

Figure S1. (A) The experimental protocol is related to Figure 1 and schematic panel illustrates the study design; (B) Western blot assay of MFN2, OPA1 p-Drp1 and Drp1 expression in total homogenate; (C) Micrographs of mitochondria observed using a transmission electron microscopy in Figure 2C and quantitative analysis of average mitochondrial length in **five CD4⁺T cells**; (D) quantitative analysis of BCL-2 and Bax. The results are shown as the mean \pm SD, n=5. *(P< 0.05) vs the sham group, ***(P< 0.001); &(P< 0.05) vs the CLP group, &&(P< 0.01).

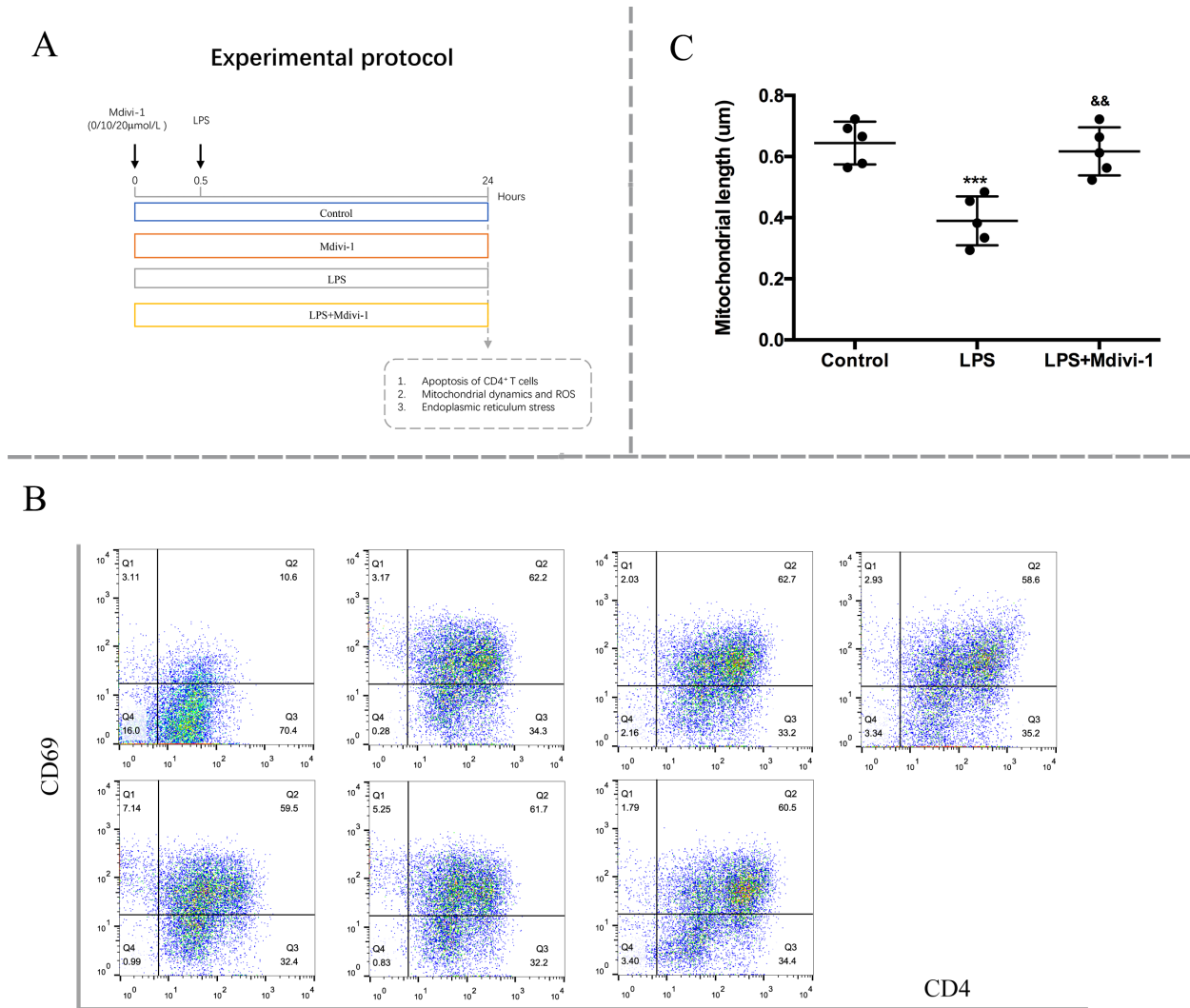


Figure S2. (A) The experimental protocol is related to Figure 4 and schematic panel illustrates the study design; (B) Expression levels of CD4 and CD69 by flow cytometric analysis in CD4⁺T cells; (C) Micrographs of mitochondria observed using a transmission electron microscopy in Figure 6A and quantitative analysis of average mitochondrial length in five CD4⁺T cells. The results are shown as the mean ± SD, n=5. *** (P < 0.001) vs the sham group; && (P < 0.01) vs the CLP group.

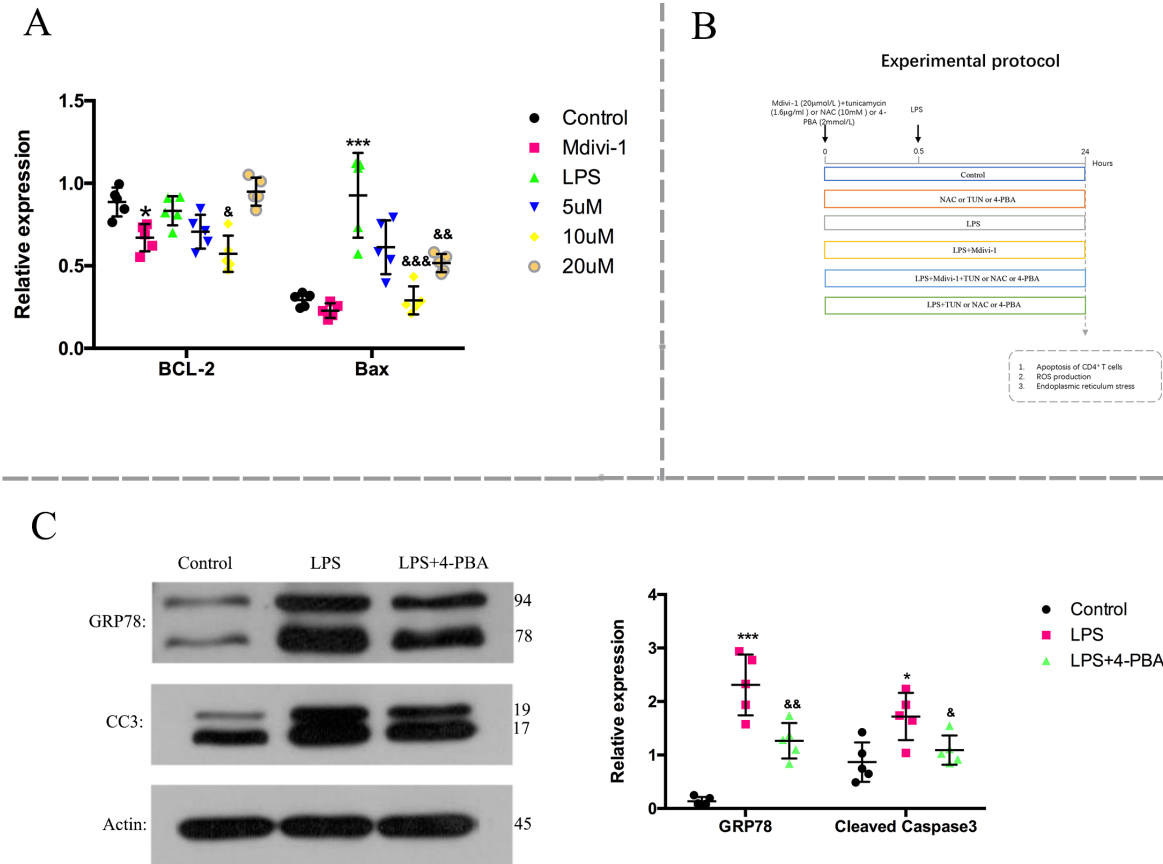


Figure S3. (A) quantitative analysis of BCL-2 and Bax; (B) The experimental protocol is related to Figure 8, 9 and schematic panel illustrates the study design; (C) Western blot assay and quantitative analysis of GRP78 and CC3 expression. The results are shown as the mean \pm SD, $n=5$. *($P < 0.05$) vs the Control group, ***($P < 0.001$); &($P < 0.05$) vs the CLP group, &&($P < 0.01$), &&& ($P < 0.001$).