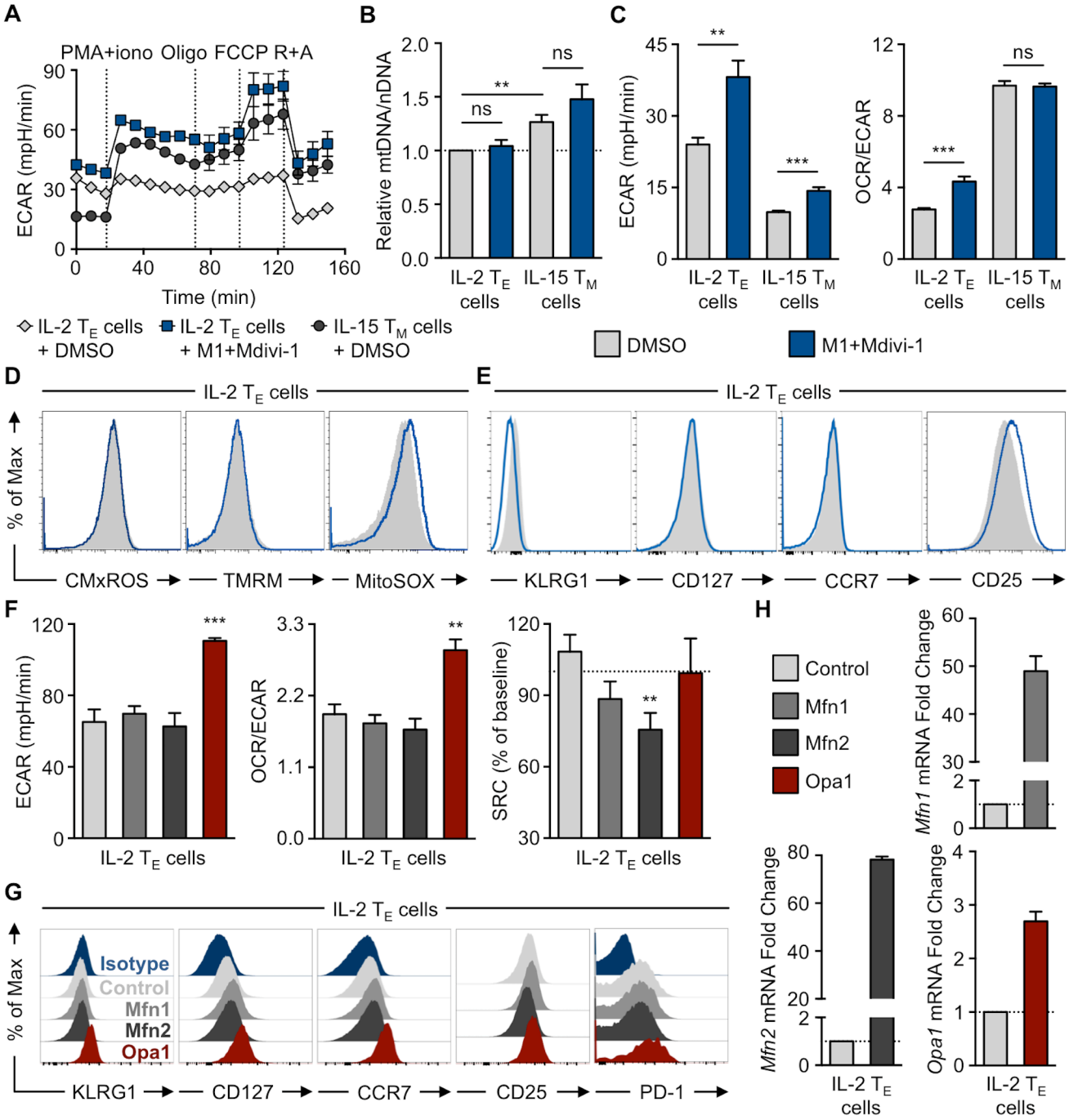

Figure S3. Assessment of T cell phenotype and metabolism following pharmacological or genetic enhancement of mitochondrial fusion (Related to Figure 3).

(**A-E**) IL-2 T_E and IL-15 T_M cells generated from OT-I mice were treated with DMSO control or M1+Mdivi-1. (**A**) ECAR of indicated cells at baseline and after PMA and ionomycin (PMA+iono) stimulation, oligomycin (Oligo), FCCP, and rotenone plus antimycin A (R+A). (**B**) qPCR analysis of relative mitochondrial DNA (mtDNA) to nuclear DNA (nDNA) ratios of indicated cells. (**C**) ECAR (left) and OCR/ECAR ratios (right) of indicated cells under basal conditions. (**D**) Histograms of membrane potential (CMxROS, TMRM) and mitochondrial ROS (MitoSOX) using indicated fluorescent dyes and (**E**) KLRG1, CD127, CCR7, and CD25 surface marker expression of indicated cells analyzed by flow cytometry. (**F-H**) OT-I IL-2 T_E cells were activated and transduced with empty vector (Control), Mfn1, Mfn2, or Opa1 expressing retrovirus. (**F**) ECAR, OCR/ECAR, and SRC analyzed by Seahorse EFA, (**G**) KLRG1, CD127, CCR7, CD25 and PD-1 surface marker expression assessed by flow cytometry, and (**H**) gene expression analysis by qPCR. (**A-G**) Data are shown as mean ± SEM and are representative or (**B-C, F**) combined from 2-3 experiments, not significant (ns), **p<0.001, ***p<0.0001.