

Description of Additional Supplementary Files

Supplementary Dataset 1: Proteomics

Z-score fold change in proteome abundance and FDR significance. TAB1: Label Free Analysis, TAB2: TMT Analysis, TAB3: Mitocarta Coverage. N/A = not a value, pink = increased, blue = decreased.

Supplementary Dataset 2: Lipidomics

Fold change (FC) in lipidome abundance and FDR significance (Pval). TAB1: Fold change in total abundance of lipid classes in Tibialis anterior (TA), TAB2: Fold change in total abundance of lipid classes in Liver, TAB3: Fold change in total abundance of lipid classes in plasma, TAB4: Fold change in cardiolipin species abundance in Tibialis anterior (TA), TAB5: Fold change in cardiolipin species abundance in liver. PI = product ion.

Supplementary Dataset 3: Bulk RNA-seq

TAB1: Base Mean and Differential Fold change RNA abundance and significance (pvalue and padj) in Tibialis anterior muscle (muscle). TAB2: Top 20 upregulated KEGG pathways from muscle differential expression analysis, TAB3: Top 20 downregulated KEGG pathways from muscle differential expression analysis, TAB4: Raw data outputs for principle component analysis

Supplementary Dataset 4: Metabolomics

Metabolomics abundance from Gastrocnemius muscles from Control (Con) and PolG Mutant (Mut) mice at varying times of study (16 weeks and 50 weeks). PBQC = quality control sample, ISTD = internal standard control.

Supplementary Dataset 5: One-carbon Metabolomics (Folate-omics)

Folate-omics abundance from Gastrocnemius muscles from Control (Con) and PolG Mutant (Mut) mice at varying times of study (Short term and Long term). TAB1: Concentration (pmol per mg muscle tissue) of the four folate metabolites in Gastrocnemius tissue in short and long term studies, TAB2: Abundance of the four metabolites measured in short term cohorts sorted by genotype, TAB3: Abundance of the four metabolites measured in long term cohorts sorted by genotype