**Supplementary data**

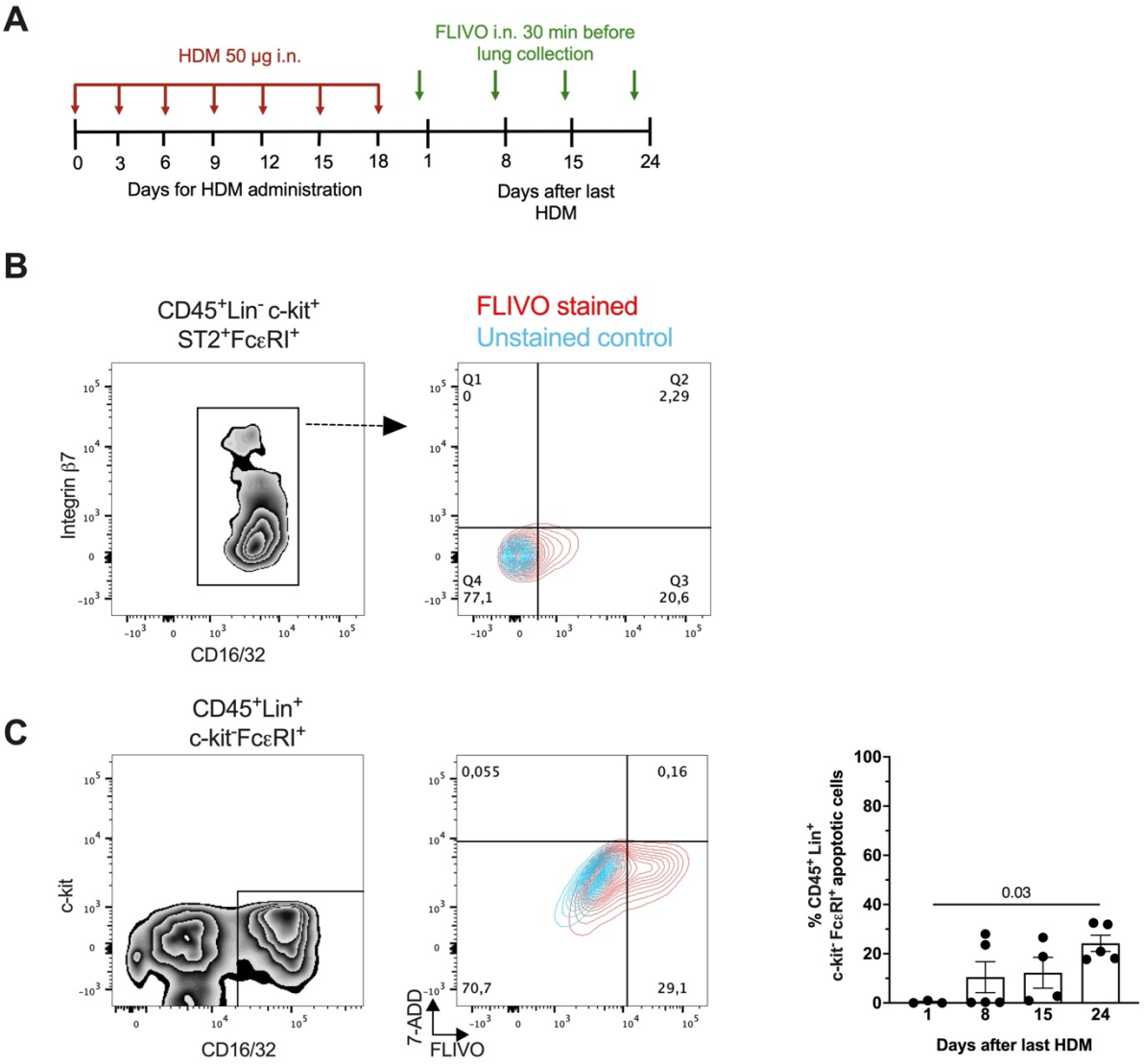


**Fig. S1. FLIVO Administration and apoptotic cell analysis in lung MCs populations. A** The fluorescently labeled poly-caspase inhibitor FLIVO was administrated 30 min before tissue collection at the indicated time points after the last HDM administration. **B-C** The proportion of apoptotic cells among the $CD45^+$ $Lin^-$ $c\text{-}kit^+$ $ST2^+$ $Fc\varepsilon RI^+$ MC populations (**B**), and among the whole $CD45^+$ $Lin^+$ $c\text{-}kit^-$ $Fc\varepsilon RI^+$ population (**C**) was investigated by flow cytometry. The lineage markers included: CD3, CD4, CD8b, CD19, B220, TER119, and Ly-6G. Bars represent the mean ± SEM of two independent experiments. Statistical differences were tested by one-way ANOVA with Tukey post-hoc test.

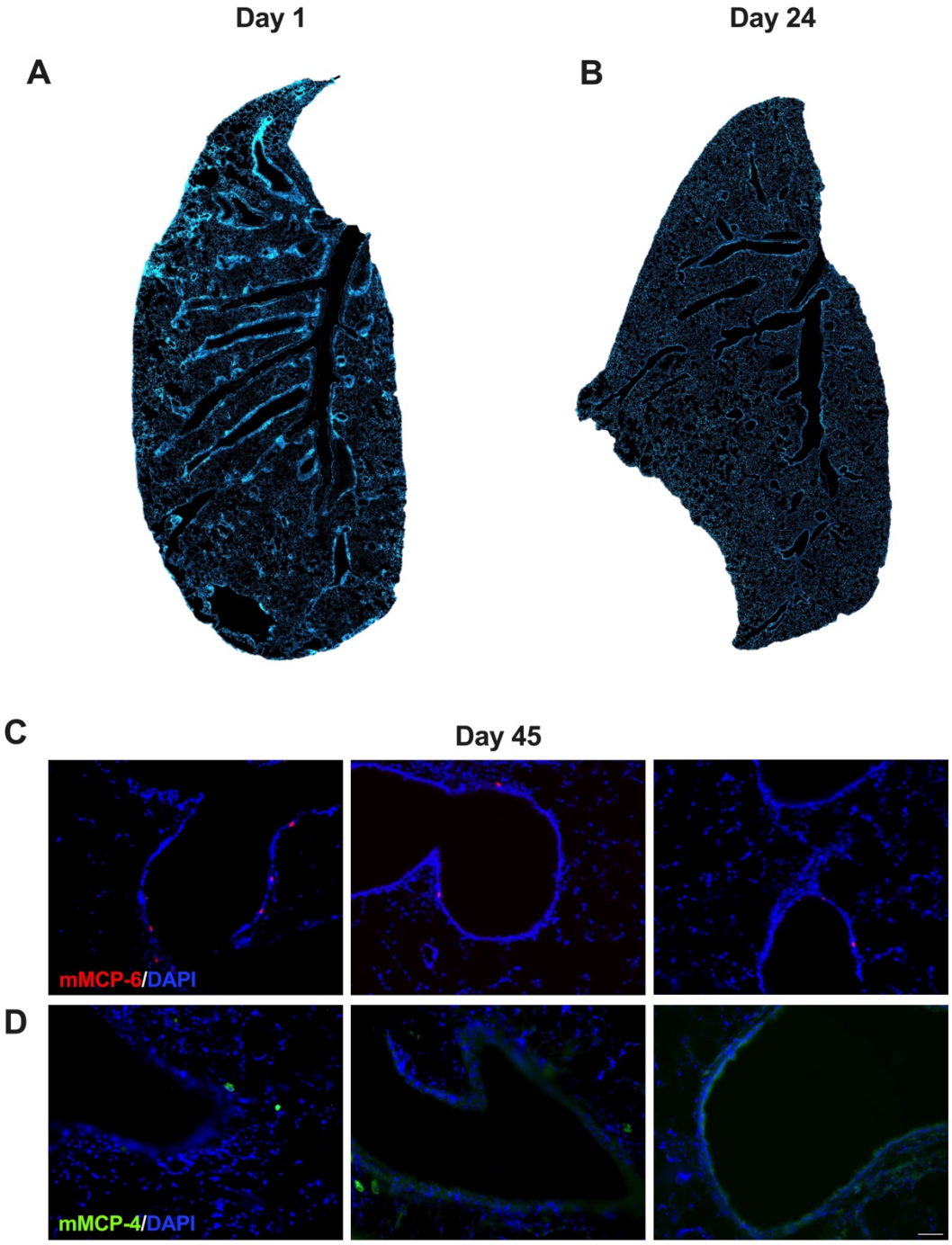


**Fig. S2. Lung inflammation is absent 24 days after the last HDM, and mMCP-6$^+$ and mMCP-4$^+$ cells can be observed even 45 days after last the HDM administration. A-B** Representative images of the left lobe lung were collected at day 1 or 24 after the last HDM administration and the general presence of inflammatory cells was visualized by DAPI. **C-D** In a single experiment, three mice subjected to the HDM protocol were left for 45 days post-HDM, and the lungs immunostained for mMCP-6$^+$ cells (**C**) and mMCP-4$^+$ cells (**D**) in the lung sections collected on day 45 after the last HDM administration. The scale bar represents 50 μm.

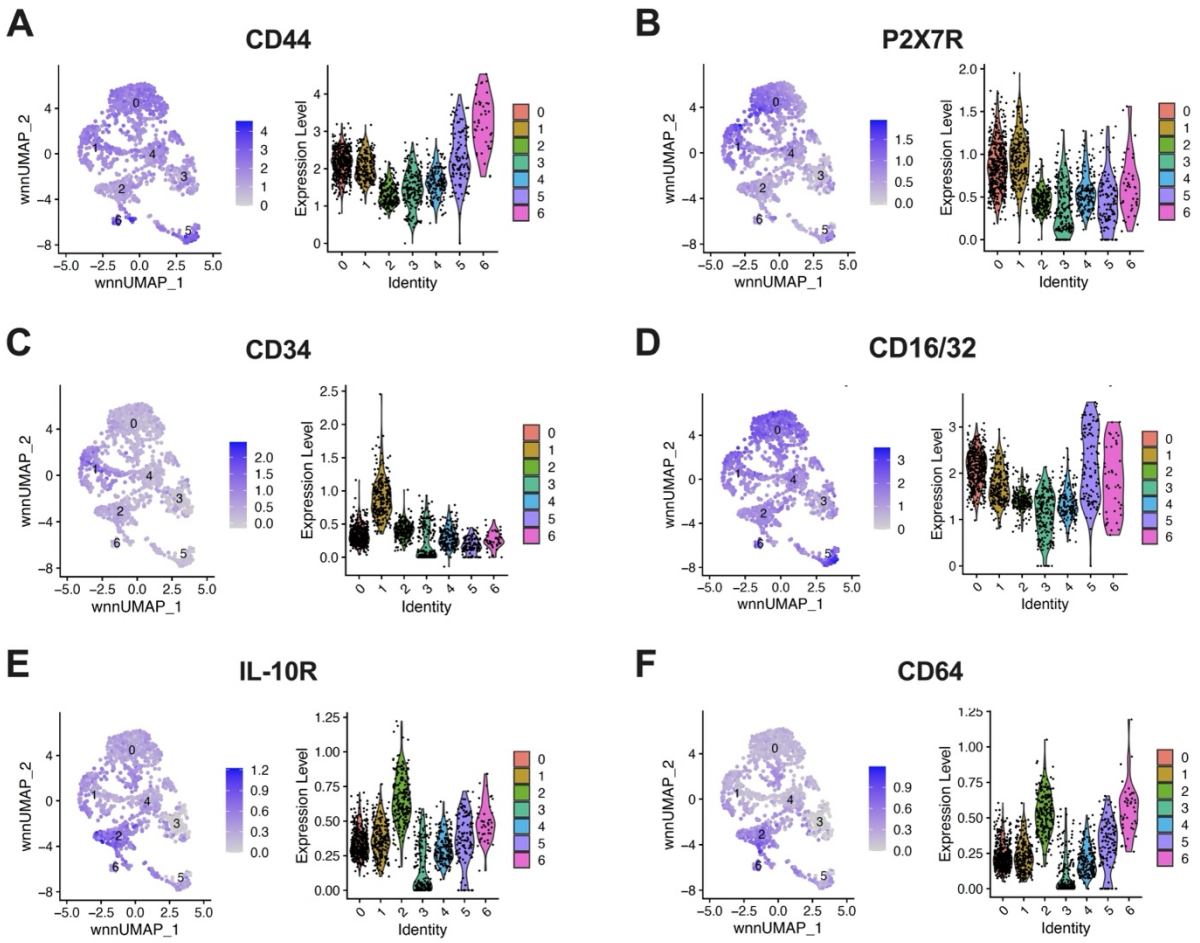


**Fig. S3. UMAPs and Violin plots illustrating additional oligo-tagged surface markers for the distinct clusters in the dataset. A-F** The UMAP highlights differentially expressed surface proteins across the CITE-seq identified cell populations, and the matching violin plots display the distribution and relative surface expression levels of CD44 (**A**), P2X7R (**B**), CD34 (**C**), CD16/32 (**D**), IL-10R (**E**), CD64 (**F**) among the seven clusters identified by CITE-seq.

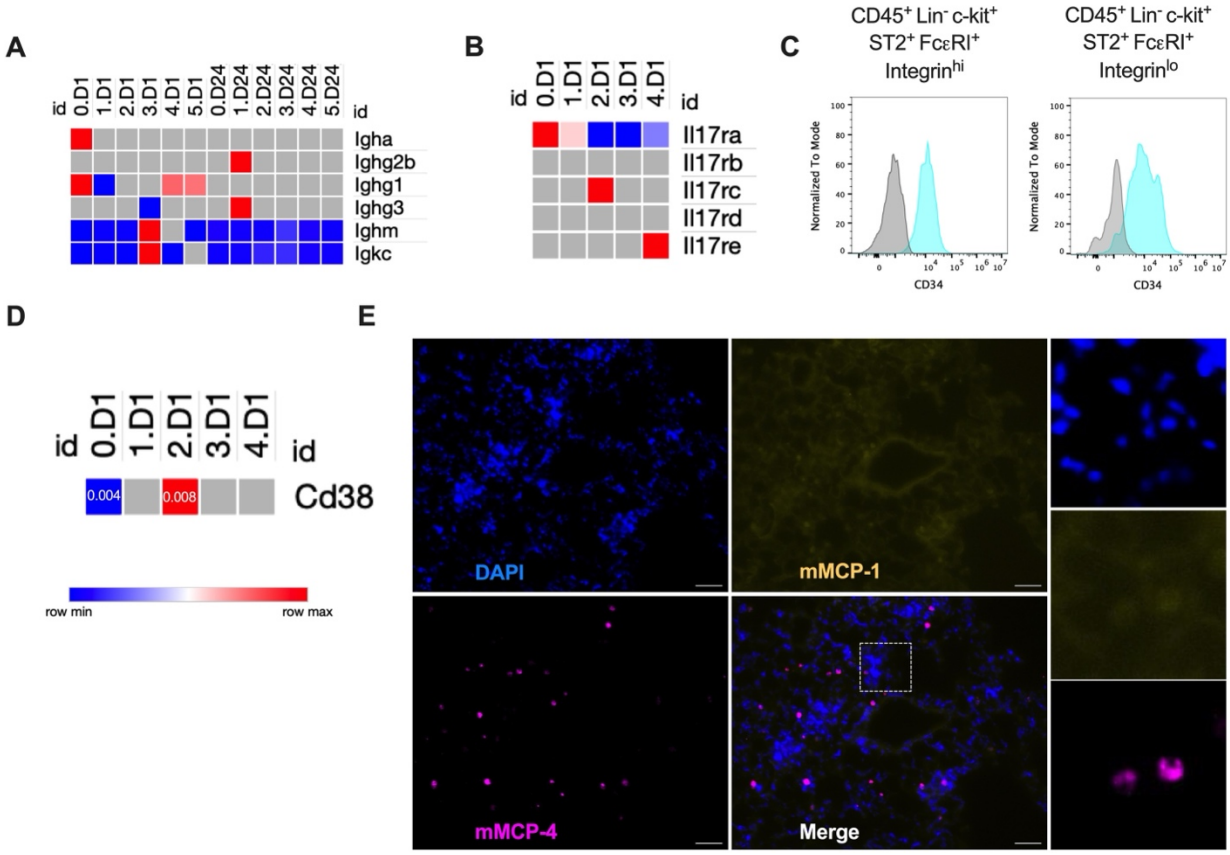


**Fig. S4. Expression profiles of immunoglobulin heavy chain genes, IL-17 receptor subunits, and transcription factors in diverse clusters, and representative visualization of co-immunostaining for mMCP-4 and mMCP-1 in MCs at day 24. A-B** Heat maps showing the average expression of different subclasses of immunoglobulin heavy chain genes (**A**) and different IL-17 receptor subunits (**B**). Grey values represent the absence of expression. **C** The expression of CD34 by flow cytometry in lung MC populations. The Lin markers included: CD3, CD4, CD8b, CD19, B220, TER119, and Ly-6G. **D** The expression of the CD38 gene in the MC clusters at day 1. The numbers within the heat map indicate the average transcript levels in each group, while grey values denote the absence of expression. **E** Representative immunostaining of lung samples collected on day 24 post-final HDM showing the absence of mMCP-1 staining within the mMCP-4$^{+}$ cells in the submucosa and parenchyma. The scale bar represents 50 μm.

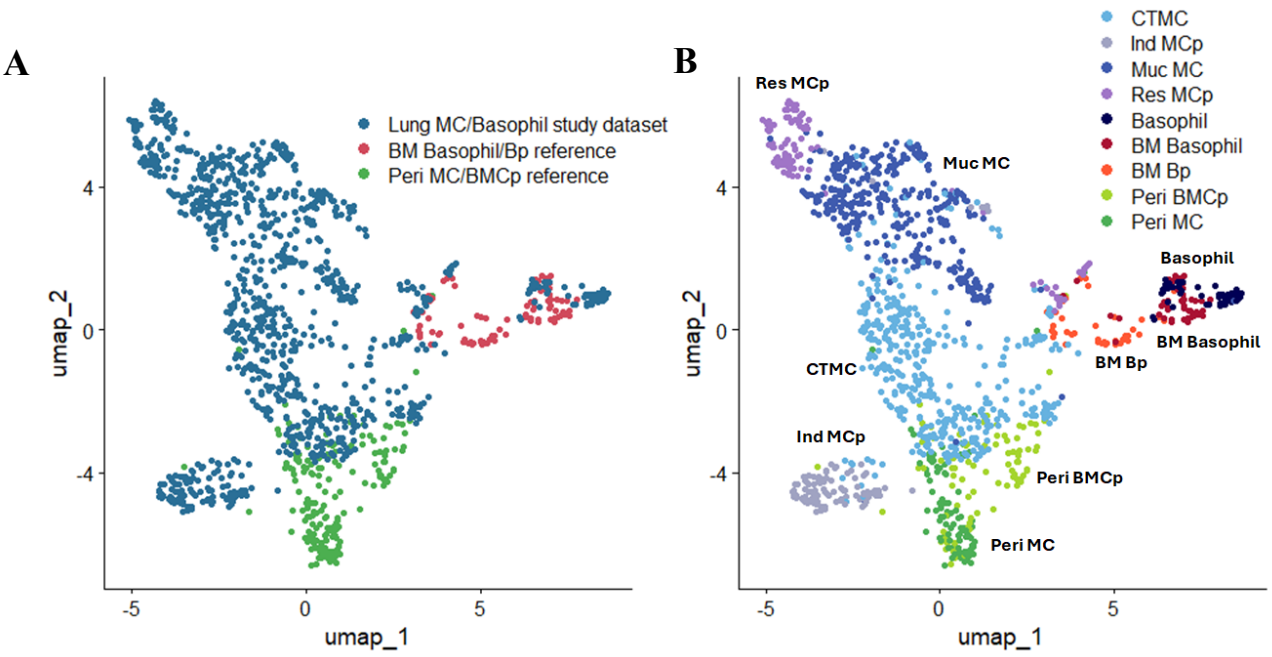


**Fig. S5: Projection of two reference datasets onto the cell type clusters identified by the scRNA-seq analysis in our study**. **A** UMAP visualization showing the integration of the dataset used in the current study (Lung MCs/basophil), and two reference datasets comprising of mouse bone marrow basophils and basophil progenitors (BM Basophil/Bp) and mouse peritoneal MCs and bipotent basophil MC progenitors (Peri MC/BMCp). **B** UMAP visualization of the clustering of the identified cell types in this study compared to those present in the reference datasets. BM, bone marrow; Peri, peritoneal; Bp, basophil progenitor; BMCp, basophil MC progenitor; MCp, MC progenitor; Ind, induced; Muc, mucosal; Res, resident.

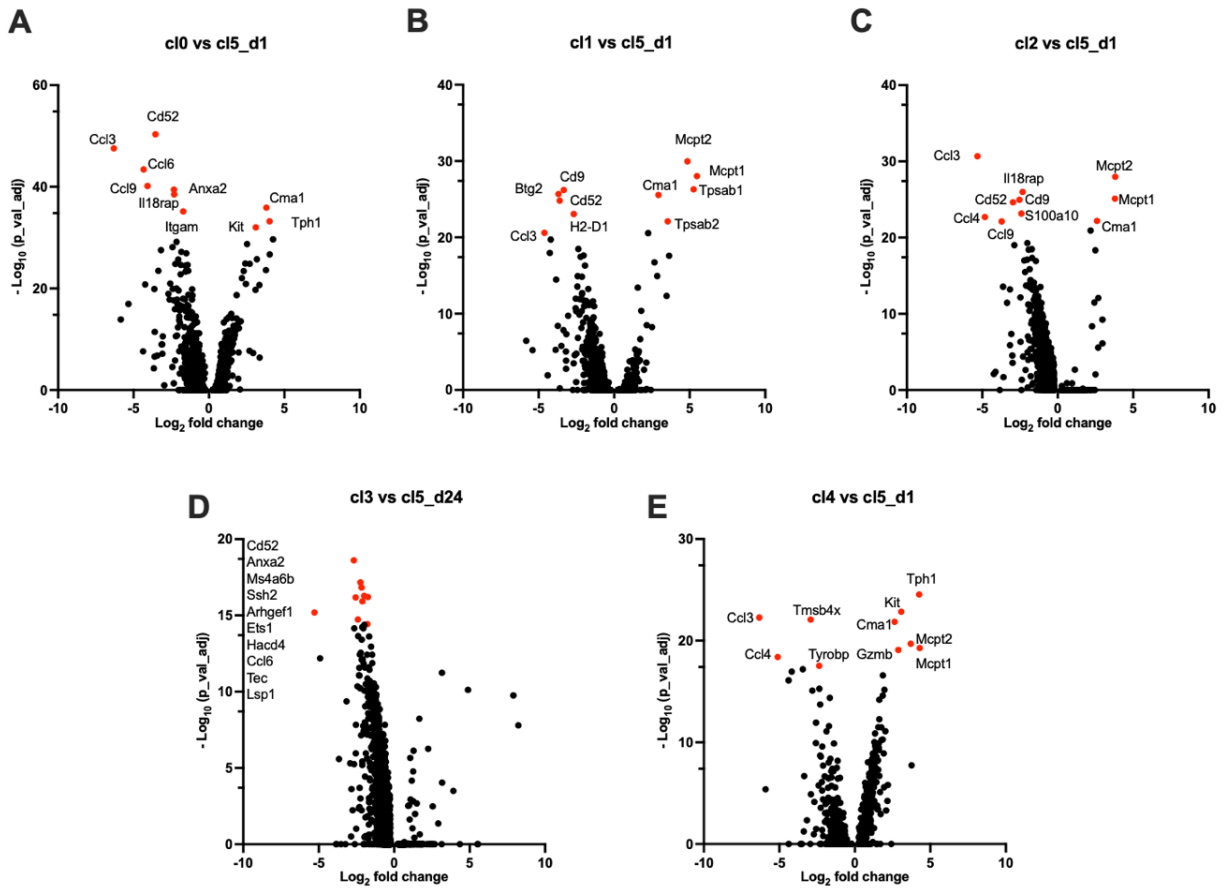


**Fig. S6. Single-cell RNA-sequencing (scRNA-seq) analysis reveals that MC proteases are upregulated in clusters 0–4 compared with basophils (Cluster 5). A–E** Volcano plots illustrating the top 10 most significantly differentially expressed genes in each cluster (cl) 0–4, relative to basophils (cl5). Differential expression was evaluated at the indicated time points, with clusters 0, 1, 2, and 4 assessed on day 1 and Cluster 3 assessed on day 24. The top 10 DEGs in each cluster are labeled in red for clarity.

**Table S1.** Please see the separate excel file.

**Table S2.** Antibodies used in flow cytometry.

| Target | Fluorochrome | Clone | Vendor |
|---|---|---|---|
| CD45 | Alexa flour 700 | 30-F11 | BD Biosciences |
| Lin: CD3 | BV510 | 17A2 | BD Biosciences |
| Lin: CD4 | BV510 | GK1.5 | eBioscience |
| Lin: CD8b | BV510 | eBioH35-17.2 | eBioscience |
| Lin: CD19 | BV510 | ebio1D3 | eBioscience |
| Lin: B220 | BV510 | RA3-6B2 | eBioscience |
| Lin: TER-119 | BV510 | TER-119 | eBioscience |
| Lin: Gr1 | BV510 | RB6-8C5 | eBioscience |
| Lin: CD11b | BV510 | M1/70 | eBioscience |
| C-kit | BV421 | 2B8 | eBioscience |
| CD16/32 | BV605 | 2.4G2 | BD Biosciences |
| Integrin β7 | PE-Cy7 | FIB504 | eBioscience |
| FcεRI | PE | MAR-1 | eBioscience |
| ST2 | BV786 | DIH9 | BioLegend |
| CD34 | BV421 | SA376A4 | BioLegend |

**Table S3.** Oligo-tagged antibodies used in the CITE-seq experiment.

| Target | Clone | Vendor |
|---|---|---|
| CD11b | M1/70 | BioLegend |
| C-kit | 2B8 | BioLegend |
| Integrin β7 | FIB504 | BioLegend |
| Integrin αE | 2E7 | BioLegend |
| CD34 | SA376A4 | BioLegend |
| IL-10R | 1B1.3a | BioLegend |
| CD64 | X54-5/7.1 | BioLegend |
| CD44 | IM7 | BioLegend |
| P2X7R | 1F11 | BioLegend |
| CD16/32 | 93 | BioLegend |

**Table S4.** Overrepresentation analysis of upregulated genes during the resolution of lung inflammation in the persistent mucosal MCs subset (cluster 1).

| Gene Set | Description | Size | Overlap | Expect | Enrichment ratio | P-value | FDR | User input |
|---|---|---|---|---|---|---|---|---|
| P00006 | Apoptosis signaling | 103 | 5 | 0.58 | 8.60 | 1.46e-4 | 0.016 | Hspa8; Jun; Nfkbia; Birc3; Hspa1b |
| P06664 | Gonadotropin-releasing hormone receptor | 215 | 6 | 1.21 | 4.94 | 5.47e-4 | 0.03 | Junb; Egr1; Nr4a1; Jund; Jun; Fosb |
| P00052 | TGF-β signaling | 83 | 4 | 0.46 | 8.53 | 8.42e-4 | 0.031 | Junb; Jund; Jun; Skil |
| P00054 | Toll receptor signaling | 36 | 2 | 0.20 | 9.84 | 0.016 | 0.46 | Jun; Nfkbia |
| P00031 | Inflammation by cytokine signaling | 210 | 4 | 1.18 | 3.37 | 0.02 | 0.54 | Junb; Jund; Jun; Nfkbia |
| P00010 | B cell activation | 54 | 2 | 0.30 | 6.56 | 0.03 | 0.66 | Jun; Nfkbia |
| P00053 | T cell activation | 64 | 2 | 0.36 | 5.53 | 0.04 | 0.77 | Jun; Nfkbia |
| P00049 | Parkinson disease | 85 | 2 | 0.47 | 4.16 | 0.08 | 1 | Hspa8; Hspa1b |
| P00020 | FAS signaling | 26 | 1 | 0.14 | 6.81 | 0.13 | 1 | Jun |
| P00017 | DNA replication | 31 | 1 | 0.17 | 5.71 | 0.16 | 1 | H3f3b |

**Table S5.** Antibodies used for immunofluorescence microscopy of mouse lung tissues.

| **Primary Antibodies** | | | | | |
|---|---|---|---|---|---|
| **Target** | **Host** | **Dilution** | **Vendor** | **Catalog number** | **Conjugation** |
| mMCP-1 | Rat | 1:200 | Thermo Fisher | 14-5503-82 | Unconjugated |
| mMCP-4 | Rabbit | 1:500 | Gift (*29*) | Whole rabbit serum | Unconjugated |
| mMCP-6 | Rabbit | 1:500 | R&D systems | MAB3736 | Unconjugated |
| mMCP-8 | Rat | 1:200 | BioLegend | 647402 | Unconjugated |
| Integrin β7 | Rat | 1:50 | BD | 551082 | APC |
| IL-17RA | Rabbit | 1:200 | Thermo Fisher | PA5-101326 | Unconjugated |
| VEGFA | Rabbit | 1:400 | Thermo Fisher | MA5-32038 | Unconjugated |
| Ki-67 | Rat | 1:1000 | Thermo Fisher | 14-5698-82 | Unconjugated |
| AHR | Rat | 1:200 | Thermo Fisher | 53-5925-80 | Alexa 488 |
| Avidin | - | 1:2000 | Vector laboratories | A-2001 | Fluorescein |
| **Secondary Antibodies** | | | | | |
| **Target** | **Host** | **Dilution** | **Vendor** | **Catalog number** | **Conjugation** |
| Rat | Donkey | 1:500 | Thermo Fisher | A48269 | Alexa 488 |
| Rat | Donkey | 1:500 | Thermo Fisher | A48272 | Alexa 647 |
| Rabbit | Donkey | 1:500 | Thermo Fisher | A10042 | Alexa 586 |