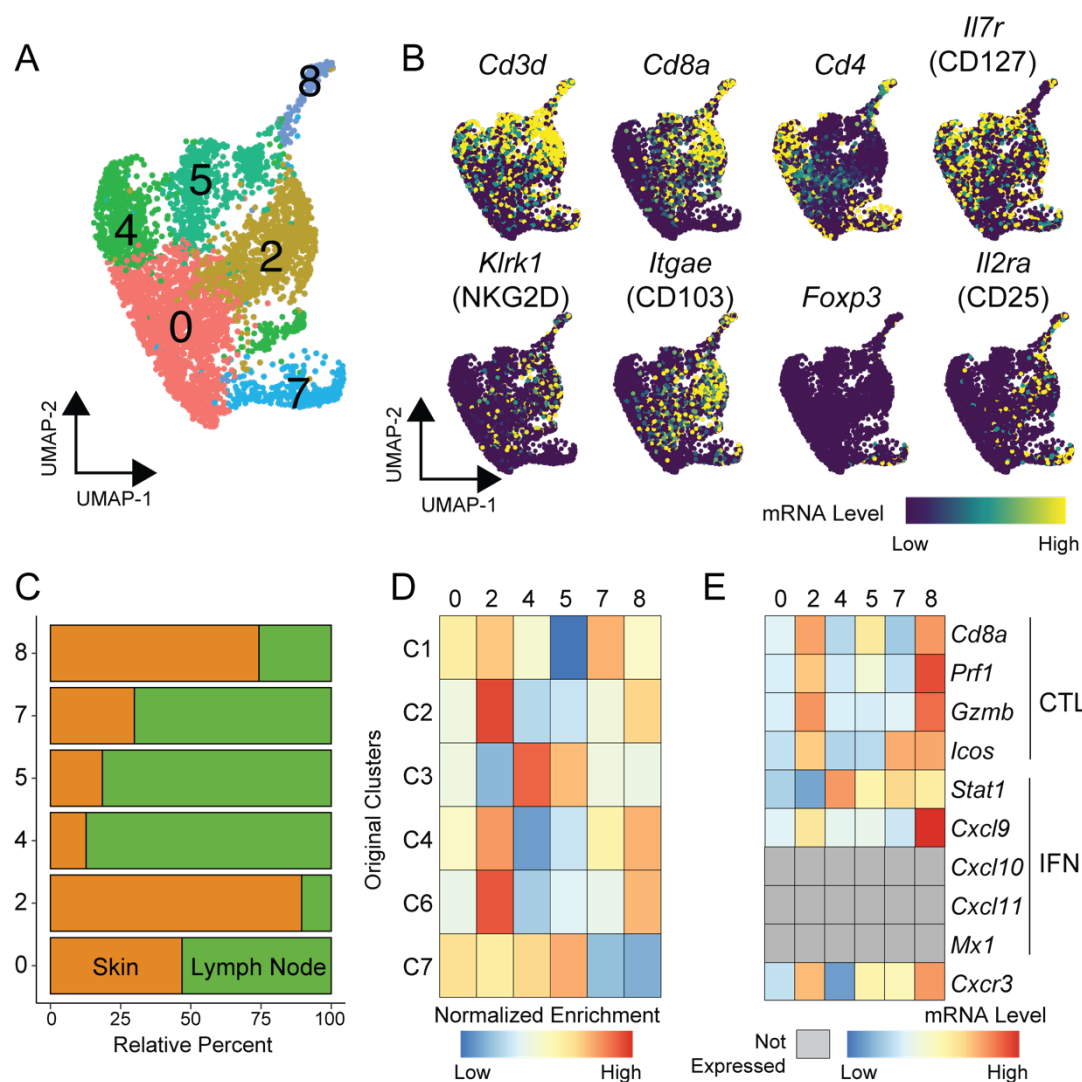
Supplemental Figures



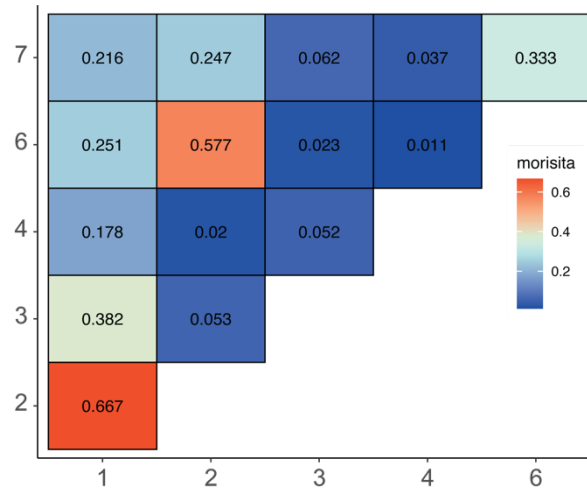
Supplemental Figure 1: A. UMAP projection for secondary murine AA single-cell cohort consisting of 5,055 and 2,671 immune cells from the lymph nodes and skin, respectively. **B.** UMAP projections demonstrating the relative distribution of murine AA cells along the UMAP projection. **C.** Normalized correlation values for predicted immune cell phenotypes based on the SingleR R package for each cluster. Cluster of columns based on Euclidean distance between normalized correlation values across all pure immune cell populations in the Immgen database. **D.** Lineage markers for T cells (*Cd4*, *Cd8a*), APC (*Itgax*, *Itgam*), and B cells (*Cd79a*, *Cd19*). **E.** Percent of assigned cell types across single immune cells isolated in the lymph nodes or skin of AA mice.



Supplemental Figure 2. A. UMAP projection for APC cells after scaling mRNA for cell cycle difference with total number of cells by condition in the table. **B** mRNA heatmap of the top 5 markers by log₂-fold change per cluster using the *FindAllMarkers* function in the Seurat R package. **C.** Differential gene expression for DC4 Skin Langerhan cells, comparing AA versus UA cells. Selected genes are labeled and have an adjusted p-value < 0.05 with plotting volcano plots on the left. **D.** Differentially-expressed MHC genes comparing AA versus UA cells across all APC clusters.



Supplemental Figure 3: **A.** UMAP projection of the flow-sorted CD45⁺ murine immune cells focusing on T cell cluster: Cluster 0 (n=1,741), Cluster 2 (n=1,039), Cluster 4 (n=793), Cluster 5 (N=671), Cluster 7 (n=381), and Cluster 8 (n=181). **B.** mRNA expression superimposed on the UMAP plot for general T cell and Treg markers. **C.** Relative contribution of cells to each cluster from lymph node versus skin. **D.** Scaled gene set enrichment scores from 50-gene signatures derived from the T cell clusters of the manuscript. **E.** Genes from the predictive ALADIN for cytotoxic T lymphocytes (CTL) and interferon (IFN). Genes not expressed in T cells are in grey.



Supplementary Figure 4: Morisita index calculations for clonotype overlap between the T cells clusters using the scRepertoire (v1.0.0) R package.

TRA: TRAV8-4.TRAJ12.TRAC
TGTGCTGTGAGTGGGATGGATAGCAGCTATAAATTGATCTTC

TRB: TRBV19.TRBJ2-1.TRBD2.TRBC2
TGTGCCAGTAGTATAGAAGGGTTAGTGGGGTACAATGAGCAGTTCTTC

TRA: TRAV16.TRAJ45.TRAC
TGTGCTCTAAGGGGGGGAGGAGGTGCTGACGGACTCACCTTT

TRB: TRBV11-2.TRBJ2-5.TRBD1.TRBC2
TGTGCCAGCAGCTCTAGGAATCTTTCTCTAGGGGGTCTGGAGACCCAGTACTTC

TRA: TRAV24.TRAJ30.TRAC
TGTGCCTCCGAGACGAACAGAGATGACAAGATCATCTTT

TRB: TRBV11-2.TRBJ2-5.TRBD1.TRBC2
TGTGCCAGCAGCTCTAGGAATCTTTCTCTAGGGGGTCTGGAGACCCAGTACTTC

TRA: TRAV24.TRAJ30.TRAC
TGTGCCTCCGAGACGAACAGAGATGACAAGATCATCTTT

TRB: TRBV11-2.TRBJ2-5.TRBD1.TRBC2
TGTGCCAGCAGCTCTAGGAATCTTTCTCTAGGGGGTCTGGAGACCCAGTACTTC

TRA: TRAV8-4.TRAJ22.TRAC
TGTGCTGTGAGTGCACCGTTTTCTGGTTCTGCAAGGCAACTGACCTTT

TRB: TRBV9.TRBJ1-6.None.TRBC1
TGTGCCAGCAGCGTAGAAATCGGGCCGGGCCCTTCACCCCTCCACTTT

Supplementary Figure 5: The top 5 clonotypes in human AA T cells defined using the scRepertoire (v1.0.0) R package.