Expanded View Figures

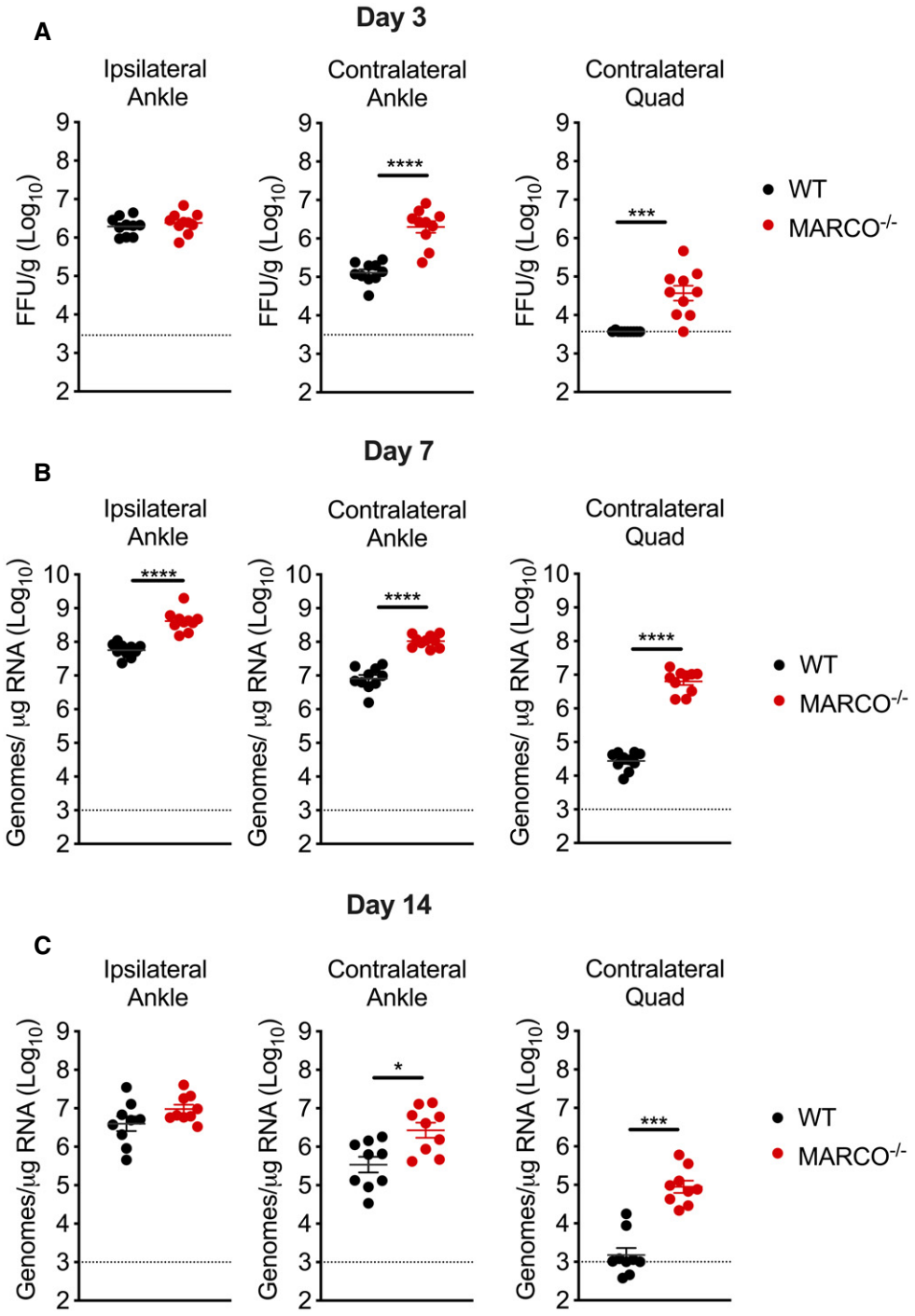

Figure EV1. CHIKV tissue burdens in distal tissues are enhanced in MARCO$^{-/-}$ mice at days 3, 7, and 14 pi.

A–C WT or MARCO$^{-/-}$ C57BL/6 mice were inoculated subcutaneously in the left-rear footpad with 10^3 PFU of CHIKV. Viral tissue burdens were analyzed at 3 (A), 7 (B), and 14 (C) days post-inoculation (dpi) by FFA (A), or RT–qPCR (B and C). Mean ± SEM. Data are pooled from two experiments for each time point, $n = 10$. Mann–Whitney test; *$P < 0.05$, ***$P < 0.001$, ****$P < 0.0001$.

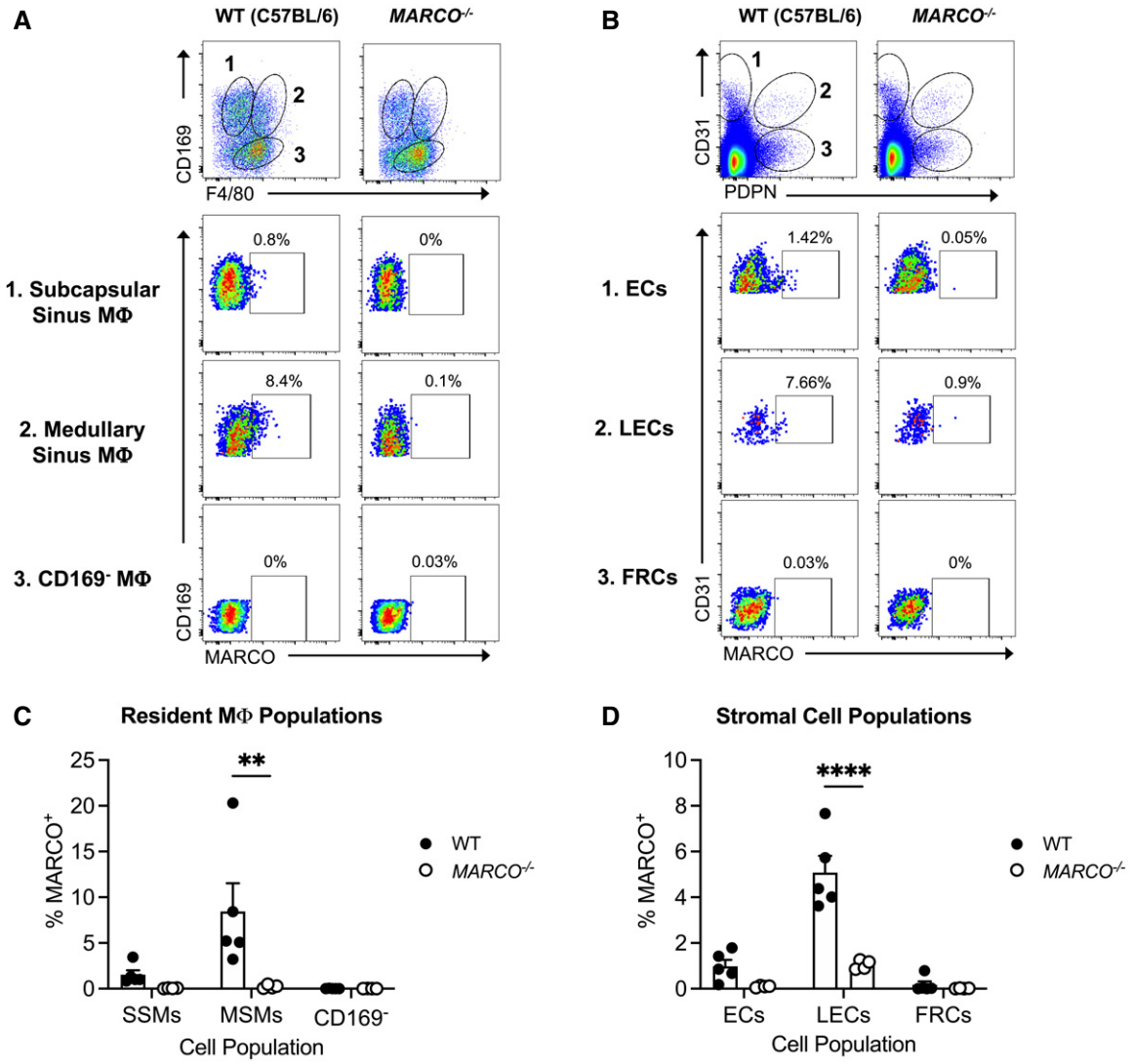

Figure EV2. MARCO is expressed by medullary sinus macrophages and LECs in LNs.

A–D LNs were pooled from uninfected WT or MARCO$^{-/-}$ C57BL/6 mice. Representative flow cytometry plots and percentages of MARCO-expressing cells by resident macrophage populations (A, C) and stromal cell populations (B, D) are shown. Mean ± SEM. Data are pooled from two experiments, $n = 4–5$. Two-way ANOVA with Bonferroni's multiple comparisons test; $^{**}P < 0.01$, $^{****}P < 0.0001$.

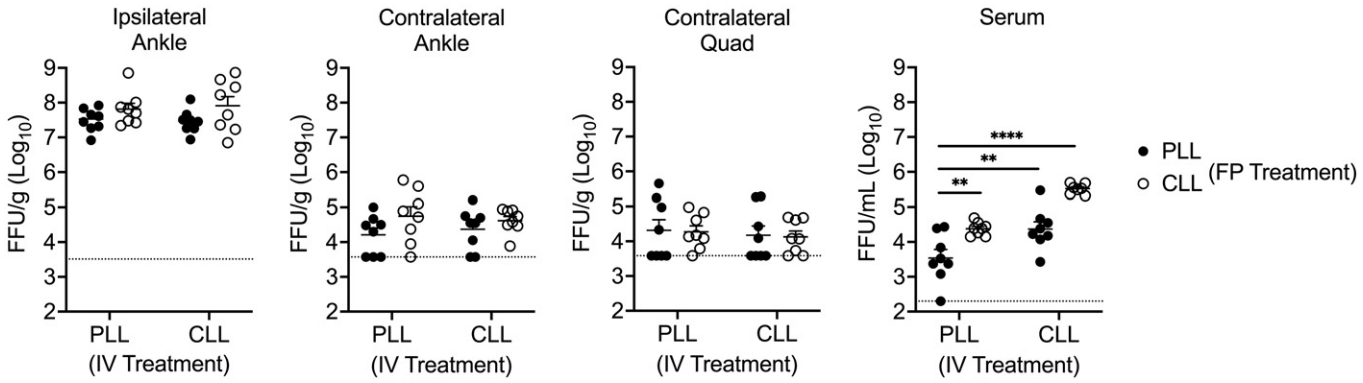

Figure EV3. Depletion of phagocytic cells in the lymph node and liver does not enhance CHIKV dissemination.

WT C57BL/6 mice were i.v. injected with PBS-loaded liposomes (PLL) or clodronate-loaded liposomes (CLL) 42 h prior to virus inoculation and subcutaneously injected in the left-rear footpad (FP) with PLL or CLL 24 h prior to virus inoculation as indicated. Mice were then inoculated s.c. with 10^3 PFU of CHIKV in the left-rear footpad, and tissues and serum were collected at 24 hpi. Infectious virus was quantified by FFA. Mean ± SEM. Data are pooled from two experiments, $n = 8$. Two-way ANOVA with Bonferroni's multiple comparison test, comparing all groups to IV PLL+ FP PLL group; $^{**}P < 0.01$, $^{****}P < 0.0001$.

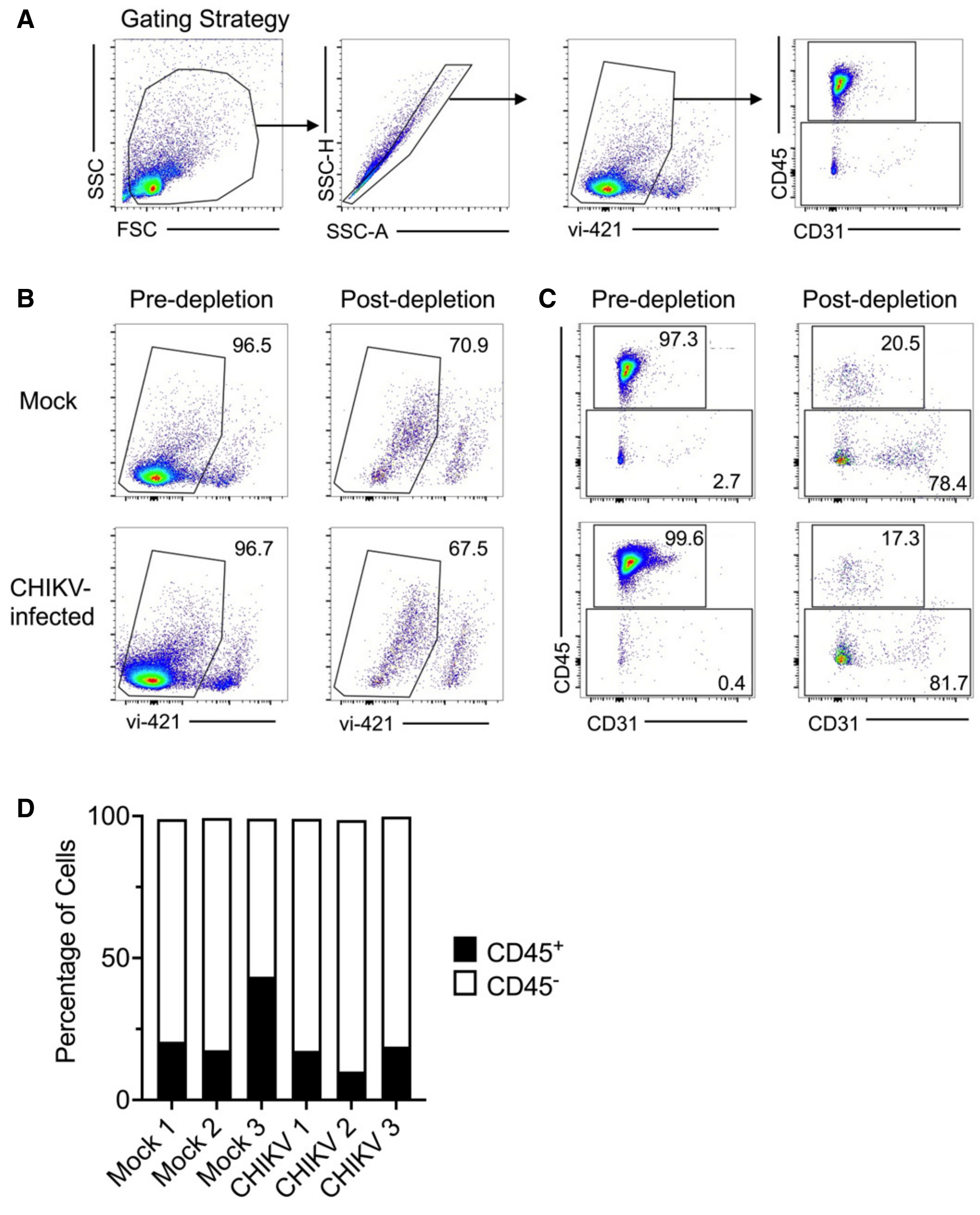

Figure EV4. CD45^{-} cell enrichment.

A Representative flow plots of gating strategy used.
Pre- and Post-CD45^{+} cell depletion cell populations were analyzed by flow cytometry.
B–C Representative flow plots of cell viability (B) and CD45^{+} and CD45^{-} cell populations (C) in pre- and post-depleted populations.
D Percentages of CD45^{+} and CD45^{-} subsets among replicates. $N = 3$, one experiment.

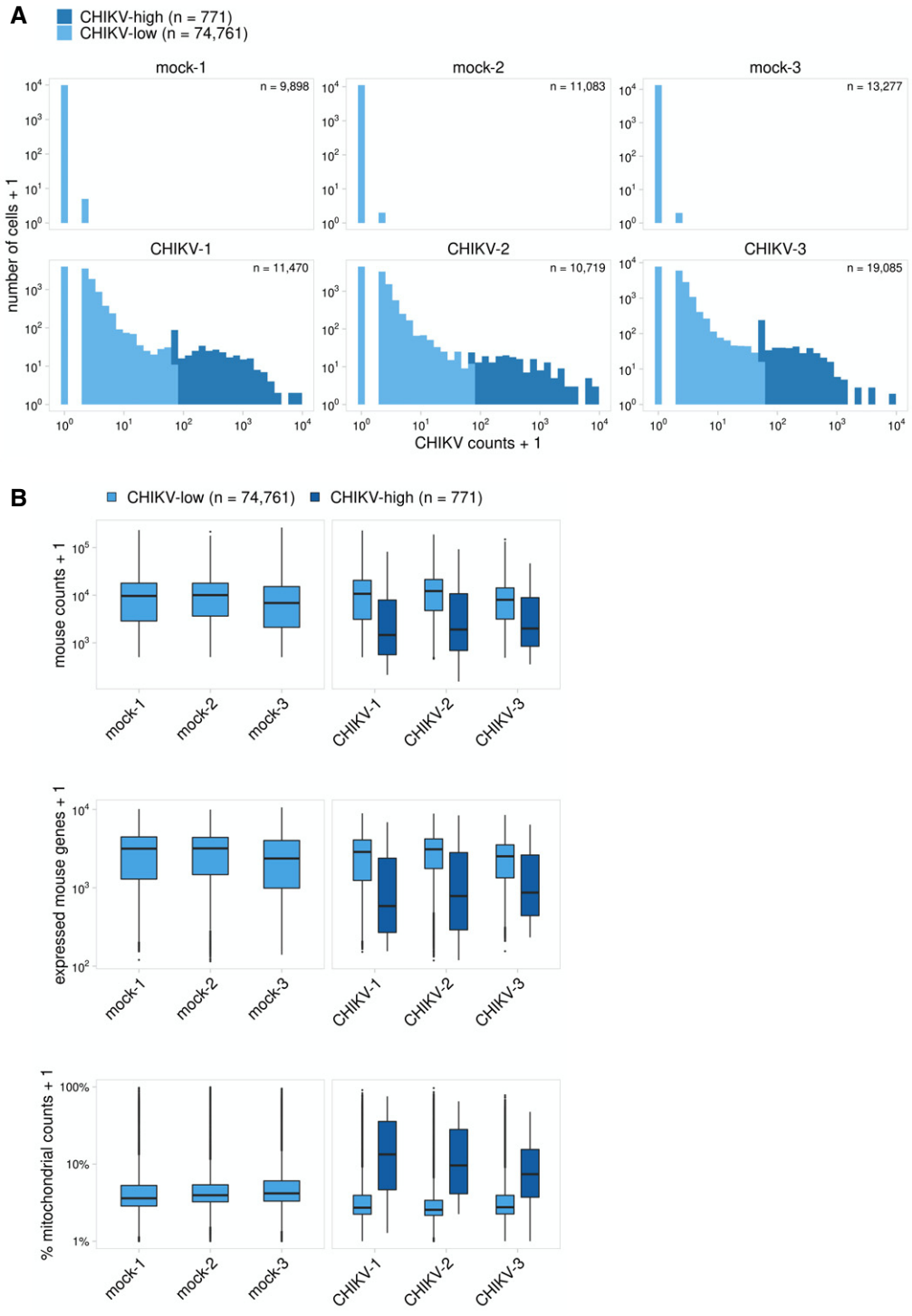

Figure EV5. CHIKV-high classification and gene expression among CHIKV-high and CHIKV-low cells.

A To identify cells with high amounts of viral RNA, cells were first filtered to only include those with > 5 CHIKV counts. K-means clustering was then used to independently group each biological replicate into CHIKV-low and CHIKV-high populations. Cells with ≤ 5 CHIKV counts are included in the CHIKV-low group. CHIKV counts are shown below for each sample before filtering low-quality cells (this includes all captured cells).

B Cell quality metrics are shown for CHIKV-low and CHIKV-high cells for each replicate. These plots include all captured cells before quality filtering. CHIKV-high cells have fewer expressed mouse genes and an increased percentage of mitochondrial counts. In the boxplot, the central lines, the box limits, and the whiskers represent medians, the interquartile range (IQR), and min/max values that are not outliers, respectively. Outliers are shown as points and include any values that are more than 1.5× IQR away from the box.