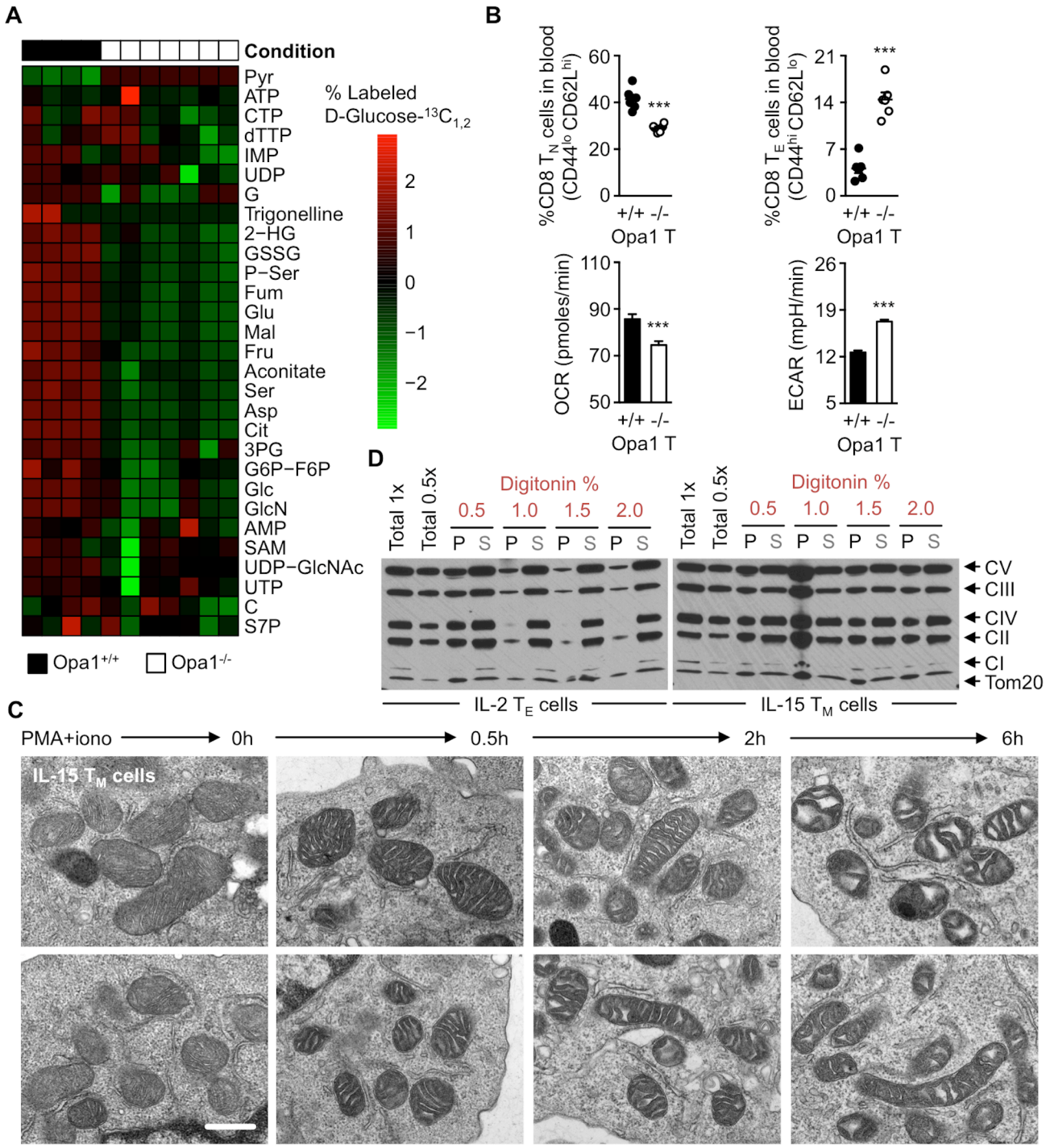

Figure S6. T cell activation induces cristae remodeling that regulates metabolism (Related to Figure 6).
(**A**) Activated Opa1$^{+/+}$ and Opa1$^{-/-}$ IL-2 T_E cells were cultured overnight with D-Glucose-$^{13}C_{1,2}$ and traced for incorporation by mass spectrometry. Heat map representation of % labeled carbons in listed metabolites. (**B**) Spleens from either polyclonal wild-type (+/+) or Opa1 deficient T cell animals (-/- Opa1 T) were isolated and surface marker expression assessed (CD44, CD62L on CD3$^+$ CD8$^+$ gates) by flow cytometry (top) or were further purified for CD8 T cells to assess OCR and ECAR at baseline (below) by Seahorse EFA. Data presented with mean ± SEM from n=6 per genotype, ***p<0.0001. (**C**) EM images of IL-15 T_M cell mitochondria over time before and after PMA and ionomycin stimulation from one experiment. Scale bar = 0.5 μm. (**D**) Immunoblot analysis of ETC complexes (CI-NDUFB8, CII-SDHB, CIII-UQCRC2, CIV-MTC01, CV-ATP5A) and OMM protein Tom20. Equivalent numbers of IL-2 T_E and IL-15 T_M cells lysed in native lysis buffer followed by digitonin solubilization of intracellular membranes. Pellet (P) and solubilized supernatant (S) fractions were resolved on a denaturing gel. Second experiment represented from **Figure 6J**.