Supplementary Fig. 5.

a, Gene set enrichment analysis of Wikipathways in the soleus muscle of Hectd1 mKO mice, numbering to the right indicates rank of the pathway when sorted by P-value. **b**, Gene set enrichment analysis of Reactome pathways in the soleus muscle of Hectd1 mKO mice, numbering to the right indicates rank of the pathway when sorted by P-value. **c**, Jaccard similarity of differential expression of the Hectd1 mKO soleus muscle RNA-seq to myopathy and atrophy datasets from Fig. 1d. **d**, Venn diagram and GO-MF overrepresentation pathway analysis for differentially expressed genes and proteins that are either common to RNA-seq and MS or uniquely appearing only in MS analysis. **e**, Heatmap showing changes in expression of mitochondrially encoded genes in RNA-seq of Hectd1 mKO mice. **f**, Heatmap showing changes in expression of genes regulating mitochondrial transcription and RNA processing in RNA-seq of Hectd1 mKO mice. **g,h**, Quantification of changes in mitochondrial genome in Hectd1 mKO mice assessed by RT-qPCR of selected mitochondrial genes normalized to genomic DNA. Linear Ct response to DNA concentration is shown in g (n = 7-8). All data are represented as mean±sd. Data in h were analyzed by Student's t-test. GSEA – gene set enrichment analysis, FDR – false discovery rate, MS – mass spectrometry, GO – Gene Ontology, MF – molecular function.