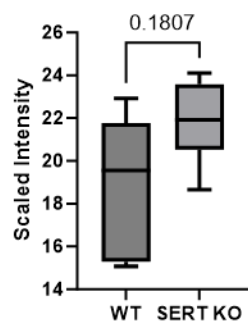


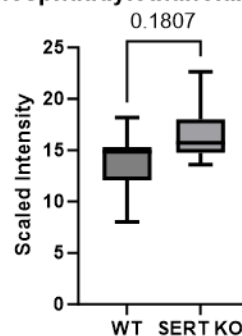
A

Phosphatidylcholine (PC)

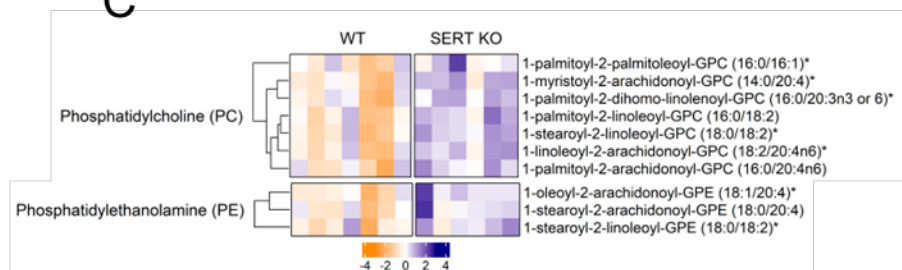


B

Phosphatidylethanolamine (PE)

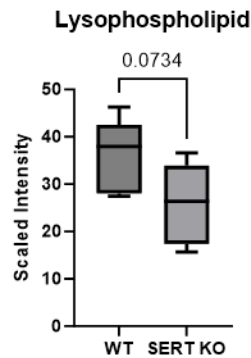


C

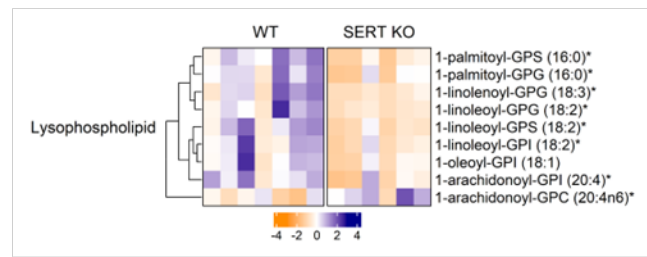


Supplemental Figure S1: **SERT KO mice have altered phosphatidylcholine (PC) and phosphatidylethanolamine (PE) metabolites.** **A.** Boxplot of overall phosphatidylcholine (PC) and **B.** phosphatidylethanolamine (PE) abundances in ileal mucosa (Welch *t*-test; WT *n* = 7; SERT KO *n* = 6). **C.** Heatmap of differentially altered PC and PE metabolites (*p* < 0.05, *q* < 0.1, Welch *t*-test; WT *n* = 7; SERT KO *n* = 6).

A

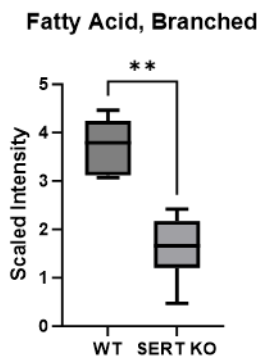


B

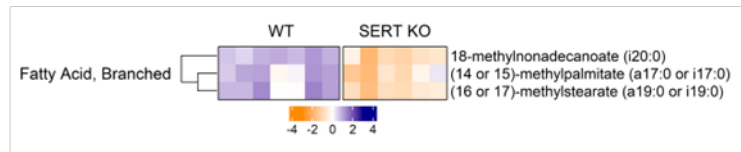


Supplemental Figure S2: **Lysophospholipid metabolites are diminished in SERT KO ileal mucosa.** **A.** Boxplot of overall lysophospholipid abundances in ileal mucosa (Welch *t*-test; WT *n* = 7; SERT KO *n* = 6) **B.** Heatmap of differentially altered lysophospholipid metabolites ($p < 0.05$, $q < 0.1$, Welch *t*-test; WT *n* = 7; SERT KO *n* = 6).

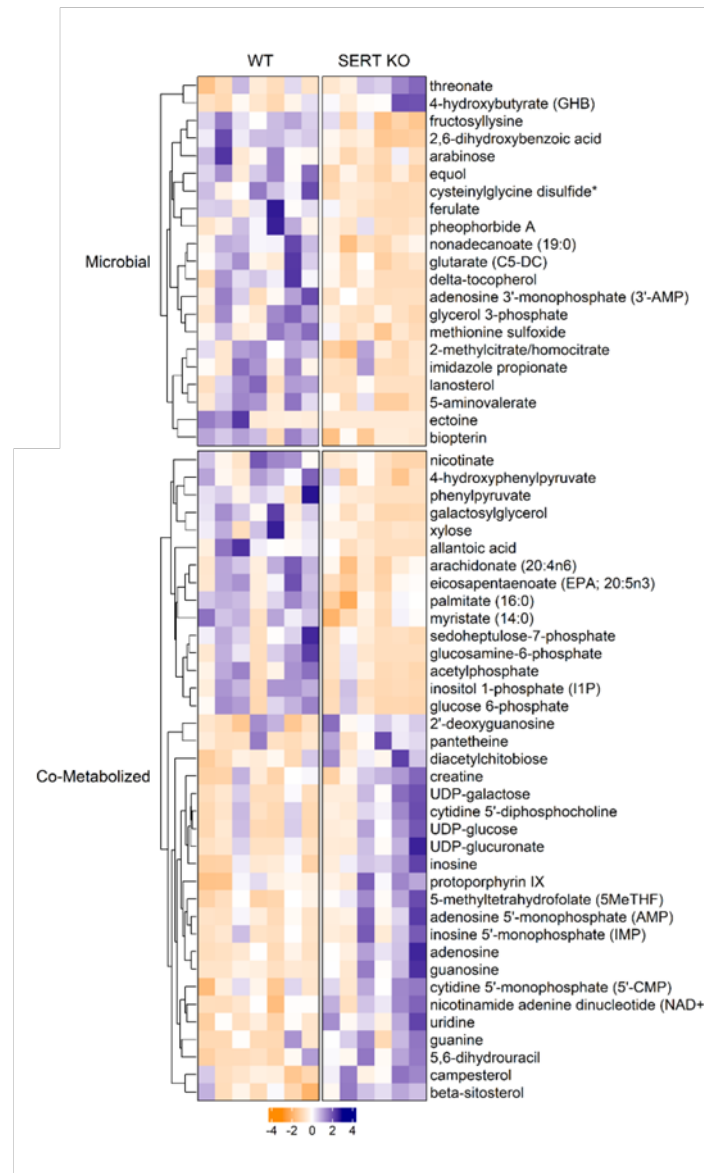
A



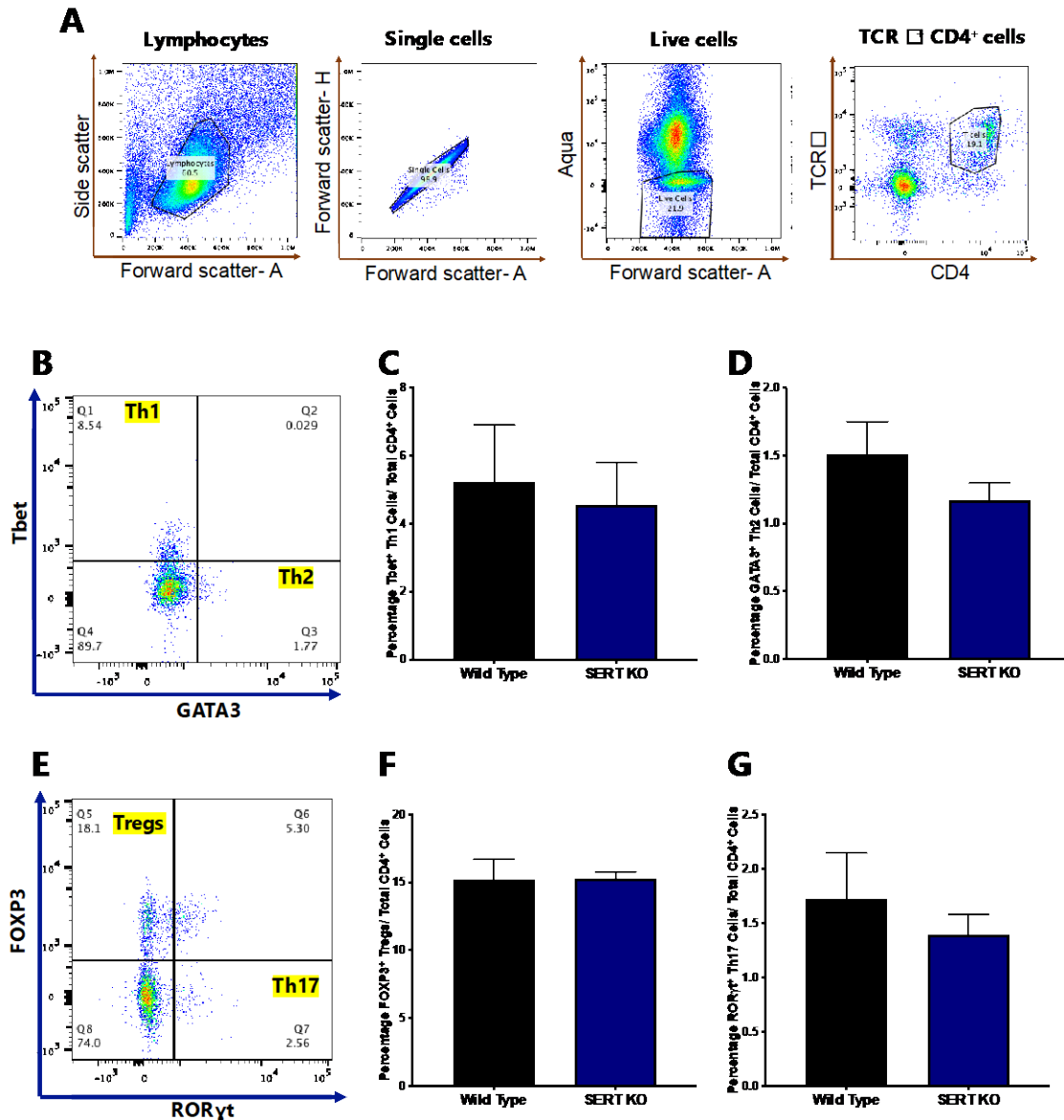
B



Supplemental Figure S3: **Ileal mucosa lacking SERT demonstrates diminished levels of branched fatty acids.** **A.** Boxplot of overall branched fatty acid abundances in ileal mucosa (Welch *t*-test; WT *n* = 7; SERT KO *n* = 6) **B.** Heatmap of differentially altered branched fatty acid metabolites ($p < 0.05$, $q < 0.1$, Welch *t*-test; WT *n* = 7; SERT KO *n* = 6). ** $p < 0.01$



Supplemental Figure S4: **Heatmap of microbial-related and co-metabolized differentially altered metabolites between WT and SERT KO mice in the ileal mucosa.** Metabolites were classified based upon MetOrigin classification. ($p < 0.05$, $q < 0.1$, Welch t-test; WT $n = 7$; SERT KO $n = 6$).



Supplemental Figure S5: **Various CD4⁺ T cell populations in ileal lamina propria of wild type and SERT KO mice.** Lamina propria lymphocytes were isolated from mice ileal tissues and 1 million cells were stained for Th cell transcription factors marking Th1 (Tbet), Th2 (GATA3), Th17 (ROR γ t) and T regulatory cells (FOXP3) **A.** Gating strategy in FACS analysis for CD4⁺ T cells. **B.** FACS dot plots identifying Th1 (Q1) and Th2 (Q3) populations. **C.** Representative bar diagram showing percentage of Th1 cells in total CD4⁺ Cell population. **D.** Representative bar diagram showing percentage of Th2 cells in total CD4⁺ Cell population. **E.** FACS dot plots identifying Tregs (Q5) and Th17 (Q7) populations. **F.** Representative bar diagram showing percentage of Treg cells in total CD4⁺ Cell population. **G.** Representative bar diagram showing percentage of Th17 cells in total CD4⁺ cell population in the ileum. Data represented as average \pm SEM, n=3.