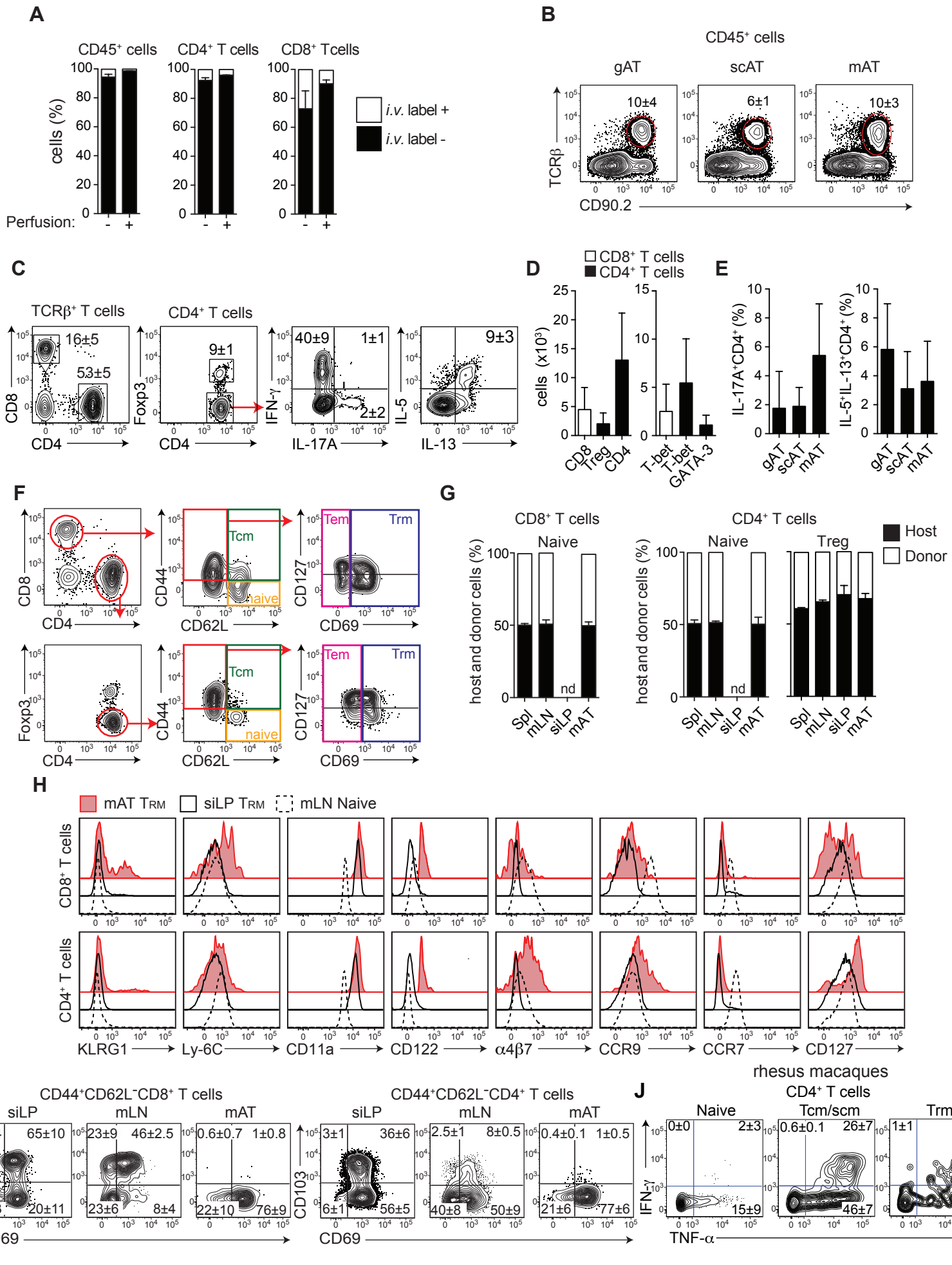
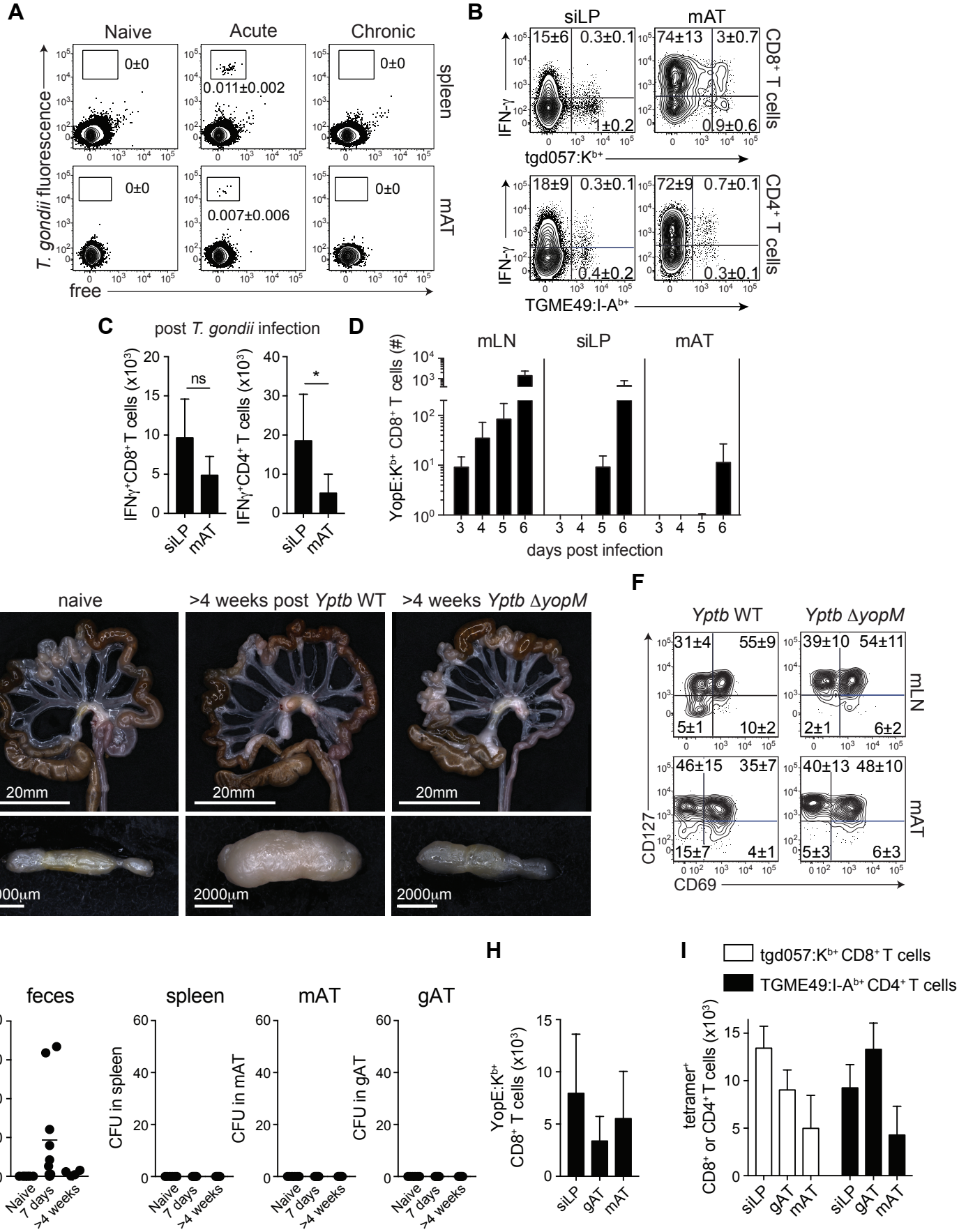


Han, Glatman Zaretsky *et al*. Supplemental Figure 1



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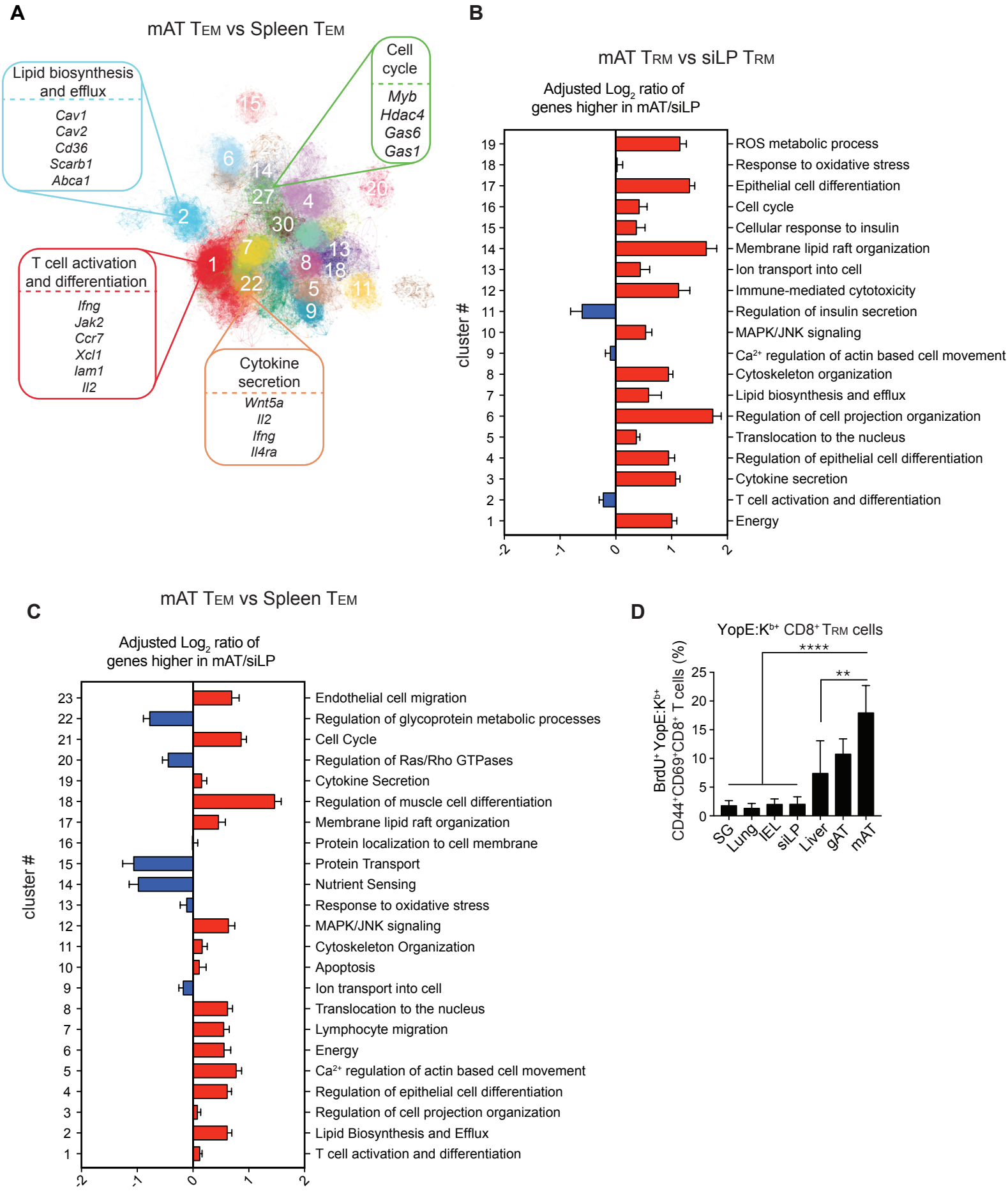
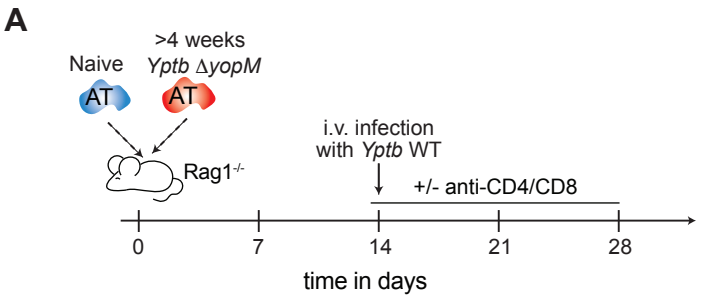
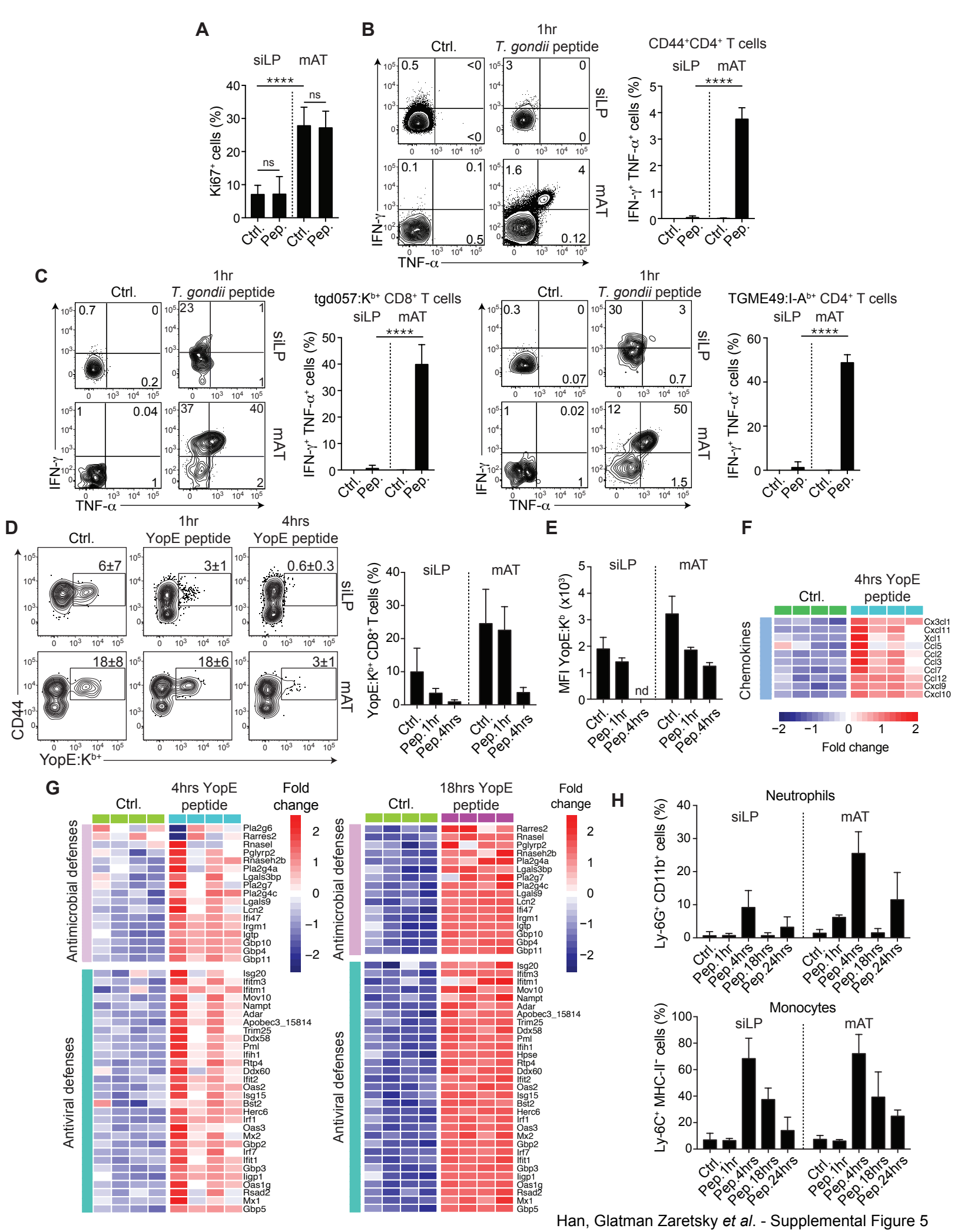
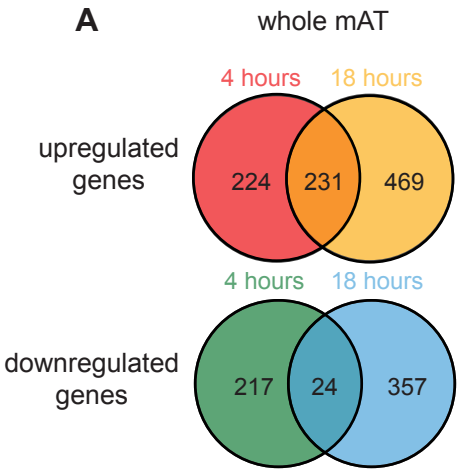

A
mAT TEM vs Spleen TEM
Lipid biosynthesis and efflux
Cav1
Cav2
Cd36
Scarb1
Abca1
Cell cycle
Myb
Hdac4
Gas6
Gas1
T cell activation and differentiation
Ifng
Jak2
Ccr7
Xcl1
Iam1
Il2
Cytokine secretion
Wnt5a
Il2
Ifng
Il4ra
B
mAT TRM vs siLP TRM
Adjusted Log2 ratio of genes higher in mAT/siLP
cluster #
ROS metabolic process
Response to oxidative stress
Epithelial cell differentiation
Cell cycle
Cellular response to insulin
Membrane lipid raft organization
Ion transport into cell
Immune-mediated cytotoxicity
Regulation of insulin secretion
MAPK/JNK signaling
Ca2+ regulation of actin based cell movement
Cytoskeleton organization
Lipid biosynthesis and efflux
Regulation of cell projection organization
Translocation to the nucleus
Regulation of epithelial cell differentiation
Cytokine secretion
T cell activation and differentiation
Energy
C
mAT TEM vs Spleen TEM
Adjusted Log2 ratio of genes higher in mAT/siLP
cluster #
Endothelial cell migration
Regulation of glycoprotein metabolic processes
Cell Cycle
Regulation of Ras/Rho GTPases
Cytokine Secretion
Regulation of muscle cell differentiation
Membrane lipid raft organization
Protein localization to cell membrane
Protein Transport
Nutrient Sensing
Response to oxidative stress
MAPK/JNK signaling
Cytoskeleton Organization
Apoptosis
Ion transport into cell
Translocation to the nucleus
Lymphocyte migration
Energy
Ca2+ regulation of actin based cell movement
Regulation of epithelial cell differentiation
Regulation of cell projection organization
Lipid Biosynthesis and Efflux
T cell activation and differentiation
D
YopE:Kb+ CD8+ TRM cells
BrdU+YopE:Kb+ CD44+CD69+CD8+ T cells (%)
****
**
SG
Lung
IEL
siLP
Liver
gAT
mAT

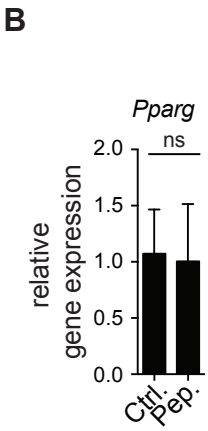


Han, Glatman Zaretsky *et al*. - Supplemental Figure 4



Han, Glatman Zaretsky *et al*. - Supplemental Figure 5





Han, Glatman Zaretsky *et al.* - Supplemental Figure 6

Supplementary Figure 1. Related to Figure 1.
(**A**) Naïve mice were injected *i.v.* with anti-CD45 AF-780 antibody. mAT was isolated from perfused (+) and non-perfused (-) mice. The frequency of $CD4^+$ and $CD8^+$ T cells labeled or not labeled by the *i.v.* injection of CD45 antibody is shown. (**B**) Representative contour plots showing total $CD90.2^+TCR\beta^+$ T cells from gonadal adipose tissue (gAT), subcutaneous adipose tissue (scAT), and mesenteric adipose tissue (mAT) isolated from naïve C57BL/6 mice. (**C-E**) Adipose tissue was isolated from naïve mice and evaluated for T cell populations, transcription factor expression and cytokine production after PMA/ionomycin restimulation with BFA. **(C)** Representative plots show $CD8^+$ and $CD4^+$ T cells and $Foxp3^+$ Treg cells and IFN-γ, IL-17A, IL-5 and IL-13 production by $CD4^+$ T cells in the mAT. (**D**) Numbers of $CD8^+$ T cells, $Foxp3^+$Treg cells and $Foxp3^-CD4^+$ T cells in mAT (left). Numbers of T-bet^+CD8^+ T cells, T-bet^+CD4^+ T cells and GATA-3^+CD4^+ T cells in mAT (right). (**E**) Frequency of IL-$17A^+$CD4 T cells and IL-5^+IL-13^+CD4 T cells in the gAT, scAT and mAT. (**F**) Gating strategy for memory T cell populations. T_{EM}, T_{RM} and T_{CM} populations were identified by their expression of CD44, CD62L, CD127 and CD69. (**G**) Frequency of $CD8^+$ T cells, $CD4^+$ T cells and Treg cells derived from host (black bars) or donor (white bars) cells in the indicated organs of parabiotic animals from **Figure 1F**. (**H-I**) Surface expression of the indicated markers on cells from the siLP, mLN, and mAT of naïve mice was determined by flow cytometry analysis. (**H**) Surface expression of indicated markers on $CD8^+$ and $CD4^+$ T_{RM} ($CD44^+CD62L^-CD69^+$) cells from the siLP and mAT and naïve $CD8^+$ and $CD4^+$ T cells ($CD44^-CD62L^+$) from the mLN. (**I**) Contour plots showing CD103 and CD69 expression on $CD44^+CD62L^-CD8^+$ (left) and $CD4^+$ (right) T cells in the indicated organs. (**J**) mAT was isolated from uninfected rhesus macaques and processed for flow cytometric analysis. Representative contour plots from concatenated samples show TNF-α and IFN-γ production by $CD3^+CD4^+$ naïve, $T_{CM/SCM}$, and T_{RM} cells. Numbers in all contour plots represent mean±SD. Error bars in all bar graphs represent standard deviation. Data are representative of at least 2 experiments with at least 4 mice, 3 pairs of parabiotic animals, or a total of 3 rhesus macaques. All cytokine production shown is after PMA/ionomycin stimulation.

Supplementary Figure 2. Related to Figure 2.
(A-C) Mice were infected with a fluorescent reporter strain of *T. gondii* by oral gavage and evaluated by flow cytometry. Numbers in representative contour plots indicate the mean±SD. **(A)** Representative contour plots of *T. gondii* fluorescence in the indicated organs of naïve, acutely (7 days post infection) or chronically (>6 weeks post infection) infected mice. **(B)** Representative contour plots showing IFN-γ production by tgd057:$K^{b+}CD8^+$ (top) and TGME49:I-$A^{b+}CD4^+$ (bottom) T cells after PMA/ionomycin stimulation in the indicated organ >6 weeks post infection. **(C)** Bar graphs show the total numbers of IFN-γ^+CD8^+ and $CD4^+$ T cells in the indicated organ >6 weeks after *T. gondii* infection. (Student's t test) **(D)** The number of $CD44^+$YopE:K^{b+} $CD8^+$ T cells in the mLN, siLP, or mAT was determined by flow cytometry at the indicated time points post-infection. **(E)** Representative images show the mLN of naïve or infected mice (>4 weeks post infection) as indicated. Top images show the mLN connected to the mAT and gastrointestinal tract. Bottom images show the isolated mLN at higher magnification. **(F)** Flow-cytometric analysis of CD127 and CD69 expression within YopE:$K^{b+}CD8^+$ T cells in the indicated organs 4 weeks post-infection with *Yptb* WT or *Yptb ΔyopM*. **(G)** Mice were infected with *Yptb ΔyopM* and bacterial burden was assessed in the indicated organs of naïve mice and mice infected 7 days or >4 weeks previously. DNA was isolated from feces and quantified by RT-qPCR (left). The indicated organs were isolated from mice at the indicated time points post-infection and bacterial burden was assessed by CFU within the tissue (right). **(H)** Quantification of $CD44^+$YopE:$K^{b+}CD8^+$ T cells in the siLP, gAT and mAT >4 weeks post-infection with *Yptb ΔyopM*. **(I)** The quantification of $CD44^+$tgd057:$K^{b+}CD8^+$ T cells (white) and TGME49:I-$A^{b+}CD4^+$ T cells (black) in the siLP, gAT and mAT >6 weeks post-infection with *T. gondii*. Numbers in representative contour plots indicate

mean±SD. Error bars in all graphs represent standard deviation. Data are representative of at least 2 experiments with at least 4 mice per group. ns not significant, *p<0.05.

Supplementary Figure 3. Related to Figure 3.
(A-B) Mice were infected with *Yptb ΔyopM* by oral gavage. >4 weeks post-infection, effector (T_{EM}: $CD44^+CD62L^-CD69^-$) and resident (T_{RM}: $CD44^+CD62L^-CD69^+$) memory $CD8^+$ T cells were sorted from the siLP, spleen, and mAT for gene expression analysis by RNA-Seq. **(A)** Pathway analysis was performed and gene pathways were organized into clusters based on shared genes, represented here as a clustergram, showing gene pathways differentially regulated between T_{EM} cells in the spleen and mAT. **(B-C)** Within each pathway cluster shown in **(A)**, the average value of the ratios of the positively or negatively regulated genes was calculated. Bar graphs show the log_2 ratio of the total number of up- or down-regulated genes in mAT T_{RM} and siLP T_{RM} (mAT/siLP)(B) or mAT T_{EM} and spleen T_{EM} (mAT/spleen)(C) for each differentially regulated cluster. **(D)** >4 weeks post-infection with *Yptb ΔyopM*, mice received BrdU i.p. daily for 12 days. The percentage of $BrdU^+YopE{:}K^{b+}CD44^+CD69^+$ $CD8^+$ T_{RM} in the indicated organ is quantified. Data are representative of at least 2 experiments with at least 3 mice per group. Error bars in bar graphs represent standard deviation. **p<0.01, ****p<0.0001

Supplementary Figure 4. Related to Figure 4.
(A) Pooled mAT, scAT and gAT isolated from either naïve donors or donors >4 weeks post-infection with *Yptb ΔyopM* were subcutaneously transplanted into *Rag1*$^{-/-}$ mice. *Rag1*$^{-/-}$ mice receiving adipose tissues from previously infected mice were either left untreated or injected with anti-CD4 and anti-CD8 depleting antibodies. 2 weeks post surgery, animals were challenged *i.v.* with 200 CFU of *Yptb* WT. A schematic of the experiment is shown.

Supplementary Figure 5. Related to Figure 5.
(A) >4 weeks post-infection with *Yptb ΔyopM*, mice injected *i.v.* with $YopE_{69\text{-}77}$ peptide or vehicle control (ctrl.) and evaluated by flow cytometry at the indicated time points post-injection. The percentage of $YopE{:}K^{b+}CD8^+$ T cells expressing Ki67 1 hour after injection is quantified in the indicated organs. **(B-C)** Mice were infected orally with a fluorescent reporter strain of *T. gondii*. 6 weeks post-infection, mice were injected *i.v.* with MHC-I and MHC-II peptides or vehicle control. **(B)** Representative contour plots (left) of IFN-γ and TNF-α expression in $CD44^+CD4^+$ T cells in the siLP or mAT. The frequency IFN-γ^+ TNF-α^+ cells within the $CD44^+CD4^+$ T cells was quantified (right). **(C)** Representative contour plots show IFN-γ and TNF-α expression in $tgd057{:}K^{b+}CD8^+$ (left) and $TGME49{:}I\text{-}A^{b+}CD4^+$ (right) T cells in the siLP or mAT. The frequency of IFN-γ^+ TNF-α^+ cells within the $CD44^+tgd057{:}K^{b+}CD8^+$ (left) or $TGME49{:}I\text{-}A^{b+}CD4^+$ (right) T cells was quantified. **(D-E)** >4 weeks post-infection with *Yptb ΔyopM*, mice injected *i.v.* with $YopE_{69\text{-}77}$ peptide or vehicle control (ctrl.) and evaluated by flow cytometry at the indicated time points post-injection. **(D)** Expression of $YopE{:}K^{b+}$ on $CD8^+$ T cells in the siLP or mAT 1 or 4 hours after injection is shown in representative contour plots (left) and quantified on the right. **(E)** MFI of $YopE{:}K^{b+}$ staining on $CD8^+$ T cells is quantified for the siLP and mAT after injection. (**F-G**) A microarray was performed on total mAT isolated from mice >4 weeks post-infection with *Yptb ΔyopM* at 4 or 18 hours post-injection with $YopE_{69\text{-}77}$ peptide or vehicle control. (**F**) Heatmap shows relative gene expression levels of chemokines 4 hours post-injection. (**G**) Heatmap represents differential antimicrobial and antiviral gene expression 4 hours (left) or 18 hours (right) post-injection. (**H**) Quantification of neutrophils (top) (gated on live, $CD45^+TCR\beta^-Siglec\ F^-NK1.1^-B220^-$ cells) or monocytes (bottom) (gated on live, $CD45^+TCR\text{-}\beta^-Siglec\ F^-NK1.1^-\ B220^-CD11b^+Ly\text{-}6G^-CD64^+CCR2^+$ cells) at the indicated time points post-vehicle control or peptide injection in the siLP or mAT. Numbers in representative contour plots indicate mean±SD. Error bars in all graphs represent standard

deviation and statistics are calculated using one way Anova adjusted for multiple comparisons. Data are representative of at least 2 experiments with at least 3 mice per group. ns not significant, ****p<0.0001.

Supplementary Figure 6. Related to Figure 6.

(**A**) >4 weeks post-infection with *Yptb ΔyopM*, mice were injected intravenously with $YopE_{69-77}$ peptide or vehicle control. At 4 or 18 hours post-injection, the total mAT was isolated for microarray analysis. The venn diagram indicates the numbers of up- (top) or down- (bottom) regulated genes at 4 and/or 18 hours post-peptide injection compared to control injected mAT. (**B**) Adipocytes were isolated from mAT 18 hours after vehicle control or peptide injection of mice >4 weeks post infection with *Yptb ΔyopM*. Expression of *Pparg* was determined by RT-qPCR. Error bars in all bar graphs represent standard deviation. Data are representative of at least 2 experiments with at least 2-6 mice per group. ns not significant.