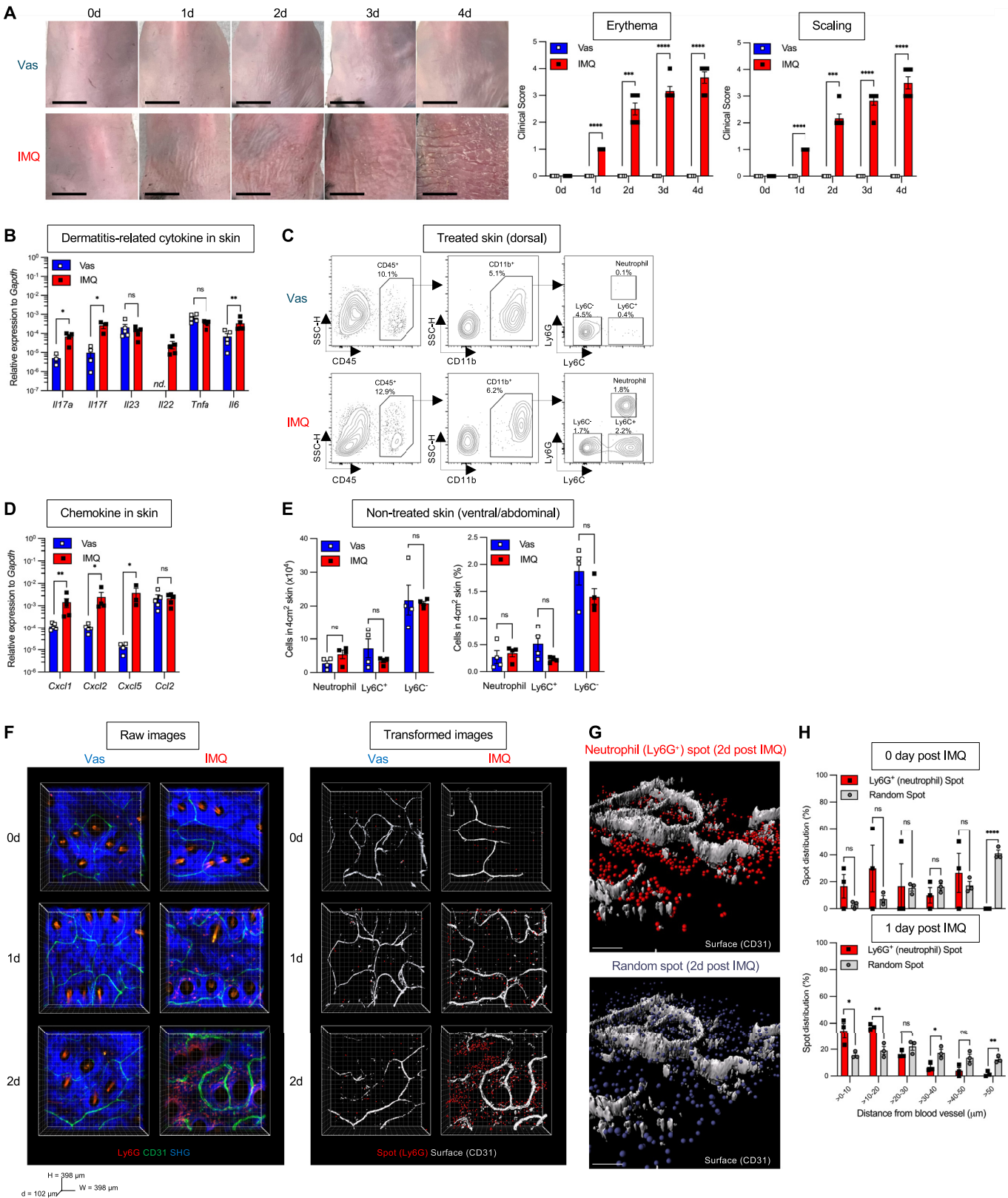


Expanded View Figures

Figure EV1. Characterization of clinical manifestations, myeloid cells, and the related factors in an imiquimod (IMQ)-induced skin psoriasis model.

(A) Upper: representative images of dorsal skin treated topically with daily Vas/IMQ from 0–3 d (4 times). Lower: Clinical score such as erythema and scaling from the dorsal skin treated with Vas/IMQ ($n = 3$ each). 2way ANOVA/Sidak comparison: $p = \text{n.d.}$ (0 d), $p < 0.0001$ (1 d), $p = 0.0005$ (2 d), $p < 0.0001$ (3 d), $p = 0.0001$ (4 d) for erythema, and $p = \text{n.d.}$ (0 d), $p < 0.0001$ (1 d), $p < 0.0002$ (2 d), $p < 0.0001$ (3 d), $p < 0.0001$ (4 d) for scaling. The scale bars in each figure represent 1 cm long. (B) mRNA expression of dermatitis-related cytokines in dorsal skin treated with Vas ($n = 3$ –5) or IMQ ($n = 3$ –5). t -test/Mann-Whitney test: $p = 0.0306$ (*Il17a*), $p = 0.0178$ (*Il17f*), $p > 0.9999$ (*Il23*), $p = \text{n.d.}$ (*Il22*), $p = 0.0526$ (*Tnfa*), $p = 0.0079$ (*Il6*). (C) Representative FACS gating strategy plots of myeloid cell fractions from dorsal skin treated with Vas or IMQ. (D) mRNA expression of chemokines in the dorsal skin treated with Vas or IMQ ($n = 3$ –5 for each). t -test/Mann-Whitney test: $p = 0.0079$ (*Cxcl1*), $p = 0.0159$ (*Cxcl2*), $p = 0.0500$ (*Cxcl5*), $p = 0.9758$ (*Ccl2*). (E) Number and percentage of myeloid cell fractions in the non-lesional abdominal skin (Vas: $n = 4$, IMQ: $n = 4$); statistical analysis t -test: $p = 0.6224$ (Neutrophil), $p = 0.0891$ (Ly6C^+), $p = 0.1634$ (Ly6C^-) for cell number, $p = 0.1255$ (Neutrophil), $p = 0.2411$ (Ly6C^+), $p = 0.8402$ (Ly6C^-) for percentage. (F) Representative 3-dimensional (3D) intravital microscopic images of dorsal skin at 0 d, 1 d, and 2 d after Vas or IMQ treatment. Left images show raw data with Ly6G^+ cells (red), CD31^+ cells (green), and SHG (second harmonic generation) (blue). Right images show spot and surface transformed data with spot (Ly6G^+) and surface (CD31^+). (G) Representative images of the transformed 3D-intravital microscopy of neutrophil (left) and random spot (right) proximity distribution to blood vessel in the 2 d IMQ-skin, scale bar = 50 μm . (H) Bar graphs showing the comparative distribution of neutrophils and random spots to the blood vessel in the IMQ-skin at 0 d (upper) and 1 d of IMQ treatment (lower) ($n = 3$ for each). Data are pooled from ≥ 2 independent experiments with each dot in the graphs representing one experimental subject. t -test: $p = 0.2027$ (> 0 –10), $p = 0.2619$ (> 10 –20), $p = 0.9444$ (> 20 –30), $p = 0.3750$ (> 30 –40), $p = 0.5581$ (> 40 –50), $p < 0.0001$ (> 50) for 0d-IMQ, $p = 0.0338$ (> 0 –10), $p = 0.0049$ (> 10 –20), $p = 0.1529$ (> 20 –30), $p = 0.0290$ (> 30 –40), $p = 0.0572$ (> 40 –50), $p = 0.0050$ (> 50) for 1d-IMQ. For 3D-intravital microscopy, experiment was done in 1 subject per group with each dot in the graphs representing individual acquired tissue plane. Data are shown as mean $\pm$ S.E. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.



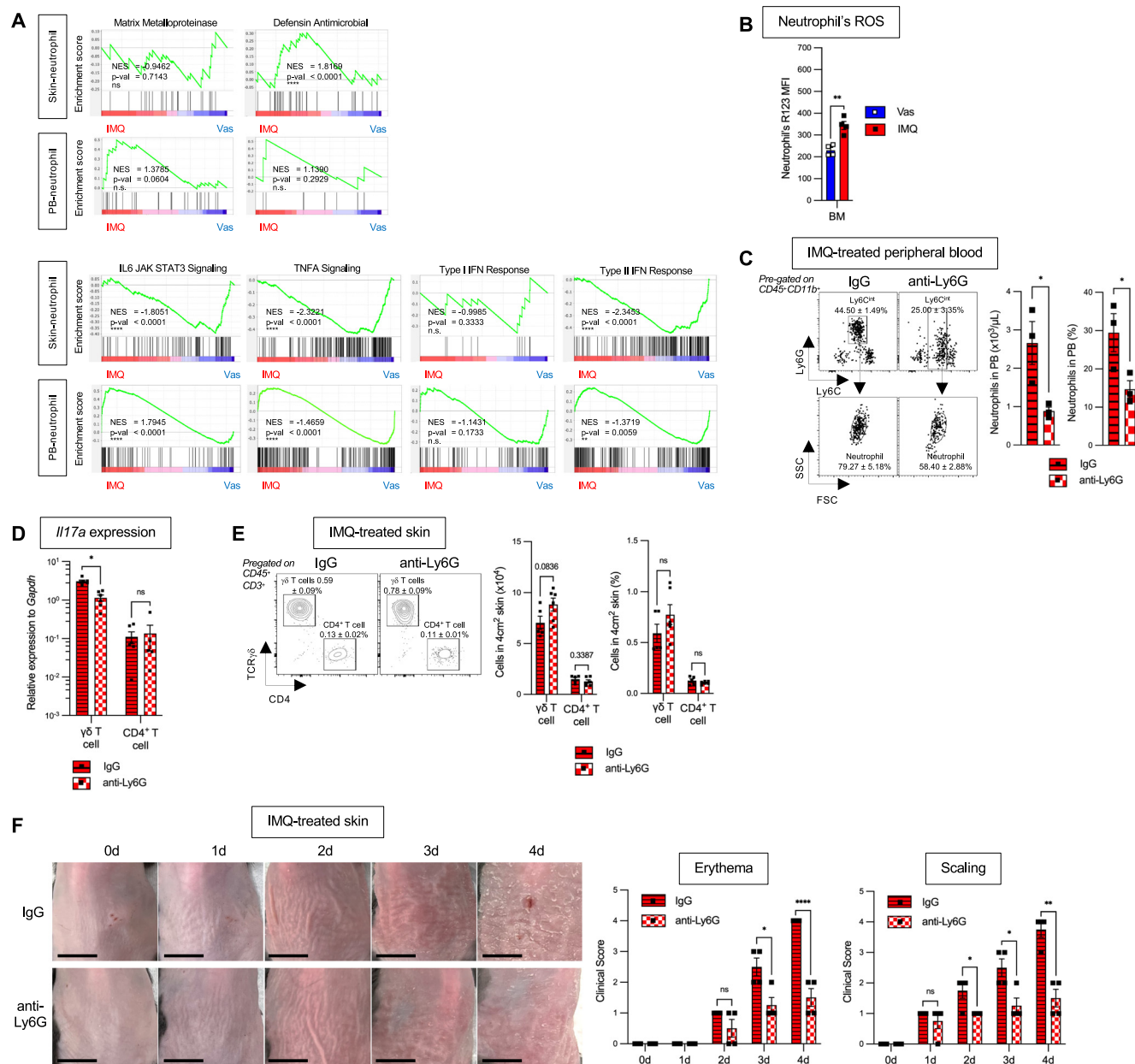


Figure EV2. Overactive neutrophils have pathological function in psoriasis.

(A) GSEA analysis of neutrophils from Vas-treated ($n = 3-5$) and IMQ-treated skin and PB ($n = 3-5$). Signal2Noise/FWER p -value: $p = 0.7143$ (Matrix Metalloproteinase), $p < 0.0001$ (Defensin Antimicrobial), $p < 0.0001$ (IL6 JAK STAT3 Signaling), $p < 0.0001$ (TNFA Signaling), $p = 0.3333$ (Type 1 IFN Response), $p < 0.0001$ (Type 2 IFN Response) for skin neutrophil and $p = 0.0604$ (Matrix Metalloproteinase), $p = 0.02929$ (Defensin Antimicrobial), $p < 0.0001$ (IL6 JAK STAT3 Signaling), $p < 0.0001$ (TNFA Signaling), $p = 0.1733$ (Type 1 IFN Response), $p = 0.0059$ (Type 2 IFN Response) for PB neutrophil. (B) ROS level in the neutrophils measured from BM of Vas- and IMQ-treated mice ($n = 4$ for each). t -test: $p = 0.0286$ (Neutrophil number), $p = 0.0286$ (Neutrophil percentage). (C) Representative FACS plot and quantification of peripheral blood neutrophils at 4 d from IgG or anti-Ly6G antibody injected IMQ-induced mice ($n = 3$ for each). Mann-Whitney test: $p = 0.0286$ (Neutrophil number), $p = 0.0286$ (Neutrophil percentage). (D) *I17a* transcript measured in sorted phenotypic $\gamma\delta$ T cells and $CD4^+$ helper T cells of IMQ-treated mice injected with either IgG control or anti-Ly6G antibody ($n = 5-6$ for each). t -test: $p = 0.0010$ ($\gamma\delta$ T-cell), $p = 0.7979$ ($CD4^+$ T-cell). (E) Percentage and absolute cell number of $\gamma\delta$ T cells and $CD4^+$ helper T cells from IMQ-treated mice administered with either IgG control or anti-G-CSF antibody ($n = 5-6$ for each). t -test: $p = 0.0836$ ($\gamma\delta$ T-cell), $p = 0.3387$ ($CD4^+$ T-cell) for cell number, $p = 0.2062$ ($\gamma\delta$ T-cell), $p = 0.2695$ ($CD4^+$ T-cell) for percentage. (F) Clinical examination of dorsal IMQ-skin at 0-4 d with IgG or anti-Ly6G treatment. Upper: representative skin images, lower: erythema and scaling scoring (IgG: $n = 4$, anti-Ly6G: $n = 4$). t -test: $p = n.d.$ (0 d), $p = n.d.$ (1 d), $p = n.d.$ (2 d), $p = 0.0170$ (3 d), $p = 0.0001$ (4 d) for erythema, $p = n.d.$ (0 d), $p = 0.3559$ (1 d), $p = 0.0240$ (2 d), $p = 0.0170$ (3 d), $p = 0.0011$ (4 d) for scaling. The black line in each picture measures 1 cm scale. Data are pooled from ≥ 2 independent experiments with each dot shown in the bar graph represents data from each individual and shown as mean $\pm$ S.E. For RNA-seq, analysis was done to the data pooled from ≥ 2 replicates. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.

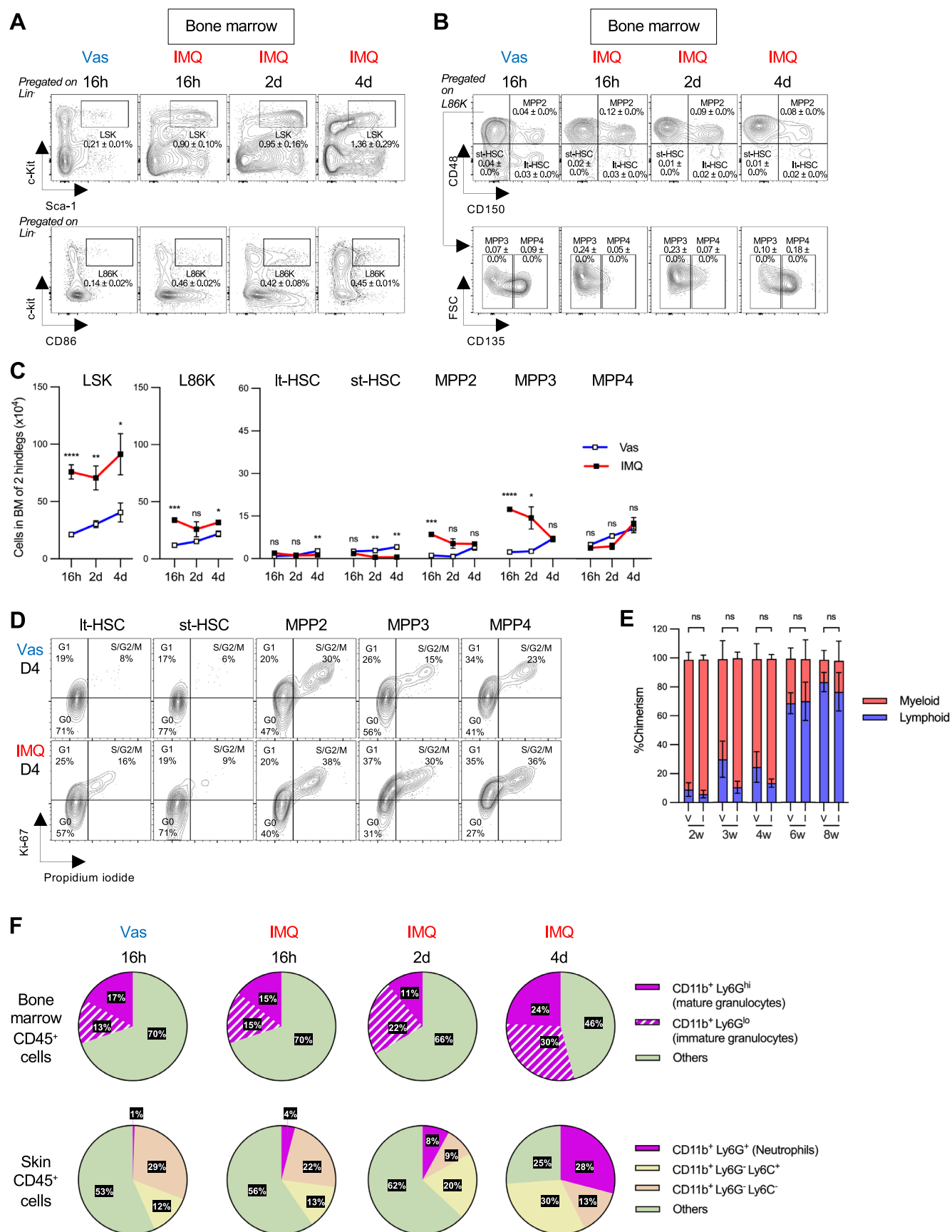
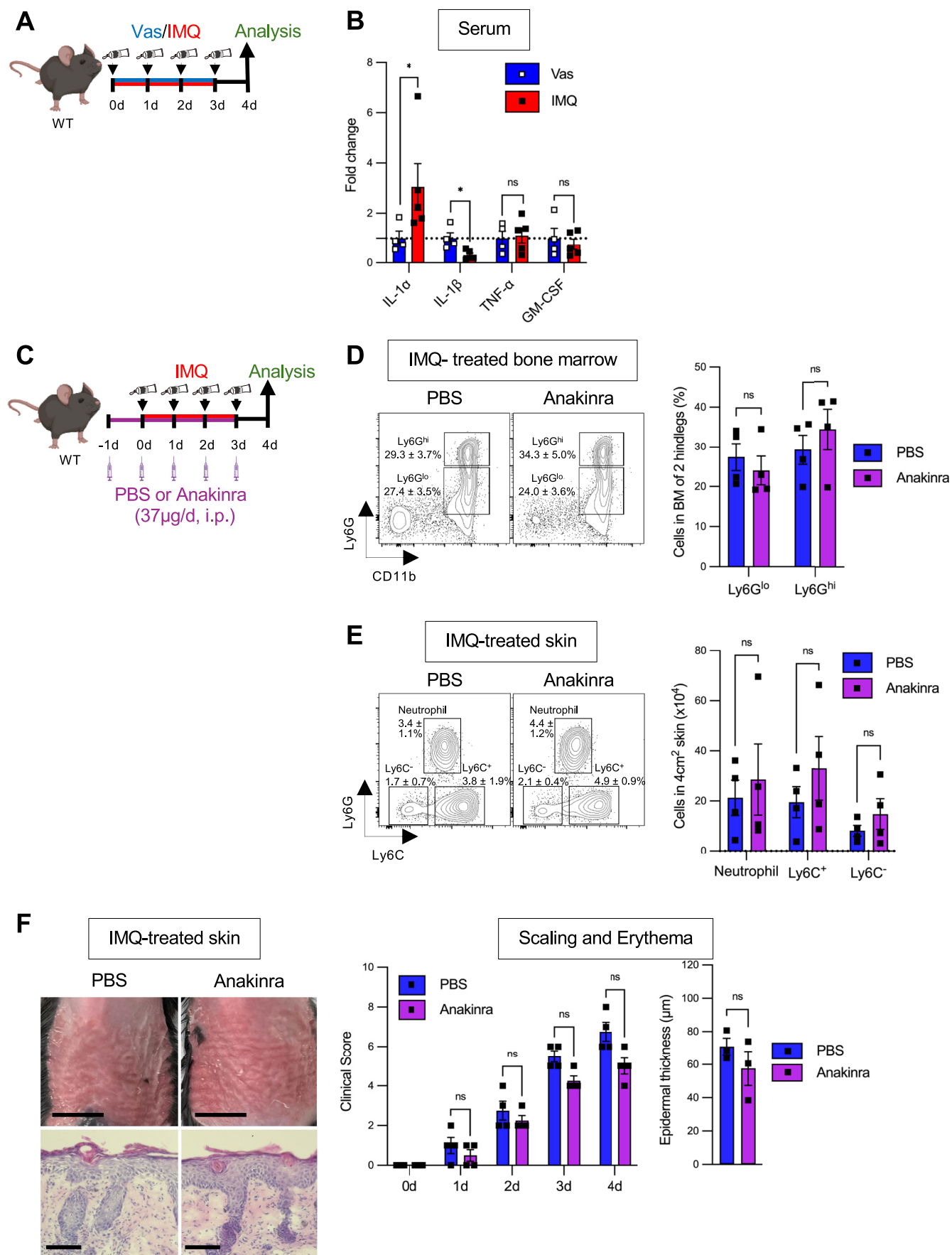


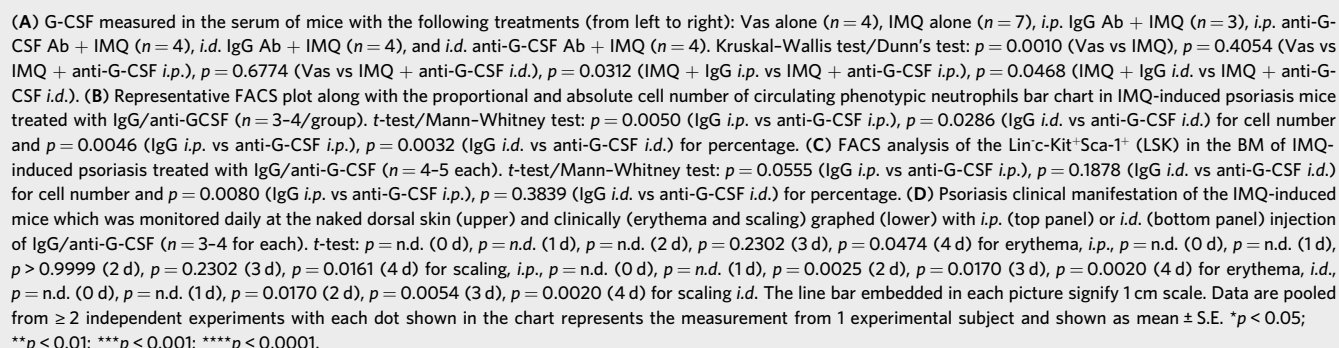
Figure EV3. Psoriasis induces HSPC expansion and granulopoiesis.

(A) FACS plots of LSK (Lin⁻ Sca-1⁺c-Kit⁺) (upper) and L86K (Lin⁻CD86⁺c-Kit⁺) cells (lower) in BM at 16 h, 2 d, and 4 d after Vas or IMQ treatment ($n = 3-6$ for each). (B) FACS plot of immunophenotypic lt-HSC, st-HSC, MPP2, MPP3, and MPP4 defined by L86K (EV3A, lower panel) in the BM of mice treated with Vas/IMQ ($n = 3-6$ each). (C) Absolute number of LSK (left), L86K (middle) and L86K-defined HSPC (lt-HSC, st-HSC, MPP2-4) (right) in the BM of mice treated with Vas/IMQ ($n = 3-6$ for each). *t*-test: $p < 0.0001$ (16 h), $p = 0.0041$ (2 d), $p = 0.0279$ (4 d) for LSK, $p = 0.0009$ (16 h), $p = 0.1934$ (2 d), $p = 0.0239$ (4 d) for L86K, $p = 0.0677$ (16 h), $p = 0.8633$ (2 d), $p = 0.0059$ (4 d) for lt-HSC, $p = 0.1845$ (16 h), $p = 0.0050$ (2 d), $p = 0.0017$ (4 d) for st-HSC, $p = 0.0001$ (16 h), $p = 0.0546$ (2 d), $p = 0.3169$ (4 d) for MPP2, $p < 0.0001$ (16 h), $p = 0.0405$ (2 d), $p = 0.8809$ (4 d) for MPP3, $p = 0.2698$ (16 h), $p = 0.0536$ (2 d), $p = 0.4749$ (4 d) for MPP4. (D) Representative FACS plots of cell cycle analysis of the HSPC fractions in Vas- and IMQ-treated BM ($n = 5$ for each). (E) Lympho-myeloid contribution in PB of transplants with donor LSK from Vas-treated ($n = 3$) or IMQ-treated ($n = 4$) BM. *t*-test: $p = 0.5751$ (2w), $p = 0.1522$ (3w), $p = 0.2866$ (4w), $p = 0.9211$ (6w), $p = 0.7372$ (8w) for Myeloid fraction. (F) Pie charts depicting relative composition of hematopoietic cells (CD45⁺) in BM (upper) and skin (lower) at 16 h, 2 d, and 4 d after Vas or IMQ treatment ($n = 3-6$ each). Data are pooled from ≥ 2 independent experiments. Each dot shown in the bar graph represents data from each individual and shown as mean $\pm$ S.E. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.



◀ **Figure EV4. IL-1 signals do not contribute to psoriasis-driven emergency granulopoiesis.**

(A) Experimental scheme for (B): Vaseline (Vas) or Imiquimod (IMQ) topically applied to the dorsal skin daily for 4 d and serum analysis was conducted at 4 d. (B) Cytokines protein measurement from the sera (Vas: $n = 4$, IMQ: $n = 5$). t -test/Mann-Whitney test: $p = 0.0317$ (IL-1 α), $p = 0.0164$ (IL-1 β), $p = 0.7905$ (TNF- α), $p = 0.5896$ (GM-CSF). (C) Experimental scheme of IMQ-induced psoriasis (0–3 d) with daily PBS/Anakinra intraperitoneal injection (from –1 d to 3 d) and analyzed at 4 d for results depicted in (D–H). (D) Representative FACS plots of immature (Ly6G^{lo}) and mature (Ly6G^{hi}) granulocytes pregated on CD45⁺ BM cells (left). The proportion of Ly6G^{lo} and Ly6G^{hi} cells ($n = 4$ for each) (right). t -test: $p = 0.5179$ (Ly6G^{lo}), $p = 0.4510$ (Ly6G^{hi}). (E) Representative FACS plots of myeloid cell fractions in the dorsal skin pregated on CD45⁺CD11b⁺ cells (left). Cell number quantification graph of the IMQ-induced mice treated with PBS/Anakinra ($n = 4$ for each) (right). t -test: $p = 0.6624$ (Neutrophil), $p = 0.3730$ (Ly6C⁺), $p = 0.3453$ (Ly6C[–]). (F) Skin clinical examination upon psoriasis disease course. Representative naked skin images with scale bar = 1 cm (left upper panel) and skin histology by HE staining with black line indicates 100 μ m (left lower panel). Daily clinical scoring (middle) and epidermal thickness measurement of IMQ-induced psoriatic skin following treatment with PBS/Anakinra ($n = 3$ –4 for each). t -test/Mann-Whitney test: $p > 0.9999$ (0 d), $p = 0.6571$ (1 d), $p = 0.7143$ (2 d), $p = 0.0857$ (3 d), $p = 0.0857$ (4 d) for clinical score, $p = 0.3123$ for epidermal thickness. Data are pooled from ≥ 2 independent experiments with each dot shown in the bar chart represents individual subject and shown as mean $\pm$ S.E. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.



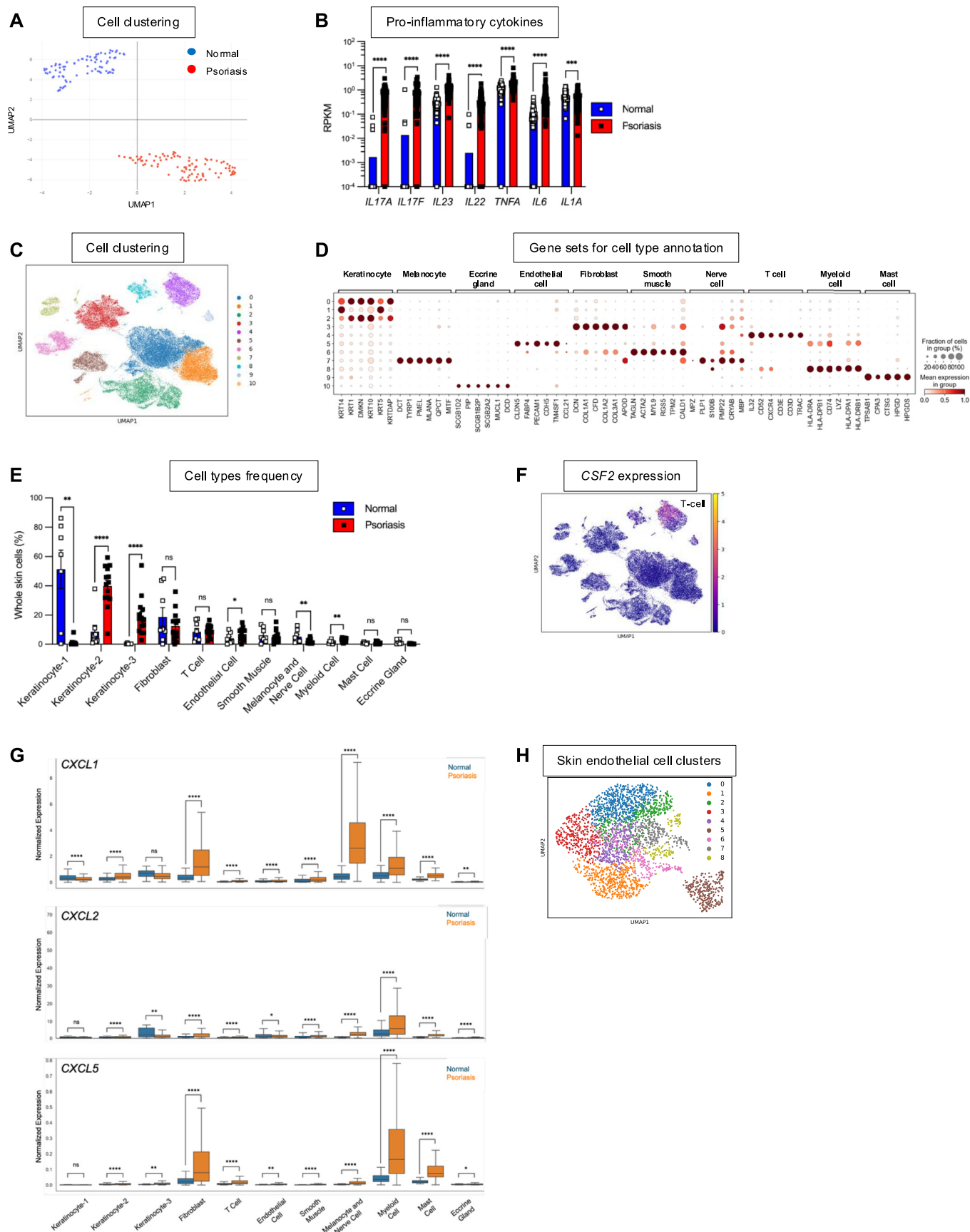


Figure EV6. Clustering and relative transcript measurement of human psoriasis skin biopsies.

(A) UMAP clustering of RNA-seq data from healthy and psoriatic human skin biopsy (normal: $n = 82$, psoriasis: $n = 92$). (B) Relative expression of dermatitis-related cytokines (normal: $n = 82$, psoriasis: $n = 92$). Mann-Whitney test: $p < 0.0001$ (*IL17A*), $p < 0.0001$ (*IL17F*), $p < 0.0001$ (*IL23*), $p < 0.0001$ (*IL22*), $p < 0.0001$ (*TNFA*), $p < 0.0001$ (*IL6*), $p = 0.0007$ (*IL1A*). (C–H) Re-analysis of single-cell RNA-seq dataset GSE173706 (normal: $n = 8$, psoriasis: $n = 14$) consisting of UMAP clustering (C), gene list for clusters annotation (D), cell frequency counting on each annotated cell types (E). t-test/Mann-Whitney test: $p = 0.0023$ (Keratinocyte-1), $p < 0.0001$ (Keratinocyte-2), $p < 0.0001$ (Keratinocyte-3), $p = 0.1568$ (Fibroblast), $p = 0.4034$ (T-cell), $p = 0.0499$ (Endothelial cell), $p = 0.3319$ (Smooth muscle), $p = 0.0083$ (Melanocyte and Nerve cell), $p = 0.0017$ (Myeloid cell), $p = 0.4803$ (Mast cell), $p = 0.1128$ (Eccrine gland), *CSF2* expression mapped in the UMAP clustering (F), *CXCL1/CXCL2/CXCL5* expression (G). t-test: $p < 0.0001$ (Keratinocyte-1), $p < 0.0001$ (Keratinocyte-2), $p = 0.0813$ (Keratinocyte-3), $p < 0.0001$ (Fibroblast), $p < 0.0001$ (T-cell), $p < 0.0001$ (Endothelial cell), $p < 0.0001$ (Smooth muscle), $p < 0.0001$ (Melanocyte and Nerve cell), $p < 0.0001$ (Myeloid cell), $p < 0.0001$ (Mast cell), $p = 0.0045$ (Eccrine gland) for *CXCL1*. $p = 0.0602$ (Keratinocyte-1), $p < 0.0001$ (Keratinocyte-2), $p = 0.0032$ (Keratinocyte-3), $p < 0.0001$ (Fibroblast), $p < 0.0001$ (T-cell), $p = 0.0129$ (Endothelial cell), $p < 0.0001$ (Smooth muscle), $p < 0.0001$ (Melanocyte and Nerve cell), $p < 0.0001$ (Myeloid cell), $p < 0.0001$ (Mast cell), $p < 0.0001$ (Eccrine gland) for *CXCL2*. $p = 0.3313$ (Keratinocyte-1), $p < 0.0001$ (Keratinocyte-2), $p < 0.0001$ (Keratinocyte-3), $p < 0.0001$ (Fibroblast), $p < 0.0001$ (T-cell), $p = 0.0021$ (Endothelial cell), $p < 0.0001$ (Smooth muscle), $p < 0.0001$ (Melanocyte and Nerve cell), $p < 0.0001$ (Myeloid cell), $p < 0.0001$ (Mast cell), $p = 0.0390$ (Eccrine gland) for *CXCL5*. Following are the detailed analytical data of each (value of Normal/value of Psoriasis): *CXCL1*: Keratinocyte-1 (min = 0.0054/0.0436, max = 2.8499/1.1675, median = 0.3033/0.2212, mean = 0.3706/0.2717, lower whisker = 0.0054/0.0436, upper whisker = 1.0234/0.6486, 95th percentile = 0.9001/0.5699), Keratinocyte-2 (min = 0.0231/0.0119, max = 1.8105/20.4381, median = 0.2590/0.4055, mean = 0.2933/0.5699, lower whisker = 0.0231/0.0119, upper whisker = 0.6936/1.3328, 95th percentile = 0.6271/1.5084), Keratinocyte-3 (min = 0.0607/0.0281, max = 1.2440/5.5007, median = 0.6806/0.4410, mean = 0.6481/0.5593, lower whisker = 0.0607/0.0281, upper whisker = 1.2440/1.2734, 95th percentile = 1.0515/1.4100), Fibroblast (min = 0.0366/0.0617, max = 5.4288/27.4380, median = 0.3219/1.1753, mean = 0.4593/1.9295, lower whisker = 0.0366/0.0617, upper whisker = 1.0833/5.3657, 95th percentile = 1.2122/6.0698), T-Cell (min = 0.0062/0.0065, max = 0.5589/6.4854, median = 0.0340/0.0861, mean = 0.0474/0.1274, lower whisker = 0.0062/0.0065, upper whisker = 0.1099/0.2845, 95th percentile = 0.1260/0.3394), Endothelial Cell (min = 0.0032/0.0052, max = 1.2288/2.6625, median = 0.0688/0.0777, mean = 0.1035/0.1456, lower whisker = 0.0032/0.0052, upper whisker = 0.2650/0.3627, 95th percentile = 0.2890/0.5058), Smooth Muscle (min = 0.0034/0.0055, max = 2.2183/4.5404, median = 0.0847/0.1834, mean = 0.1913/0.3389, lower whisker = 0.0034/0.0055, upper whisker = 0.5502/0.8210, 95th percentile = 0.7248/1.1467), Melanocyte and Nerve Cell (min = 0.0194/0.0716, max = 1.8830/16.2340, median = 0.4136/2.6095, mean = 0.4975/3.4355, lower whisker = 0.0194/0.0716, upper whisker = 1.2674/9.2033, 95th percentile = 1.2372/9.1966), Myeloid Cell (min = 0.0104/0.0032, max = 1.8229/19.2280, median = 0.4934/1.0720, mean = 0.5847/1.4393, lower whisker = 0.0104/0.0032, upper whisker = 1.2988/3.9222, 95th percentile = 1.3739/3.7889), Mast Cell (min = 0.0732/0.1191, max = 0.5190/10.0436, median = 0.2052/0.4905, mean = 0.2128/0.5765, lower whisker = 0.0732/0.1191, upper whisker = 0.4121/1.0925, 95th percentile = 0.3820/1.0138), Eccrine Gland (min = 0.0012/0.0017, max = 0.0873/0.3837, median = 0.0158/0.0232, mean = 0.0201/0.0424, lower whisker = 0.0012/0.0017, upper whisker = 0.0588/0.0966, 95th percentile = 0.0487/0.1275) for *CXCL1*; Keratinocyte-1 (min = 0.0054/0.0436, max = 2.8499/1.1675, median = 0.3033/0.2212, mean = 0.3706/0.2717, lower whisker = 0.0054/0.0436, upper whisker = 1.0234/0.6486, 95th percentile = 0.9001/0.5699), Keratinocyte-2 (min = 0.0231/0.0119, max = 1.8105/20.4381, median = 0.2590/0.4055, mean = 0.2933/0.5699, lower whisker = 0.0231/0.0119, upper whisker = 0.6936/1.3328, 95th percentile = 0.6271/1.5084), Keratinocyte-3 (min = 0.0607/0.0281, max = 1.2440/5.5007, median = 0.6806/0.4410, mean = 0.6481/0.5593, lower whisker = 0.0607/0.0281, upper whisker = 1.2440/1.2734, 95th percentile = 1.0515/1.4100), Fibroblast (min = 0.0366/0.0617, max = 5.4288/27.4380, median = 0.3219/1.1753, mean = 0.4593/1.9295, lower whisker = 0.0366/0.0617, upper whisker = 1.0833/5.3657, 95th percentile = 1.2122/6.0698), T-Cell (min = 0.0062/0.0065, max = 0.5589/6.4854, median = 0.0340/0.0861, mean = 0.0474/0.1274, lower whisker = 0.0062/0.0065, upper whisker = 0.1099/0.2845, 95th percentile = 0.1260/0.3394), Endothelial Cell (min = 0.0032/0.0052, max = 1.2288/2.6625, median = 0.0688/0.0777, mean = 0.1035/0.1456, lower whisker = 0.0032/0.0052, upper whisker = 0.2650/0.3627, 95th percentile = 0.2890/0.5058), Smooth Muscle (min = 0.0034/0.0055, max = 2.2183/4.5404, median = 0.0847/0.1834, mean = 0.1913/0.3389, lower whisker = 0.0034/0.0055, upper whisker = 0.5502/0.8210, 95th percentile = 0.7248/1.1467), Melanocyte and Nerve Cell (min = 0.0194/0.0716, max = 1.8830/16.2340, median = 0.4136/2.6095, mean = 0.4975/3.4355, lower whisker = 0.0194/0.0716, upper whisker = 1.2674/9.2033, 95th percentile = 1.2372/9.1966), Myeloid Cell (min = 0.0104/0.0032, max = 1.8229/19.2280, median = 0.4934/1.0720, mean = 0.5847/1.4393, lower whisker = 0.0104/0.0032, upper whisker = 1.2988/3.9222, 95th percentile = 1.3739/3.7889), Mast Cell (min = 0.0732/0.1191, max = 0.5190/10.0436, median = 0.2052/0.4905, mean = 0.2128/0.5765, lower whisker = 0.0732/0.1191, upper whisker = 0.4121/1.0925, 95th percentile = 0.3820/1.0138), Eccrine Gland (min = 0.0012/0.0017, max = 0.0873/0.3837, median = 0.0158/0.0232, mean = 0.0201/0.0424, lower whisker = 0.0012/0.0017, upper whisker = 0.0588/0.0966, 95th percentile = 0.0487/0.1275) for *CXCL2*; Keratinocyte-1 (min = 0.0054/0.0436, max = 2.8499/1.1675, median = 0.3033/0.2212, mean = 0.3706/0.2717, lower whisker = 0.0054/0.0436, upper whisker = 1.0234/0.6486, 95th percentile = 0.9001/0.5699), Keratinocyte-2 (min = 0.0231/0.0119, max = 1.8105/20.4381, median = 0.2590/0.4055, mean = 0.2933/0.5699, lower whisker = 0.0231/0.0119, upper whisker = 0.6936/1.3328, 95th percentile = 0.6271/1.5084), Keratinocyte-3 (min = 0.0607/0.0281, max = 1.2440/5.5007, median = 0.6806/0.4410, mean = 0.6481/0.5593, lower whisker = 0.0607/0.0281, upper whisker = 1.2440/1.2734, 95th percentile = 1.0515/1.4100), Fibroblast (min = 0.0366/0.0617, max = 5.4288/27.4380, median = 0.3219/1.1753, mean = 0.4593/1.9295, lower whisker = 0.0366/0.0617, upper whisker = 1.0833/5.3657, 95th percentile = 1.2122/6.0698), T-Cell (min = 0.0062/0.0065, max = 0.5589/6.4854, median = 0.0340/0.0861, mean = 0.0474/0.1274, lower whisker = 0.0062/0.0065, upper whisker = 0.1099/0.2845, 95th percentile = 0.1260/0.3394), Endothelial Cell (min = 0.0032/0.0052, max = 1.2288/2.6625, median = 0.0688/0.0777, mean = 0.1035/0.1456, lower whisker = 0.0032/0.0052, upper whisker = 0.2650/0.3627, 95th percentile = 0.2890/0.5058), Smooth Muscle (min = 0.0034/0.0055, max = 2.2183/4.5404, median = 0.0847/0.1834, mean = 0.1913/0.3389, lower whisker = 0.0034/0.0055, upper whisker = 0.5502/0.8210, 95th percentile = 0.7248/1.1467), Melanocyte and Nerve Cell (min = 0.0194/0.0716, max = 1.8830/16.2340, median = 0.4136/2.6095, mean = 0.4975/3.4355, lower whisker = 0.0194/0.0716, upper whisker = 1.2674/9.2033, 95th percentile = 1.2372/9.1966), Myeloid Cell (min = 0.0104/0.0032, max = 1.8229/19.2280, median = 0.4934/1.0720, mean = 0.5847/1.4393, lower whisker = 0.0104/0.0032, upper whisker = 1.2988/3.9222, 95th percentile = 1.3739/3.7889), Mast Cell (min = 0.0732/0.1191, max = 0.5190/10.0436, median = 0.2052/0.4905, mean = 0.2128/0.5765, lower whisker = 0.0732/0.1191, upper whisker = 0.4121/1.0925, 95th percentile = 0.3820/1.0138), Eccrine Gland (min = 0.0012/0.0017, max = 0.0873/0.3837, median = 0.0158/0.0232, mean = 0.0201/0.0424, lower whisker = 0.0012/0.0017, upper whisker = 0.0588/0.0966, 95th percentile = 0.0487/0.1275) for *CXCL5*, and re-clustering of annotated endothelial cell subset (H). Each dot shown in the chart represents the measurement from 1 experimental subject and shown as mean $\pm$ S.E. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$.