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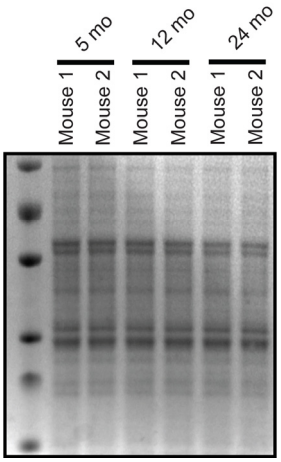
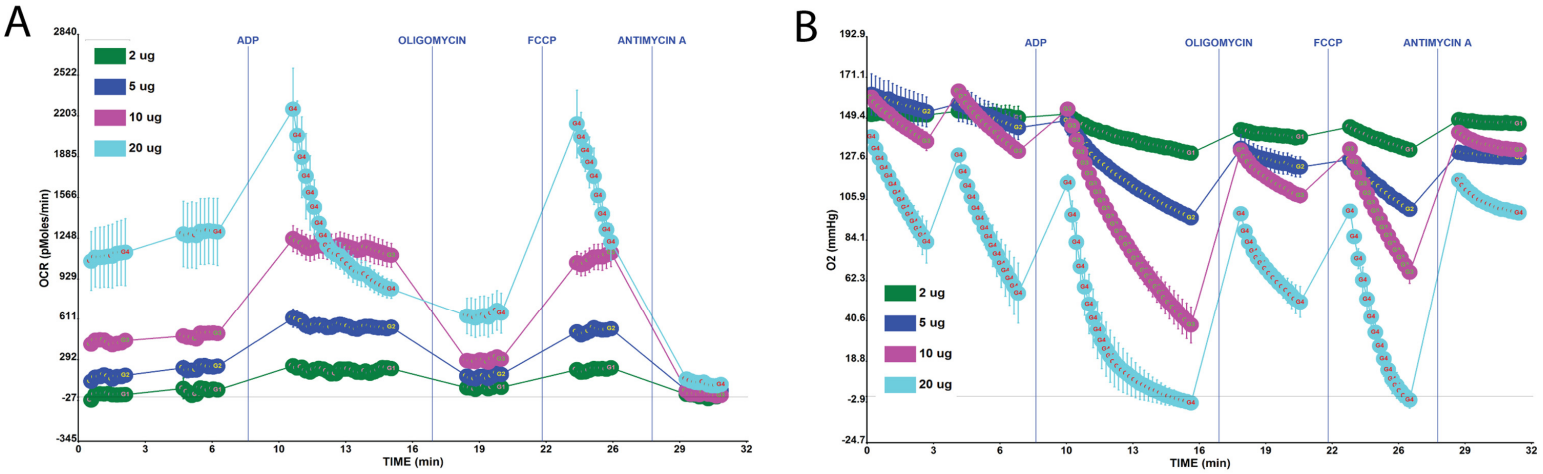
SUPPLEMENTAL DATA

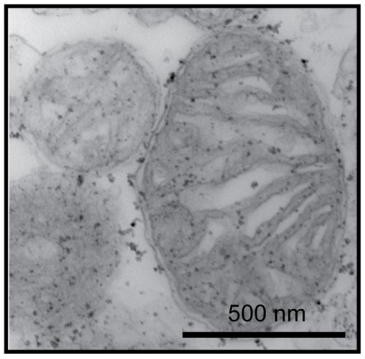
Please browse full text version to see the Supplemental Tables of this manuscript. Supplementary File 1. Complete list of the 898 common identified and quantified proteins. Supplementary File 2. Complete MitoMiner annotation output.



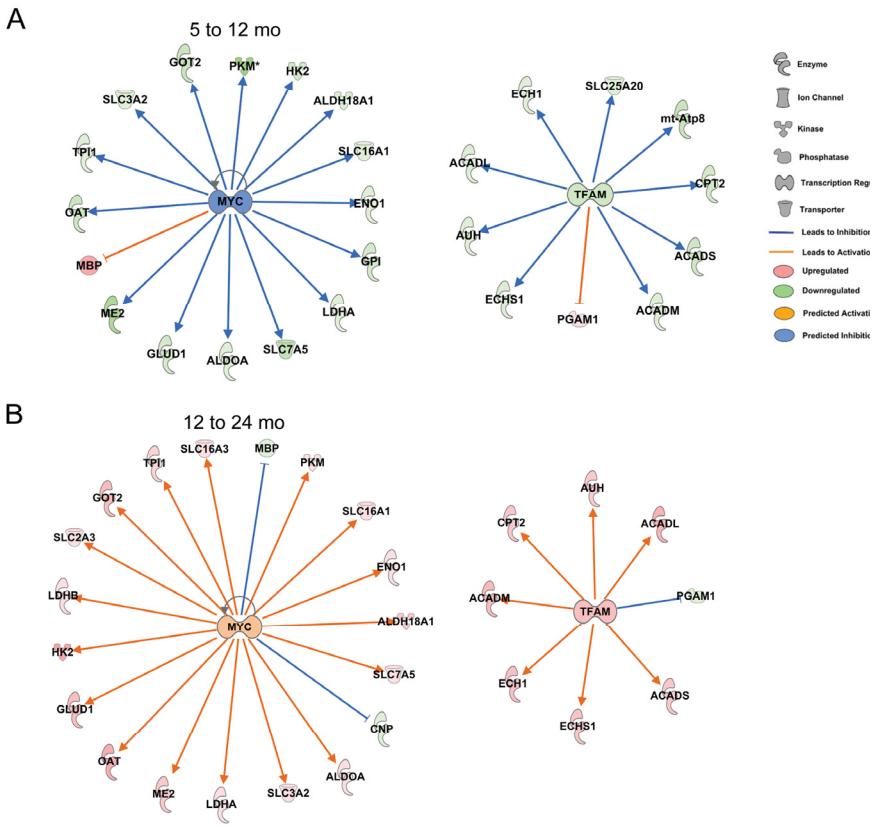
Supplemental Figure 1. Confirmation of equal loading for immunoblots. Coomassie staining of 10 µg total protein for each synaptic mitochondrial sample loaded for electrophoresis.



Supplemental Figure 2. Optimization of Seahorse XF24 with isolated mouse synaptic mitochondria. (**A**) OCR is shown for coupling assay with 2, 5, 10 and 20 µg of synaptic mitochondria. ADP, FCCP, oligomycin, and antimycin A were added as described in the Materials and Methods. (**B**) Absolute levels of O_2 in the wells are shown from the same assay in (**A**).



Supplemental Figure 3. Electron microscopy of the pure isolated synaptic mitochondria. Electron dense spots indicate the TOM22 magnetic beads, which remain after the immunomagnetic affinity purification step. Magnification shown is 52,000x.



Supplemental Figure 4. Proteomics predicts changes in a PGC1A-independent mitochondrial transcriptional regulatory pathway with aging. IPA generated MYC and TFAM upstream regulator networks overlaid with our proteomic expression data for synaptic mitochondria from (**A**) 5 to 12 month and (**B**) 12 to 24 month old mice. MYC and TFAM activity was predicted based on proteomic expression data. All proteins shown (except MYC) were found in the proteomic analysis.