

Supplementary Material:

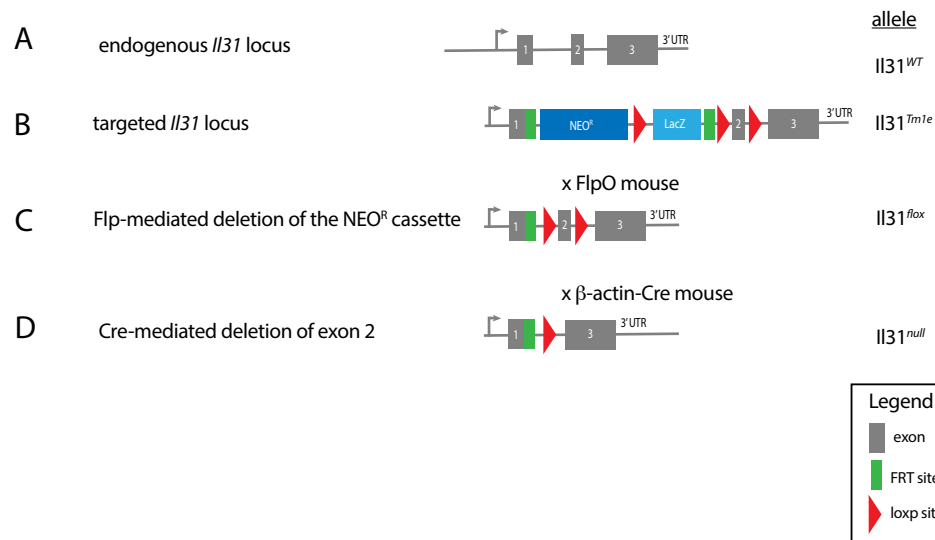


Fig. S1. Transgene schematic and serial crosses to generate *Il31*^{null} allele

(A) Endogenous 3-exon *Il31* allele

(B) The *Il31*^{Tm1e} transgene interrupts exon 1 of the endogenous *Il31* locus with a neomycin resistance/LacZ cassette.

(C) Mice containing an *Il31*^{lox} allele were generated by crossing an *Il31*^{Tm1e} transgenic mouse with a Flp-recombinase expressing strain (FlpO), resulting in germline excision of the region between FRT sites (green rectangles).

(D) Mice containing an *Il31*^{null} allele were generated by crossing an *Il31*^{lox} transgenic mouse with a ubiquitous Cre recombinase-expressing strain (β -actin Cre), resulting in germline excision of the region between loxp sites (red triangles).

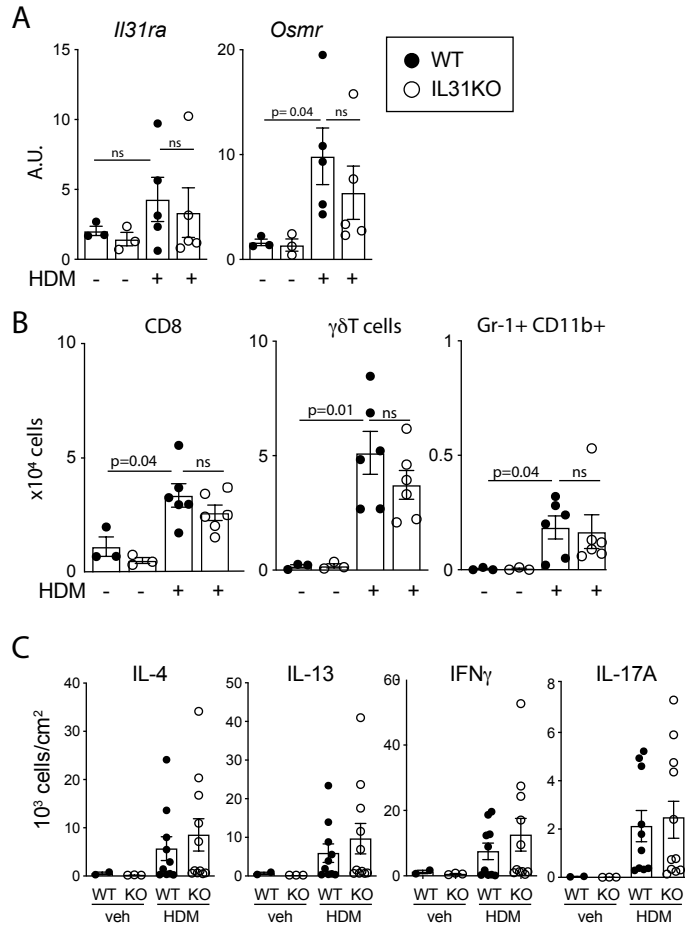


Fig. S2. Supplementary data to accompany Figure 2

(A) Taqman-based qPCR detection of *Il31ra* and *Osmr* in control and HDM-treated skin.

(B) CD45⁺ (hematopoietic) populations increased in HDM-treated skin include CD8 T cells, dermal $\gamma\delta$ T cells, and CD11b⁺Gr1⁺ cells (combined monocytes and neutrophils).

(C) Flow cytometry data from Figure 2F enumerated as cytokine-producing CD4 T cells per mouse. Both vehicle (control) and HDM-treated samples are included for comparison.

WT, black circles; IL31KO, open circles. Data reflect n=3 animals per control group and n \geq 5 per HDM treatment group, and are representative of 3 independent experiments (A, B), or pooled from 2 independent experiments with n \geq 5 mice per treatment group (C). Bars indicate mean \pm SD. Statistical significance determined by unpaired student's t-test.

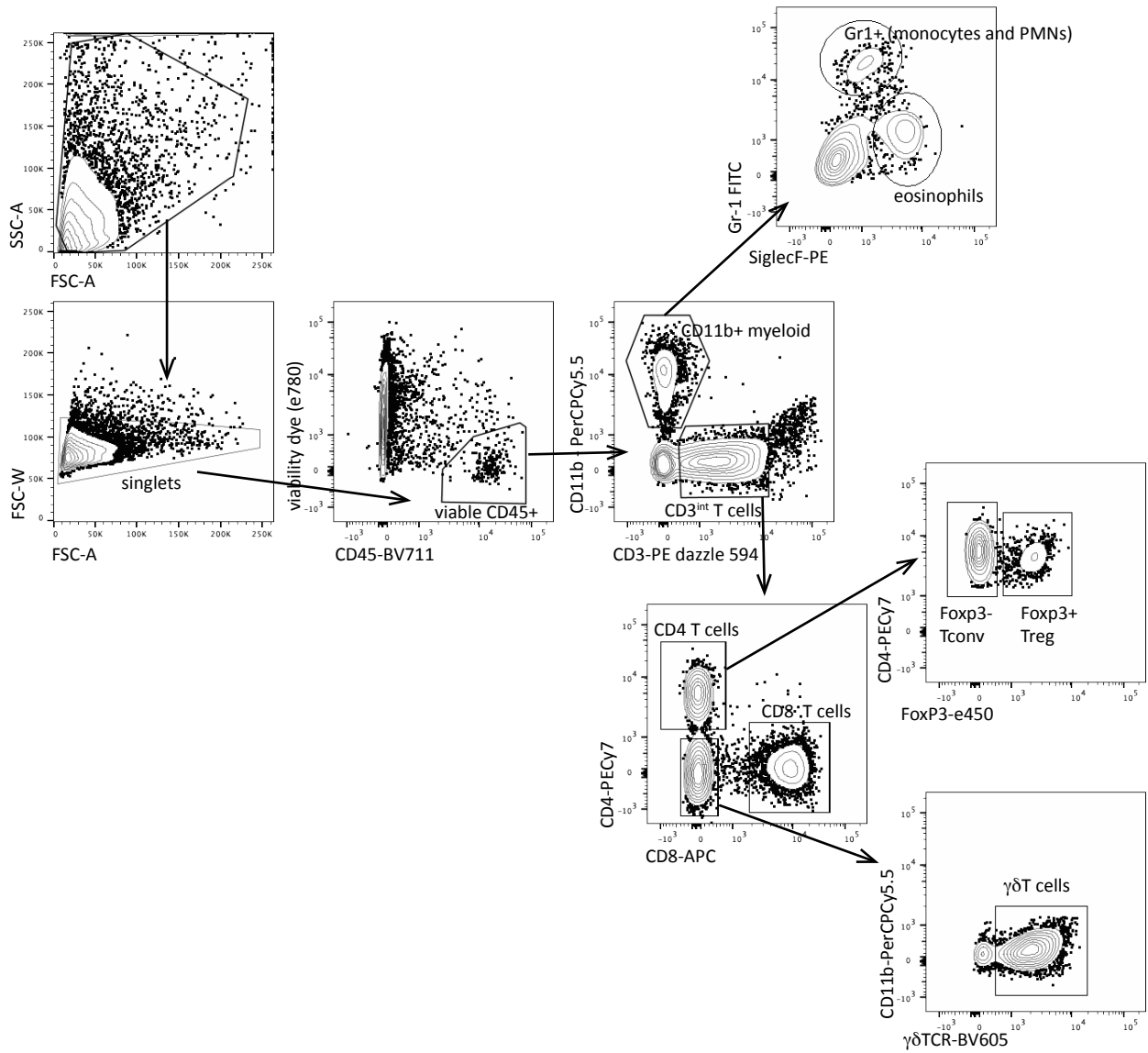


Fig. S3. Gating strategy for cutaneous CD45+ (hematopoietic) subsets

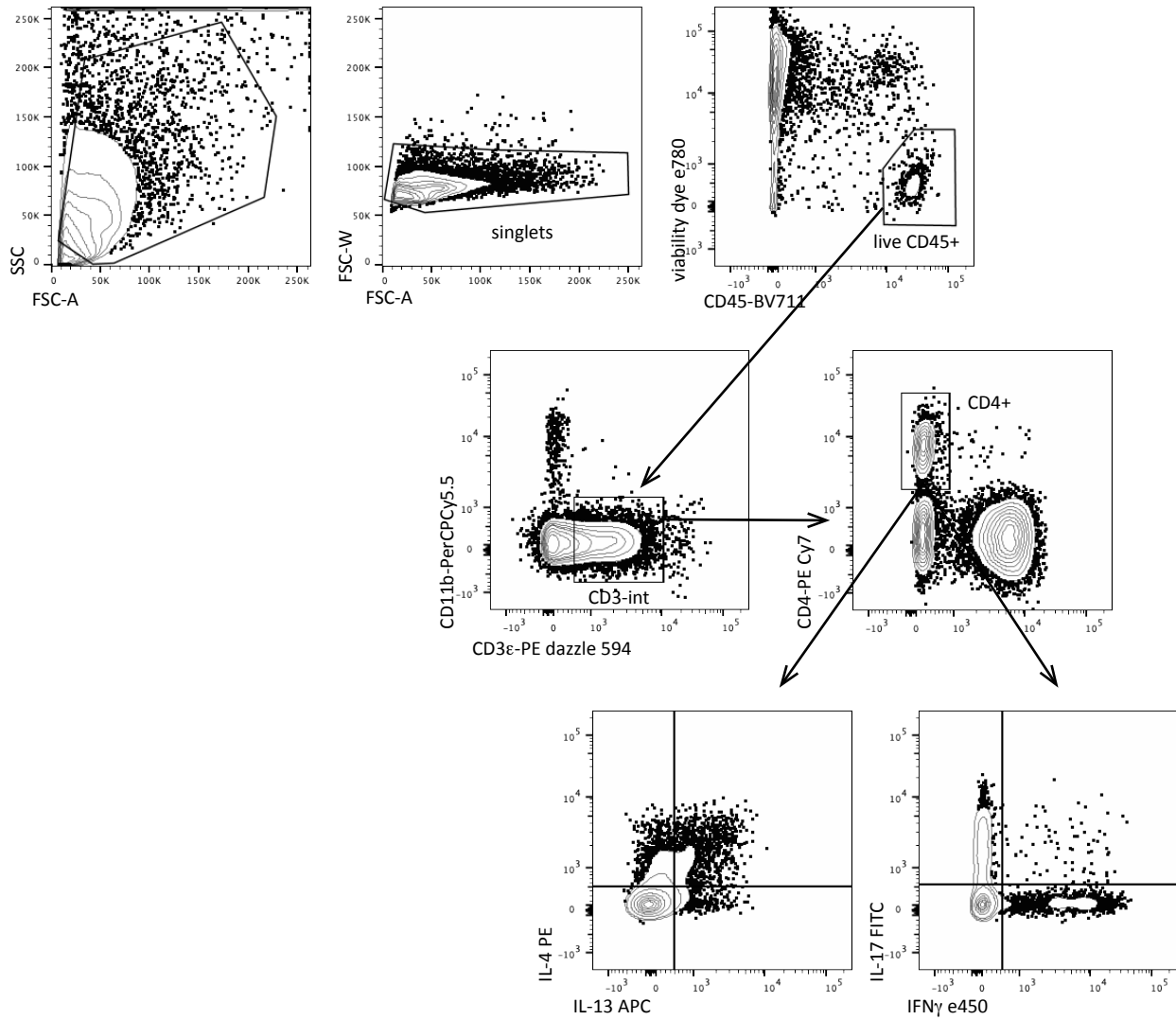
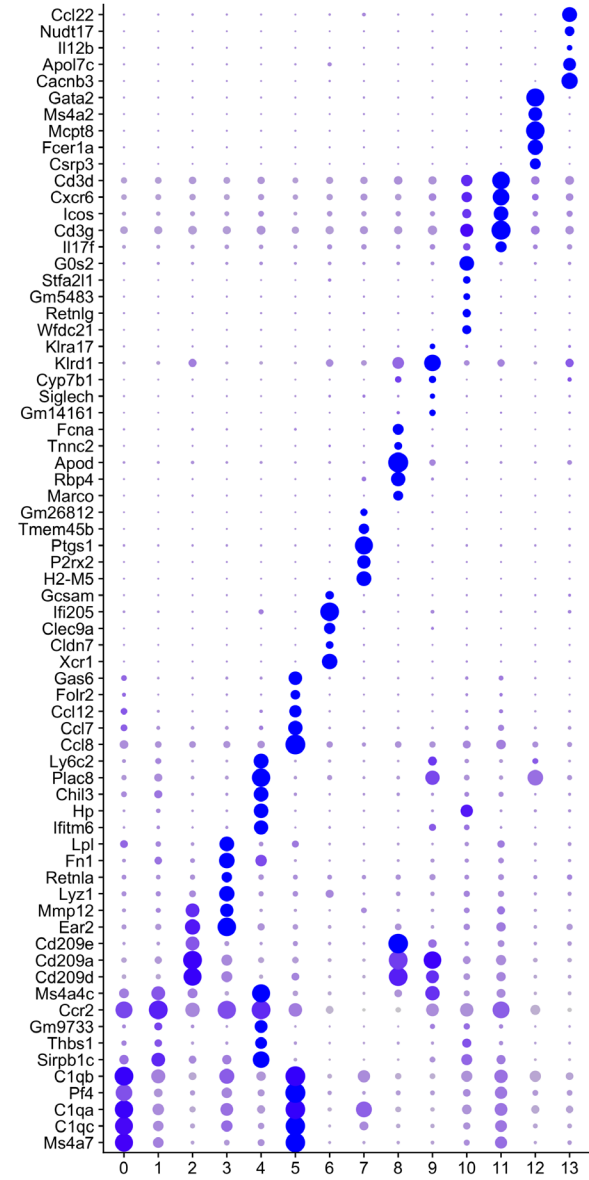


Fig. S4. Gating strategy for CD4 T cell intracellular cytokine detection

A Cluster Marker Genes (defined by LFC)



B Cluster Marker Genes (defined by LFC x PCT)



C

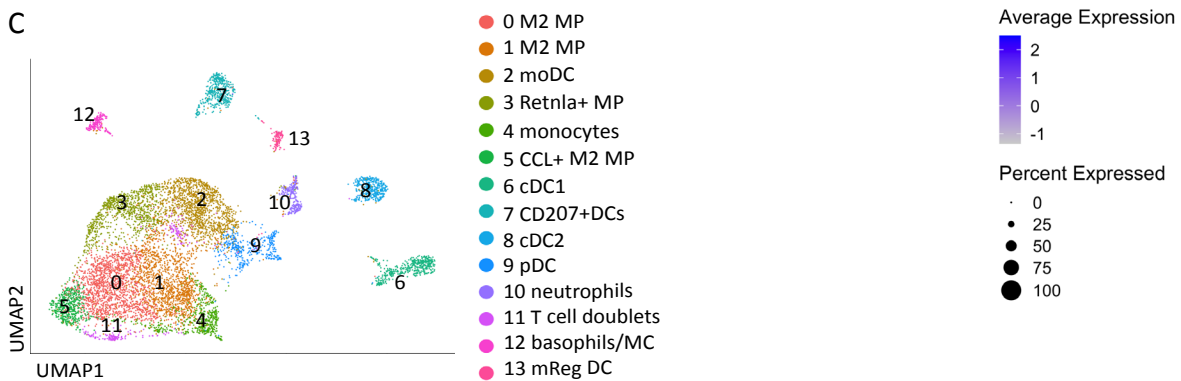


Fig. S5. Cell Marker genes for the 13 myeloid clusters

(A) Dot plot of top 5 differentially-expressed genes defined by average log fold change (LFC)

(B) Dot plot of top 5 differentially-expressed genes defined as the product of the average log fold change (LFC) and the cluster specificity (PCT ratio).

(C) UMAP plot and cluster identities from Figure 4 reproduced for reference

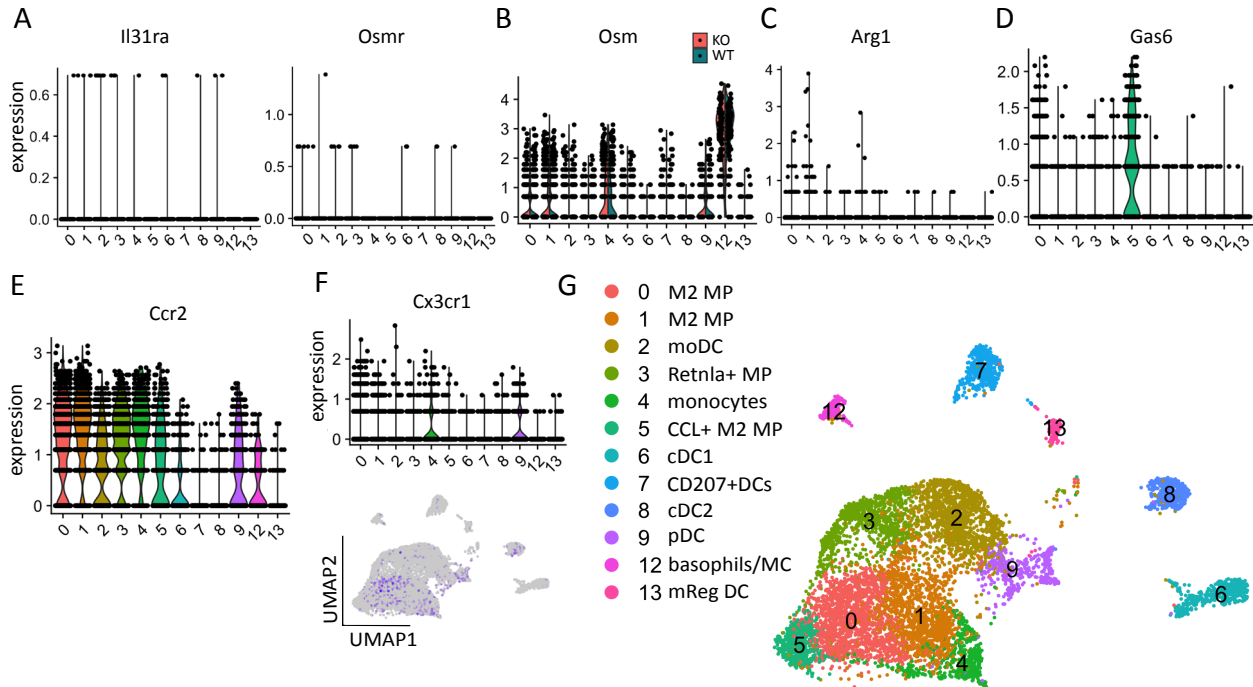


Fig. S6. Supplementary data to accompany Figures 4-5.

(A) *Il31ra* and *Osmr* only detected in scattered cells

(B) Split violin plot demonstrates similar *Osm* expression in WT and IL31RAKO across clusters (turquoise = WT, salmon = IL31RAKO).

(C) Rare cells express M2 marker *Arg1*

(D) Expression of Mertk ligand and cluster 5 marker *Gas6*.

(E) *Ccr2* is broadly expressed by macrophages (clusters 0,1,3,4,5) and monocyte-derived DCs (cluster 2).

(F) Distribution of *Cx3cr1* across myeloid clusters (top: violin plot; bottom, feature plot)

(G) UMAP plot and cluster identities from Figure 5 reproduced for reference