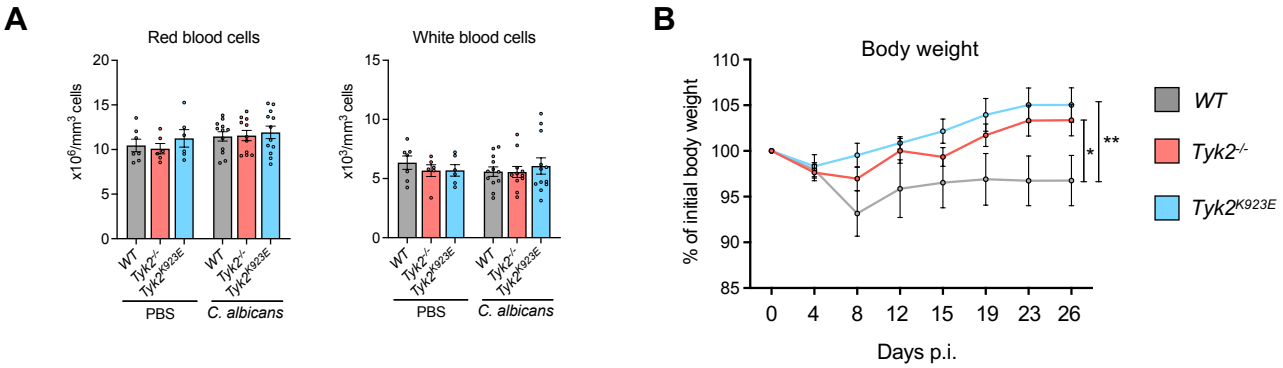
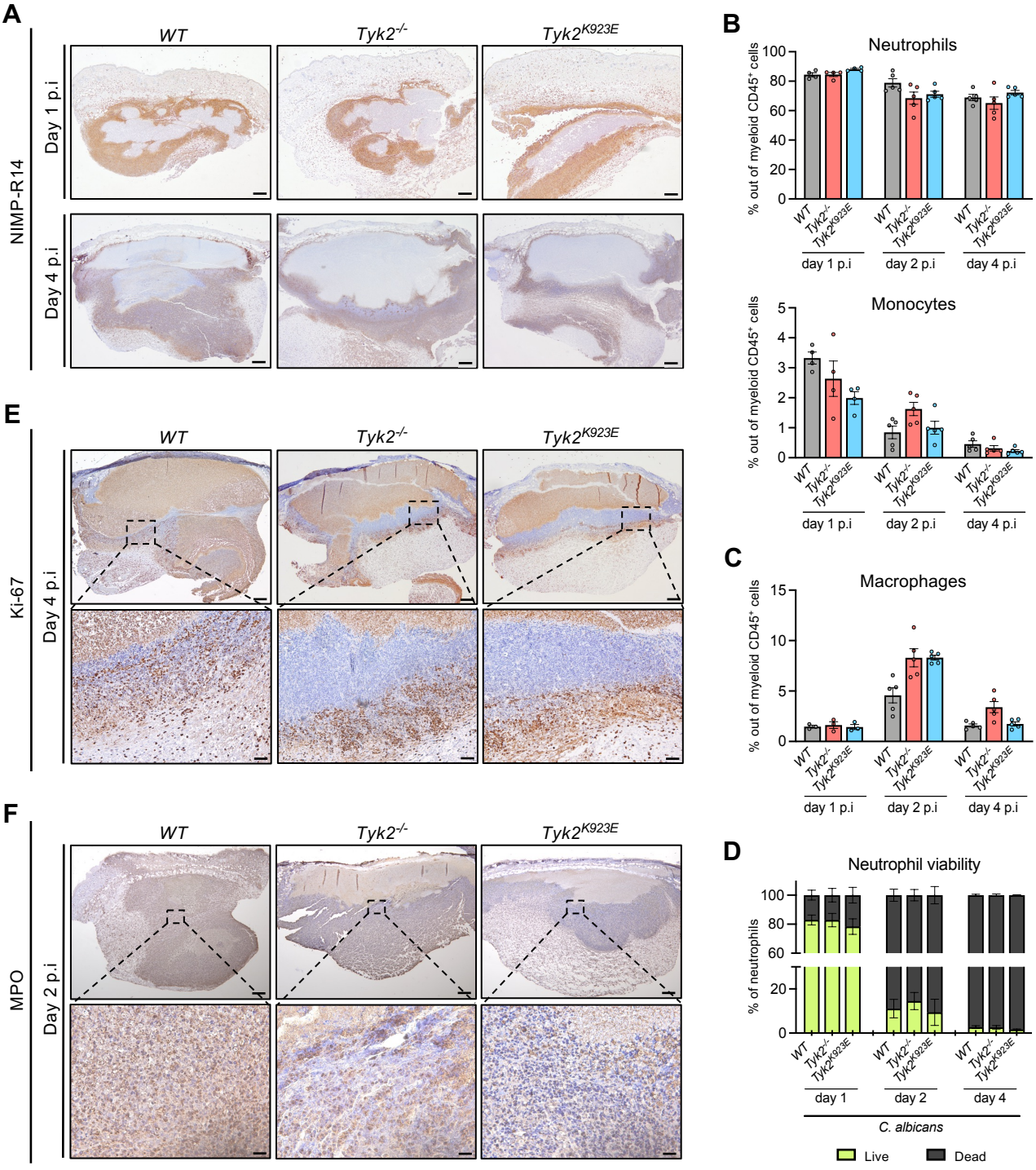


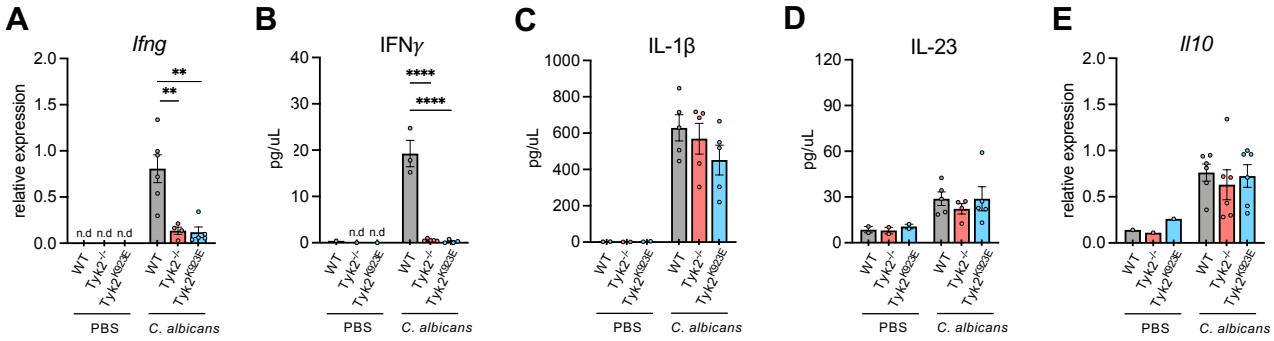
Supplementary Figure 1. **(A)** Blood cell composition on day 4 p.i was determined with a Vet ABC analyzer. The total numbers of red and white blood cells are shown. For each cell population, 2 independent experiments are shown, n=2-4 (PBS) and n=5-6 (*C. albicans*)/genotype/experiment. **(B)** Body weight of infected *WT, Tyk2*$^{-/-}$ and *Tyk2*^{K923E} mice was measured every 3 to 4 days and the difference relative to the initial weight on the day before the infection is plotted. One representative experiment out of 2 is shown, n=5-7/genotype/experiment.

Statistical significance is only given for the comparison between the genotypes: *p < 0.05, **p < 0.01,***p < 0.001, and ****p < 0.0001; Mean values ± SEM are given; n, biological replicates.



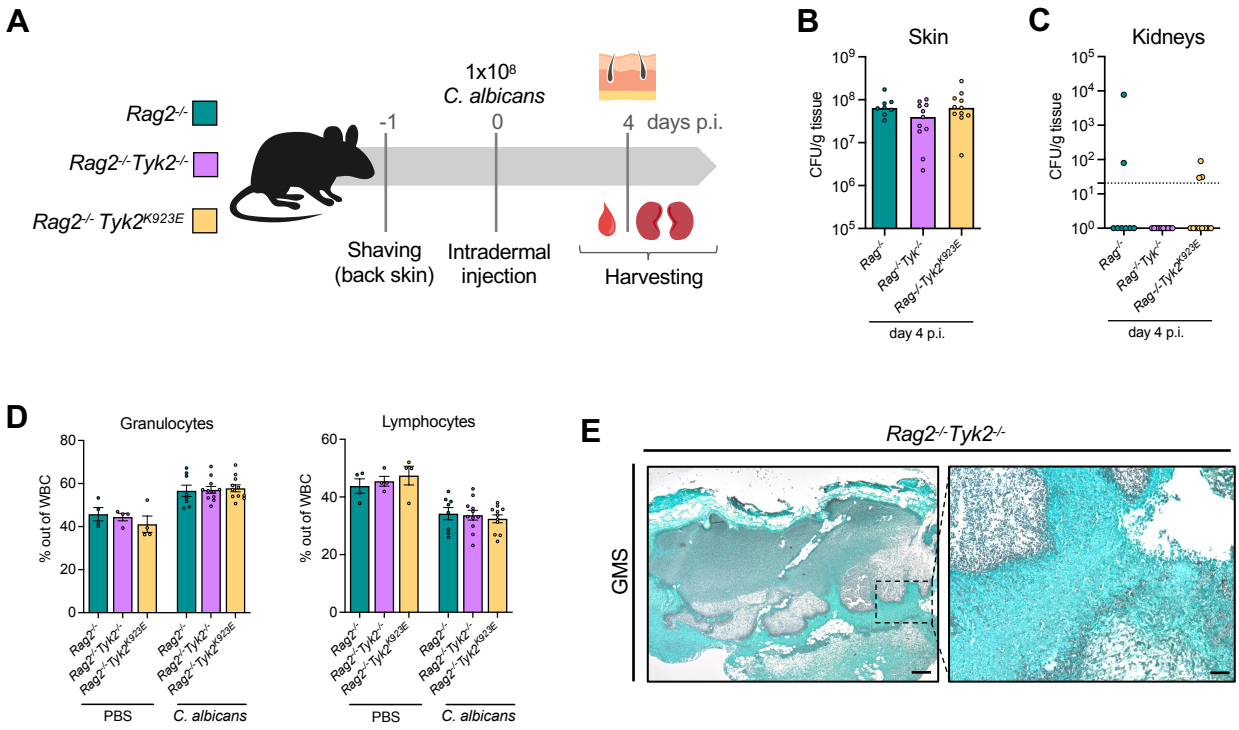
Supplementary Figure 2. **(A)** Skin sections obtained from infected *WT, Tyk2*$^{-/-}$ and *Tyk2*^{K923E} mice on day 1 and 4 p.i were stained with a NIMP-R14 antibody. Scale bar indicates 200 µm. **(B)** Skin-infiltrating neutrophils (gated as CD45^{+}CD11b^{+}Ly6C^{+}Ly6G^{+} cells), monocytes (gated as CD45^{+}CD11b^{+}Ly6G^{-}Ly6C^{high}F4/80^{-} cells) and **(C)** macrophages (gated as CD45^{+}CD11b^{+}Ly6G^{-}F4/80^{+} cells) were quantified by flow cytometry at day 1, 2 and 4 p.i. The percentage of each of these populations out of myeloid CD45^{+} cells (gated as live CD3^{-}CD19^{-}NK1.1^{-}CD45^{+} cells) is shown. **(D)** The viability of skin infiltrating neutrophils was quantified based on flow cytometry analysis with live/dead staining. For each time-point, a representative experiment out of 2 is shown, n=3-4 (PBS) and n=4 (*C. albicans*)/genotype/experiment. **(E)** Skin sections obtained from infected *WT, Tyk2*$^{-/-}$ and *Tyk2*^{K923E} mice on day 4 p.i were stained with a Ki-67 antibody. Scale bar indicates 200 µm (top) and 50 µm (bottom). **(F)** Skin sections obtained from infected *WT, Tyk2*$^{-/-}$ and *Tyk2*^{K923E} mice on day 2 p.i were stained with a MPO antibody. Scale bar indicates 200 µm (top) or 20 µm (bottom).

Mean values ± SEM are given; n, biological replicates.

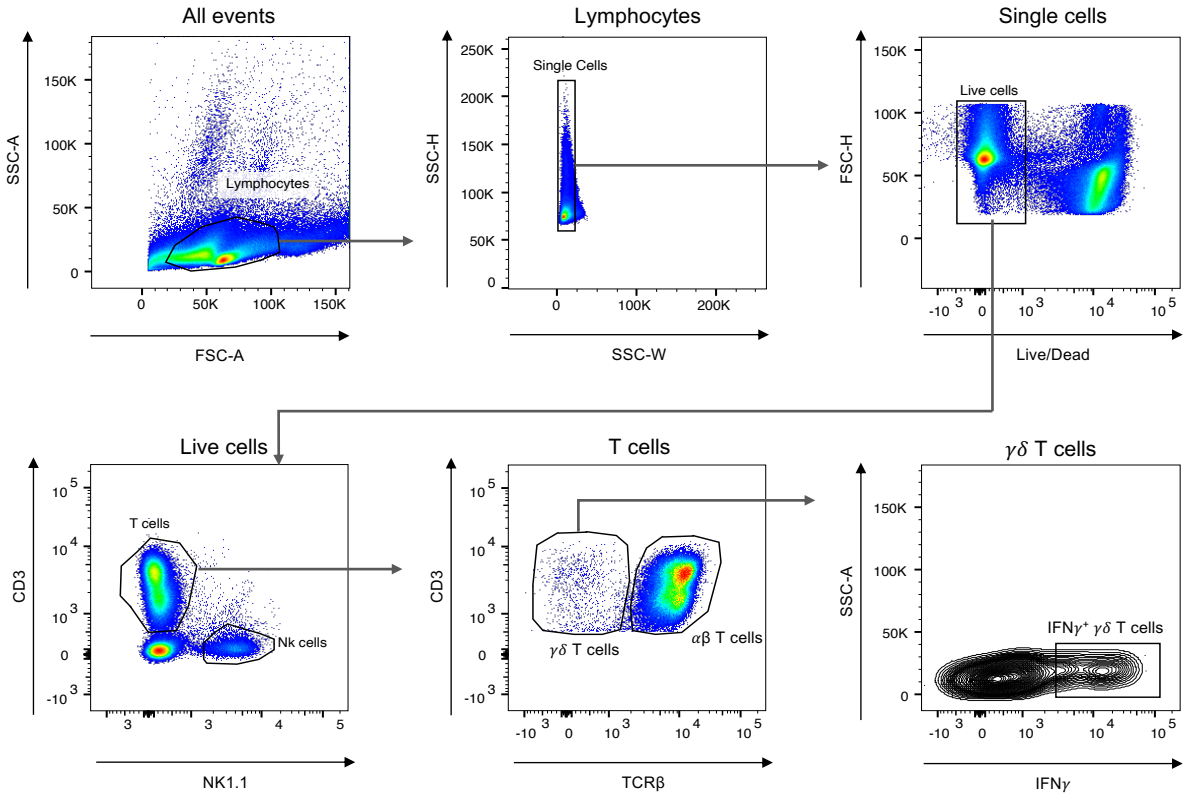


Supplementary Figure 3. mRNA levels of *Ifng* **(A)** and *Il10* **(E)** in the infected skin on day 4 p.i were measured by RT-qPCR. IFNγ **(B)**, IL-1β **(C)** and IL-23 **(D)** in the skin on day 2 p.i were measured using a Luminex assay. One representative experiment out of 2 is shown, n=1-2 (PBS) and n=4-6 (*C. albicans*)/genotype.

Statistical significance is only given for the comparison between the genotypes: *$p < 0.05$, **$p < 0.01$,***$p < 0.001$, and ****$p < 0.0001$; Mean values ± SEM are given; n, biological replicates; n.d, not detectable



Supplementary Figure 4. *Rag2*$^{-/-}$, *Rag2*$^{-/-}$*Tyk2*$^{-/-}$ and *Rag2*$^{-/-}$*Tyk2*^{K923E} mice were infected as described in Figure 1 legend **(A)**. Fungal load in the skin **(B)** and kidneys **(C)** was measured on day 4 p.i. Two independent experiments are shown, n=3-6/genotype/experiment. The dotted line indicates the assay detection limit. **(D)** Blood cell composition on day 4 p.i was determined with a Vet ABC analyzer. The percentage of granulocytes and lymphocytes out of total white blood cells (WBC) is shown. For each cell population, two independent experiments are shown, n=2 (PBS) and n=3-6 (*C. albicans*)/genotype/experiment. **(E)** Representative pictures of the infected skin on day 4 p.i. A GMS staining of the skin sections is shown. Scale bar represents 200 µm (left) or 50 µm (right). Mean values ± SEM are given. n, biological replicates.



Supplementary Figure 5. The gating strategy used to determine the number of IFNγ^+ $\gamma\delta$ T cells is shown. Spleens of *WT, Tyk2*$^{-/-}$ and *Tyk2*^{K923E} mice were collected and single cell suspensions were prepared. 1x10^6 splenocytes were incubated for 24 hours with heat-killed *C. albicans* or IL-12 and stained for flow cytometry analysis.