

SUPPLEMENTARY MATERIAL

SUPPLEMENTARY FIGURE LEGENDS

Supplemental Figure 1. *Atp6V0d1* expression changes during differentiation in 3T3-L1 cells, and adipogenesis is affected by *Atp6V0d1* inhibition. **A-D**, Fold change in expression of *Atp6V0d1*, *Pparg*, *Cebpa* and *Cebpb* genes during 3T3-L1 adipocyte differentiation. Gene expression is normalized by the geometric mean of the expression of β -actin, *Gapdh* and *36b4* (n = 3 per group). **E**, Representative western blot of ATP6V0D1 and PPAR- γ in 3T3-L1 adipocytes from Days 0–12 of differentiation (n = 3 per group). **F**, Representative image of lipid droplets stained by Oil Red O and fluorescent dye in 3T3-L1 adipocytes. **G**, Representative western blot of ATP6V0D1, PPAR- γ and CEBP α expression in 3T3-L1 adipocytes treated with shRNA targeting *Atp6v0d1* or control shRNA (n = 3 per group). **H-I**, Representative immunoblots and quantification of ATP6V0D1 protein levels in normal chow diet (NCD) and high fat diet (HFD) mice. A-D and I were analyzed by two-tailed unpaired Student's *t*-test. Data represent the mean \pm SEM.

Supplemental Figure 2. Loss of adipose *Atp6v0d1* induces hepatosteatosis and lipodystrophy. **A**, Construction strategy for adipocyte-specific *Atp6v0d1* knockout mice (*Atp6v0d1*^{AKO}). **B**, Representative gel electrophoresis image showing genomic excision of *Atp6v0d1* region in adipose tissues of *Atp6v0d1*^{AKO}. **C**, Representative western blot of ATP6V0D1 in adipose tissues of control and *Atp6v0d1*^{AKO}. **D**, Representative images of control and *Atp6v0d1*^{AKO} mice. **E**, Representative images of liver, inguinal WAT (iWAT), epidermal white adipose tissue (eWAT), retroperitoneal WAT (rWAT), and brown adipose tissue (BAT). **F**, H&E staining of liver and adipose tissue sections. **G**, Plasma leptin. **H**, Plasma adiponectin. **I**, Liver weight. **J**, Hepatic cholesterol. **K**, Hepatic triglyceride. **L**, Hepatic non-esterified fatty acids. **M**, AST to ALT ratio.

Supplemental Figure 3. *Atp6v0d1*^{AKO} mice aged 36 weeks exhibit fatty liver,

lipodystrophy and insulin resistance. A, Plasma cholesterol. **B,** Plasma triglycerides. **C,** Plasma non-esterified fatty acids. **D,** Intraperitoneal glucose tolerance test (IPGTT). **E,** Insulin tolerance test (ITT). **F,** Liver weight.

Supplemental Figure 4. A, Heart rate data of control and *Atp6v0d1*^{AKO} mice in cardiac function examination by echocardiography in 8, 12, 16, 20, 24, 28 and 36 weeks. **B,** EF% and FS% of control and *Atp6v0d1*^{AKO} mice aged 8, 12, 16, 20, 24, 28 and 36 weeks. **C,** qPCR quantification of the mRNA levels of *Nppa*, *Nppb*, *Myh6* and *Myh7* from control and *Atp6v0d1*^{AKO} heart tissues. Data represent the mean ± SEM (n = 4 - 5 per group; two-tailed unpaired Student's t-test)

Supplemental Figure 5. A, Representative images of adult mice cardiomyocytes isolated from WT and *Atp6v0d1*^{AKO} hearts. **B,** Representative immunoblots of individual respiratory chain complexes.

Supplemental Figure 6. A, Differentially expressed genes analyzed by volcano plots between control and *Atp6v0d1*^{AKO} mice hearts. **B,** The top 10 (a ranking by P-value) significantly enriched GO terms in biological process group (BP), cellular component group (CC) and molecular function group (MF). **C,** The 15 most relevant Reactome pathways (<https://reactome.org>) according to the upregulated and downregulated subgroups of DEGs.

Supplemental Figure 7. Rosiglitazone ameliorates cardiomyopathy in *Atp6v0d1*^{AKO} mice. A, Schematic illustration of Rosiglitazone treatment (50 µg per 10 g mouse weight), delivered via intragastric gavage to control and *Atp6v0d1*^{AKO} mice. **B,** Echo measurement of left ventricular ejection fraction (EF%) and fractional shortening (FS%) of control and *Atp6v0d1*^{AKO} mice with or without Rosiglitazone treatment. **C,** Representative images of hearts from control and *Atp6v0d1*^{AKO} mice with or without Rosiglitazone treatment. **D-E,** Heart weight (HW)

to tibia ratio and lung weight to tibia ratio of control and *Atp6v0d1*^{AKO} mice with or without Rosiglitazone treatment. **F-H**, Representative immunoblots and quantification of IRS1 and IRS2 protein levels. Data are normalized to GAPDH. **I**, Representative immunoblots of FOXO1, AMPK, p-AMPK and PPAR γ protein levels for each group. **J-L**, Quantification of specified densitometric ratios. **M**, Representative immunoblots of CD36, PDH and p-PDH protein levels. **N-O**, Quantification of specified densitometric ratios (n = 4–6 per group). Data represent the mean \pm SEM (one-way ANOVA).

Supplemental Figure 8. A, Echocardiographic evaluation of systolic function of control and *Atp6v0d1*^{AKO} mice after tail vein injection of AAV9-cTnt-myocardin or AAV9-vectors. n = 4-6 mice per group. Data are presented as mean \pm SEM. **B**, The myocardin protein expression in mice cardiomyocyte by immunostaining, cardiomyocyte size and fibrosis in *Atp6v0d1*^{AKO} mice after tail vein injection of AAV9-cTnt-myocardin or AAV9-vectors. Left: Immuno-fluorescence imaging of myocardin. Middle: Representative images of WGA stain. Right: Representative transverse sections with Masson trichrome staining. **C-D**, Representative immunoblots and quantification of IRS1 protein levels in NCD and HFD mice. Data represent the mean \pm SEM (n = 4 per group; two-tailed unpaired Student's t-test). **E-F**, Representative immunoblots and quantification of IRS2 protein levels in NCD and HFD mice. Data represent the mean \pm SEM (n = 3 per group; two-tailed unpaired Student's t-test).

Supplemental Figure 9. Representative immunoblots and quantification of ANP protein levels in rat neonatal cardiomyocytes infected with myocardin siRNA (si-myocardin) or scrambled siRNA (si-Scramble) as a control. Data represent the mean \pm SEM (n = 7 per group; two-tailed unpaired Student's t-test)

Supplementary Table 1. Antibodies used in the study

| Target | Species originated | Dilution | Brand | Catalog number |
|------------------|--------------------|----------|-------------|----------------|
| ATP6V0d1 | Rabbit | 1:2000 | Abcam | ab202897 |
| PPAR γ | Rabbit | 1:1000 | CST | #2435 |
| CEBP α | Rabbit | 1:500 | Proteintech | 18311-1-AP |
| FASN | Rabbit | 1:500 | Proteintech | 10624-2-AP |
| β -tubulin | Mouse | 1:5000 | Proteintech | 66240-1-Ig |
| β -actin | Mouse | 1:5000 | Proteintech | 60008-1-Ig |
| ANP | Rabbit | 1:1000 | Abclonal | A1609 |
| α MHC | Rabbit | 1:1000 | ABclonal | A12964 |
| β MHC | Rabbit | 1:1000 | Santa cruz | Sc-168678 |
| CD36 | Rabbit | 1:1000 | Abcam | ab133625 |
| Glut1 | Rabbit | 1:1000 | Proteintech | 21829-1-AP |
| Glut4 | Mouse | 1:1000 | Proteintech | 66846-1-Ig |
| PDH | Rabbit | 1:1000 | Proteintech | 18068-1-AP |
| p-PDH | Rabbit | 1:1000 | Absin | Abs140331 |
| IRS1 | Rabbit | 1:1000 | CST | #2390 |
| IRS2 | Rabbit | 1:1000 | CST | #3089 |
| FoxO1 | Rabbit | 1:1000 | CST | #2880 |
| PPAR α | Rabbit | 1:1000 | Abcam | ab215270 |
| PPAR δ | Rabbit | 1:1000 | Abcam | ab178866 |
| Pgc1 α | Rabbit | 1:1000 | Abcam | ab191838 |
| AMPK | Rabbit | 1:1000 | CST | #5831 |
| p-AMPK | Rabbit | 1:1000 | CST | #2535 |
| PI3K | Rabbit | 1:1000 | CST | #4257 |
| p-PI3K | Rabbit | 1:1000 | CST | #4228 |
| AKT | Rabbit | 1:1000 | CST | #9272 |
| p-AKT-S473 | Rabbit | 1:1000 | CST | #9271 |

| | | | | |
|------------|--------|--------------|---------------|------------|
| p-AKT-T308 | Rabbit | 1:5000 | CST | #9275 |
| MYOCD | Rabbit | 1:1000 | sigma-aldrich | SAB4200539 |
| SRF | Rabbit | 1:100 (ChIP) | CST | #5147 |
| GAPDH | Rabbit | 1:5000 | CST | #2118 |

Supplementary Table 2. Primers used in the study

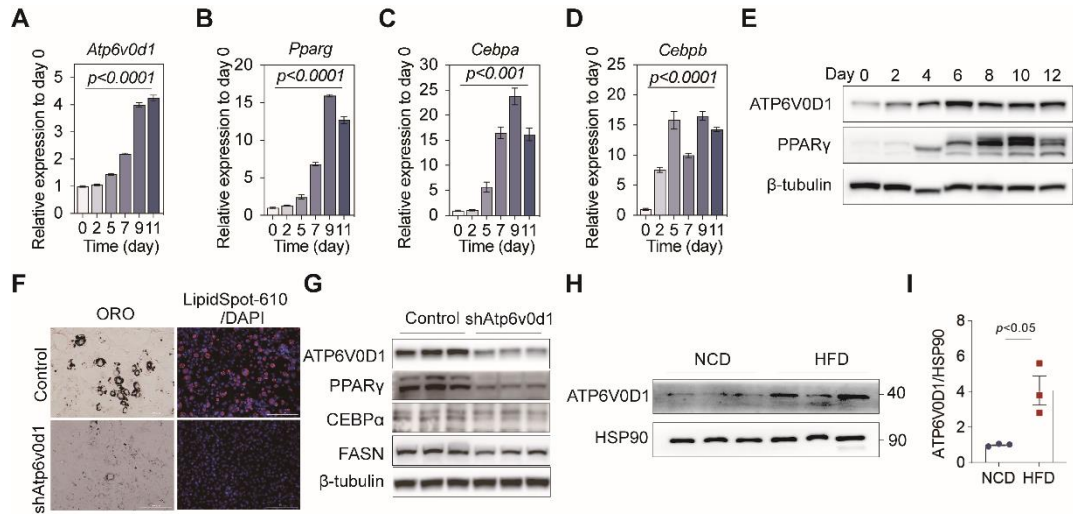
| Gene | | |
|------------|---------|---------------------------------|
| Atp6v0d1-m | Forward | 5'-CAATGCCATTCTGGTGGAC-3' |
| | Reverse | 5'-TTTCGGATTATCTCGATGTTCA-3' |
| Pparg-m | Forward | 5'-GAAAGACAACGGACAAATCACC-3' |
| | Reverse | 5'-GGGGGTGATATGTTTGAACCTTG-3' |
| Cebpa-m | Forward | 5'-CAAGAACAGCAACGAGTACCG-3' |
| | Reverse | 5'-GTCACTGGTCAACTCCAGCAC-3' |
| Cebpb-m | Forward | 5'-CTGCGGGGTTGTTGATGT-3' |
| | Reverse | 5'-ATGCTCGAAACGGAAAAGGT-3' |
| Fasn-m | Forward | 5'-TGGGTCTAGCCAGCAGAGT-3' |
| | Reverse | 5'-ACCACCAGAGACCGTTATGC-3' |
| Scd1-m | Forward | 5'-GCGATACTCTGGTGCTCA-3' |
| | Reverse | 5'-CCCAGGGAAACCAGGATATT-3' |
| Dgat1-m | Forward | 5'-TTCCGCCTCTGGGCATT-3' |
| | Reverse | 5'-AGAATCGGCCCAATCCA-3' |
| Dgat2-m | Forward | 5'-GGCGCTACTTCCGAGACTAC-3' |
| | Reverse | 5'-TGGTCAGCAGGTTGTGTGTC-3' |
| Fabp4-m | Forward | 5'-GGATGGAAAGTCGACCACAA-3' |
| | Reverse | 5'-TGGAAGTCACGCCTTTCATA-3' |
| Fatp1-m | Forward | 5'-AGGTCAATGAGGACACGATGGAG-3' |
| | Reverse | 5'-CTGGTACATTGAGTTAGGGTCCAAC-3' |
| Lipe-m | Forward | 5'-GCGCTGGAGGAGTGTTTTT-3' |
| | Reverse | 5'-CGCTCTCCAGTTGAACCAAG-3' |
| Lpl-m | Forward | 5'-GGGAGTTTGGCTCCAGAGTTT-3' |
| | Reverse | 5'-TGTGTCTTCAGGGGTCCTTAG-3' |
| Plin1-m | Forward | 5'-AACGTGGTAGACACTGTGGTACA-3' |
| | Reverse | 5'-TCTCGGAATTCGCTCTCG-3' |
| Plin2-m | Forward | 5'-GACCTTGTGTCCTCCGCTTAT-3' |

| | | |
|------------------|---------|-------------------------------|
| | Reverse | 5'-CAACCGCAATTTGTGGCTC-3' |
| Plin3-m | Forward | 5'-GGAGGAACCTGTTGTGCAG-3' |
| | Reverse | 5'-ACCATCCCATACGTGGAAC-3' |
| Adpoq-m | Forward | 5'-GGAGAGAAAGGAGATGCAGGT-3' |
| | Reverse | 5'-CTTTCCTGCCAGGGGTTC-3' |
| Pepck-m | Forward | 5'-ATGTGTGGGCGATGACATT-3' |
| | Reverse | 5'-AACCCGTTTTCTGGGTTGAT-3' |
| 36b4-m | Forward | 5'-ACTGGTCTAGGACCCGAGAAG-3' |
| | Reverse | 5'-CTCCCACCTTGTCTCCAGTC-3' |
| β -actin-m | Forward | 5'-CTAAGGCCAACCGTGAAAAG-3' |
| | Reverse | 5'-ACCAGAGGCATACAGGGACA-3' |
| Gapdh-m | Forward | 5'-AGCTTGTCATCAACGGGAAG-3' |
| | Reverse | 5'-TTTGATGTTAGTGGGGTCTCG-3' |
| Myh6-m | Forward | 5'-GCCCAGTACCTCCGAAAGTC-3' |
| | Reverse | 5'-GCCTTAACATACTCCTCCTTGTC-3' |
| Myh7-m | Forward | 5'-CGTGCCAATGACGACC-3' |
| | Reverse | 5'-CACTGCCTCCTCTACTTCTG-3' |
| Nppa-m | Forward | 5'-GCTTCCAGGCCATATTGGAG-3' |
| | Reverse | 5'-GGGGGCATGACCTCATCTT-3' |
| Nppb-m | Forward | 5'-GAGGTCACCTATCCTCTGG-3' |
| | Reverse | 5'-GCCATTCCTCCGACTTTTCTC-3' |
| Cd36-m | Forward | 5'-ACAGACGCAGCCTCCT-3' |
| | Reverse | 5'-GATTCAGATCCGAACA-3' |
| Acadl-m | Forward | 5'-TTTCCTCGGAGCATGACATTTT-3' |
| | Reverse | 5'-GCCAGCTTTTTCCAGACCT-3' |
| Acadm-m | Forward | 5'-TGATGTGGCGGCCATTAAGA-3' |
| | Reverse | 5'-GGGTTAGAACGTGCCAACAAGAA-3' |
| Acads-m | Forward | 5'-AAGTTTGGATCCGCACAGCAG-3' |
| | Reverse | 5'-CAAGCTTTGGTGCCGTTGAG-3' |

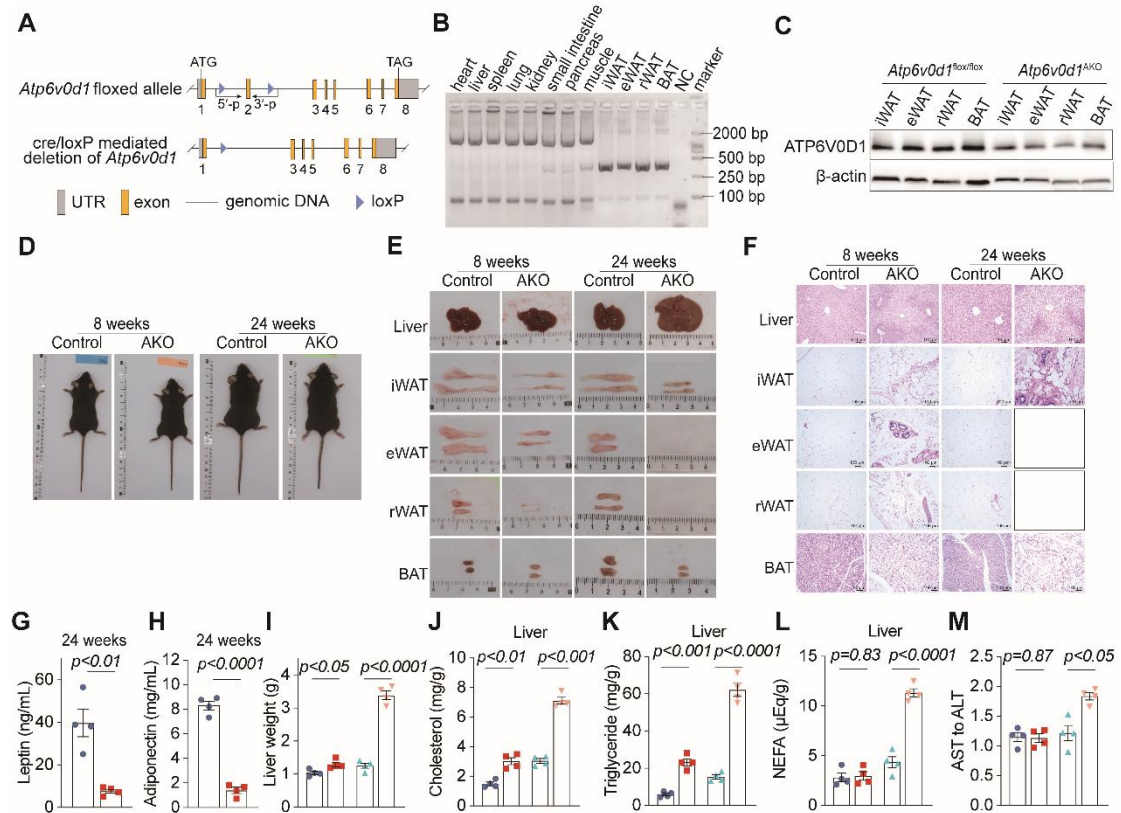
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|---------|---------|-------------------------------|
| Cpt1a-m | Forward | 5'-CTCCGCCTGAGCCATGAAG-3' |
| | Reverse | 5'-CACCAGTGATGATGCCATTCT-3' |
| Cpt1b-m | Forward | 5'-GTCGCTTCTTCAAGGTCTGG-3' |
| | Reverse | 5'-AAGAAAGCAGCACGTTTCGAT-3' |
| Cpt1c-m | Forward | 5'-GATTTTCTGTACGTCACCCCC-3' |
| | Reverse | 5'-AGGTGGTCTTTTTCCACCCC-3' |
| Fasn-m | Forward | 5'-GGAGGTGGTGATAGCCGGTAT-3' |
| | Reverse | 5'-TGGGTAATCCATAGAGCCCAG-3' |
| Acsl1-m | Forward | 5'-TGCCAGAGCTGATTGACATTC-3' |
| | Reverse | 5'-GGCATAACCAGAAGGTGGTGAG-3' |
| Acsl3-m | Forward | 5'-AACCACGTATCTTCAACACCATC-3' |
| | Reverse | 5'-AGTCCGGTTTGGAAGTACAG-3' |
| Acsl5-m | Forward | 5'-TCCTGACGTTTGGAACGGC-3' |
| | Reverse | 5'-CTCCCTCAATCCCCACAGAC-3' |
| Fabp3-m | Forward | 5'-ACCTGGAAGCTAGTGGACAG-3' |
| | Reverse | 5'-TGATGGTAGTAGGCTTGGTCAT-3' |
| Pk-m | Forward | 5'-GTTCTCACGGAGTCTGGC-3' |
| | Reverse | 5'-GAGTCACGGCAATGATAGG-3' |
| Pfk-m | Forward | 5'-CTGTGGTCCGAGTTGGTAT-3' |
| | Reverse | 5'-ACGTGGCCTCCCTGAT-3' |
| Hk1-m | Forward | 5'-GGCAGATTGAGGAAACCC-3' |
| | Reverse | 5'-GGATGCTCCGAACATAAGAA-3' |
| Hk2-m | Forward | 5'-ATCGCCTGCTTATTCACG-3' |
| | Reverse | 5'-CCATTGTCTGTCACCCTTACT-3' |
| Pdk1-m | Forward | 5'-GATGGCTATGAGAACGC-3' |
| | Reverse | 5'-GTATTGTCTGTCCTGGTGAT-3' |
| Pdk2-m | Forward | 5'-CTCCATCCGAATGCTAATC-3' |
| | Reverse | 5'-TGGGAAGGGACATAGACC-3' |
| Pdk3-m | Forward | 5'-CTCAACTGCTCCTCGTCC-3' |

| | | |
|--------------------|---------|------------------------------|
| | Reverse | 5'-GGCAAGCCATAACCAAAT-3' |
| Pdk4-m | Forward | 5'-TGTGGTCCCTACAATGGC-3' |
| | Reverse | 5'-AATGTGGCTTGGGTTTCC-3' |
| Cs-m | Forward | 5'-AATCAGGAGGTGCTTGTCT-3' |
| | Reverse | 5'-AGGAATAGCGAGGGTCAG-3' |
| Slc2a1-m | Forward | 5'-CGTCGTTGGCATCCTTA-3' |
| | Reverse | 5'-CCTTCTTCTCCCGCATC-3' |
| Slc2a4-m | Forward | 5'-GCCTGCCCGAAAGAGT-3' |
| | Reverse | 5'-TGAAGACCGTATTGACCACA-3' |
| Myocd-m | Forward | 5'-ACACTCCTGGGGTCTGAACA-3' |
| | Reverse | 5'-GCGGTATTAAGCCTTGGTTAGC-3' |
| FoxO1-m | Forward | 5'-TCAAGGATAAAGGGCGACAGC-3' |
| | Reverse | 5'-CCTCCCTCTGGATTGAGCATC-3' |
| Irs1-m | Forward | 5'-CGATGGCTTCTCAGACGTG-3' |
| | Reverse | 5'-CAGCCCGCTTGTTGATGTTG-3' |
| Irs2-m | Forward | 5'-CTGCGTCCTCTCCCAAAGTG-3' |
| | Reverse | 5'-GGGGTCATGGGCATGTAGC-3' |
| Myocd-r | Forward | 5'-GATAGTAAGAACCGCCACAA-3' |
| | Reverse | 5'-TGAAGCAGCCGAGCAT-3' |
| Irs1-r | Forward | 5'-CCTGGAGTATTATGAGAACGAG-3' |
| | Reverse | 5'-CCGCAATGGCAAAGTGT-3' |
| Irs2-r | Forward | 5'-CCCCTGTGGGTCGGATTT-3' |
| | Reverse | 5'-TGAGTGATGAGGCTGGGTATG-3' |
| FoxO1-r | Forward | 5'-GGATAAGGGCGACAGCAACA-3' |
| | Reverse | 5'-TCTTGCCTCCCTCTGGATTG-3' |
| ChIP CArG region-r | Forward | 5'-TTTTGATGGCAAGACGACTT-3' |
| | Reverse | 5'-TTCTGTTCCCTAAGACACCTAT-3' |
| ChIP Ctrl1-r | Forward | 5'-TAGCACCAACAGGACCCA-3' |
| | Reverse | 5'-GCATCGTGAAGAAGGCATA-3' |

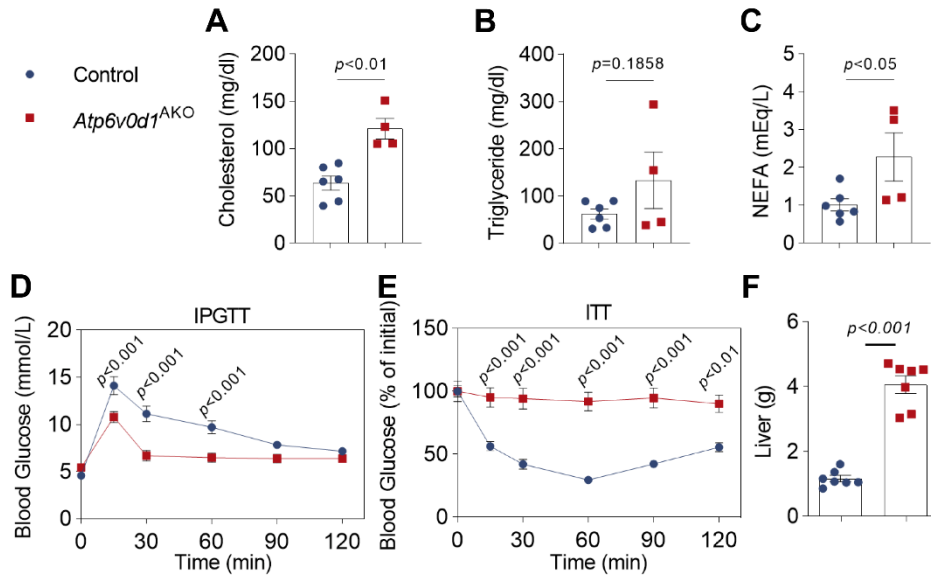
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| ChIP Ctrl2-r | Forward | 5'-AGCAACCGCAAAGGAAA-3' |
| | Reverse | 5'-AGCAACTACCACTGGGAGAC-3' |



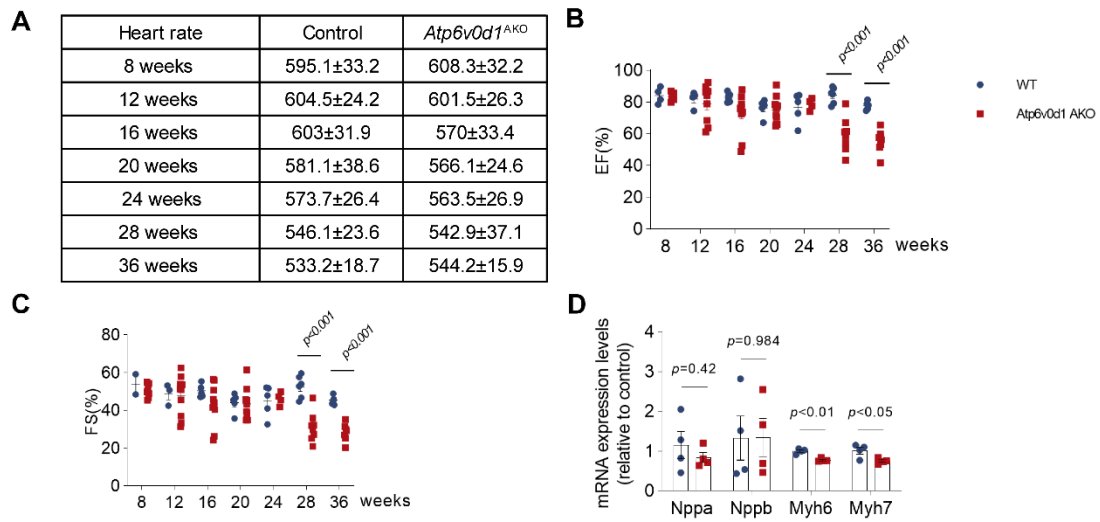
Supplementary Figure 1



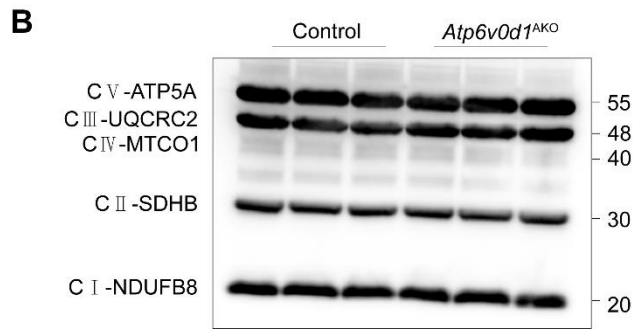
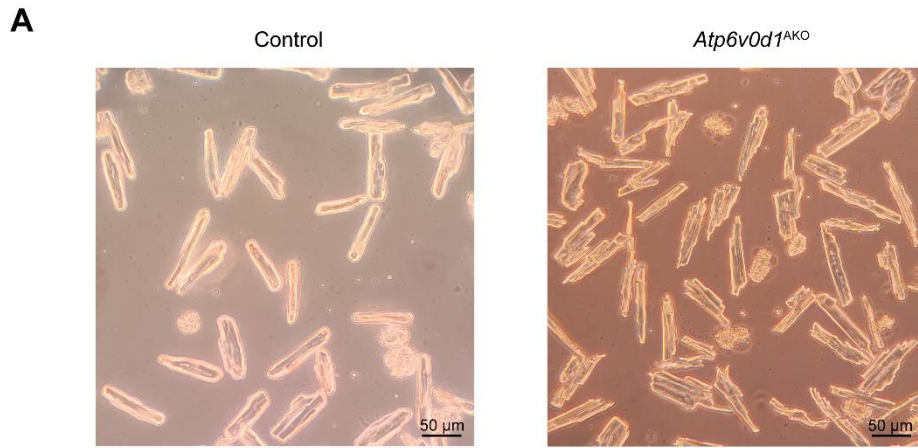
Supplementary Figure 2



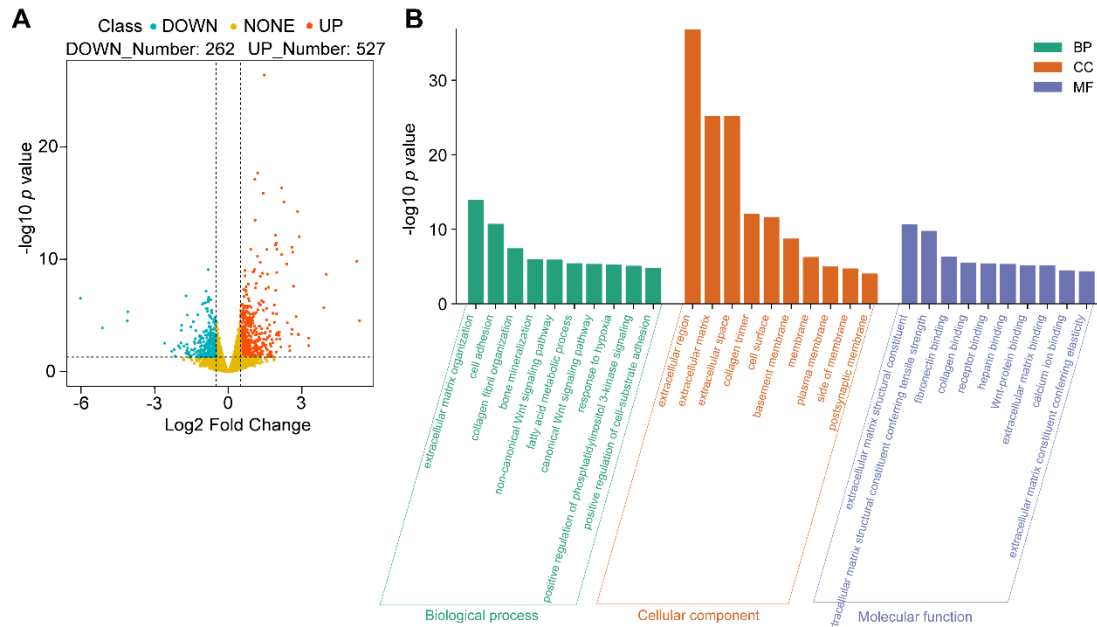
Supplementary Figure 3



Supplementary Figure 4

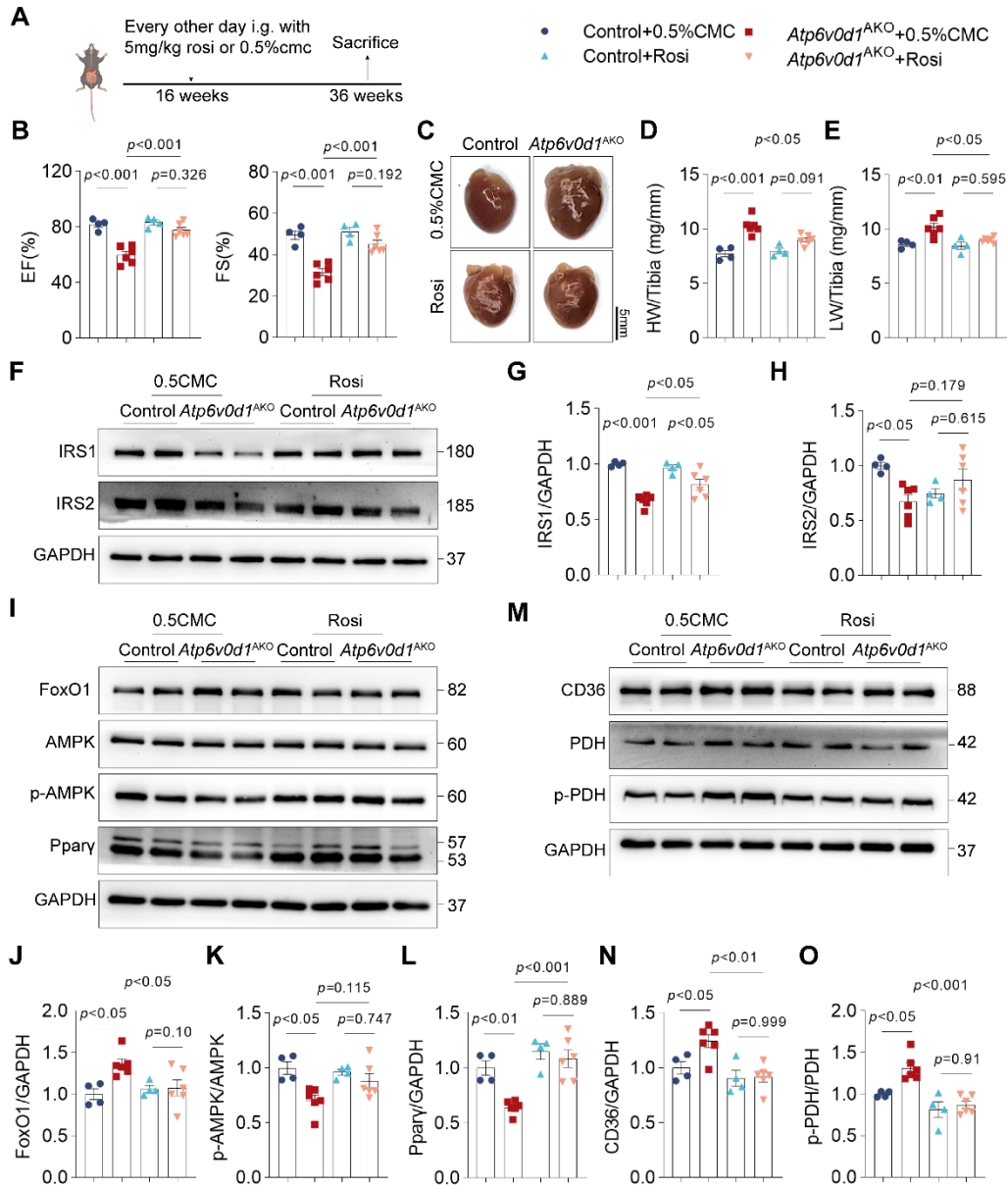


Supplementary Figure 5



| Term | Input Number | Background Number | P-Value | Corrected P-Value |
|--|--------------|-------------------|----------|-------------------|
| Upregulated Genes | | | | |
| Extracellular matrix organization | 39 | 263 | 2.81E-26 | 1.55E-23 |
| Metabolism | 71 | 1609 | 2.63E-17 | 7.27E-15 |
| Degradation of the extracellular matrix | 20 | 128 | 1.74E-14 | 3.22E-12 |
| Collagen formation | 16 | 78 | 1.85E-13 | 2.57E-11 |
| Collagen degradation | 14 | 55 | 4.78E-13 | 5.30E-11 |
| Integrin cell surface interactions | 15 | 70 | 6.09E-13 | 5.63E-11 |
| Assembly of collagen fibrils and other multimeric structures | 13 | 54 | 6.01E-12 | 4.76E-10 |
| Collagen biosynthesis and modifying enzymes | 13 | 57 | 1.08E-11 | 7.50E-10 |
| Collagen chain trimerization | 11 | 38 | 4.78E-11 | 2.94E-09 |
| Metabolism of lipids | 30 | 585 | 2.39E-09 | 1.32E-07 |
| Fatty acid metabolism | 16 | 167 | 5.14E-09 | 2.53E-07 |
| Signal Transduction | 68 | 2305 | 5.47E-09 | 2.53E-07 |
| ECM proteoglycans | 9 | 43 | 3.22E-08 | 1.37E-06 |
| Hemostasis | 25 | 497 | 7.38E-08 | 2.92E-06 |
| Molecules associated with elastic fibres | 8 | 35 | 1.05E-07 | 3.87E-06 |
| Downregulated Genes | | | | |
| Metabolism | 27 | 1609 | 1.98E-05 | 6.75E-03 |
| Attenuation phase | 3 | 13 | 1.60E-04 | 2.72E-02 |
| Receptor-type tyrosine-protein phosphatases | 3 | 18 | 3.71E-04 | 3.27E-02 |
| Neuronal System | 9 | 314 | 3.85E-04 | 3.27E-02 |
| HSF1-dependent transactivation | 3 | 22 | 6.29E-04 | 4.28E-02 |
| Interleukin-7 signaling | 3 | 26 | 9.80E-04 | 4.85E-02 |
| Regulation of HSF1-mediated heat shock response | 4 | 61 | 9.99E-04 | 4.85E-02 |
| IRS activation | 2 | 6 | 1.24E-03 | 4.98E-02 |
| Protein-protein interactions at synapses | 4 | 66 | 1.32E-03 | 4.98E-02 |
| Cytokine Signaling in Immune system | 10 | 477 | 1.91E-03 | 6.06E-02 |
| PI3K/AKT activation | 2 | 9 | 2.40E-03 | 6.06E-02 |
| Cellular response to heat stress | 4 | 79 | 2.47E-03 | 6.06E-02 |
| Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding | 3 | 37 | 2.51E-03 | 6.06E-02 |
| Protein folding | 3 | 38 | 2.69E-03 | 6.06E-02 |
| Chaperonin-mediated protein folding | 3 | 38 | 2.69E-03 | 6.06E-02 |

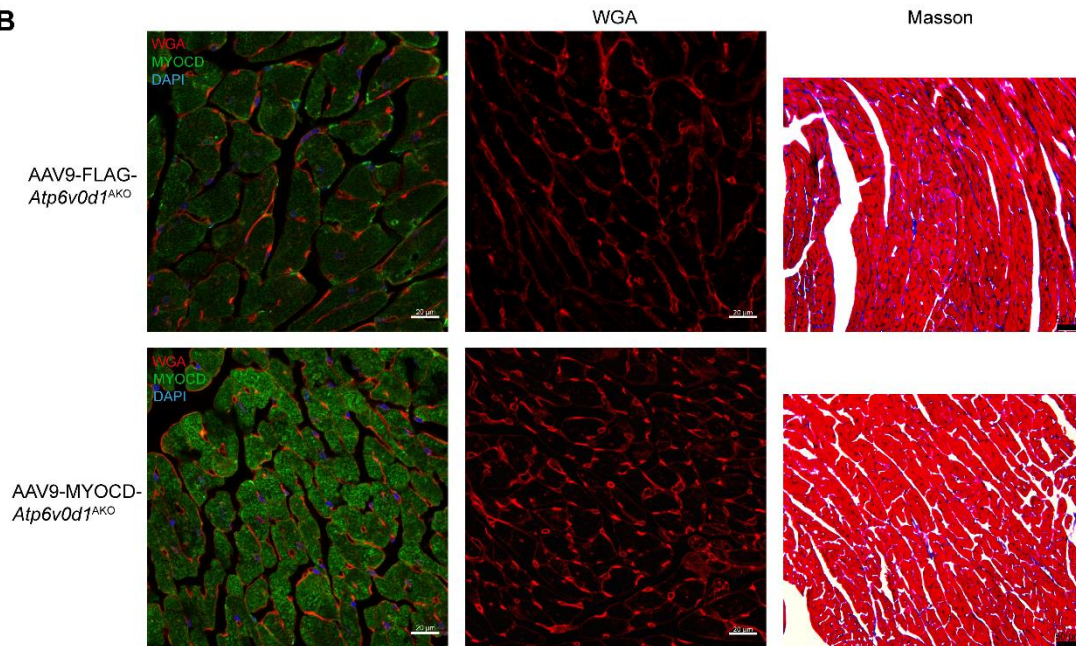
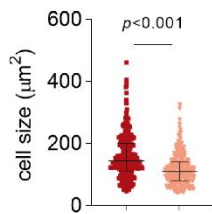
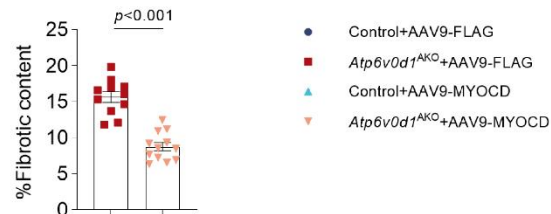
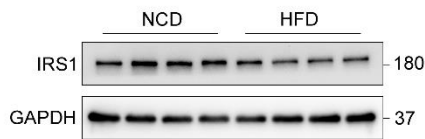
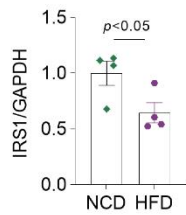
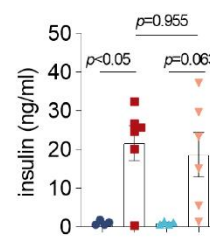
Supplementary Figure 6

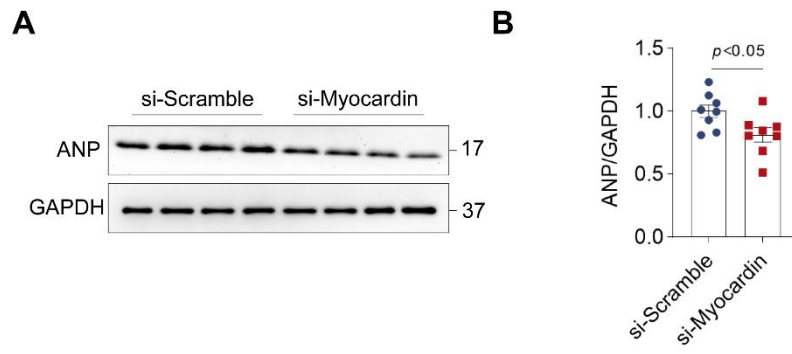


Supplementary Figure 7

A

| | AAV9-FLAG | | AAV9-MYOCD | |
|---------------------|------------|--------------------------------|------------|--------------------------------|
| | Control | <i>Atp6v0d1</i> ^{AKO} | Control | <i>Atp6v0d1</i> ^{AKO} |
| LVAW;d | 1.2±0.1 | 1.3±0.1 | 1.2±0.2 | 1.3±0.3 |
| LVAW;s | 1.9±0 | 1.8±0.2 | 1.9±0.1 | 1.8±0.3 |
| LVID;d | 3.3±0.2 | 4.1±0.5 | 3.4±0.5 | 3.4±0.3 |
| LVID;s | 1.6±0.2 | 2.8±0.4 | 1.8±0.4 | 1.8±0.2 |
| LVPW;d | 1±0.1 | 1±0.2 | 1±0.2 | 1±0.1 |
| LVPW;s | 1.6±0.1 | 1.4±0.2 | 1.7±0.1 | 1.7±0.1 |
| EF | 83±3 | 62.4±2.6 | 80.9±3.7 | 79.3±3.6 |
| FS | 50.8±3.3 | 33.3±1.8 | 48.6±3.5 | 47±3.6 |
| LV Mass | 139.7±16.3 | 205.3±28.6 | 144.8±7.5 | 160.1±16.8 |
| LV Mass (Corrected) | 111.8±13 | 164.2±22.9 | 115.9±6 | 128.1±13.4 |
| LV Vol;d | 43.7±7.3 | 77.1±21 | 50.3±17.6 | 48.1±9.8 |
| LV Vol;s | 7.5±2 | 29.2±8.7 | 10.1±5.1 | 10.1±3.3 |
| Heart Rate | 608.5±15.8 | 557.7±26.2 | 580.2±23.8 | 612.5±19.9 |

B**C****D****E****F****G****Supplementary Figure 8**



Supplementary Figure 9