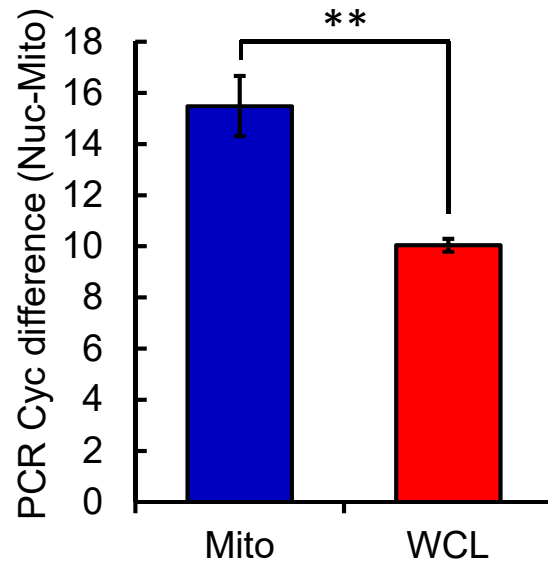


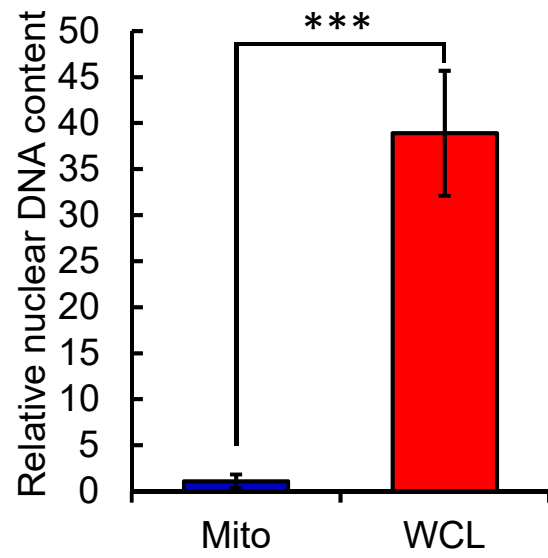
### **Supplementary Fig. 1. Subcellular distribution of PARP1**

Western blot evaluation of PARP1 in subcellular fractions from HeLa WT cells. Purified nuclear, cytoplasm, and mitochondria were probed for western blot with indicated antibodies.

**(a)**



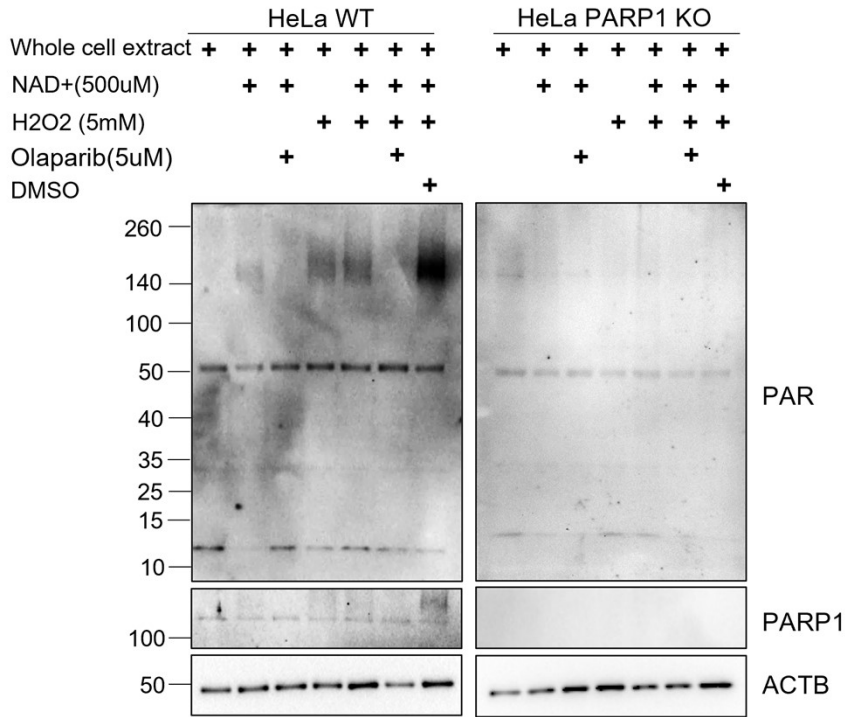
**(b)**



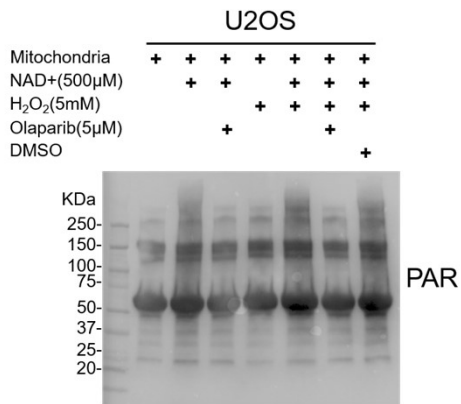
**Supplementary Fig. 2. Estimation of nuclear contamination by realtime PCR.**

Whole cell lysates (WCL) and purified mitochondria from WT/PARP1 KO HeLa were prepared for ChIP/ChAP. Purified DNAs were evaluated for nuclear contamination using five mitochondria and three nuclear specific genes (n=3). (a) Average PCR CT value differences between average mitochondrial and nuclear genes were compared. (b) Comparison of nuclear DNA contamination in purified mitochondria versus WCL. Relative nuclear DNA contaminations are calculated by normalization with the amount of nuclear DNA in purified mitochondria. Error bars represent standard deviation. \*\*, <0.01; \*\*\*, <0.001.

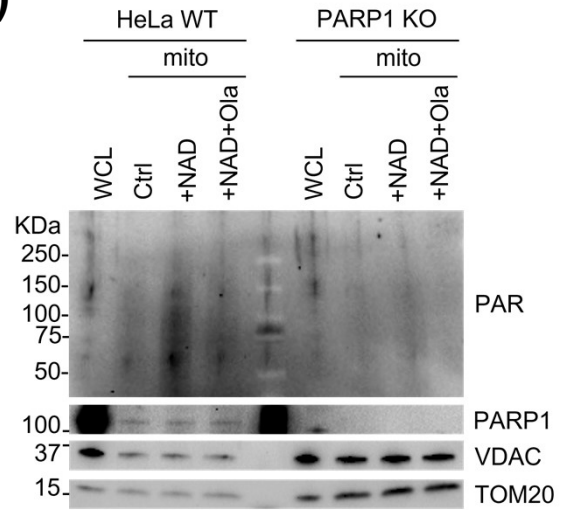
**(a)**



**(b)**

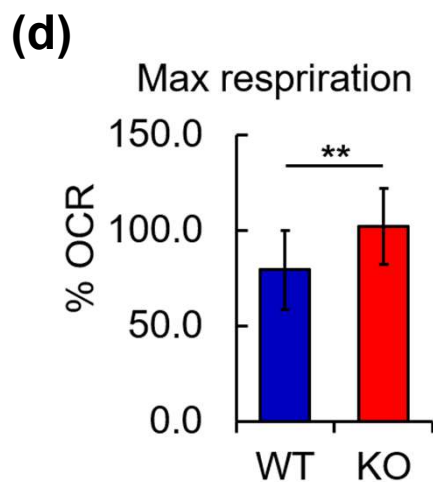
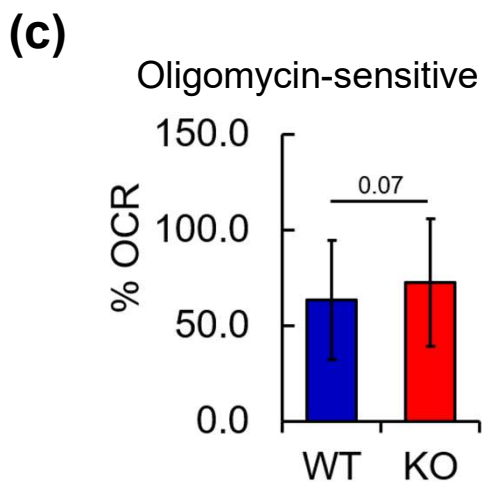
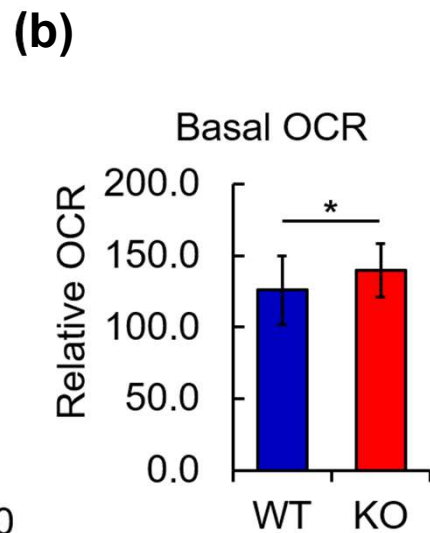
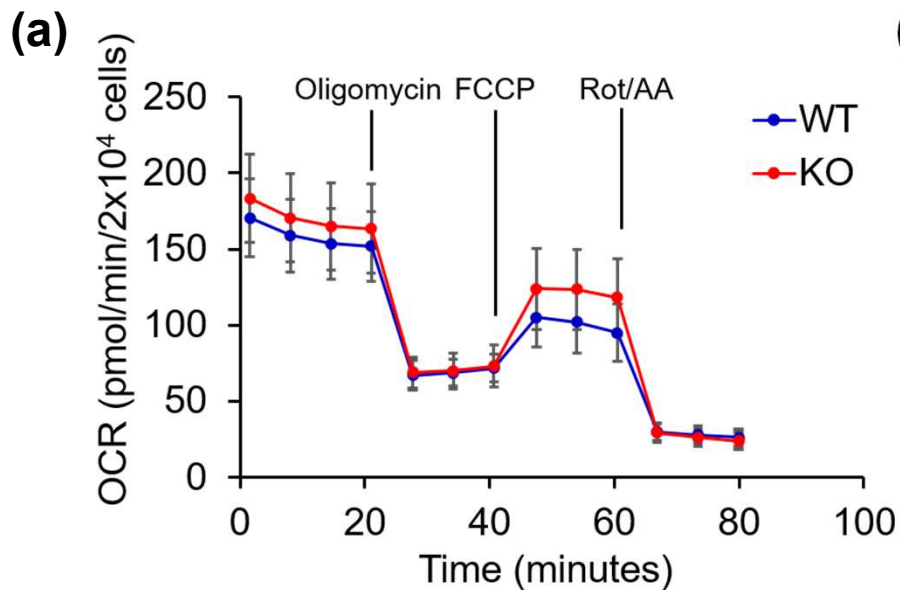


**(c)**



### **Supplementary Fig. 3. NAD<sup>+</sup> stimulates mitochondrial PAR by PARP1**

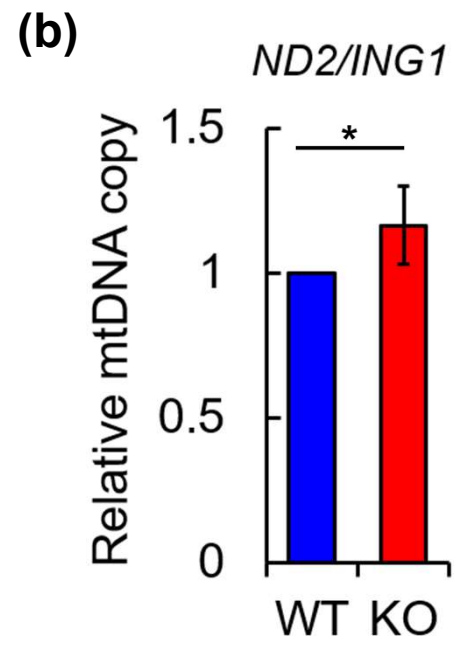
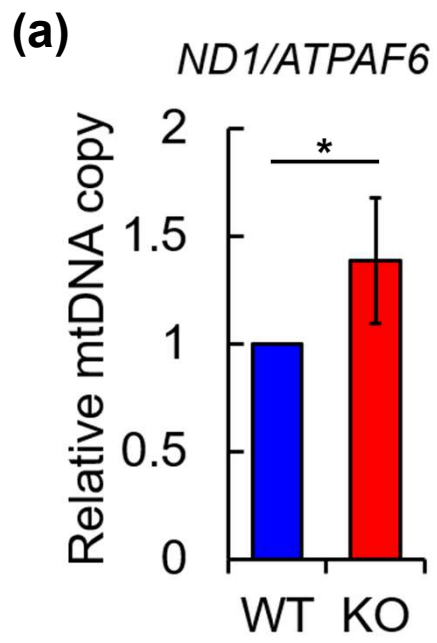
(a) HeLa WT and PARP1 KO cells were treated with indicated combinations of reagents for 30 minutes at 37 °C and whole cell extracts were subjected for western blot, probed with indicated antibodies. (b) NAD<sup>+</sup> stimulates mitochondrial PAR by PARP1. Purified mitochondria from U2OS cells were treated with indicated combinations of reagents for 30 minutes at 37 °C and 1.3ug of mitochondrial samples were subjected for western blot, probed with PAR specific antibody. (c) Western blot evaluation of purified mitochondria for ChIP/ChAP. Isolated mitochondria from WT/KO cells were treated with NAD<sup>+</sup> with/without olaparib for 30 minutes at 37 °C. After reaction, mitochondrial samples were resuspended in ChIP/ChAP buffer B. mtDNAs were digested, DNA concentrations were measured and normalized. Same amount mtDNA containing mitochondrial samples were probed for western blot with indicated antibodies. Whole cell lysates for each cell were loaded as a control. Error bars represent SD.



#### **Supplementary Fig. 4. Seahorse extracellular flux analysis of intact cells**

OCR was measured in WT and KO HeLa cells using Seahorse extracellular flux analysis, according to Materials and Methods (n=5). (a) Seahorse extracellular flux analysis representative trace. (b) Basal respiration was calculated and normalized to the number of cells in each well. (c) and (d) Oligomycin-sensitive respiration and Maximal respiration capacity are measured via the calculation of relative changes between FCCP and Rotenone/Antimycin A injection. Error bars represent SD. \*, <0.05; \*\*, <0.01.





### **Supplementary Fig. 5. mtDNA copy number assessment**

Total cellular DNA were purified from WT/KO cells, mitochondria specific genes were estimated by realtime PCR and normalized with control nuclear DNA specific targets.

Two nuclear DNA encoded genes, (a) *ATPAF* and (b) *ING1* were used to normalize mtDNA encoded genes *ND1* and *ND2*, respectively, to calculate mtDNA copy number (n=6). Error bars represent SD. \*,<0.05.