**Actin-microtubule cytoskeletal interplay mediated by MRTF-A/SRF signaling promotes dilated cardiomyopathy caused by *LMNA* mutations**

**Supplementary information**

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## SUPPLEMENTARY FIGURES

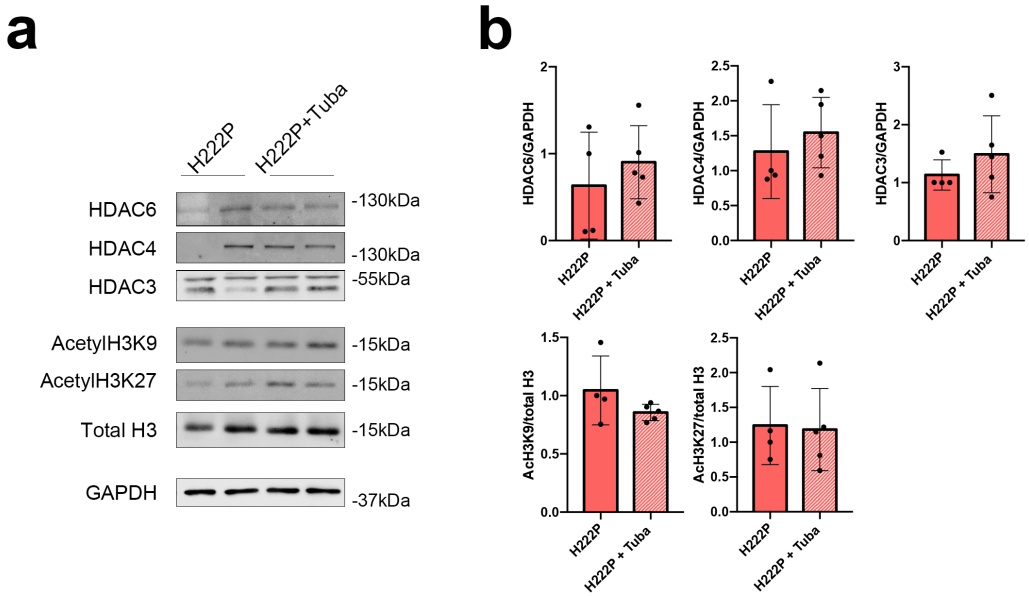


**Figure S1| Tubastatin A treatment has no effect on HDAC expression and acetylation of histone H3. (a)** Representative immunoblots showing expression of histone deacetylases: HDAC6, HDAC4, HDAC3, and acetylation levels of histone H3 (AcH3K9 and AcH3K27) in hearts from *Lmna*$^{p.H222P/H222P}$ mice (H222P) treated with tubastatin A (+Tuba) as compared with treated with DMSO. **(b)** Bar graph showing quantification of expression of HDAC6, HDAC4 and HDAC3 normalized to GAPDH and expression of acetylated H3K9 and H3K27 normalized to total H3 in hearts from *Lmna*$^{p.H222P/H222P}$ (H222P) mice treated with tubastatin A (+Tuba) (n=5) compared to mice treated with DMSO (n=4) (mean ± SD). Source data are provided as a Source Data file.

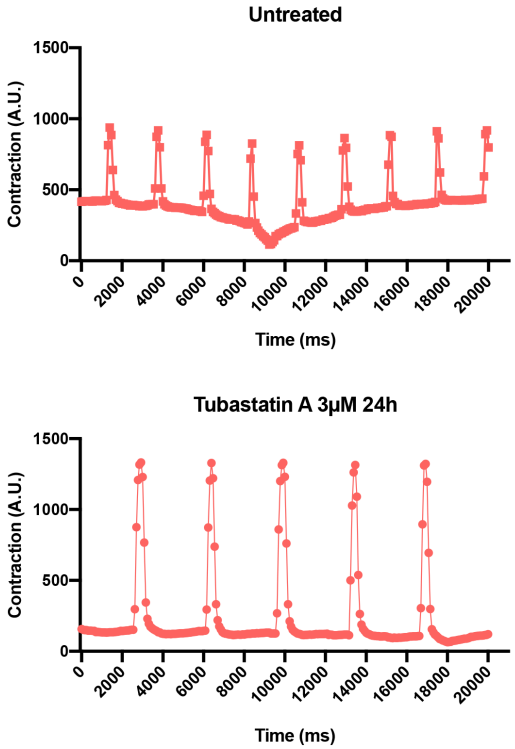


**Figure S2| Tubastatin A treatment ameliorates contraction profile of iPS-CM carrying *LMNA* p.H222P mutation.** Representative contraction profile obtained after analysis with MuscleMotion ImageJ macro of iPS-CM carrying *LMNA* p.H222P mutation, cultured in monolayer, matured for 40 days post differentiation and spontaneously beating, treated (lower panel) or not (upper panel) with tubastatin A 3µM for 24h.

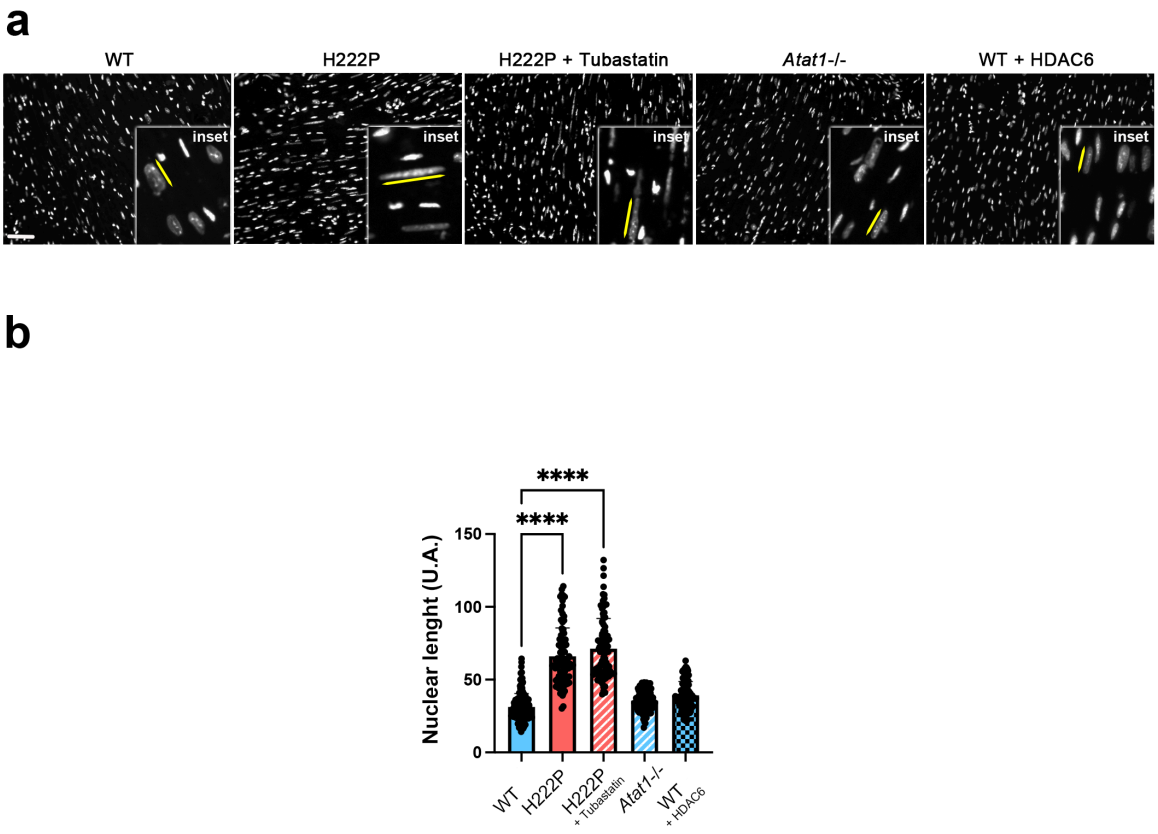


**Figure S3| α-Tubulin acetylation is not affecting nuclear shape. (a)** Representative micrographs showing the nucleus labeling (dapi staining) of heart sections from WT mice and *Lmna*$^{p.H222P/H222P}$ mice, *Lmna*$^{p.H222P/H222P}$ mice treated with tubastatin A, *Atat1*$^{-/-}$ mice and WT mice transduced with AAV-HDAC6. Scale bar: 50 μm. **(b)** Graph showing the quantification of cardiac nuclear length from cardiomyocytes from the different mouse models (n=170 WT, n=90 H222P, n=92 H222P + Tubastatin A, n=117 *Atat1*$^{-/-}$, n=131 WT+HDAC6 nuclei, mean ± SD), One-Way ANOVA followed by Tukey's multiple comparison test, ****p≤0.0001. Source data are provided as a Source Data file.

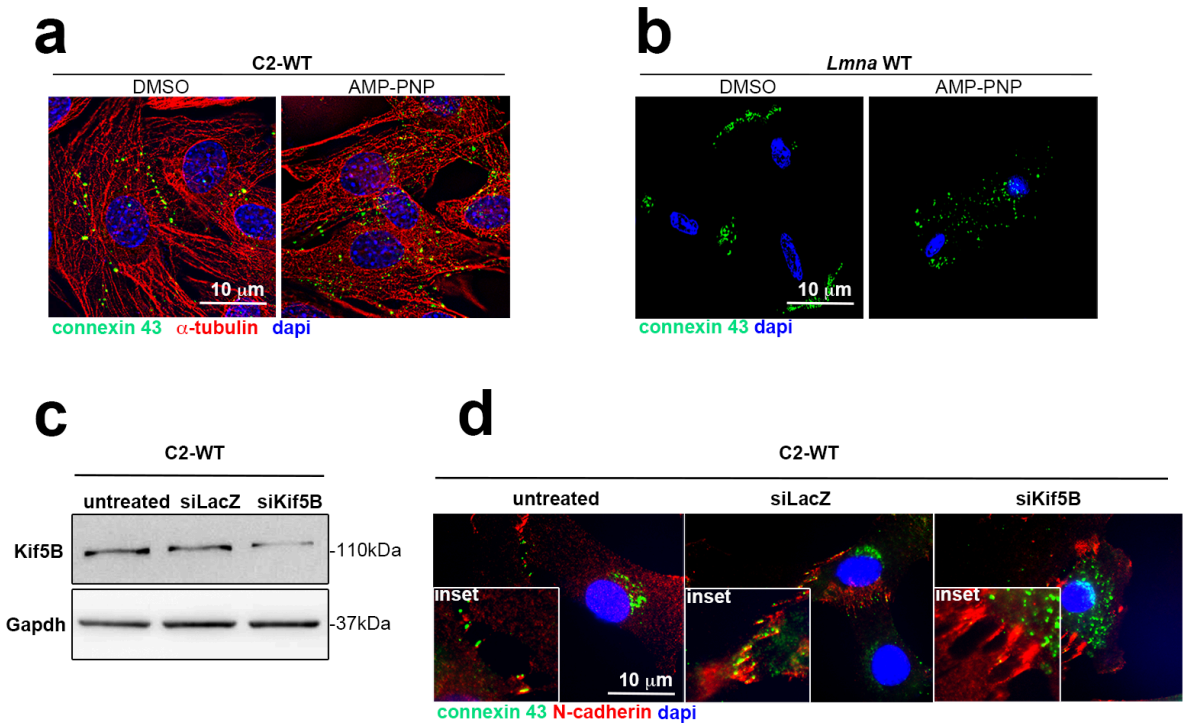


**Figure S4| Cx43 localization depends on kinesin motor proteins. (a)** Fluorescence micrographs showing Cx43 and α-actinin labeling of C2-WT cells. Nuclei counter-stained with dapi are also shown. **(b)** Fluorescence micrographs showing Cx43 labeling of isolated adult cardiomyocytes from WT mice. Nuclei counter-stained with dapi are also shown. **(c)** Immunoblot showing Kif5B expression from C2-WT cells treated or not with siRNA against Kif5B. **(d)** Fluorescence micrographs showing Cx43 and N-cadherin labeling of C2-WT cells treated or not with siRNA against Kif5B. Nuclei counter-stained with dapi are also shown. **(a,b,c,d)** A representative of three independent repeats is shown. Source data are provided as a Source Data file.

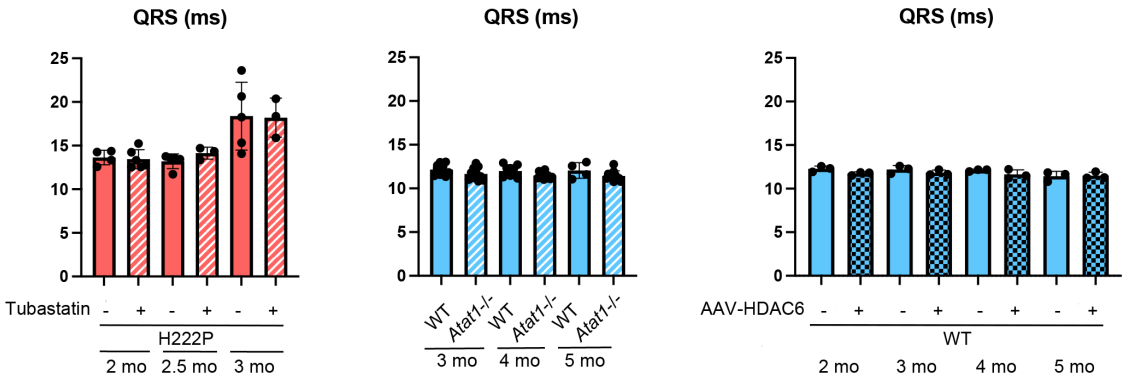


**Figure S5| α-Tubulin acetylation is not affecting intraventricular conduction.** Graph showing QRS interval from (left panel) *Lmna*$^{p.H222P/H222P}$ mice treated with tubastatin A from 2 (n=6) to 3 (n=3) month of age as compared with DMSO-treated (n=5), (middle panel) *Atat1*$^{-/-}$ mice at 3, 4 and 5 month of age (n=11) as compared with WT mice (n=10) and (right panel) WT mice transduced with AAV-HDAC6 (n=3) as compared with PBS-injected mice (n=3). Results are means ± SEM.

## SUPPLEMENTARY TABLES

**Table S1| Echocardiographic data for *Lmna*$^{+/+}$ (WT) mice transduced or not transduced with AAV-cofilin-1 or AAV-cofilin-1-T25A at 6 months of age.** IVS, inter ventricular septum; LVD, left ventricular diameter; LVPW, left ventricular posterior wall; LVED, left ventricular end diastolic; LVES, left ventricular end systolic; EF, ejection fraction; FS, fractional shortening; s, systole; d, diastole. Values are means ± SEM. *p≤0.05, **p≤0.01 and ***p≤0.001 between *Lmna*$^{+/+}$ mice transduced and *Lmna*$^{+/+}$ mice not transduced. Values for *Lmna*$^{p.H222P/H222P}$ mice are shown as comparison.

| | ***Lmna* WT NT** | ***Lmna* WT AAV-cofilin WT** | ***Lmna* WT AAV-cofilin T25A** | ***Lmna* H222P NT** |
|---|---|---|---|---|
| **age** | 6 months | 6 months | 6 months | 6 months |
| **n** | 3 | 3 | 3 | 3 |
| **time (ms)** | 93,033 ± 1,86 | 101,82 ± 2,37 ** | 108,13 ± 1,66 *** | 96,11 ± 2,88 |
| **heart rate (bpm)** | 645,07 ± 12,80 | 589,53 ± 13,61 ** | 554,9 ± 8,6 *** | 624,6 ± 18,51 |
| **cardiac output (l/min)** | 0,06 ± 0 | 0,05 ± 0,01 | 0,06 ± 0,02 | 0,07 ± 0,01 |
| **IVSd (cm)** | 0,07 ± 0 | 0,06 ± 0,005 | 0,07 ± 0,005 | 0,06 ± 0 |
| **LVDd (cm)** | 0,35 ± 0,01 | 0,36 ± 0,03 | 0,37 ± 0,04 | 0,47 ± 0,07 * |
| **LVPWd (cm)** | 0,07 ± 0 | 0,06 ± 0 | 0,07 ± 0,011 | 0,06 ± 0,005 |
| **IVSs (cm)** | 0,12 ± 0,01 | 0,09 ± 0,01 ** | 0,13 ± 0,005 | 0,09 ± 0,01 ** |
| **LVDs (cm)** | 0,18 ± 0,005 | 0,23 ± 0,025 | 0,19 ± 0,025 | 0,37 ± 0,09 ** |
| **LVPWs (cm)** | 0,12 ± 0,01 | 0,09 ± 0,005 | 0,11 ± 0,015 | 0,08 ± 0 ** |
| **LVED vol (ml)** | 0,113 ± 0,005 | 0,12 ± 0,026 | 0,13 ± 0,04 | 0,26 ± 0,11 |
| **LVES vol (ml)** | 0,02 ± 0 | 0,036 ± 0,01 | 0,02 ± 0,01 | 0,14 ± 0,10 |
| **EF (%)** | 84,4 ± 0,58 | 71,12 ± 3,67 * | 84,28 ± 1,58 | 48,760 ± 16,50 ** |
| **FS (%)** | 47,32 ± 0,67 | 35,01 ± 2,89 * | 47,22 ± 1,68 | 21,54 ± 9,27 *** |
| **LV eject vol (ml)** | 0,09 ± 0,005 | 0,08 ± 0,015 | 0,11 ± 0,03 | 0,11 ± 0,02 |
| **h/r** | 0,39 ± 0,007 | 0,34 ± 0,032 | 0,40 ± 0,03 | 0,26 ± 0,03 ** |

**Table S2| Top scoring gene ontology (Biological Functions) in hearts from *Lmna*$^{+/+}$ (WT) mice transduced or not transduced with AAV-cofilin-1 or AAV-cofilin-1-T25A at 6 months of age. Values for *Lmna*$^{p.H222P/H222P}$ mice are shown as comparison.**

The most statistically significant functions identified are listed according to their p value. In red are biological functions related to cytoskeleton.

| Diseases and Biological Functions | *p*-value | | |
|---|---|---|---|
| | ***Lmna* H222P NT** | ***Lmna* WT AAV-cofilin WT** | ***Lmna* WT AAV-cofilin T25A** |
| Cell movement of muscle cells | 2,47E-13 | 3,71E-09 | N.S. |
| Endothelial cell development | 1,44E-07 | 9,86E-09 | N.S. |
| Migration of muscle cells | 4,28E-13 | 1,39E-08 | N.S. |
| Organization of fibrils | 2,05E-10 | 1,73E-06 | N.S. |
| Organization of filaments | 3,44E-09 | 1,76E-06 | N.S. |
| Morphology of filaments | 5,64E-08 | 4,94E-06 | N.S. |
| Morphology of skeleton | 1,86E-06 | 1,38E-05 | N.S. |
| Cell spreading | 1,11E-10 | 2,52E-05 | N.S. |
| Fibrosis | 1,20E-14 | 3,68E-05 | N.S. |
| Accumulation of macrophages | 5,14E-07 | 6,52E-05 | N.S. |
| Organization of actin cytoskeleton | 3,73E-10 | 1,17E-04 | N.S. |
| Cell movement of fibroblast cell lines | 1,06E-09 | 1,44E-04 | N.S. |
| Migration of endothelial cells | 2,51E-07 | 1,54E-04 | N.S. |
| Formation of filopodia | 1,05E-07 | 1,55E-04 | N.S. |
| Fibrogenesis | 1,35E-12 | 1,58E-04 | N.S. |
| Activation of antigen presenting cells | 7,97E-09 | 1,66E-04 | N.S. |
| Differentiation of connective tissue cells | 1,58E-11 | 1,76E-04 | N.S. |
| Cell movement of connective tissue cells | 2,80E-08 | 2,85E-04 | N.S. |
| Quantity of connective tissue | 5,27E-13 | 6,04E-04 | N.S. |
| Cell-cell contact | 1,80E-08 | 7,45E-04 | N.S. |
| Organization of cytoskeleton | 7,40E-17 | 7,66E-04 | N.S. |
| Morphology of connective tissue cells | 3,24E-08 | 8,62E-04 | N.S. |
| Cell viability | 2,52E-08 | 1,27E-03 | N.S. |
| Quantity of connective tissue cells | 3,59E-10 | 1,37E-03 | N.S. |
| Cell movement of fibroblasts | 4,46E-09 | 1,74E-03 | N.S. |
| Morphology of heart ventricle | 2,69E-07 | 1,85E-03 | N.S. |
| Formation of filaments | 1,63E-10 | 2,22E-03 | N.S. |
| Migration of antigen presenting cells | 4,23E-11 | 4,88E-03 | N.S. |
| Binding of fibroblasts | 3,25E-08 | 6,85E-03 | N.S. |
| Cellular infiltration | 8,81E-19 | 7,27E-03 | N.S. |
| Attachment of cells | 1,74E-12 | 7,97E-03 | N.S. |
| Quantity of adipose tissue | 3,57E-07 | 8,31E-03 | N.S. |

**Table S3| Top scoring gene ontology (Canonical Pathways) in hearts from *Lmna*$^{+/+}$ (WT) mice transduced or not transduced with AAV-cofilin-1 or AAV-cofilin-1-T25A at 6 months of age. Values for *Lmna*$^{p.H222P/H222P}$ mice are shown as comparison.**

The most statistically significant canonical pathways identified are listed according to their p value. In red are the canonical pathways of interest in this study.

| Canonical Pathways | *p*-value | | |
|---|---|---|---|
| | ***Lmna* H222P NT** | ***Lmna* WT AAV-cofilin WT** | ***Lmna* WT AAV-cofilin T25A** |
| **ERK/MAPK Signaling** | **1,53E-02** | **3,20E-04** | **N.S.** |
| Leukocyte Extravasation Signaling | 4,34E-05 | 4,78E-04 | N.S. |
| Oxidative Ethanol Degradation III | 6,61E-03 | 5,88E-04 | N.S. |
| Dendritic Cell Maturation | 2,94E-03 | 6,14E-04 | N.S. |
| Fatty Acid α-oxidation | 3,53E-02 | 6,88E-04 | N.S. |
| Putrescine Degradation III | 1,12E-02 | 7,97E-04 | N.S. |
| Tryptophan Degradation X (Mammalian, via Tryptamine) | 3,23E-03 | 9,17E-04 | N.S. |
| Ethanol Degradation IV | 4,27E-03 | 1,05E-03 | N.S. |
| Phospholipases | 1,68E-02 | 1,60E-03 | N.S. |
| Ethanol Degradation II | 1,52E-04 | 1,88E-03 | N.S. |
| Noradrenaline and Adrenaline Degradation | 3,93E-04 | 2,53E-03 | N.S. |
| VEGF Signaling | 1,16E-02 | 2,59E-03 | N.S. |
| Integrin Signaling | 1,81E-05 | 2,79E-03 | N.S. |
| Gαq Signaling | 7,45E-03 | 2,80E-03 | N.S. |
| Phospholipase C Signaling | 2,30E-02 | 3,17E-03 | N.S. |
| Axonal Guidance Signaling | 2,53E-04 | 3,43E-03 | N.S. |
| Phagosome Formation | 1,94E-08 | 3,67E-03 | N.S. |
| Fc Epsilon RI Signaling | 2,10E-02 | 4,54E-03 | N.S. |
| Role of NFAT in Regulation of the Immune Response | 1,74E-02 | 5,02E-03 | N.S. |
| IL-17 Signaling | 1,62E-02 | 7,36E-03 | N.S. |
| Fcγ Receptor-mediated Phagocytosis in Macrophages and Monocytes | 2,39E-04 | 8,28E-03 | N.S. |
| VEGF Family Ligand-Receptor Interactions | 2,83E-02 | 9,27E-03 | N.S. |
| Serotonin Degradation | 1,99E-02 | 1,03E-02 | N.S. |
| **Actin Cytoskeleton Signaling** | **1,94E-05** | **1,35E-02** | **N.S.** |
| FAK Signaling | 4,85E-03 | 1,45E-02 | N.S. |
| Superpathway of Inositol Phosphate Compounds | 8,79E-03 | 1,55E-02 | N.S. |
| p38 MAPK Signaling | 2,76E-02 | 1,59E-02 | N.S. |
| Apelin Cardiac Fibroblast Signaling Pathway | 1,27E-05 | 1,59E-02 | N.S. |
| Alanine Biosynthesis II | 8,99E-03 | 1,76E-02 | N.S. |
| Alanine Degradation III | 8,99E-03 | 1,76E-02 | N.S. |
| Signaling by Rho Family GTPases | 2,50E-02 | 2,17E-02 | N.S. |
| Sphingosine-1-phosphate Signaling | 8,95E-03 | 2,18E-02 | N.S. |
| ILK Signaling | 8,77E-09 | 2,47E-02 | N.S. |
| Role of Pattern Recognition Receptors in Recognition of Bacteria and Viruses | 4,79E-03 | 2,75E-02 | N.S. |
| Glioma Invasiveness Signaling | 1,63E-06 | 3,07E-02 | N.S. |
| Regulation of Actin-based Motility by Rho | 5,62E-04 | 3,60E-02 | N.S. |
| Inhibition of Matrix Metalloproteases | 3,37E-06 | 4,21E-02 | N.S. |
| Macropinocytosis Signaling | 1,41E-06 | 4,29E-02 | N.S. |
| Granulocyte Adhesion and Diapedesis | 6,41E-04 | 4,86E-02 | N.S. |
| PKCθ Signaling in T Lymphocytes | 3,60E-02 | 4,86E-02 | N.S. |

**Table S4| Top scoring Upstream Regulators in hearts from *Lmna*$^{+/+}$ (WT) mice transduced or not transduced with AAV-cofilin-1 or AAV-cofilin-1-T25A at 6 months of age. Values for *Lmna*$^{p.H222P/H222P}$ mice are shown as comparison.**

The most statistically significant upstream regulators identified are listed according to their p value. In red is the upstream regulator of interest in this study.

| Upstream Regulators | *p*-value | | |
|---|---|---|---|
| | ***Lmna* H222P NT** | ***Lmna* WT AAV-cofilin WT** | ***Lmna* WT AAV-cofilin T25A** |
| INHBB | 2,96E-06 | 4,45E-08 | N.S. |
| ITGB6 | 4,44E-05 | 3,11E-06 | N.S. |
| EGR1 | 2,55E-09 | 3,39E-06 | N.S. |
| RETNLB | 1,59E-10 | 5,42E-06 | N.S. |
| C3AR1 | 2,85E-04 | 5,89E-06 | N.S. |
| SPTLC2 | 1,06E-06 | 6,20E-06 | N.S. |
| MAP3K1 | 1,86E-05 | 8,30E-06 | N.S. |
| TBX5 | 2,80E-02 | 8,30E-06 | N.S. |
| GLIS2 | 2,20E-08 | 1,11E-05 | N.S. |
| C5AR1 | 2,04E-05 | 3,40E-05 | N.S. |
| CTGF | 8,27E-06 | 4,24E-05 | N.S. |
| SEMA7A | 1,98E-07 | 4,28E-05 | N.S. |
| ADA | 5,22E-03 | 5,15E-05 | N.S. |
| ERBB4 | 8,22E-08 | 2,92E-04 | N.S. |
| CYR61 | 6,13E-04 | 3,48E-04 | N.S. |
| ERBB3 | 9,30E-13 | 3,62E-04 | N.S. |
| DCN | 1,86E-06 | 4,27E-04 | N.S. |
| KLF4 | 1,79E-07 | 6,89E-04 | N.S. |
| BMP2 | 5,69E-03 | 1,44E-03 | N.S. |
| TGFB2 | 1,94E-04 | 1,58E-03 | N.S. |
| SPARC | 2,29E-03 | 1,86E-03 | N.S. |
| SRC | 2,42E-04 | 2,46E-03 | N.S. |
| TNFRSF1A | 2,78E-03 | 3,63E-03 | N.S. |
| TLR3 | 2,66E-03 | 3,95E-03 | N.S. |
| SOX4 | 1,72E-04 | 4,32E-03 | N.S. |
| HMGA1 | 1,05E-03 | 4,53E-03 | N.S. |
| RELA | 3,96E-05 | 4,57E-03 | N.S. |
| TNFRSF1B | 1,70E-02 | 5,38E-03 | N.S. |
| JUN | 5,08E-06 | 6,35E-03 | N.S. |
| **SRF** | **1,04E-02** | **8,97E-03** | **N.S.** |
| STAT3 | 1,75E-12 | 1,04E-02 | N.S. |
| EGF | 2,15E-06 | 1,06E-02 | N.S. |
| CDKN2A | 2,72E-02 | 1,65E-02 | N.S. |
| WNT3A | 3,50E-05 | 2,22E-02 | N.S. |
| OGA | 5,05E-05 | 2,37E-02 | N.S. |
| STAT6 | 1,12E-06 | 3,92E-02 | N.S. |
| SHH | 1,05E-02 | 4,02E-02 | N.S. |
| ACOX1 | 8,43E-07 | 4,20E-02 | N.S. |

**Table S5| SRF target genes regulation in hearts from *Lmna*$^{+/+}$ (WT) mice transduced or not transduced with AAV-cofilin-1 or AAV-cofilin-1-T25A at 6 months of age. Values for *Lmna*$^{p.H222P/H222P}$ mice are shown as comparison. (green: down-regulation, red: up-regulation).**

| EntrezGeneID | Gene | Description | Fold | | |
|---|---|---|---|---|---|
| | | | ***Lmna* H222P NT** | ***Lmna* WT AAV-cofilin WT** | ***Lmna* WT AAV-cofilin T25A** |
| 12721 | *CORO1A* | coronin 1A | -1.07837 | -1.08182 | 1.00244 |
| 56431 | *DSTN* | destrin, actin depolymerizing factor | -1.46583 | -1.11139 | 1.02303 |
| 11475 | *ACTA2* | actin, alpha 2, smooth muscle, aorta | -1.14666 | -1.3521 | 1.02515 |
| 22003 | *Tpm1* | tropomyosin 1, alpha | -1.06179 | -1.01997 | 1.01253 |
| 59091 | *JPH2* | junctophilin 2 | -1.1997 | -1.03441 | 1.1358 |
| 14200 | *FHL2* | four and a half LIM domains 2 | -2.51028 | -1.64494 | 1.0339 |
| 17929 | *MYOM1* | myomesin 1 | -1.22636 | -1.07403 | 1.02004 |
| 225115 | *SVIL* | supervillin | -1.06002 | -1.1449 | 1.02517 |
| 17698 | *MSN* | moesin | -2.23618 | -1.25362 | 1.17429 |

**Table S6| ECG parameters.** Baseline values of ECG parameters measured in *Lmna*$^{p.H222P/H222P}$ mice treated with Tubastatin A as compared with DMSO-treated (top table); in *Atat1*$^{-/-}$ (KO) mice as compared with wild-type mice (WT) (middle table) and in mice transduced with AAV overexpressing HDAC6 as compared with WT mice (bottom table).

| | H222P | H222P | H222P | H222P | H222P | H222P |
|---|---|---|---|---|---|---|
| | **DMSO** | **Tubastatin** | **DMSO** | **Tubastatin** | **DMSO** | **Tubastatin** |
| **age** | 2 months | 2 months | 2,5 months | 2,5 months | 3 months | 3 months |
| **n** | 4 | 5 | 4 | 3 | 4 | 3 |
| RR (ms) | 80.55 ± 1.9 | 80.84 ± 0.9 | 80.3 ± 1.2 | 78.9 ± 0.6 | 78.61 ± 1.1 | 79.3 ± 0.8 |
| PR (ms) | 34.23 ± 0.7 | 35.1 ± 0.6 | 33.7 ± 0.6 | 32.82 ± 0.77 | 34.08 ± 0.7 | 32.55 ± 0.38 |
| QRS (ms) | 13.64 ± 0.42 | 13.44 ± 0.44 | 13.20 ± 0.37 | 14.136 ± 0.39 | 18.38 ± 1.7 | 18.20 ± 1.29 |

| | WT | Atat1 KO | WT | Atat1 KO | WT | Atat1 KO |
|---|---|---|---|---|---|---|
| **age** | 3 months | 3 months | 4 months | 4 months | 5 months | 5 months |
| **n** | 10 | 11 | 10 | 11 | 4 | 11 |
| RR (ms) | 80.55 ± 1.9 | 80.84 ± 0.9 | 80.3 ± 1.2 | 78.9 ± 0.6 | 78.61 ± 1.1 | 79.3 ± 0.8 |
| PR (ms) | 34.23 ± 0.7 | 35.1 ± 0.6 | 33.7 ± 0.6 | 32.82 ± 0.77 | 34.08 ± 0.7 | 32.55 ± 0.38 |
| QRS (ms) | 12.16 ± 0.19 | 11.66 ± 0.2 | 11.99 ± 0.19 | 11.46 ± 0.11 | 12.05 ± 0.44 | 11.43 ± 0.17 |

| | WT | AAV-HDAC6 | WT | AAV-HDAC6 | WT | AAV-HDAC6 | WT | AAV-HDAC6 |
|---|---|---|---|---|---|---|---|---|
| **age** | 2 months | 2 months | 3 months | 3 months | 4 months | 4 months | 5 months | 5 months |
| **n** | 3 | 3 | 3 | 3 | 3 | 3 | 3 | 3 |
| RR (ms) | 78.8 ± 0.32 | 79.72 ± 0.46 | 78.77 ± 0.8 | 81.58 ± 1.3 | 79.20 ± 1.6 | 83.11 ± 3.4 | 83.05 ± 1.6 | 86.14 ± 4.7 |
| PR (ms) | 33.2 ± 0.7 | 33.24 ± 0.7 | 32.67 ± 0.37 | 34.16 ± 0.9 | 33.15 ± 1.58 | 34.56 ± 1.2 | 36.168 ± 1.07 | 34.41 ± 1.14 |
| QRS (ms) | 12.27 ± 0.18 | 11.74 ± 0.11 | 12.20 ± 0.26 | 11.81 ± 0.18 | 12.11 ± 0.07 | 11.63 ± 0.31 | 11.44 ± 0.32 | 11.49 ± 0.23 |

**Table S7| Clinical parameters of patients whose iPS-derived cardiomyocytes were used in this study.**

| *LMNA* mutation | Age | Sex | Diagnosis | Echocardiography | Electrocardiography | Reference |
|---|---|---|---|---|---|---|
| p.S143P | 30-35 | F | DCM | DCM | 1st degree AV block and paroxysmal flutter | Kärkkäinen et al., 2004; West et al., 2016; Shah et al., 2019 |
| p.R190W | 35-40 | M | DCM | DCM | ventricular ectopic beats | Salvarani et al. 2009 |
| p.H222P | 20-25 | M | EDMD | normal | arrhythmias | Bonne et al. 2000 |

**Table S8| Listing of primers used in this study**

| Gene | Forward | Reverse |
|---|---|---|
| ***Srf*** | 5' cccaccacagaccagagaat 3' | 5' agttggtgatggggaaggag |
| ***Acta2*** | 5' aggaaccctgagacgctgct 3' | 5' ccattccaaccattactccc 3' |
| ***Fhl2*** | 5' acgagacctgcttcacctgt 3' | 5' tgctcccggtaagtaacacc 3' |
| ***Myom1*** | 5' gccctcagaaacgactgaag 3' | 5' gagcagtcgtcagtccatga 3' |
| ***Svil*** | 5' gccctacaagaagctcatgc 3' | 5' ccaagctccctctttgtctg 3' |
| ***Tnnc1*** | 5' gacggtgacaagaacaacga 3' | 5' ggaatggggagagaaagtcg 3' |
| ***Msn*** | 5' tggagcagcacaaactcaac 3' | 5' atgttgagacccaaggcatc 3' |
| ***Rplp0*** | 5' ctccaagcagatgcagcaga 3' | 5' atagccttgcgcatcatggt 3' |
| ***Atat1*** | 5' ggaacaggaagcggaggata 3' | 5' ctggcgttcattatgtcccc 3' |