

Supplementary Data to:

Phosphorylation of the chromatin remodeling factor DPF3a induces cardiac hypertrophy through releasing HEY repressors from DNA

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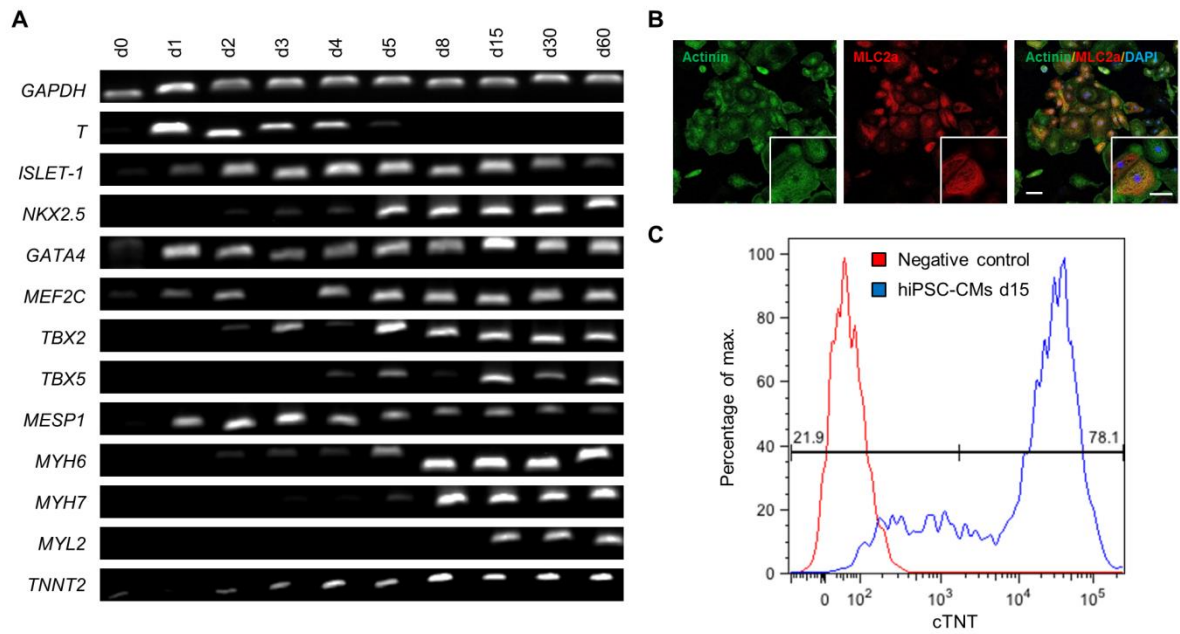
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Supplementary Figure S1. Characterization of successful differentiation of human-induced pluripotent stem cells to cardiomyocytes.

- (A) Analysis of mesodermal and cardiac gene expression during differentiation from day 0 to day 60.
- (B) Immunostaining for characteristic cardiac markers. Scale bars indicate 50 and 20 μ M, respectively.
- (C) Cardiac Troponin T expression was analyzed at day 15 by flow cytometry.

MATVIHNPLK ALGDQFYKEA IEHCRSYNSR LCAERSVRLP FLDSQTGVAQ NNCYIWMEKR 60
 HRGPGLAPGQ LYTYPARCWR KRRRLHPPED PKLRLLLEIKP EVELPLKKGD FTSESITLEA 120
 LLRGEGVEKK VDAREEESIQ EIQRVLENDE NVEEGNEEED LEEDIPIKRKN RTRGRARGSA 180
 GGRRRHDAAS QEDHDKPYVC DICGKRYKNR PGLSYHYAHT HLASSEEGDEA QDQETRSPPN 240
 HRNENHRPQK GPDGTVIPNN YCDFCLGGSN MNKSGRPEE LVSCADCGRS AHLGGEGRKE 300
 KEAAAAARTT EDLFGSTSES DTSTFHGFDE DDLEEPRSCR GRRSGRGSPT ADKKGSC 357

- Netphos 2.0 score > 0.5
- CK2 KinasePhos 2.0 score > 0.5

Supplementary Figure S2. Phosphorylation prediction of DPF3a.

Prediction of phosphorylation sites within the human DPF3a sequence (NP_036206) using the prediction tools Netphos 2.0 and KinasePhos 2.0.

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M.musculus      MATVIHNPLKALGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYIWM EKR 60
R.norvegicus    MATVIHNPLKALGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYIWM EKR 60
H.sapiens       MATVIHNPLKALGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYIWM EKR 60
M.mulatta       MATVIHNPLKALGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYIWM EKR 60
G.gallus1       MATVIHNPLKALGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYIWM EKR 60
G.gallus2       MATVIHNPLKALGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYIWM EKR 60
*****

M.musculus      HRGPGGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIKPEVELPLKKGDF TSESTTLEA 120
R.norvegicus    HRGPGGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIKPEVELPLKKGDF TSESTTLEA 120
H.sapiens       HRGPGGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIKPEVELPLKKGDF TSESTTLEA 120
M.mulatta       HRGPGGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIKPEVELPLKKGDF TSESTTLEA 120
G.gallus1       HRGPGGLAPGQLYTYPARCWRKKRRLHPPEDSRKLLLEIKPEVDLPLKKGDF TSESTTLEA 120
G.gallus2       HRGPGGLAPGQLYTYPARCWRKKRRLHPPEDSRKLLLEIKPEVDLPLKKGDF TSESTTLEA 120
*****. : * : ***** : *****

M.musculus      LLRGEVVEKKVDAREEESIQEIQRVLENDENV EEGNEEDLEEDVPKRKNRTRGR----- 175
R.norvegicus    LLRGEVVEKKVDAREEESIQEIQRVLENDENV EEGNEEDLEEDIPKRKNRTRGR----- 175
H.sapiens       LLRGEVVEKKVDAREEESIQEIQRVLENDENV EEGNEEDLEEDIPKRKNRTRGR----- 175
M.mulatta       LLRGEVVEKKVDAREEESIQEIQRVLENDENV EEGNEEDLEEDIPKRKNRTRGR----- 175
G.gallus1       LLRGEI EKKMDTK EEDPIQEIQRVLENDEN ADEVNEEDLEEDIPKRKNRPRGR----- 175
G.gallus2       LLRGEI EKKMDTK EEDPIQEIQRVLENDEN ADEVNEEDLEEDIPKRKNRPRGRPKTPT 180
*****. *** : * : * : * : ***** : * ***** : ***** : ***

M.musculus      -----ARGSAGGRRRHDAASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEG 227
R.norvegicus    -----ARGSAGGRRRHDAASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEG 227
H.sapiens       -----ARGSAGGRRRHDAASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEG 227
M.mulatta       -----ARGSAGGRRRHDAASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEG 227
G.gallus1       -----ARGSGGRRRHDAASQDDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEG 227
G.gallus2       WKKIFQKNARGSGGRRRHDAASQDDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEG 240
*****. ***** : ***** : *****

M.musculus      DEAQDQETRSPPNHRNENHRPQKPGDGTVIPNNYCDFCLGGSNMNKKSGRPEELVSCADC 287
R.norvegicus    DEAQDQETRSPPNHRNENHRPQKPGDGTVIPNNYCDFCLGGSNMNKKSGRPEELVSCADC 287
H.sapiens       DEAQDQETRSPPNHRNENHRPQKPGDGTVIPNNYCDFCLGGSNMNKKSGRPEELVSCADC 287
M.mulatta       DEAQDQETRSPPNHRNENHRPQKPGDGTVIPNNYCDFCLGGSNMNKKSGRPEELVSCADC 287
G.gallus1       DEAREQETRSSPVHRNENHKPQKPGDGVIIIPNNYCDFCLGGSNMNKKSGRPEELVSCSDC 287
G.gallus2       DEAREQETRSSPVHRNENHKPQKPGDGVIIIPNNYCDFCLGGSNMNKKSGRPEELVSCSDC 300
*** : ***** * ***** : ***** : *****

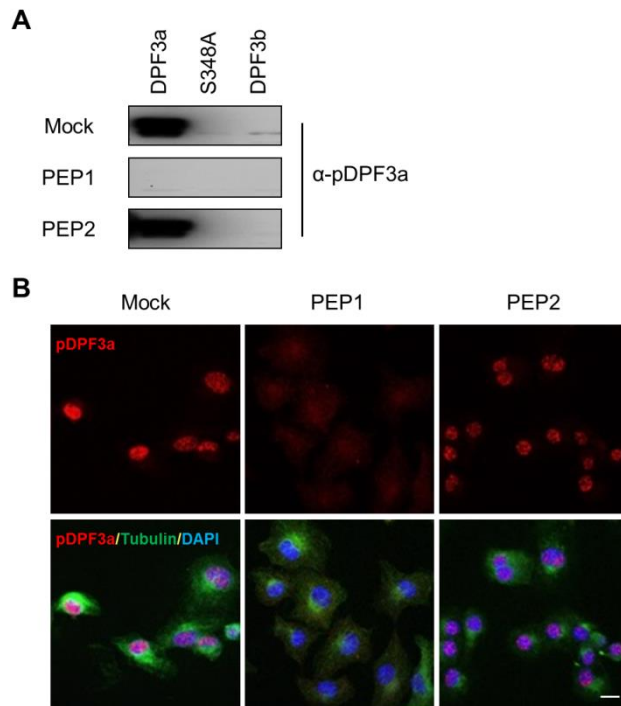
M.musculus      GRSAPHLGGEGRKEKEAAAAARTTEDLFGSTSESDTSTFYGFDEDDLEEPRSCRGRSSGRG 347
R.norvegicus    GRSAPHLGGEGRKEKEAAAAARTTEDLFGSTSESDTSTFYGFDEDDLEEPRSCRGRSSGRG 347
H.sapiens       GRSAPHLGGEGRKEKEAAAAARTTEDLFGSTSESDTSTFHGFDEDDLEEPRSCRGRSSGRG 347
M.mulatta       GRSAPHLGGEGRKEKEAAAAARTTEDLFGSTSESDTSTFHGFDEDDLEEPRSCRGRSSGRG 347
G.gallus1       GRSAPHLGREGRDE--AAPRTTEDLFGSTSESDTSTFHGFDEDDAEPLSSRGGGCGGS 345
G.gallus2       GRSAPHLGREGRDE--AAPRTTEDLFGSTSESDTSTFHGFDEDDAEPLSSRGGGCGGS 358
***** ** : : * : ***** : ***** ** * * * . * .

M.musculus      SPTADKKGSC 357
R.norvegicus    SPTADKKGSC 357
H.sapiens       SPTADKKGSC 357
M.mulatta       SPTADKKGSC 357
G.gallus1       SPSADKKGSC 355
G.gallus2       SPSADKKGSC 368
** : ***** . *

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Supplementary Figure S3. Conservation analysis of DPF3a.

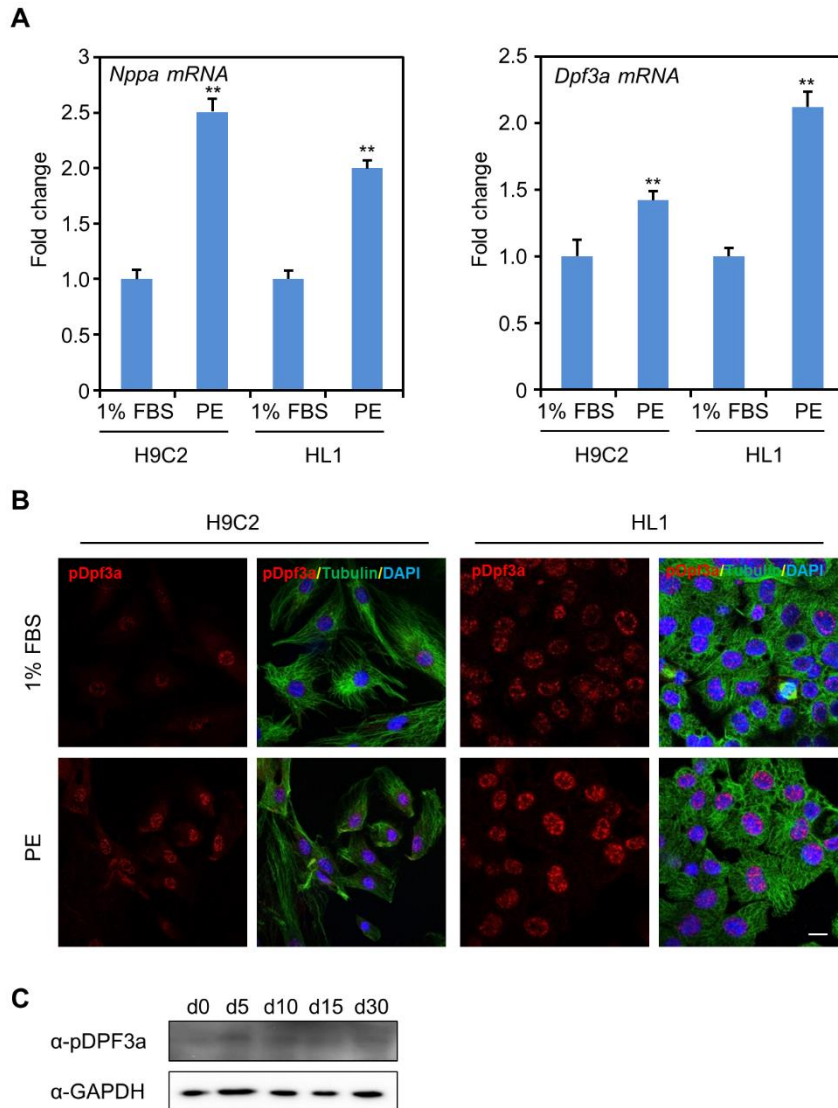
Protein sequence conservation analysis of DPF3a using ClustalW2 in *H. sapiens* (NP_036206), *M. mulatta* (AFE80282), *M. musculus* (NP_001254555), *R. norvegicus* (NP_001178747) and *G. gallus* (AAK51969.1 and AAK51970).



Supplementary Figure S4. Specificity of anti-pDPF3a.

(A) Flag-tagged DPF3a WT, S348A, and DPF3b from lysates of transiently transfected HEK293 cells were electrophoresed on a SDS-polyacrylamide gel and probed using the anti-pDPF3a antibody, pre-incubated with either PEP1 or PEP2 control peptide. PEP1: GRRSGRGS^(P)PTADKKGS; PEP2: GRRSGRGSPTADKKGS.

(B) HL1 cells were fixed and stained with antibody against pDPF3a (red) and antibody against Tubulin (green). Anti-pDPF3a antibody was pre-incubated with either PEP1 or PEP2 control peptide. Scale bar, 20 μm.

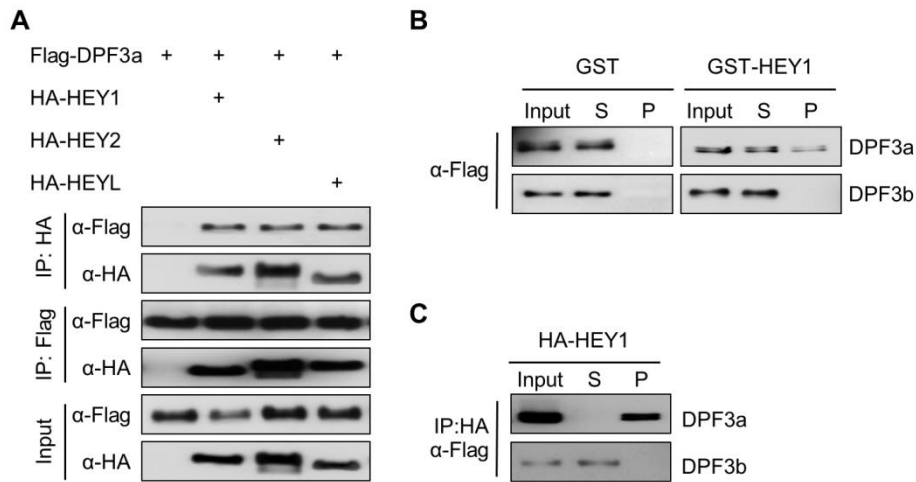


Supplementary Figure S5. DPF3a expression and phosphorylation in cardiac cells.

(A) *Nppa* and *Dpf3a* mRNA expression were analyzed in HL1 and H9C2 cardiomyocytes after phenylephrine (PE) treatment for 24 hours. 1% FBS was used as control.

(B) Nuclear localization of pDPF3a was increased by phenylephrine (PE) in HL1 and H9C2 cardiomyocytes. Red: pDPF3a; green: Tubulin. Scale bar, 20 μ m.

(C) The protein level of phosphorylated DPF3a during differentiation of human-induced pluripotent stem cells to cardiomyocytes. Immunoblotting were performed on samples obtained from different day during cardiac differentiation.

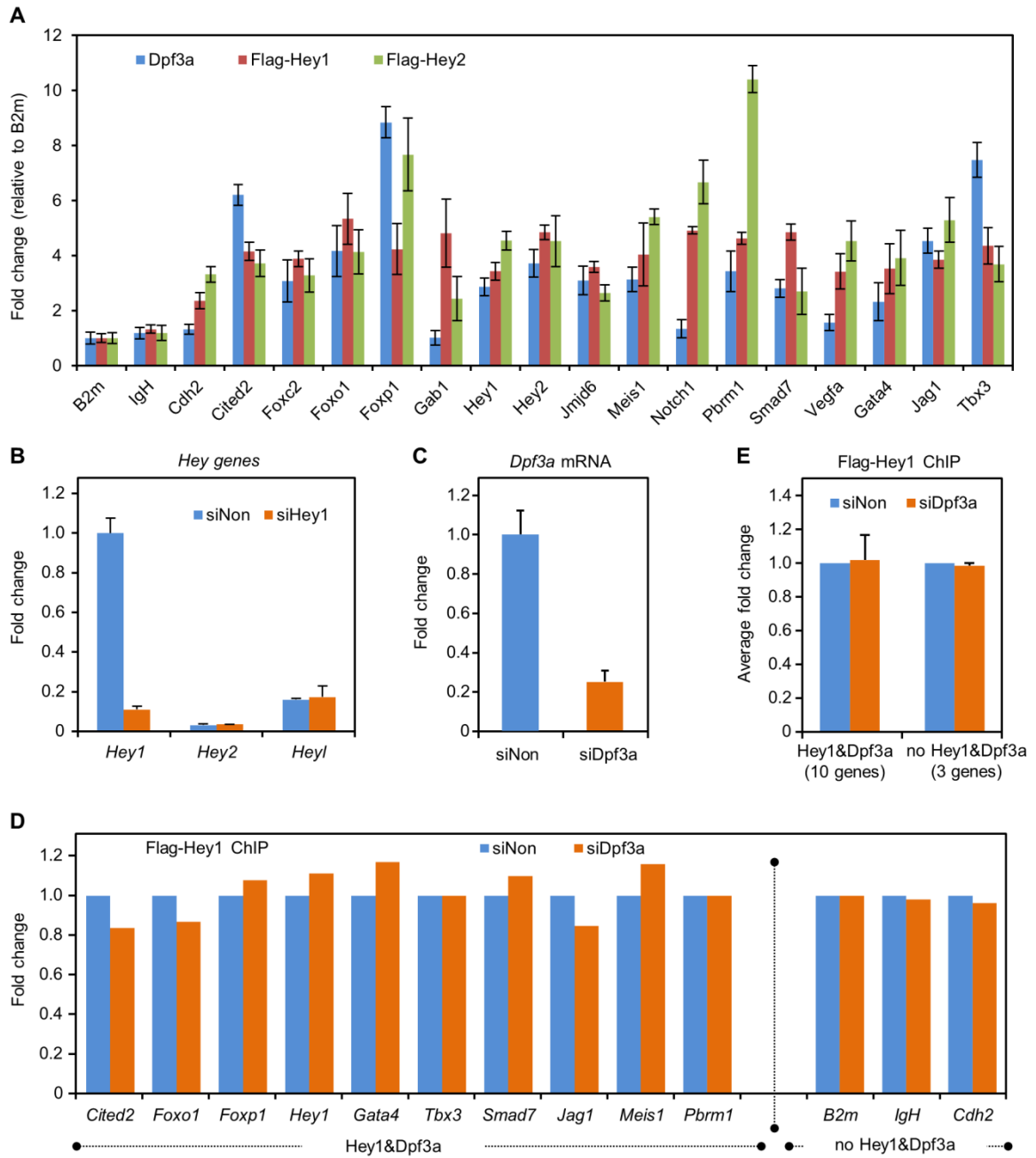


Supplementary Figure S6. Interactions between DPF3a/b and HEY proteins.

(A) DPF3a interacts with all HEY proteins. HEK293 cells were transiently transfected with Flag-tagged DPF3a and with HA-tagged HEY1, HEY2 or HEYL. Cell lysates were incubated with an anti-HA matrix to pull down HA-tagged protein together with interacting proteins, which were further probed with anti-Flag antibody in immunoblotting.

(B) GST pull-down with GST-HEY1 and Flag-DPF3a and DPF3b. GST vector was used as a negative control. S: supernatant, P: immunoprecipitation pellet.

(C) Co-immunoprecipitation of HA-tagged HEY1 with Flag-tagged DPF3a and DPF3b from lysates of transiently transfected HEK293 cells.



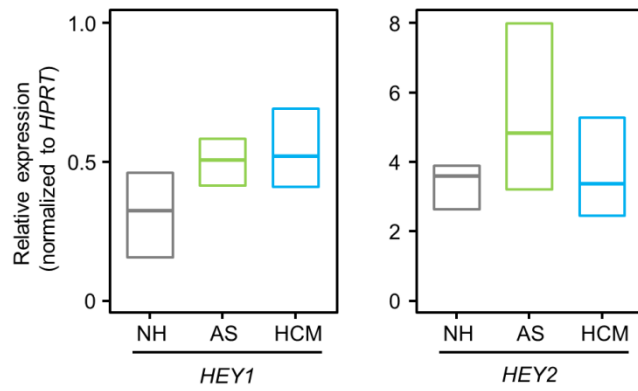
Supplementary Figure S7. ChIP-qPCR and siRNA knockdown in C2C12 cells

(A) Co-occurrence of Dpf3a, Hey1 and Hey2 binding. Dpf3a, Hey1 and Hey2 enrichment at selected promoters was analyzed using ChIP and qPCR.

(B) Expression levels of *Hey1*, *Hey2* and *Heyl* genes before and after siHey1 knockdown.

(C) Knockdown efficiency of *Dpf3a* in C2C12 cells was analyzed by qPCR.

(D-E) Hey1 enrichment at selected promoters in siDpf3a knockdown was compared to siNon control. Binding of Hey1 was quantified by ChIP and qPCR (triplicate experiments).



Supplementary Figure S8. HEY1 and HEY2 expression in human hearts.

Expression of *HEY1* and *HEY2* in aortic stenosis (AS), hypertrophic cardiomyopathy (HCM) and normal heart (NH) was analyzed using qPCR. Results represent median expression levels with 25% and 75% quartiles. Expression levels were analyzed by a two-sided Wilcoxon test and resulted in no significant findings between the analyzed groups.

Supplementary Table S1. Antibodies used in different experiments.

Antibodies used in chromatin immunoprecipitation (ChIP), Immunofluorescence (IF), Western blot (WB) and fluorescence-activated cell sorting (FACS), and their respective amounts/dilutions applied in the experiments are given.

| Primary antibodies | Company | Used amount/dilution |
|---|------------------------------|--|
| Anti-SNF2 β /BRG1, rabbit antiserum | Upstate (07-478) | ChIP: 5 μ g |
| Anti-CK2 alpha, rabbit polyclonal | Abcam (ab10466) | WB: 1:500 |
| Anti-Gapdh, mouse monoclonal | Ambion (AM4300) | WB: 1:5000 |
| Anti-Flag, rabbit polyclonal | AnaSpec (29674) | IF: 1:500 |
| Anti-Flag M2, mouse monoclonal | Sigma (F3165) | WB: 1:1000, IF: 1:400, ChIP: 2 μ g |
| Anti-GST, rabbit polyclonal | Invitrogen (71-7500) | WB: 1:500 |
| Anti-HA, rat monoclonal | Roche (11867423001) | WB: 1:2000 |
| Anti-Hey1, rabbit polyclonal | Abcam (ab22614) | WB: 1:100 |
| Anti-His HRP, mouse monoclonal | Macs Molecular (130-092-785) | WB: 1:5000 |
| Anti-pDPF3a, rabbit polyclonal | Self-made | WB: 1:500, IF: 1:100, ChIP: 5 μ g |
| Anti-Thiophosphate Ester, rabbit monoclonal | Epitomics (2686-1) | WB: 1:5000 |
| Anti-Troponin I, goat polyclonal | HyTest (4T21/2) | IF: 1:200 |
| Anti- Troponin T, mouse monoclonal | Lab Vision (MS-295) | FACS: 1:500 |
| Anti- Mlc2a, mouse monoclonal | Synaptic Systems (311011) | IF: 1:200 |
| Anti-Tubulin, mouse monoclonal | Sigma (T9026) | IF: 1:800 |
| Anti-Actinin, mouse monoclonal | Sigma (A7811) | IF: 1:400 |
| Anti-Vinculin, mouse monoclonal | Sigma (V9131) | WB: 1:25000 |
| Normal Mouse IgG preimmuneserum | Santa Cruz Biotech (sc-2027) | ChIP: 5 μ g |
| Normal Rabbit IgG preimmuneserum | Santa Cruz Biotech (sc-1237) | ChIP: 5 μ g |
| Secondary antibodies | | |
| Anti-mouse IgG (HRP) | Sigma(A0168) | WB: 1:10000 |
| Anti-mouse IgG (Alexa Flour 488) | Invitrogen (A11029) | IF: 1:2000 |
| Anti-rabbit IgG (Alexa Flour 568) | Invitrogen (A11036) | IF: 1:2000 |
| Anti-rabbit IgG(Biotin) | Jackson lab(711-065-152) | IF: 1:500 |
| Anti-goat IgG (Alexa Flour 568) | Invitrogen (A11057) | IF: 1:500 |
| Anti-rabbit IgG (HRP) | Sigma (A2074) | WB: 1:10000 |
| Anti-rat IgG (HRP) | Sigma (A9542) | WB: 1:20000 |

Supplementary Table S2. siRNAs used for knockdown experiments.

Sequences of siRNAs used in knockdown experiments.

| Name | Target | Species | Company | Accession NO. | Target sequence |
|-------------|---------------|----------------|----------------|----------------------|---|
| siDpf3a | Dpf3a | mouse | Invitrogen | NM_058212 | TGACTCTGGTCATTGTTCTAGTTCT |
| siHey1 | Hey1 | mouse | Invitrogen | NM_010423 | CGACGAGACCGAATCAATATT |
| siCk2a1 | Ck2a1 | mouse | Invitrogen | NM_007788 | GATTATAGTTTGGATATGTTT |
| siNon | Synthetic | mouse | Invitrogen | Synthetic | Not provided |
| siFITC | Synthetic | mouse | Invitrogen | Synthetic | Not provided |
| siDPF3 | DPF3 | human | Qiagen | NM_012074 | AAGGGAAATCAAAGAATCGA AAGAGGATATTCCCAAGCGAA AACAGACTCTCTGGGCAATTA AAGAAACGTATCAATACCCAT |
| siNON | Synthetic | human | Qingen | Synthetic | Not provided |

Supplementary Table S3. Sequences of qPCR expression primers

| Gene | Species | Accession Number | Forward Sequence (5' - 3') | Reverse Sequence (5' - 3') |
|----------------|---------|------------------------|----------------------------|----------------------------|
| <i>Dpf3a</i> | mouse | NM_058212 | CAGACGGGACAGTCATTCCTAAT | CTCCCAAATGAGCAGAGCGT |
| <i>Dpf3</i> | mouse | NM_058212/NM_001267625 | ACAACTGCTACATCTGGATGG | GTCGTAGTTTTGGGCCTCTG |
| <i>Hey1</i> | mouse | NM_010423 | TGAGCTGAGAAGGCTGGTAC | ACCCCAAACCTCCGATAGTCC |
| <i>Hey2</i> | mouse | NM_013904 | TGAGAAGACTAGTGCCAACAGC | TGGGCATCAAAGTAGCCTTTA |
| <i>HeyL</i> | mouse | NM_013905 | CGTGGATCACTTGAAGATGC | CATTCGCCGAAACCCAATACT |
| <i>Ck2a1</i> | mouse | NM_007788 | GATAGCCAAGTTCTGGGAA | CATCGCTTACGGGAGTGC |
| <i>Hprt</i> | mouse | NM_013556 | AAACAATGCAAACTTTGCTTTCC | GGTCTTTTACCAGCAAGCT |
| <i>Dpf3a</i> | rat | NM_001191818 | AAGGCAGGAAGGAGAAGGAG | AGGCTCTTCCAATCGTCCT |
| <i>Nppa</i> | rat | NM_012612 | AGGGCTTCTTCTCTTCTG | TGTTGGACACCGCACTGTAT |
| <i>Hprt</i> | rat | NM_012583 | TGCTGGTGAAAAGGACCTCTC | CCACTTTCGCTGATGACACAA |
| <i>DPF3</i> | human | NM_012074/NM_001280542 | GGCTGCTGGAGATAAAAACCTGA | TTCTGGATGCTTTCTCCTC |
| <i>DPF3a</i> | human | NM_012074 | GACGATTTGGAAGAGCCTCG | GAGTCTGTTCCGTGGGTTTAGC |
| <i>DPF3b</i> | human | NM_001280542 | CGAGGCTGTCAAGACCTACAAG | CGCAGAAGAGTAGCTGGTCATC |
| <i>HEY1</i> | human | NM_012258 | ACGGGATGACCGTGATCACCTGAAA | GCGTGCGCGTCAAAGTAAC |
| <i>HEY2</i> | human | NM_012259 | ACGGGTTGAAGATGCTTCAGGCAACA | TCAGGTACCGGCAACTTCT |
| <i>NPPA</i> | human | NM_006172 | ACGGGTACAATGCCGTGTCCAACG | TTCTTCAAATGGTCCAGCAA |
| <i>TBX3</i> | human | NM_005996 | AAGGAGAATGGGACCTCTGA | CCTCGCTGGGACATAAATCT |
| <i>FOXO1</i> | human | NM_002015 | CTGGCTCTCACAGCAATGAT | CACCATAGAATGCACATCCC |
| <i>SMAD7</i> | human | NM_001190821 | CAGATTCCTCAACTTCTTCTGG | CCCCTCTCGTCTTCTCCTC |
| <i>HPRT</i> | human | NM_000194 | GGTGGAGATGATCTCTCAACTTTAA | AGGAAAGCAAAGTCTGCATTGTT |
| <i>GAPDH</i> | human | NM_002046.5 | ACCCACTCCTCCACCTTTGA | TTGCTGTAGCCAAATTCGTTG |
| <i>OCT4</i> | human | NM_002701 | AGTTTGTGCCAGGGTTTTTG | ACTTCACCTTCCCTCCAACC |
| <i>NANOG</i> | human | NM_024865 | TTTGAAGCTGCTGGGGAAG | GATGGGAGGAGGGGAGAGGA |
| <i>T</i> | human | NM_003181 | CTCACCATGAGATGATCGTGAC | AGGAAGGAGTACATGGCGTTG |
| <i>ISLET-1</i> | human | NM_002202 | AGCAGCCCAATGACAAAATAA | CGTGTCTCTCTGGACTGGCA |
| <i>NKX2.5</i> | human | NM_001166175 | CACCTCAACAGCTCCCTGACT | ATCGCCGCCACAACTCT |
| <i>GATA4</i> | human | NM_002052 | ATCTCACTACGGGCACAGCA | TTTGAGGAGGGAAGAGGGGAAG |
| <i>TBX2</i> | human | NM_005994 | ACCCTGAGATGCCAAAC | CAGTGACGGCGATGAAGT |
| <i>MEF2C</i> | human | NM_002397 | TCAGGGACGAGAGAGAGAAGAAA | ACAGTCACACAGCAGCTCA |
| <i>TBX5</i> | human | NM_000192 | CAGAAACTCAAGCTCACCAACAA | TGCTATAAACGCAGTCTCAGGAA |
| <i>MYH6</i> | human | NM_002471 | GGTCATTGCTGAAACCGAGA | GCTCCTTGAGGTTGAAAAGCA |
| <i>MESP1</i> | human | NM_018670 | ACGTGCTGGCTCTGTTG | GTCAGTTGTCCCTTGTCACTT |
| <i>MYH7</i> | human | NM_000257 | GGATGTCTTCGTGCCTGATG | GGTCTCCTTACGGTCACT |
| <i>MYL2</i> | human | NM_000432 | GGCGAGTGAACGTGAAAAAT | CAGCATTTCCCGAACGTAAT |
| <i>MYL7</i> | human | NM_021223 | GAGGAGAATGGCCAGCAGGAA | GCGAACATCTGCTCCACCTCA |
| <i>TNNT2</i> | human | NM_000364 | TTCACCAAAGATCTGCTCCTCGCT | TTATTACTGGTGTGGAGTGGGTGTTG |

Supplementary Table S4. Primer sequences used for ChIP-qPCR in C2C12 cells

| Gene | Accession NO. | Forward sequence (5' - 3') | Reverse sequence (5' - 3') |
|---------------|----------------------|-----------------------------------|-----------------------------------|
| <i>B2m</i> | NM_009735 | TGCCAAACCCTCTGTACTTCT | TTAGGCCTCTTTGCTTTACCA |
| <i>Chd2</i> | NM_001081345 | CCGAGAAGTGTGTGTGTGTG | ACCTCCGTATCCTCCATCC |
| <i>IgH</i> | NG_005838 | TGGTGGGGCTGGACAGAGTGT | GCCGATCAGAACCAGAACACC |
| <i>Jag1</i> | NM_013822 | CAGCAAGCGAGCCCAGAG | TTCAAAGTTCCCAGCAGAG |
| <i>Smad7</i> | NM_001042660 | GCCAAAGGTCACCACCAT | TTGAGTTTCTTGAGCACCGA |
| <i>Gata4</i> | NM_008092 | CTACCTGGCCAGCTCCAGT | CCTTGCACGTGACTCCCTTA |
| <i>Gab1</i> | NM_001301298 | CCCAGAGGACGTCTCAGATT | CCGATCGAGTTCTCTTCAG |
| <i>Notch1</i> | NM_008714 | CGTTAGGCAGAGCAAGGG | GTGGTGTGCGTCAACGTC |
| <i>Tbx3</i> | NM_011535 | TGACATAAACGCAGGACAGG | ACCAATTGTGTGGCTGCATA |
| <i>Cited2</i> | NM_010828 | ATGGGCGAGCACATACTA | ACCCATGAACTGGGAGTTGT |
| <i>Foxc2</i> | NM_013519 | AGAAGAAGGATGTGCCAAG | CCTCGCTCTTAACCACGACT |
| <i>Foxo1</i> | NM_019739 | GTCGTACGCCGACCTCAT | GACAGGGTGAGCCTCTTCTC |
| <i>Foxp1</i> | NM_001197321 | CAGGCGAGAAACGGAGAG | AGCTCTTCTCTGCGACACG |
| <i>Vegfa</i> | NM_001025250 | TTGAATATCAAATCCCAGAGCA | GCAGCGACAAGGCAGACTAT |
| <i>Hey1</i> | NM_010423 | GGGTGAGCTCTTTCATGGT | GCAGTTAACTCCTCCTTGCC |
| <i>Hey2</i> | NM_013904 | AGGAGGAGCAGCTACTGTGCG | CAGCGTGGGAAAGAACCT |
| <i>Meis1</i> | NM_010789 | AGACACTCCACAAATTCGCA | GCTGCAGCCTGTATTTGTGT |
| <i>Pbrm1</i> | NM_001081251 | GCGCACACACATACACTGTC | CCCAGTGCTGCCGTAAAT |

Supplementary Table S5. Demography of human subjects.

NH: normal heart, HCM: hypertrophic cardiomyopathy, AS: aortic stenosis

| Clinical diagnosis | Age | Gender |
|---------------------------|------------|---------------|
| NH | 55 | male |
| | 43 | male |
| | 57 | female |
| | 37 | female |
| AS | 64 | male |
| | 68 | male |
| | 81 | female |
| | 68 | female |
| HCM | 50 | male |
| | 42 | male |
| | 53 | female |
| | 57 | female |
| | 51 | female |
| | 42 | female |
| | 50 | female |
| 49 | female | |

Supplementary Table S6. E-box motif identified within DPF3a peaks.

For ChIP-chip, C2C12 cells were transfected with Flag-DPF3a and ChIP was performed using anti-Flag antibody.

| Method | Cell type | Antibody for ChIP | Total peaks | Peaks with E-box |
|---------------|------------------------|--------------------------|--------------------|-------------------------|
| ChIP-chip | C1C12 undifferentiated | Flag | 134 | 88 |
| ChIP-seq | C1C12 undifferentiated | pDPF3a | 777 | 709 |
| ChIP-seq | C1C12 differentiated | pDPF3a | 821 | 782 |