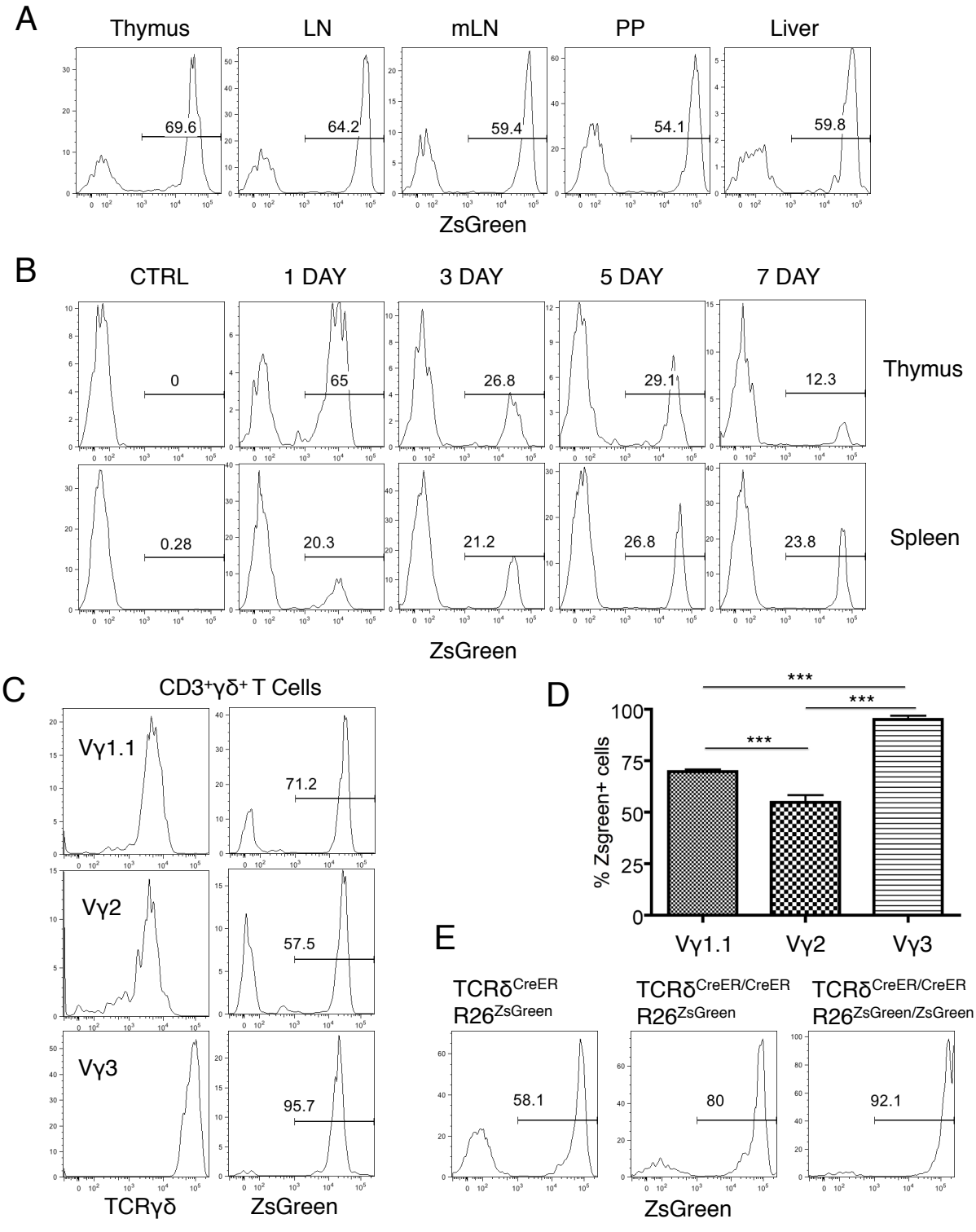
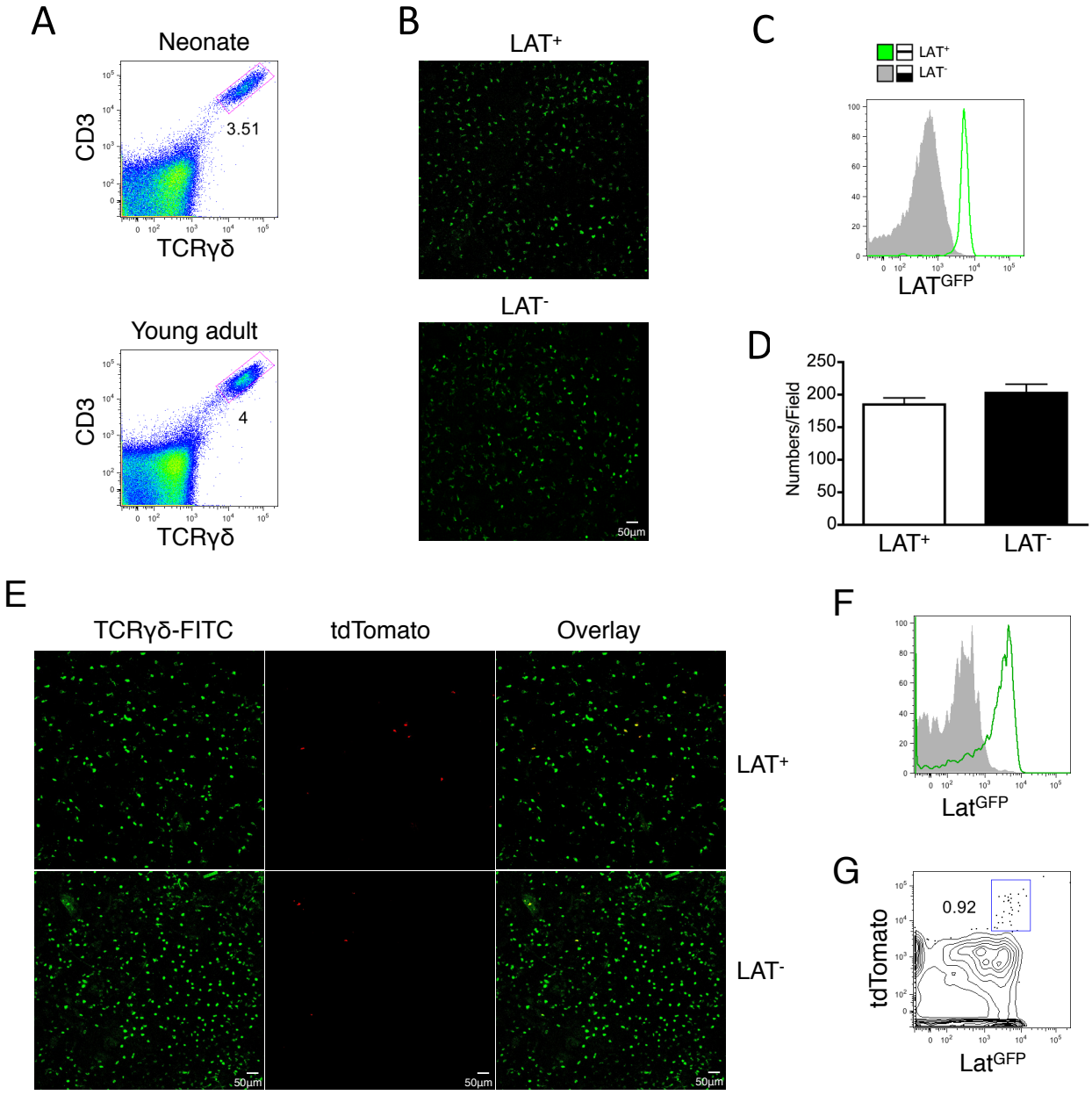


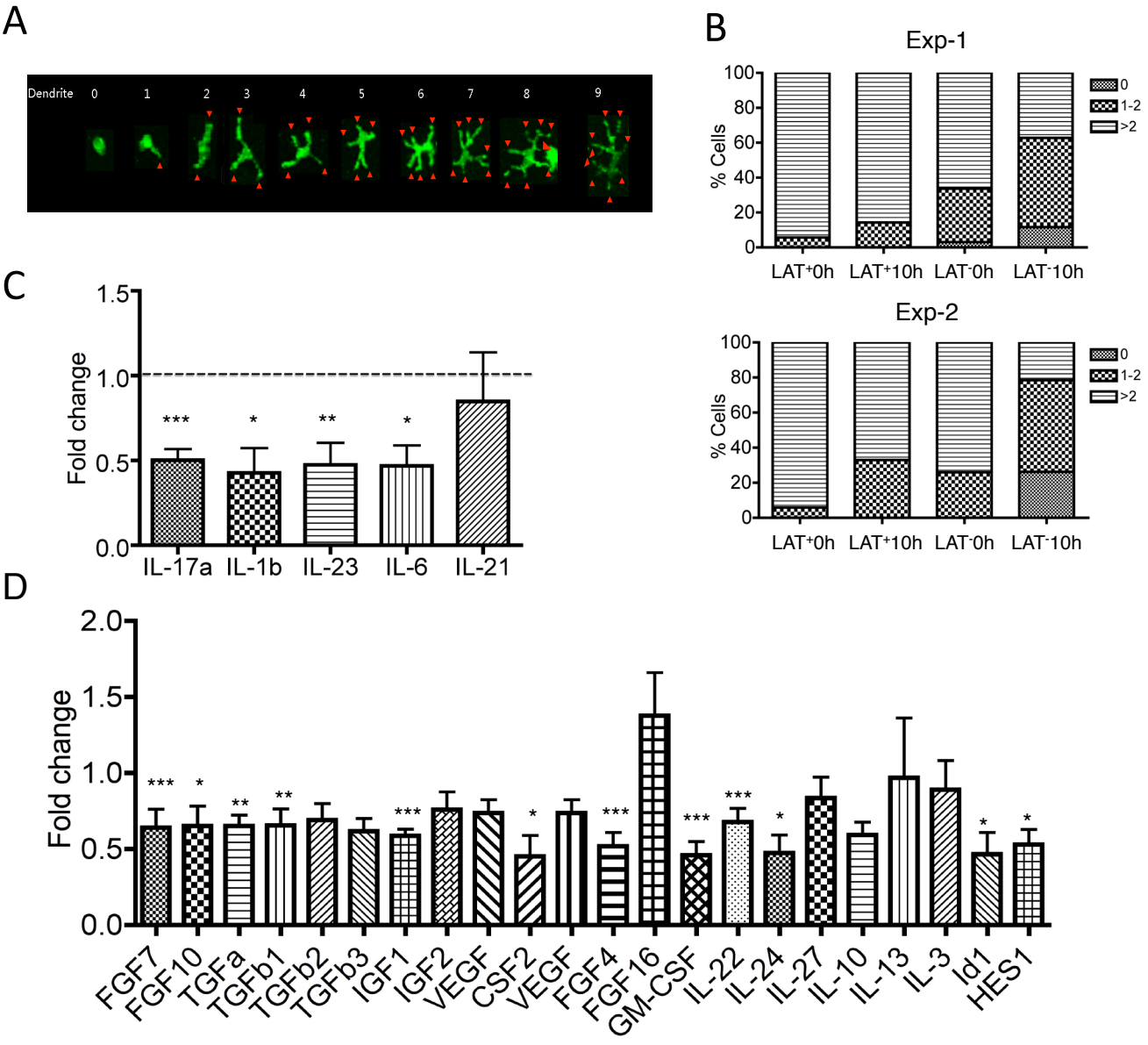
Supplemental Fig.1 Induced Cre activation among γδ T cells in various lymphoid organs. (A) Representative FACS plots for ZsGreen expression in γδ T cells in thymus, LNs, mLN, Peyer's Patch (PP), and liver. FACS analysis of γδ T cells were performed three days post 3-dose tamoxifen treatment of *TCRδ^{CreER}R26^{ZsGreen}* mice. (B) Representative FACS plots for ZsGreen expression in γδ T cells (thymus and spleen) in a time course following single dose tamoxifen treatment.. (C) ZsGreen expression in different subsets of γδ T cells after 3 doses of tamoxifen treatment. (D) Bar graph summary of ZsGreen expression in different subsets of γδ T cells after 3 doses of tamoxifen treatment. Data is based on analysis of 3 mice. *** P<0.001. (E) Representative FACS analysis of ZsGreen expression in splenic γδ T cells from indicated genotypes (n = 3).

Supplemental Fig.2



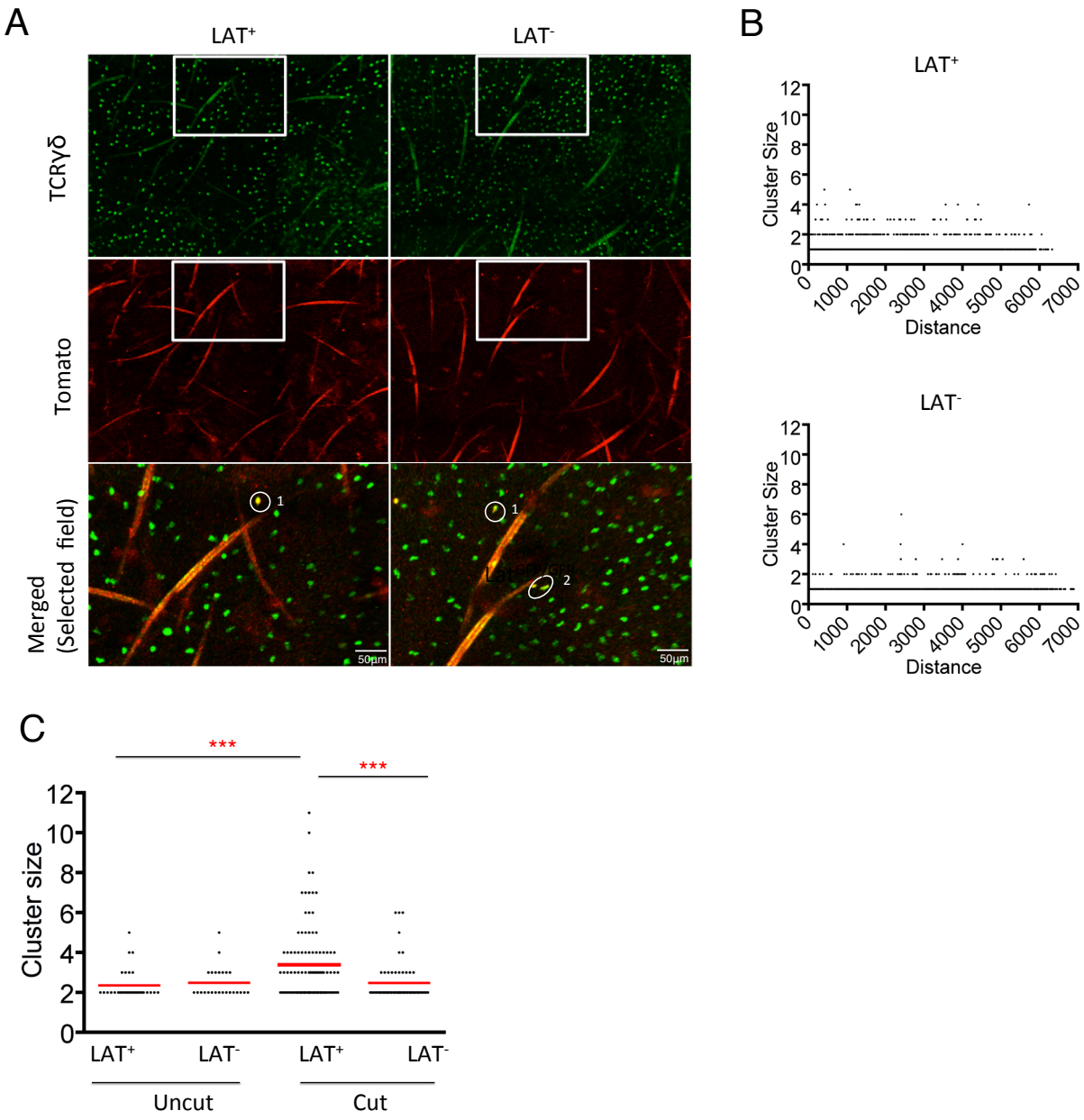
Supplemental Fig.2 Analysis of DETC density and individual DETC clones. (A) Representative FACS analysis of the density of γδ T cells from 8-day neonates (n = 2) and one-month young adults (n > 3). Total cell suspension was stained with anti-CD3 and anti TCRγδ Abs. (B) Representative confocal images of γδ T cells from one month-old *TCRδ^{CreER}Lat$^{GFP/GFP}$* (LAT$^-$) and *Lat$^{GFP/GFP}$* (LAT$^+$) control mice (n = 3 for each) treated with tamoxifen during Day 1-5 after birth. (C) GFP expression among DETCs isolated from mice used in (B). (D) Cell counts based on images as shown in (B). Each bar represents 10 randomly chosen fields (830μm×830μm/field). (E) Representative confocal images of mouse epidermal sheets prepared 3 days post tamoxifen treatment of newborns for 5 days. FITC-anti TCRγδ and Tomato fluorescent images were collected with appropriate filters. (F) Representative histogram showing GFP in DETCs at one month post tamoxifen treatment. (G) Representative FACS plots showing Tomato expression in LAT-deficient DETCs. Data are representative of 3 mice of each genotype.

Supplemental Fig.3



Supplemental Fig.3 Effect of TCR signaling on function of DETCs in wound healing. (A) Representative image of DETCs with varying numbers of dendrites. Dendrite counting is highlighted with triangles. (B) The distribution of DETCs based on their dendrite numbers. Numbers of dendrites in each DETC at wound edge were counted according to (A) at 10 hours post wounding. DETCs with 0, 1-2, and >2 dendrites were separated into three corresponding groups. Each graph is based on an independent experiment involving separate group of mice. (C&D) qPCR analysis of the expression of IL-17 pathway-related molecules (C) and growth factor genes (D). DETCs were isolated from *Lat*$^{GFP/GFP}$ (LAT^{+}) (n=3) and *TCRδ*^{CreER}*Lat*$^{GFP/GFP}$ (LAT^{-}) (n=3) mice one week post tamoxifen treatment and stimulated with anti-CD3 and anti-CD28 antibodies for 24 hours. Results are fold change between LAT^{-} and LAT^{+} samples. *P<0.05, **P<0.01, and *** P<0.001.

Supplemental Fig.4



Supplemental Fig.4 TCR signaling is required for clonal expansion at the wound edge. (A) Clone distributions revealed by Tomato tracking in the uncut ears of *TCRd^{CreER};R26^{tdTomato}* (LAT^{+}) and *TCRd^{CreER};LAT$^{GFP/GFP}$;R26^{tdTomato}* (LAT^{-}) mice at 4 days post tamoxifen treatment. Merged images (bottom panel) were from the highlighted areas shown in upper and middle panels. Representative Tomato^{+} DETC clones were highlighted with circles and labeled with cell counts. (B) Clone size distribution along the length of the ear. (C) Clone distribution of labeled Tomato^{+} DETC clusters containing two or more cells within 500μm of wound edge of the cut ear or the corresponding area in the uncut ear. Red lines indicate the averages of clone size. The average with SD for each sample is: uncut LAT^{+} 2.35±0.75, uncut LAT^{-} 2.48±0.77, cut LAT^{+} 3.38±1.83, cut LAT^{-} 2.48±1.01. Results were based on 3 LAT^{+} and 5 LAT^{-} mice. *** P<0.001.