Supplementary Information

Phosphomimetic cardiac myosin-binding protein C partially rescues a cardiomyopathy phenotype in murine engineered heart tissue

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Primer	Sequence (5' to 3')
Mybpc3 S282D F	GAGCAGGTCGGAGAACCGATGACAGCCATGAAGATG
Mybpc3 S282D R	CATCTTCATGGCTGTCATCGGTTCTCCGACCTGCTC

Suppl. Table S1: Primer sequences for site-directed mutagenesis

Suppl. Table S2: Primer sequences for RT-PCR and RT-qPCR with SYBR-Green

Primer	Sequence (5' to 3')
FLAG F	GGATTACAAGGATGACGACGA
Gapdh F	ATTCAACGGCACAGTCAAG
Gapdh R	TGGCTCCACCCTTCAAGT
<i>Mybpc3 ex.1</i> F	CACCCCTGGTGTGACTGTTCTCAA
<i>Mybpc3 ex.2</i> R	GTCATCAGGGCTCGCATC
<i>Mybpc3 ex.2</i> R	CTGACCGCTCCGTCTCAG
<i>Mybpc3 ex.4</i> F	TCTTTCTGATGCGACCACAG
<i>Mybpc3 ex.9</i> R	TCCAGAGTCCCAGCATCTTC

Suppl. Table S3: Primers and probes sequences for RT-qPCR

Gene acronym	Full name	Primers/Probe	Sequence (5' to 3')
Gnas	Guanine	F	CAAGGCTCTGTGGGAGGAT
	nucleotide-	R	CGAAGCAGGTCCTGGTCACT
	binding protein,	Probe	FAM-GCTGATTGACTGTGCCCAGTACTTCCT-TAMRA
	alpha		
	stimulating		
Mybpc3	Myosin-binding	WT/Mut1 F	GTGTCTACCAAGGACAAATTTGACA
	protein C,	WT/Mut1 R	CCAGGTCTCCAGAACCAATG
	cardiac	WT Probe	FAM-AACCTCACTGTCCATGAG-MGB
		Mut1 Probe	VIC-CTCACTGTCCATAAGG-MGB
		Mutant 2/3 F	TGGACCTGAGCAGCAAAGTG
		Mutant 2/3 R	GGTCCAGGTCTCCAGAACCA
		Mutant 2/3 Probe	FAM-CCAGCAAGAGGCCA-MGB

	Gene acronym	Gene full name	wт	KI-NT	KI-S282	KI-D282
~	Actc1	Actin, alpha, cardiac muscle 1	1.00	2.03	1.32	1.49
	Ctgf	Connective tissue growth factor	1.00	1.39	1.22	1.21
hqo	Fhl1	Four-and-a-half-LIM-domains 1	1.00	1.78	1.16	1.49
Ť	Meox	Mesenchyme homeobox 1	1.00	2.16	2.21	2.13
ype	Myh7	Myosin, heavy polypeptide 7, cardiac muscle, beta	1.00	3.58	1.24	2.63
–	Nppb	Natriuretic peptide B	1.00	1.94	0.65	1.04
	Rcan1	Regulator of calcineurin 1	1.00	1.63	1.05	1.30
ğ	Cacna1c	Calcium channel, voltage-dependent, L type, alpha 1C subunit	1.00	1.44	1.20	1.29
dli	Cacna1g	Calcium channel, voltage-dependent, T type, alpha 1G subunit	1.00	1.57	1.82	1.36
Jan	Gja1	Gap junction protein, alpha 1, 43kDa	1.00	1.47	1.07	1.16
a [,]	Pln	Phospholamban	1.00	1.44	1.39	1.42
Ű	Ryr2	Ryanodine receptor 2, cardiac	1.00	11.33	1.17	6.02
+ 5	Kcnb1	Potassium voltage gated channel, Shab-related subfamily, member 1	1.00	1.36	1.46	1.40
Na-	Kcnip2	Kv channel-interacting protein 2	1.00	3.55	0.78	2.17
K+/	Kcnj2	Potassium inwardly-rectifying channel, subfamily J, member 2	1.00	nd	1.17	nd
– e	Scn5a	Sodium channel, voltage-gated, type V, alpha	1.00	1.39	1.10	1.54
	Actn2	Actinin alpha 2	1.00	1.47	1.30	1.32
	Cryab	Crystallin, alpha B	1.00	1.57	1.28	1.41
mere	Csrp3	Cysteine and glycine-rich protein 3	1.00	1.61	1.27	1.55
	Des	Desmin	1.00	2.53	1.07	1.42
	Flnc	FilaminC	1.00	1.48	0.95	1.43
	Ldb3	LIM domain binding 3	1.00	1.69	1.36	1.46
	Myl2	Myosin, light polypeptide 2, regulatory, cardiac	1.00	1.71	1.75	1.76
	Myl3	Myosin, light polypeptide 3, essential, cardiac	1.00	1.69	1.48	1.54
arco	Myoz2	Myozenin 2	1.00	1.60	1.44	1.36
Sa	Mypn	Myopalladin	1.00	2.18	1.45	1.20
	Муzap	Myocardial zonula adherens protein	1.00	2.05	1.34	1.24
	Nexn	Nexilin	1.00	1.52	1.28	1.49
	Obscn	Obscurin	1.00	1.53	1.17	1.77
	Тсар	Telethonin	1.00	1.34	1.87	1.41
	Tnnc1	Troponin C, cardiac	1.00	1.46	1.31	1.33
	Ttn	Titin	1.00	1.62	1.29	1.60

Suppl. Table S4: Gene acronym, full name and expression level in WT, KI-NT, KI-S282 and KI-D282 EHTs

Values in KI-NT, KI-S282 and KI-D282 are given in fold-change over WT. nd: not-determined.



Suppl. Fig. 1 Immunofluorescence images of KI EHTs transduced with AAV6 encoding wild-type cMyBP-C **(S282) or phosphomimetic cMyBP-C (D282)** KI EHTs were transduced at MOI of 1,000 vg/cell. After fixation EHTs were co-stained with antibodies directed against the FLAG-tag for exogenous cMyBP-C (green) and total cMyBP-C (red). Nuclei were stained with DRAQ5 (blue). Scale bars 20 μm. Higher magnifications (zoom-in) images are shown on the right side. Scale bars 5 μm.



Suppl. Fig. 2 Contraction velocity (CV) and relaxation velocity (RV) measured on the day of highest force development [a]-[b] Contraction and relaxation velocities under spontaneous contraction. Numbers of EHTs/batches: WT 51/5; KI-NT 61/7; KI-S282 26/5; KI-D282 20/5. [c]-[d] Contraction and relaxation velocities calculated under electrical stimulation. WT n = 15; KI-NT n = 8; KI-S282 n = 6; KI-D282 n = 7. Data are expressed as mean \pm SEM. ***P*<0.01 vs. WT, one-way ANOVA plus Dunnett's multiple comparisons test.



Suppl. Fig. 3 Effect of isoprenaline on relaxation time (T2_{20%}) under electrical stimulation. EHTs of all groups were treated 15 min with 100 nM isoprenaline at submaximal external [Ca²⁺] in Tyrode's solution and paced at 6 Hz. T2_{20%} was decreased in WT, S282 (*P <0.05 Student's t-test) and D282 EHTs.

Full agarose gels. Red rectangles show the selected part, red arrow shows displayed bands in the figures



Fig. 1a upper panel



Fig. 1a middle panel

Fig. 1a bottom panel

kDa den one Fig.1g FLAG 150 100 3 kDa 150 Fig.1g α -Actinin 100 1.







Fig.1i pSer-282 cMyBP-C



Fig.1i α-Actinin