

## SUPPLEMENTARY FIGURES

**Figure S1.** (a, b) Relative mRNA expression for indicated genes in dorsal skin of WT, CIKS  $\Delta$ KC (a) and IL-19 KO mice (b) after IMQ or control treatment as indicated (\* $p < 0.05$ ; mean  $\pm$  SEM;  $n = 6$  mice per group).

**Figure S2.** (a) Immunofluorescence images of sections from IMQ- or control- treated dorsal skin from WT and IL-20RB KO mice stained with DAPI (blue), anti-K5 (red) and anti-Ki67 (green). Epidermal Ki67<sup>+</sup> cells were quantitated by counting fluorescent dots in  $200 \times 200 \mu\text{m}$  areas from different sections per mouse ( $n = 6-10$  mice per group; Scale bar  $100\mu\text{m}$ ). (b, c) Relative mRNA expression for indicated genes in dorsal skin (b) and skin-draining LNs (c) of IMQ- or control-treated WT and IL-20RB KO mice ( $n = 8-12$  mice per group). (d, e) Representative flow cytometric analyses of IMQ- or control-treated skin-draining LNs cells from WT and IL-20RB KO mice analyzed for expression of markers as shown. Numbers and percentages of IL-17A<sup>+</sup>  $\gamma\delta$ T cells (d) and neutrophils (e) generated from flow cytometric analyses. ( $n = 6-12$  mice per group) (\* $p < 0.05$ , \*\* $p < 0.01$ ; mean  $\pm$  SEM).

**Figure S3.** (a) CCR2 expression on dendritic epidermal T cells (DETC, TCR $\gamma\delta^{\text{hi}}$ ), dermal  $\gamma\delta$ T cells (CD45<sup>+</sup>, TCR $\gamma\delta^{\text{intermediate}}$ , TCR $\nu\gamma 4^+$ ) from IMQ-treated WT and CCR2 KO mice. (b) Representative flow cytometric analyses of IMQ- or control-treated dorsal skin cells from WT and CCR2 KO mice analyzed for expression of markers as shown. Numbers and percentages of IL-17A<sup>+</sup>  $\gamma\delta$ T cells generated from flow cytometric analyses. (\*\* $p < 0.01$ ; mean  $\pm$  SEM;  $n = 3-6$  mice per group).





