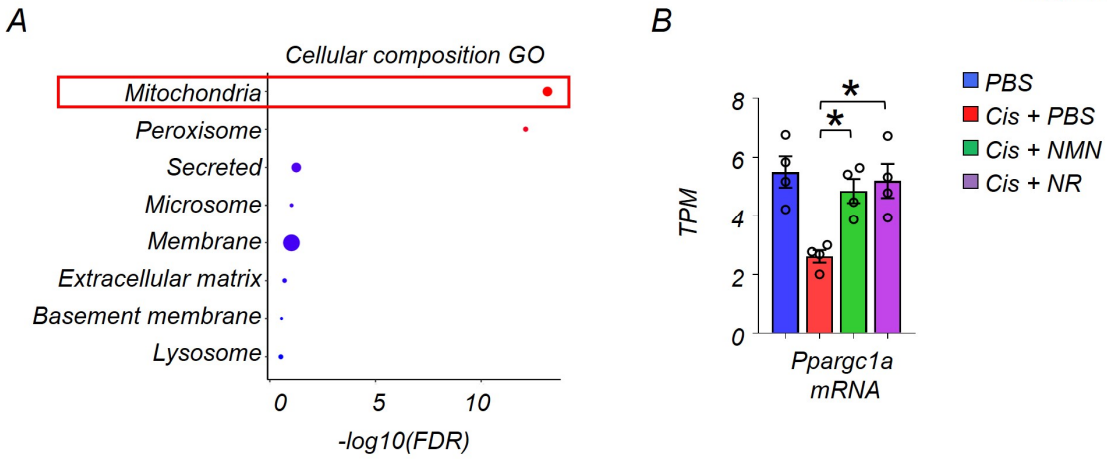
SUPPLEMENTARY MATERIALS

Supplementary Figures 1-2

Uncropped image for Supplementary Fig2 B

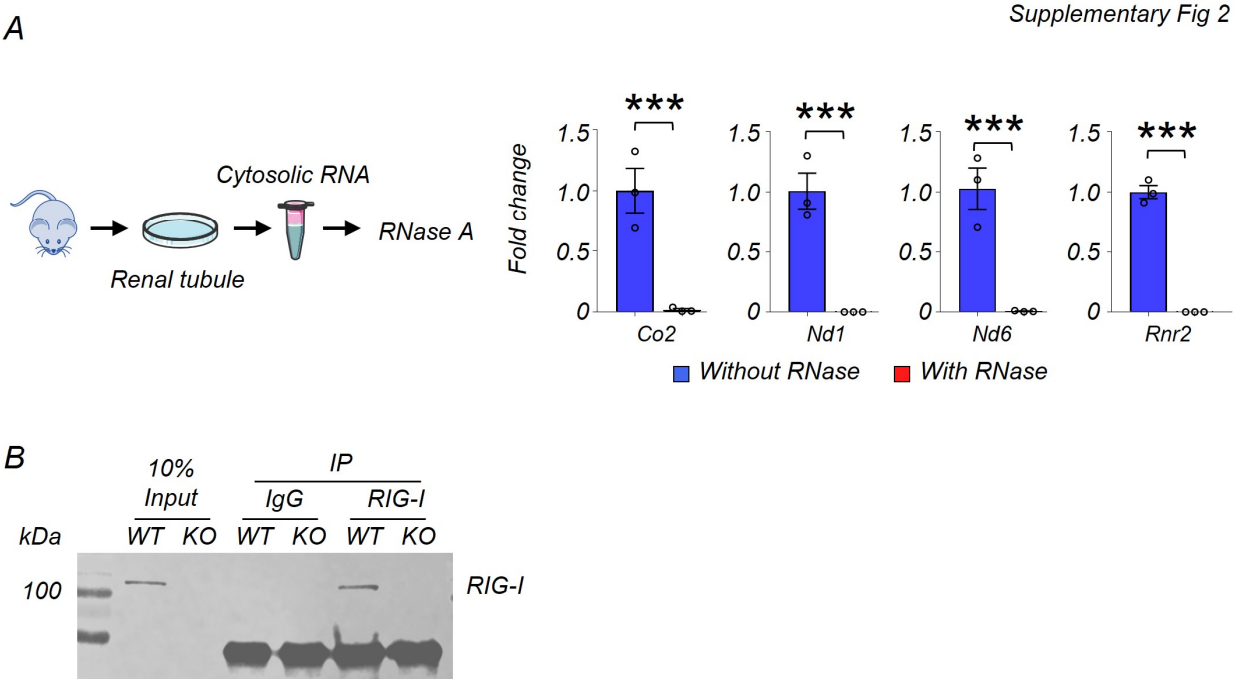


Supplementary Fig 1. Gene ontology analysis of cellular localization of genes normalized by NMN and NR supplementation.

(A) GO analysis of cellular localization. Red box highlighted the enrichment for mitochondria fraction. Dot color indicates significance, and dot size indicates the gene counts in the pathway.

(B) Relative transcript levels of *Ppargc1a* in kidneys of the experimental groups.

Data are presented as mean ± s.e.m. and were analyzed using a one-way ANOVA followed by Tukey post hoc test for multigroup comparison.



Supplementary Fig 2. Effect of RNAse treatment on gene expression and immunoprecipitation of RIG-I
(A) (Left) Cytosolic RNA extracted from renal tubule cells were incubated with RNase A. (Right) Relative transcript levels of mitochondria genes (*Co2, Dd1, Nd6* and *Rnr2)* in cytosolic fraction with or without RNase (n=3 each). Gene expression levels were normalized using *Gapdh*. ***p<0.001. Data are presented as mean ± s.e.m. and were analyzed using a two-tailed Student's t-test. (B) Western blot image of RIG-I in renal tubule cells as indicated (IP: immunoprecipitation). 2 experiments were repeated independently.

Uncropped image for Supplementary Fig2 B