

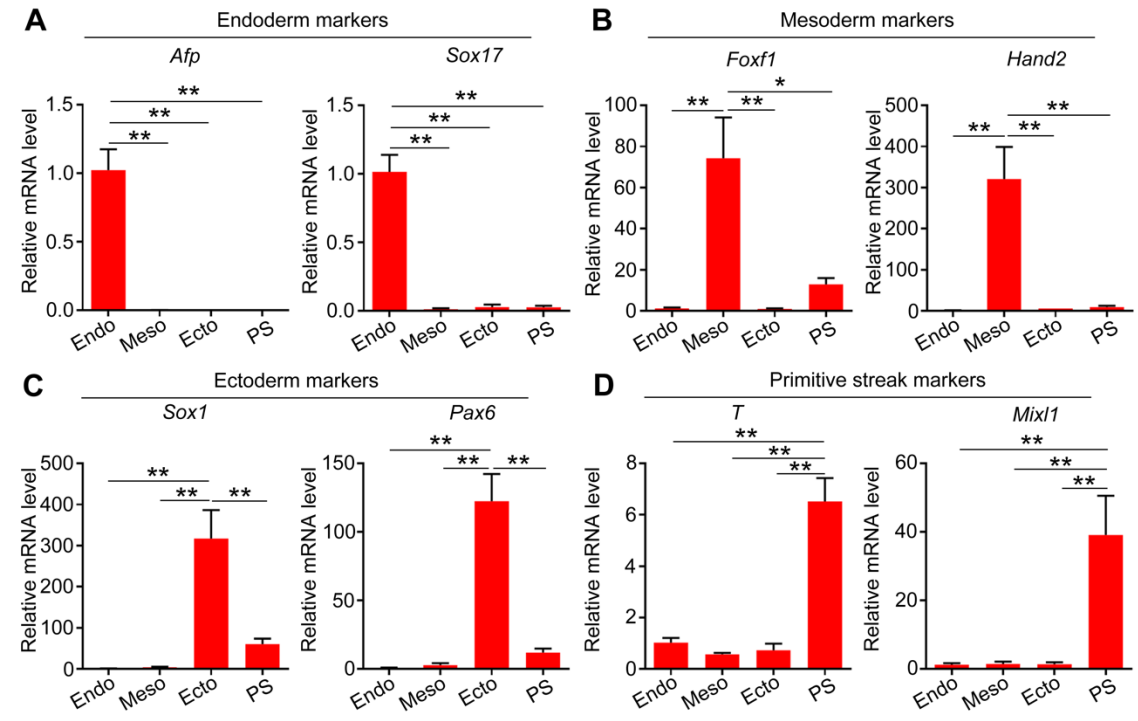
## SUPPLEMENTAL INFORMATION

### **Retinoic acid promotes metabolic maturation of human embryonic stem cell-derived cardiomyocytes**

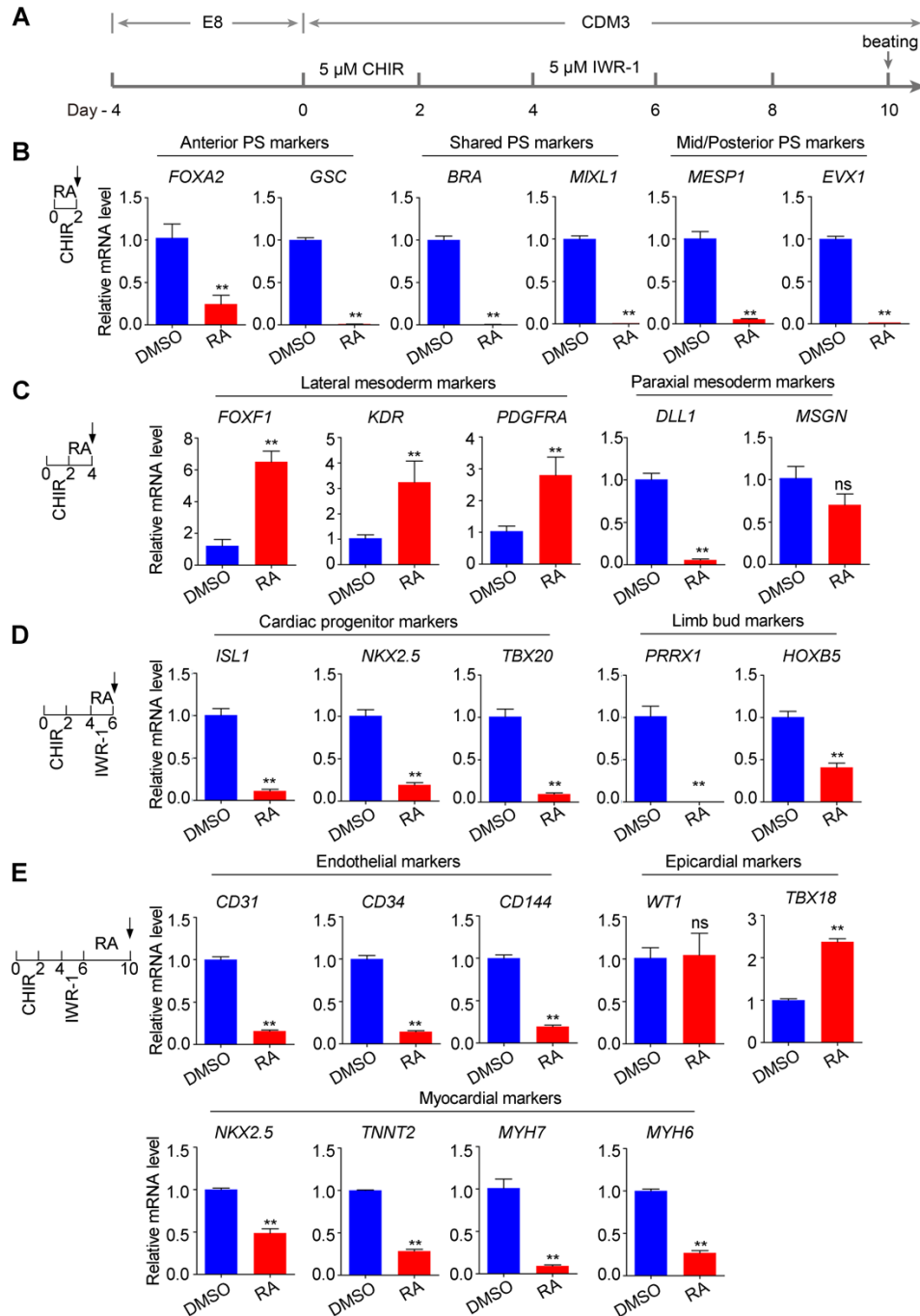
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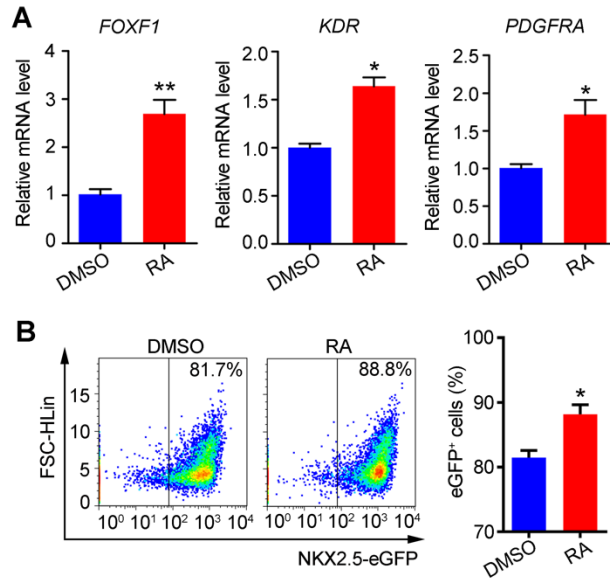
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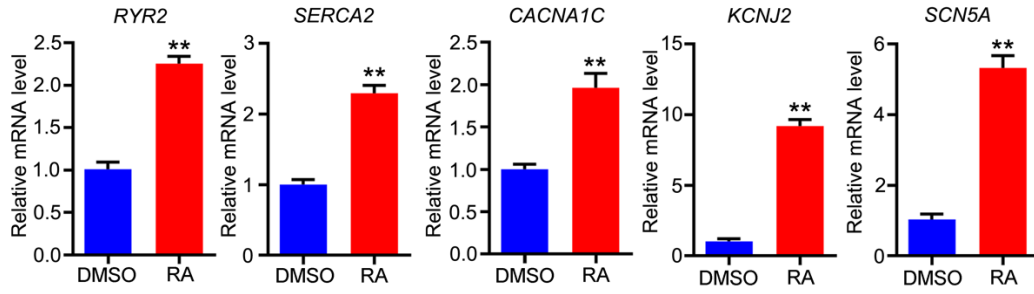
**Figure S1. Germ layer marker expressions in dissected mouse embryo tissues.** (A) Expression patterns of endoderm markers *Afp* and *Sox17*. (B) Expression patterns of mesoderm markers *Foxf1* and *Hand2*. (C) Expression patterns of ectoderm markers *Sox1* and *Pax6*. (D) Expression patterns of primitive streak markers *T* and *Mixl1*. Endo: endoderm; Meso: mesoderm; Ecto: ectoderm; PS: primitive streak. Student's *t*-test; \* $p < 0.05$ ; \*\* $p < 0.01$ .



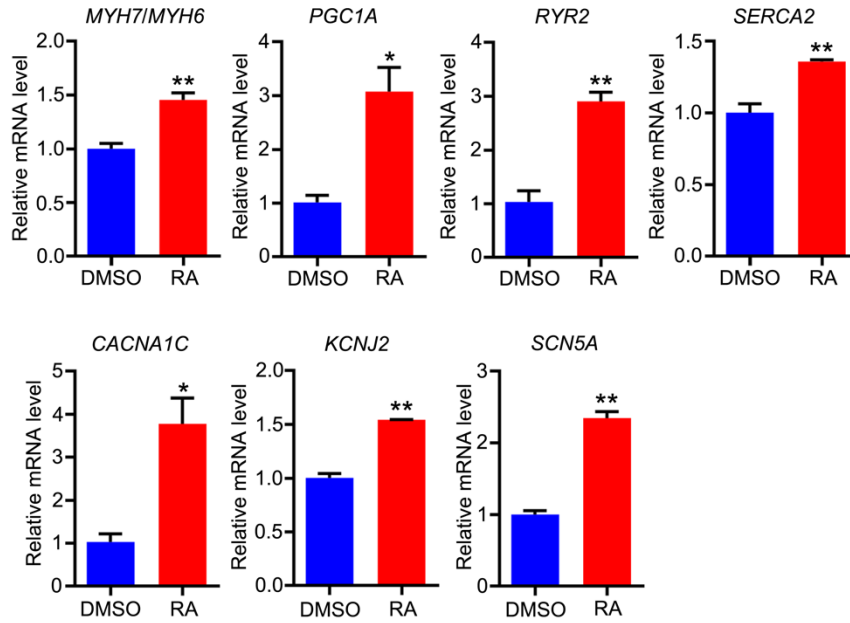
**Figure S2. RA treatment during cardiomyocyte differentiation.** (A) Schematic diagram of cardiomyocyte differentiation from hESCs. (B) Real-time PCR showed the expression levels of anterior PS, shared PS and mid/posterior PS markers in the DMSO- or RA-treated hESC-derived cells on day 2 of differentiation. PS: primitive streak. The downward arrow indicates the time point for qPCR detection. (C) Real-time PCR showed that RA promoted lateral mesoderm differentiation but not paraxial mesoderm differentiation. (D) Real-time PCR showed that cardiac progenitor markers and limb bud markers were significantly inhibited after RA treatment on days 4-6. (E) Real-time PCR showed that RA treatment on days 6-10 mainly inhibited the expression levels of endothelial and myocardial markers. Student's *t*-test; \*\**p*<0.01, and ns, not significant.



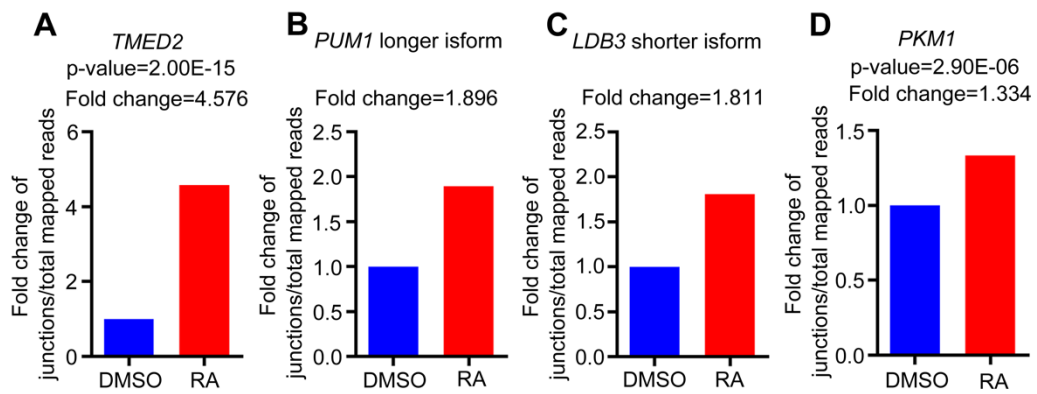
**Figure S3. RA treatment on days 2-4 induces lateral mesoderm and cardiomyocyte differentiation in the NKX2.5<sup>eGFP/w</sup> hES3 line.** (A) Real-time PCR showed that RA significantly increased lateral mesoderm markers on day 4 of differentiation. (B) Flow cytometry analysis of differentiated cardiomyocytes (day 10) showed that the proportion of NKX2.5-eGFP<sup>+</sup> cells was increased after RA treatment. Student's *t*-test; \**p*<0.05; \*\**p*<0.01.



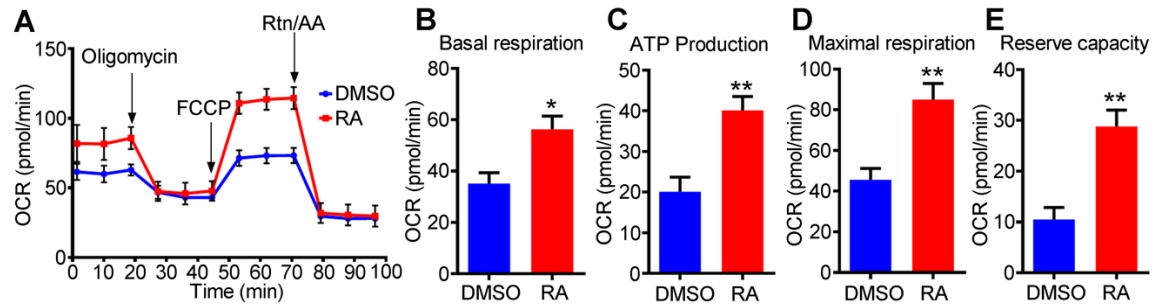
**Figure S4. The effect of RA (days 15-20) on maturation marker expressions in cardiomyocytes derived from NKX2.5<sup>eGFP/w</sup> hES3 line on day 30. Student's *t*-test; \*\*  $p < 0.01$ .**



**Figure S5. The effect of RA (days 15-20) on maturation marker expressions in cardiomyocytes derived from H1 hESC line on day 30. Student's *t*-test; \**p*<0.05; \*\**p*<0.01.**

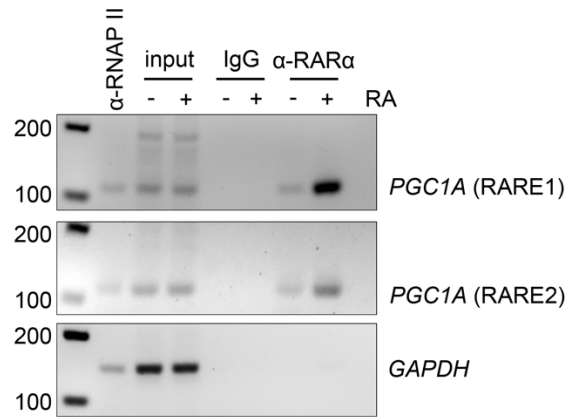


**Figure S6. Quantification of RNA splicing.**

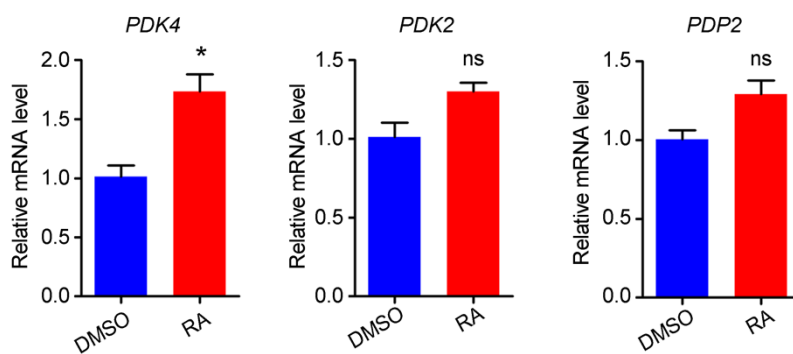


**Figure S7. RA promotes the oxidative phosphorylation of cardiomyocytes derived from H1 hESC line.** (A) Representative OCR traces of the DMSO- and RA-treated hESC-CMs derived from H1 ESCs in the presence of both glucose and pyruvate obtained using a Seahorse XF24 Extracellular Flux Analyzer. (B-E) Quantification of basal respiration (B), ATP production (C), maximal respiration (D) and reserve capacity (E). Student's *t*-test; \**p*<0.05; \*\**p*<0.01.





**Figure S8. ChIP-PCR reveals the direct binding of RAR $\alpha$  to RAREs in *PGC1A* promoter after RA treatment in hESC-CMs.** The two RAREs in *PGC1A* promoter were named as RARE1 (-229 bp ~ -212 bp: 5'-AGGGTTATCTGGGGGCGA-3') and RARE2 (-70 bp ~ -53 bp: 5'-TGA CTCTGAGATGCCCTC-3'), respectively.



**Figure S9. The effects of RA (days 15-20) on the expression of mitochondrial genes related to pyruvate metabolism.** *PDK4*: pyruvate dehydrogenase kinase 4; *PDK2*: pyruvate dehydrogenase kinase 2; *PDP2*: pyruvate dehydrogenase phosphatase catalytic subunit 2. Student's *t*-test; \* $p < 0.05$ , and ns, not significant.

SUPPLEMENTAL TABLES

Table S1. Mouse primer sequences used for quantitative real-time PCR.

<b>Genes</b>	<b>Forward</b>	<b>Reverse</b>
<i>Rbp1</i>	AGGCATAGACGACCGCAAGT	ATCCACTGCGTCCAGCCAC
<i>Aldh1a2</i>	ATCGCTTCTCACATCGGCATAG	CCTCCGAGTTCAGGGTCA
<i>Crabp1</i>	CATGCTGAGGAAGGTGGCC	TGAAGTTGATCTCCGTGGTGC
<i>Cyp26a1</i>	GGGTTTCGGGTTGCTCTG	CGGGATTAAATTCCTCCTTG
<i>Rbp4</i>	ACGAGTCCGTCTTCTGAGCAA	TGGAGAAAGGAGGCTACACCC
<i>Stra6</i>	TCGCCAAGCCATAGTCAGC	GCAGTAAAGGCACAAACACCAG
<i>Afp</i>	CAGCCAAAGTGGAGTGGAAG	GGAAACTGGAAGGGTGGGAC
<i>Sox17</i>	CTTTATGGTGTGGGCCAAAG	TTCCAAGACTTGCCTAGCATC
<i>Foxf1</i>	GCATCCCTCGGTATCACTCAC	ATCCTCCGCCTGTTGTATGC
<i>Hand2</i>	TCCCCACCTCCCTCTCCA	CACACAGAGAATGACGGGGGT
<i>Sox1</i>	AGACTTCGAGCCGACAAGAG	AACTGTGCAAACAGGTGCAG
<i>Pax6</i>	TAACGGAGAAGACTCGGATGAAGC	CGGGCAAACACATCTGGATAATGG
<i>T</i>	CCAGAATGAGGAGATTACAGCC	TGGTCGTTTCTTTCTTTGGC
<i>Mixl1</i>	CGCTCCCTCAGTAACAACGC	GCTGCCACAGACTTCCAAATG
<i>Gapdh</i>	CCCAATGTGTCCGTCGTG	TGCCTGCTTCACCACCTTCT

**Table S2. Human primer sequences used for quantitative real-time PCR.**

<b>Genes</b>	<b>Forward</b>	<b>Reverse</b>
<i>STRA6</i>	CCTACACGCTGCTGCACAA	GGAACATGCCTCAGCACAGA
<i>FOXA2</i>	AGGGCCAGAGTTCACAAATC	GGGTATCCCTCCCTCCTTCTT
<i>GSC</i>	GAGGAGAAAGTGGAGGTCTGGTT	CTCTGATGAGGACCGCTTCTG
<i>BRA</i>	ACTACACACCCCTCACCCAT	GTACTGGCTGTCCACGATGT
<i>MESPI</i>	CCTGAAGGGCAGGCGATG	CCTTGTCACTTGGGCTCCTC
<i>EVX1</i>	AGTGACCAGATGCGTCGTTAC	TGGTTTCCGGCAGGTTTAG
<i>FOXF1</i>	AGCAGCCGTATCTGCACCAGAA	CTCCTTTCGGTCACACATGCTG
<i>KDR</i>	ATGTCAGAAAAGGAGATGCTCGC	TTTCCACAGCAAAAACACCAA
<i>PDGFRA</i>	AGAGGAACAGACACAGCTCG	TTCCACCAGGTCTGAAGAGTC
<i>DLL1</i>	ACTCCGCGTTCAGCAACCCCAT	TGGGTTTTCTGTTGCGAGGTCATCAGG
<i>MSGN</i>	CGGAATTACCTGCCACCTGT	GGTCTGTGAGTTCCCGGATG
<i>ISL1</i>	TACTGAGCGACTTCGCCTTG	GTGGAATTAGAGCCCGGTCC
<i>NKX2.5</i>	CTATCCGGGTACGGCGG	TGAACCGCATTCAAGTCCCC
<i>TBX20</i>	TGCGGTGGGGAATAGAGG	GGGAGACAAAGACCCGAAAC
<i>PRRX1</i>	TGATGCTTTTGTGCGAGAAGA	AGGGAAGCGTTTTTATTGGCT
<i>HOXB5</i>	AACTCCTTCTCGGGGCGTTAT	CATCCCATTGTAATTGTAGCCGT
<i>WT1</i>	GCCTCACTCCTTCATCAAACA	GGCCGAAAAGTGGACAGT
<i>TNNT2</i>	AGCGGAAAAGTGGGAAGAGG	CACAGCTCCTTGGCCTTCTC
<i>MYH7</i>	ACCTGTCCAAGTCCGCAAG	TCATTCAAGCCCTTCGTGCC
<i>MYH6</i>	CAAGAGCCGTGACATTGGTG	AGGTTGGCAAGAGTGAGGTT
<i>MYL7</i>	GCCTTACACTGCTCTTTGGG	CAGATGAAGGGTGACGGGAG
<i>IRX4</i>	CAGGATAGCCGGAGACGC	TTAGGAGGTGGCTGAGACGG
<i>SLN</i>	AGTTAGATGAAGACCTACAGCAGC	GAAGGCGGCTATGTAAGATGAG
<i>CD31</i>	TTGAGACCAGCCTGATGAAACCCT	TCCGTTTCTGGGTTCAAGCGATA
<i>CD34</i>	CAAGCCACCAGAGCTATTCC	TAGCCAGTGATGCCCAAGAC
<i>CD144</i>	CATCTTCCCAGGAGGAACAG	AGAGCTCCACTCACGCTCAG
<i>TBX18</i>	TCTGGCGACCATCACTACGG	GGGTGAGTGGCAGGAACG
<i>PGC1A</i>	GTCTAACTATGCAGACCTAGATTCA	CTGTCATCCTCAGCTAGGGAAC
<i>ENO1</i>	GGAGCAGGTTTACCACAA	CCTTCTTTATTCTCCAGGATGTT
<i>ALDOA</i>	GGCCTCCGTCTGGATTTC	GGGCATGGTGCTGGTAGTAG
<i>LDHA</i>	GACTTCTGAGGAAGAGGCC	CATGCACAACCTCCACCTAGA
<i>BPGM</i>	AGGGAGAAAATGGCTTTGAATC	TCGTGGAAGTAGGGATGAGACT
<i>PDK4</i>	GAACCTGGCAAAGAAGTGGC	AGGAGTTTTCTGTTGCTGTCG
<i>PDK2</i>	ATGGCAGTCCTCCTCTCTGA	CACCCACCCTCTTCTAACA
<i>PDP2</i>	GGTAGACGCTTATACTCCAGGT	CACATGGGGAAGTGTTAGGG
<i>SERCA2</i>	ACCTGGAACCTGTTCTTAGCTC	CATCACAGATGACAATTAGTGCC
<i>RYR2</i>	TCCGGAACAGTATGAAGACCA	CACACAACGCTGGCAATTCA
<i>CACNA1C</i>	CATGCTCACGGTGTTC	TCCTACGGCATCATTGACC
<i>KCNJ2</i>	TGTCACGGATGAATGCCAA	CTGCGCCAATGATGAAAGCA
<i>SCN5A</i>	TTCAGGGCTGAAGACCATCG	GCACTTGTGCCTTAGGTTGC
<i>18S</i>	GTAACCCGTTGAACCCATT	CCATCCAATCGGTAGTAGCG
<i>ND1</i>	AACCTCAACCTAGGCCTCCT	GAGTTTGATGCTCACCTGA
<i>(mtDNA)</i>		
<i>mtCO1</i>	ACGTTGTAGCCCACTTCCAC	CATCGGGTAGTCCGAGTAA
<i>(mtDNA)</i>		
<i>RNA18S5</i>	GCTGAGAAGACGGTCGAACT	CGCAGGTTACCTACGGAAA
<i>(genomic DNA)</i>		

**Table S3. Antibodies used in this study.**

<b>Antibody</b>	<b>Company</b>	<b>Catalog Number</b>	<b>Immunostaining</b>	<b>Flow cytometry</b>	<b>ChIP</b>
Troponin T (TNNT2)	Thermo Scientific	MS-295-P1	1:200	1:200	
Sarcomeric Alpha Actinin ( $\alpha$ -actinin)	Abcam	ab9465	1:200		
RAR $\alpha$	Abcam	ab41934			1: 1000
Alexa Fluor® 594	Jackson	711-585-152	1:1000		
AffiniPure Donkey Anti- Mouse IgG (H+L)	ImmunoResearch				
Alexa Fluor® 488	Jackson	715-545-151	1:1000		
AffiniPure Donkey Anti- Mouse IgG (H+L)	ImmunoResearch				
Alexa Fluor® 647	Jackson	715-605-151	1:1000		
AffiniPure Donkey Anti- Mouse IgG (H+L)	ImmunoResearch				

**Table S4. Human primer sequences used for ChIP-PCR.**

Target Region	Primer Sequence (5'→3')	Product Length (bp)
Predicated RARE1	Forward: ATAACATGTATGCATGCC	119
	Reverse: GTGAGTGTTCCCTCATCTCAT	
Predicated RARE2	Forward: GTGCCCTATTGTGGAGTTC	119
	Reverse : ATGAGATGAGGGAACACTCAC	