

## Appendix

**Figure S1. Quantification of mtRNA transcripts in whole-body *Tefm* and *Polrmt* double-heterozygous knockout mice.**

**Figure S2. Normalized read counts from RNA sequencing of mitochondrial transcripts in *Tefm* knockout mice.**

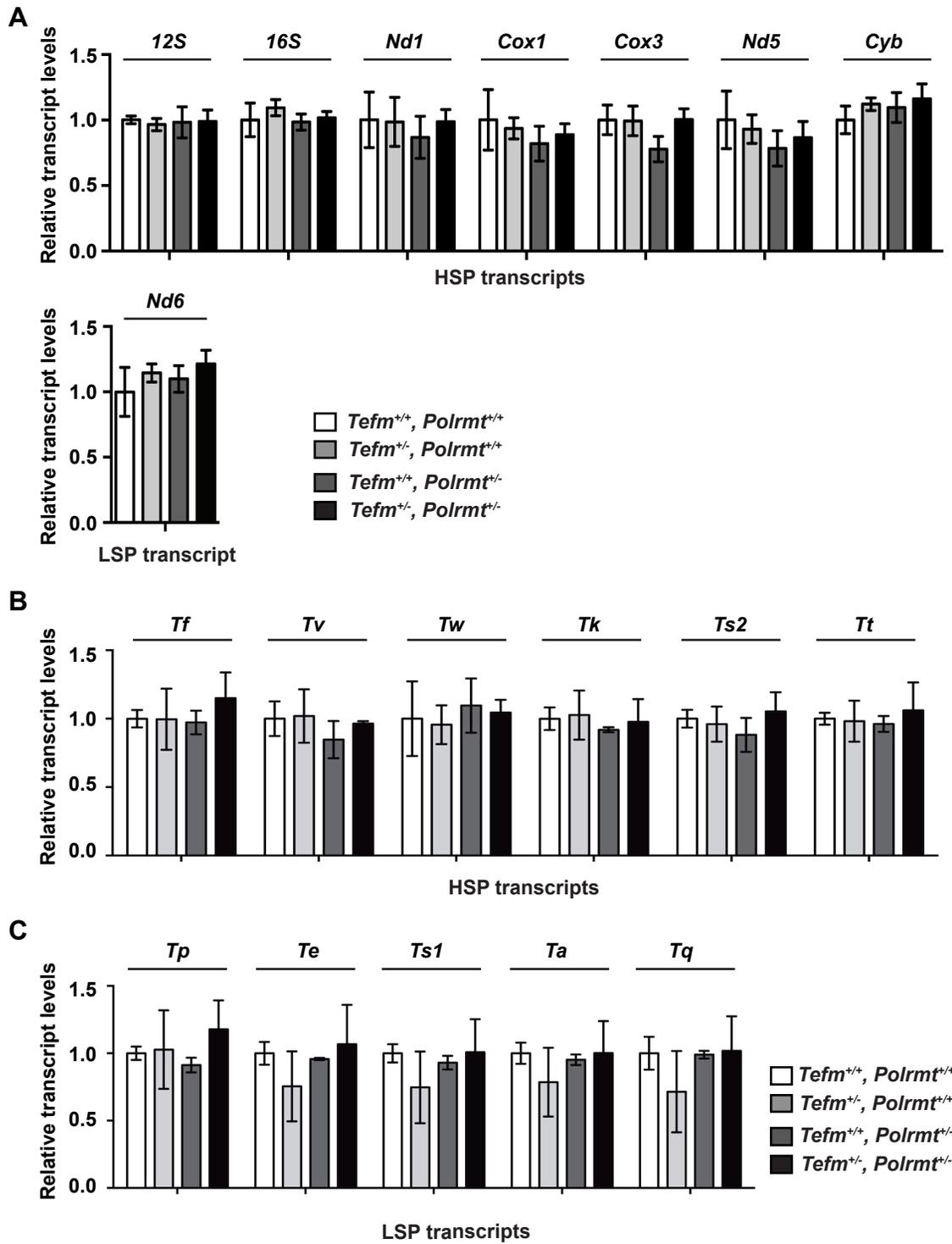
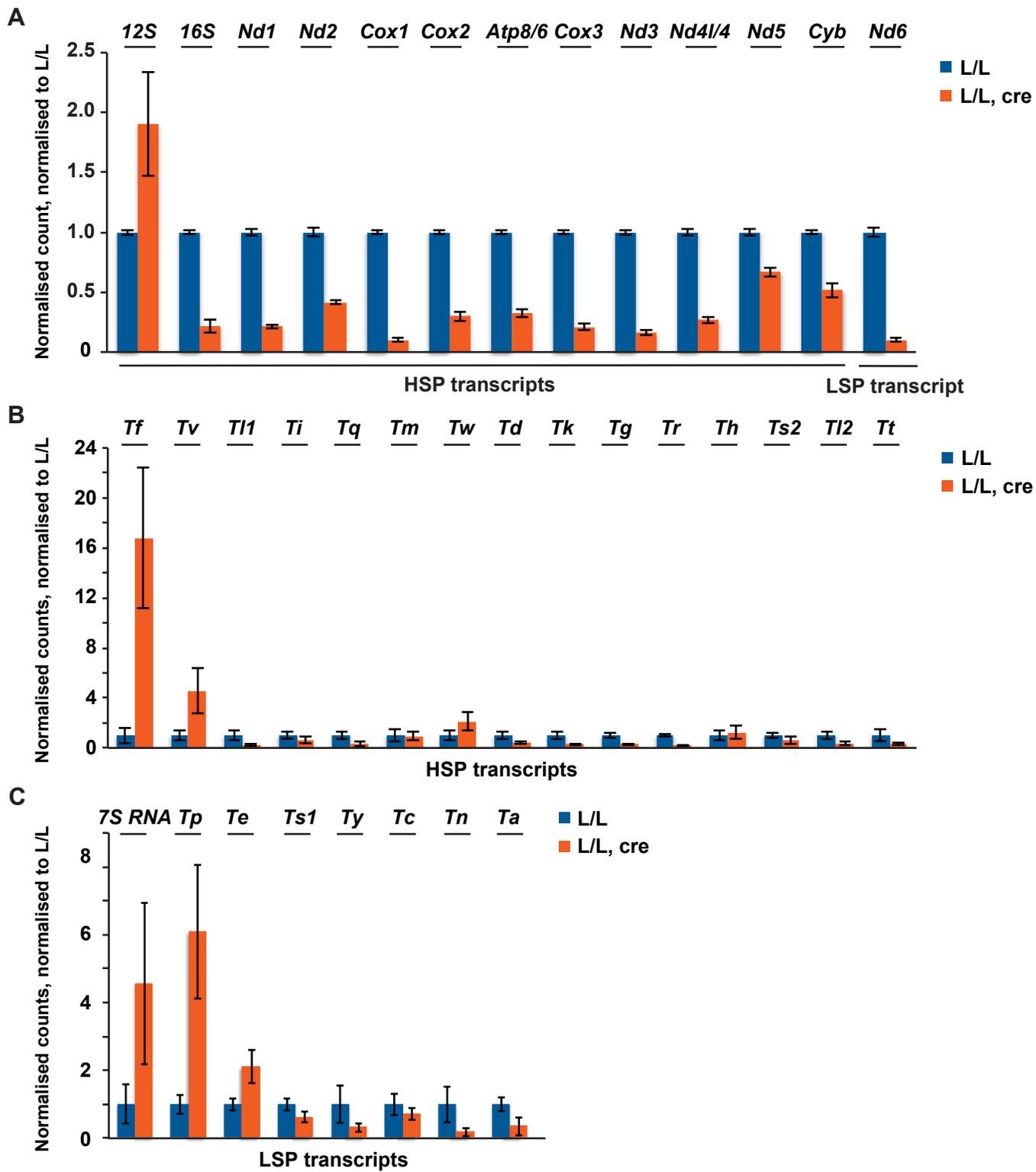


Figure S1



**Figure S2**

## Appendix Figure Legend

**Figure S1. Quantification of mtRNA transcripts in whole-body *Tefm* and *Polrmt* double-heterozygous knockout mice.** Quantification of northern blot of mtRNA transcripts in 16-week-old *Tefm* and/or *Polrmt* double-heterozygous/heterozygous knockout mouse hearts (n= 8 mice for each group). (A) mt-rRNAs and mt-mRNAs transcripts; (B) HSP mt-tRNAs transcripts. (C) LSP mt-tRNA transcripts.

Data information: In (A-C), data are presented as mean  $\pm$  SEM. Statistical analysis was performed using one-way analysis of variance (ANOVA). There is no difference between groups.

**Figure S2. Normalized read counts from RNA sequencing of mitochondrial transcripts in *Tefm* knockout mice.** (A) mt-rRNAs and mt-mRNAs. (B) mt-tRNAs from HSP transcripts. (C) 7S RNA and mt-tRNAs from LSP transcripts. (D) The 7S RNA read counts at LSP from small RNA sequencing. *Tefm* knockout mice n= 4, control mice n= 3.

Data information: In (A-C), data are presented as mean  $\pm$  SEM. Differential expression was performed using DESeq2 and the Wald test to determine significance (the adjusted *p* value for 12S rRNA is < 0.05, and all others are < 0.01).