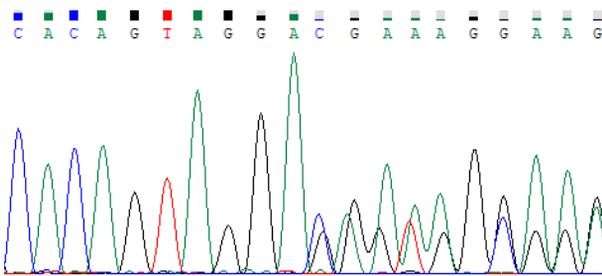
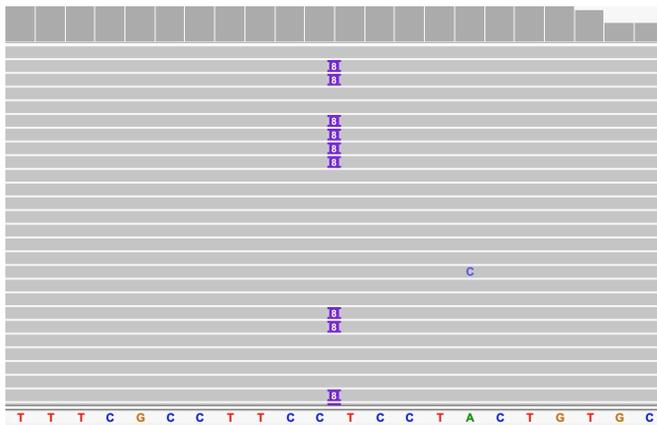
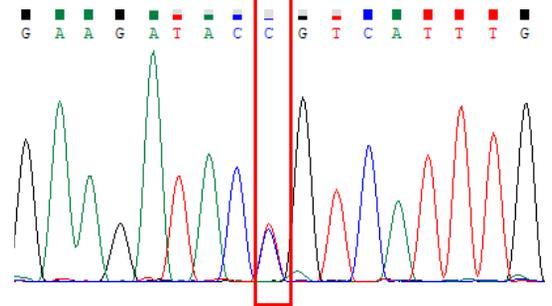
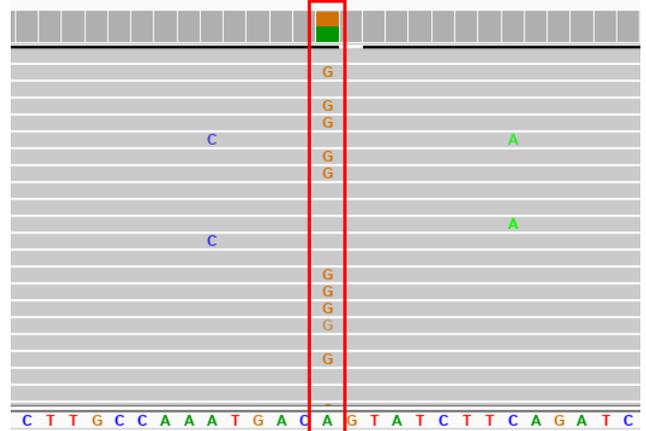


A

c.377_384dup

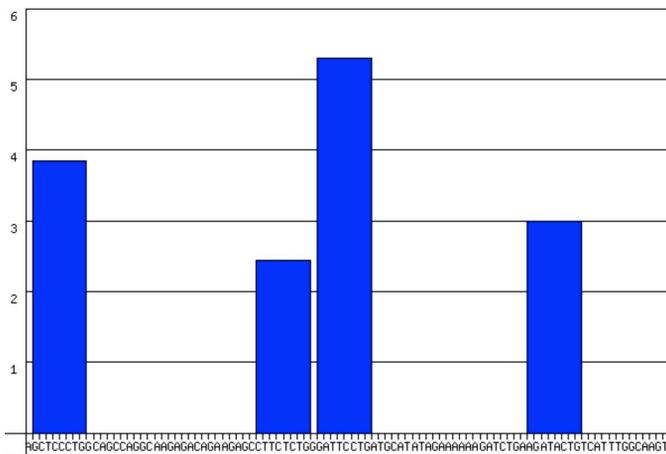


c.243+1548T>C

**B**

agCTCCCTG-----CTTCTCTGGGATTCTCTG-----AGATACT/CG-----gt
 ag **PSEUDOEXON** gt

wild-type



c.243+1548T>C

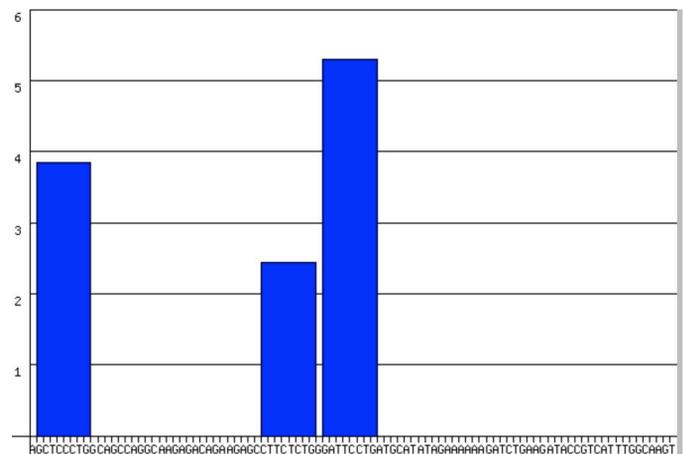


Figure S1 Genetics findings in our Patient. (A) Integrated Genomics Viewer (IGV) screenshots and sequence electropherograms displaying the *SGCB* variants detected in the Patient described in the manuscript. (B) ESE-finder 3.0 screenshots showing the prediction of the Serine And Arginine Rich Splicing Factor 2 (SRSF2) splicing factor binding sites (in blue in the sequence) in wild-type and mutated (c.243+1548T>C) sequence.

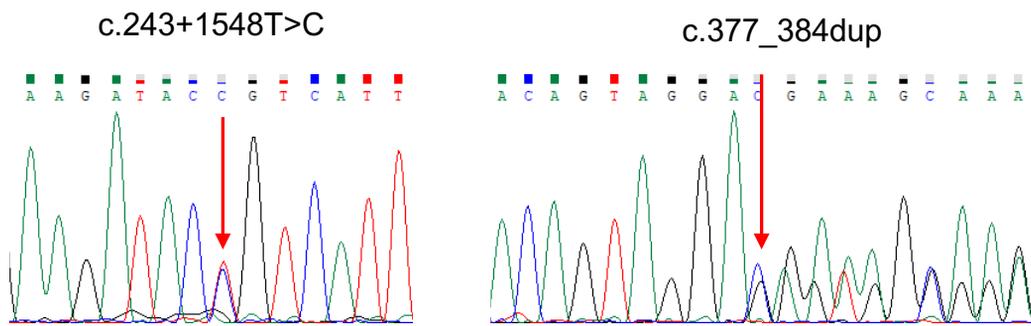
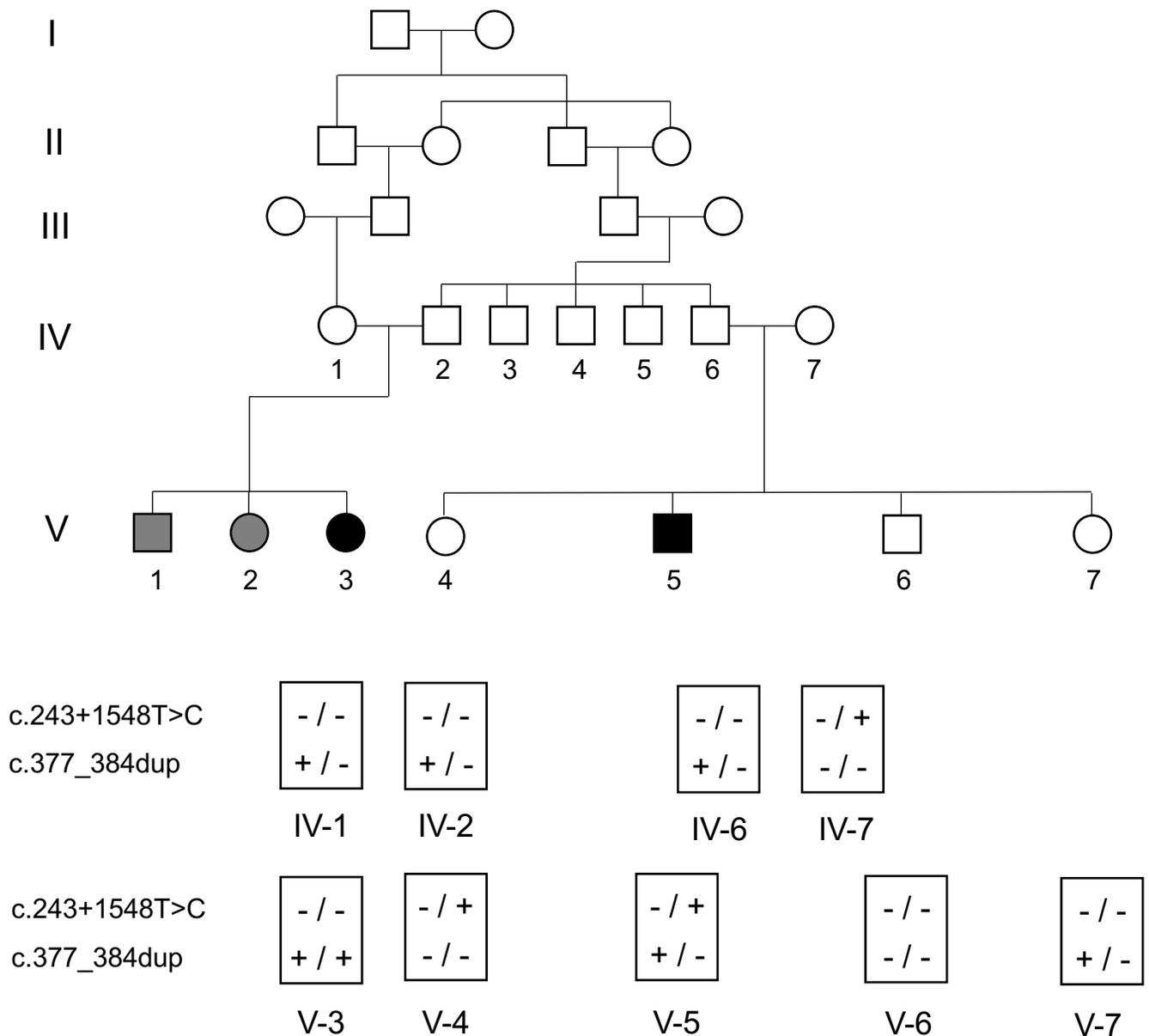
A**B**

Figure S2 Genetic findings in a previously reported LGMDR4 patient. (A) Sequence electropherograms displaying the *SGCB* variants detected in the Patient V-A described in Barresi *et al.*, 2000. (B) Pedigree of the family described in Barresi *et al.*, 2000 now reporting the genotype of the *SGCB* c.243+1548T>C and c.377_384dup variants in available family members.

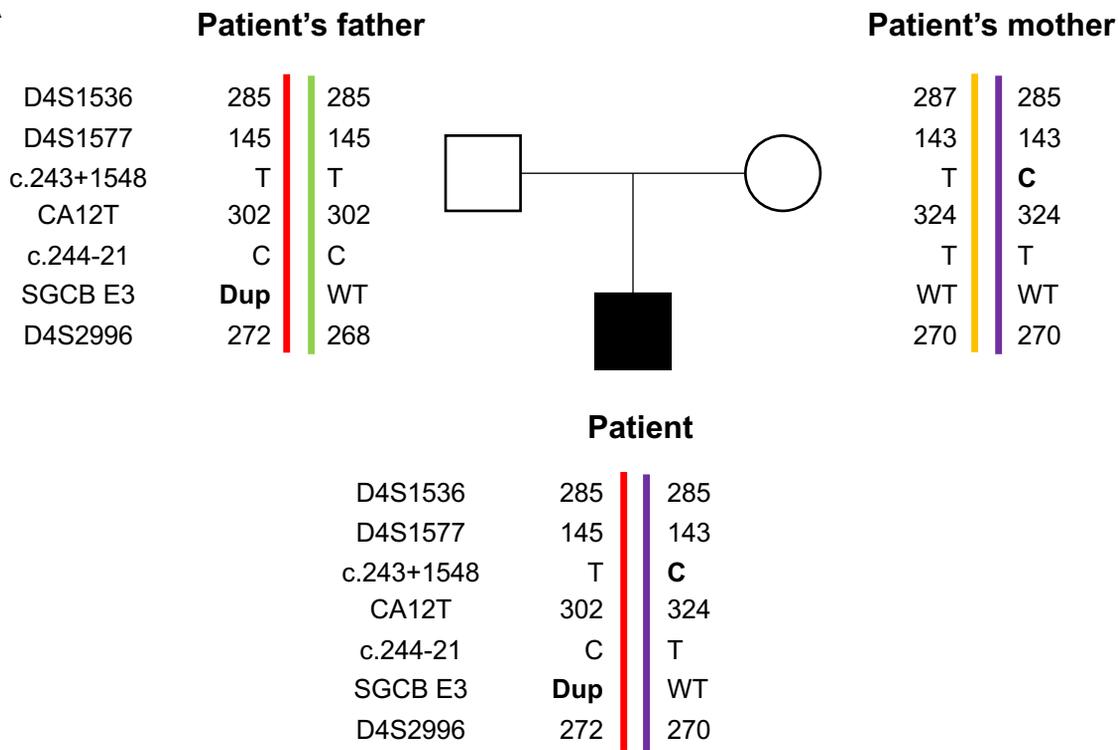
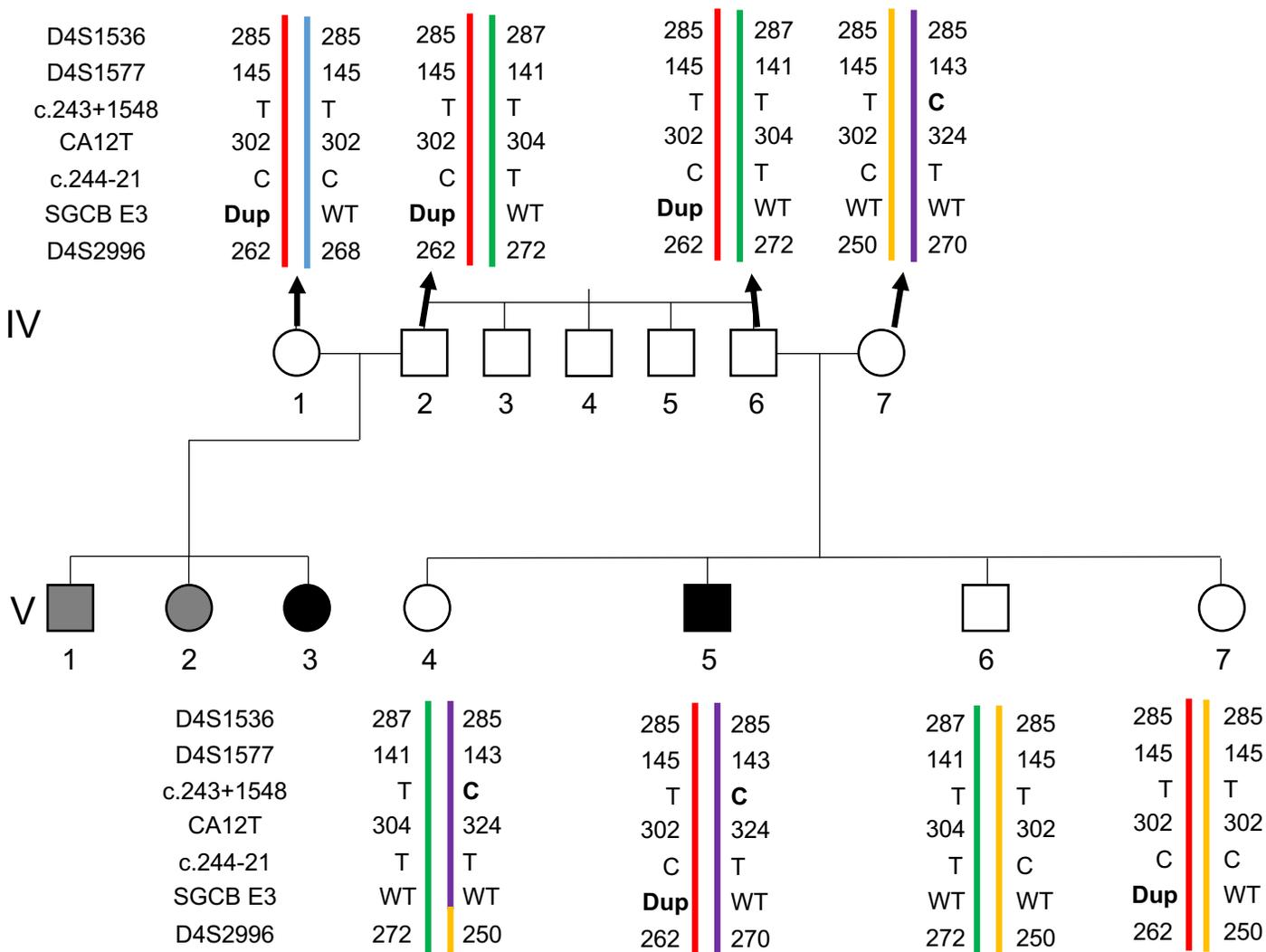
A**B**

Figure S3 Microsatellite analysis around SGCB locus in the pedigrees described. Microsatellite markers analysis in the family described in the manuscript (A) and in the pedigree previously reported by Barresi *et al.*, 2000 (B). "Dup" indicates an allele harboring the c.377_384dup mutation.

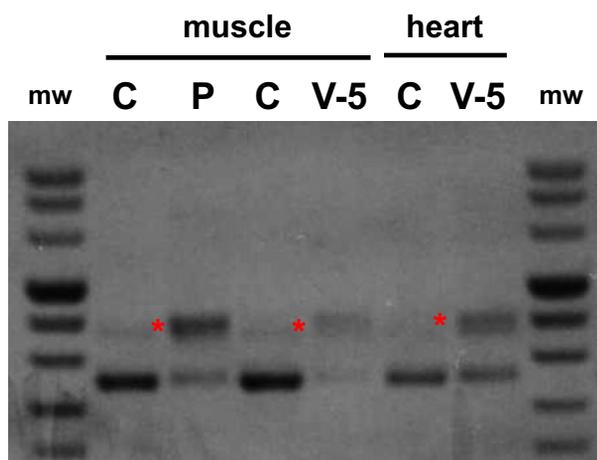
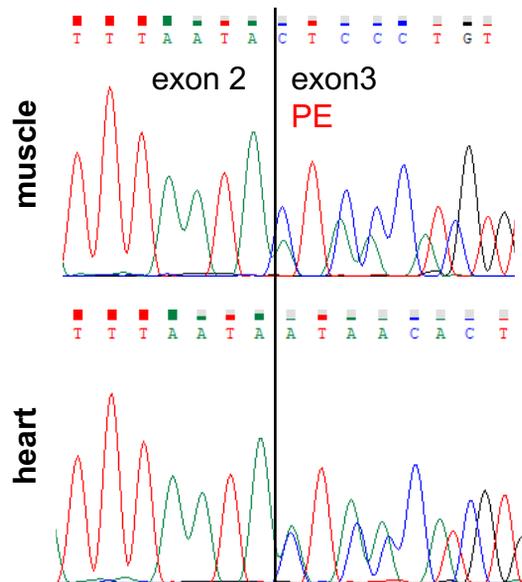
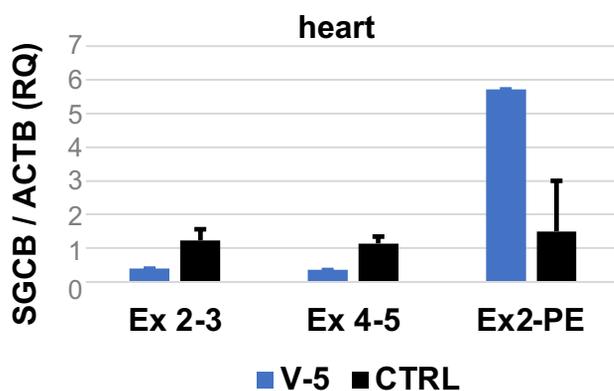
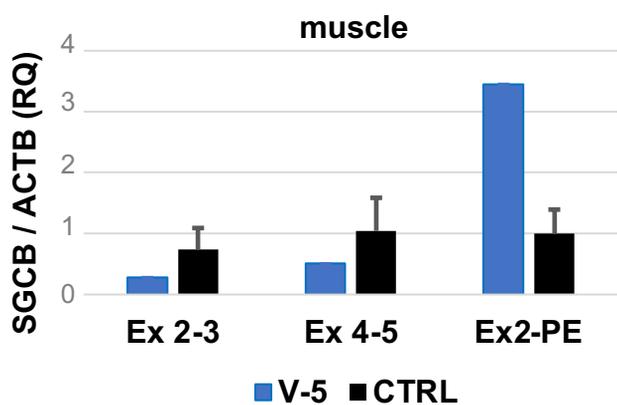
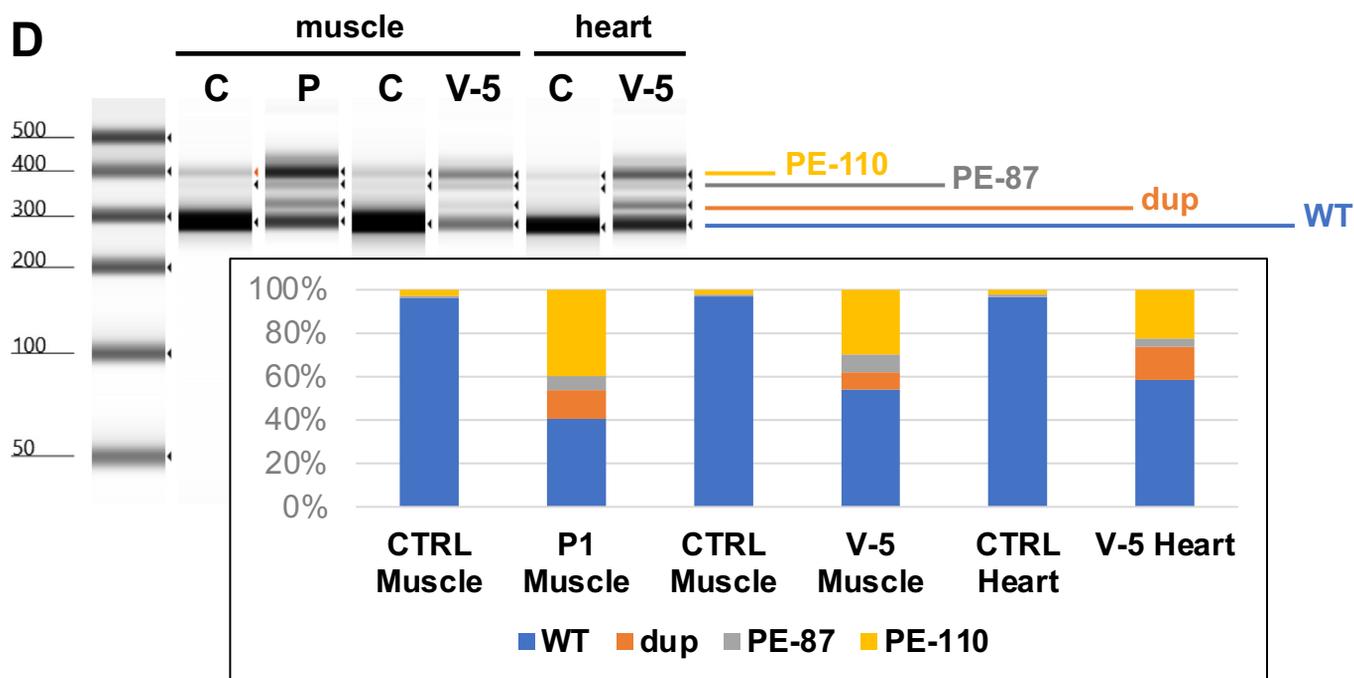
A**B****C****D**

Figure S4 Transcript analysis of SGCB in a previously described LGMDR4 patient. (A) RT-PCR analysis of *SGCB* transcripts in tissues collected from the patient described in the manuscript (P), the previously-reported patient V-5 and controls (C). (B) Sequence electropherograms displaying the abnormal Exon2-PE junction in Patient V-5's tissues. (C) Quantitative RT-PCR experiments evaluating physiological (Ex2-Ex3, Ex4-Ex5) and abnormal (Ex2-PE) splicing junctions in Patient V-5's tissues and control biopsies (n=3). (D) Tape station analysis of RT-PCR amplicons showed in panel A documenting the presence of different levels of aberrant and physiological splicing products in patients' and control tissues.

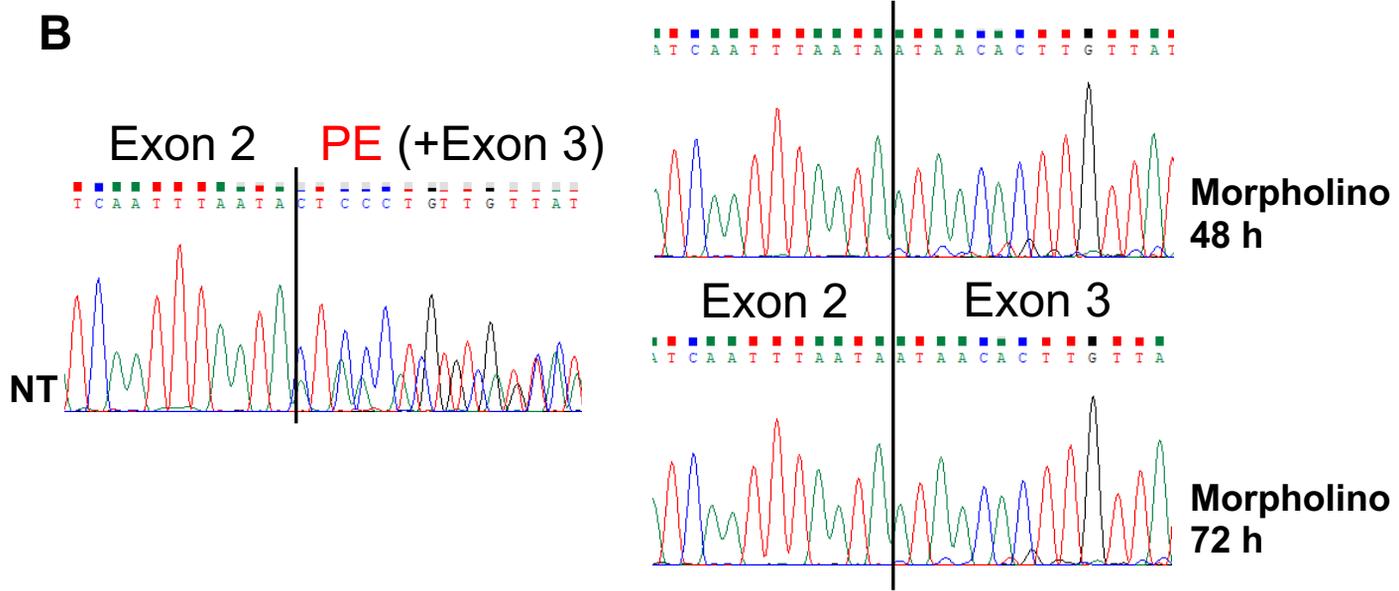
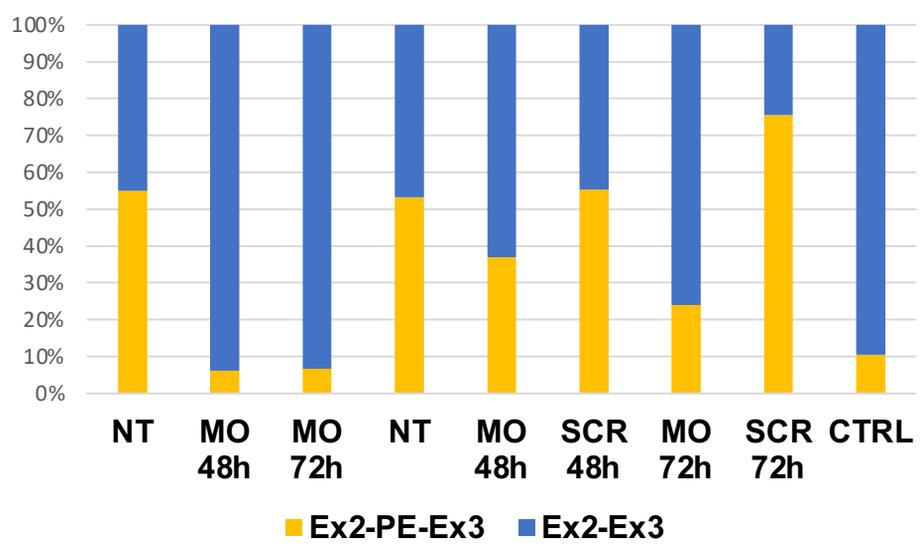
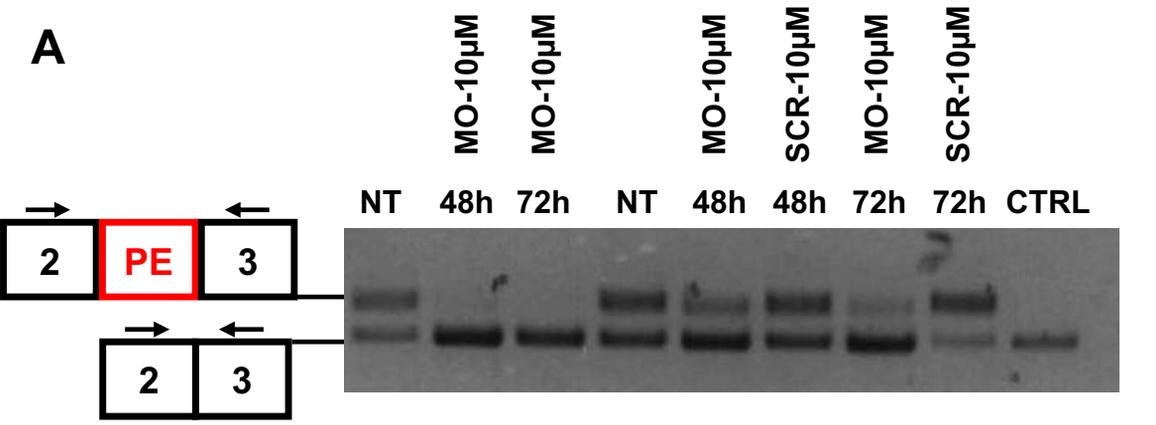


Figure S5 In vitro correction of splicing defect after Morpholino treatment. (A) RT-PCR analysis of *SGCB* transcript in patient's derived iPSC before (NT, untreated) and after the delivery of Morpholino 10 μ M (MO) documenting the correction of the splicing defect in treated cells. The delivery of a morpholino scrambled sequence (SCR) did not result in splicing correction. A control cell line was also included (CTRL). Bars under the gel represents the proportion of normally spliced (Ex2-Ex3) and abnormally-spliced (Ex2-PE-Ex3) *SGCB* transcripts, as calculated after densitometry. (B) Sequence electropherograms displaying the restoration of the physiological splicing after Morpholino delivery.

Gene	Inheritance	OMIM	Locus
ANO5	AD, Ar	166260, 613319, 611307	11p14.3
B3GALNT2	Ar	615181	1q42.3
B4GAT1	Ar	615287	11q13.2
BVES	Ar	616812	6q21
CACNA1S	AD	170400, 601887, 188580	1q32.1
CAPN3	AD, Ar	618129, 253600	15q15.1
CAV3	AD, DD	192600, 123320, 611818, 614321, 606072	3p25.3
CLCN1	AD, Ar	160800, 255700	7q34
COL6A1	AD, Ar	158810, 254090	21q22.3
COL6A2	Ar, AD	255600, 158810, 254090	21q22.3
DAG1	Ar	616538, 613818	3p21.31
DMD	XLr	300376, 302045, 310200	Xp21.2-p21.1
DNAJB6	AD	603511	7q36.3
DPM3	Ar	618992, 618992	1q22
DYSF	Ar	254130, 253601, 606768	2p13.2
FKRP	Ar	613153, 606612, 607155	19q13.32
FKTN	Ar	611615, 253800, 613152, 611588	9q31.2
GAA	Ar	232300	17q25.3
GFPT1	Ar	610542	2p13.3
GMPPB	Ar	615350, 615351, 615352	3p21.31
POMGNT2	Ar	614830, 618135	3p22.1
HNRPDL	AD	609115	4q21.22
CRPPA	Ar	614643, 616052	7p21.2
KCNJ2	AD	170390, 613980, 609622	17q24.3
LAMA2	Ar	607855, 618138	6q22.33
LARGE1	Ar	613154, 608840	22q12.3
LMNA	AD, Ar	115200, 605588, 181350, 616516, 610140, 176670, 151660, 212112, 248370, 613205, 619793	1q22
MYOF	AD	619366	10q23.33
PLEC	Ar, AD	616487, 131950, 226670, 612138, 613723	8q24.3
POGLUT1	Ar, AD	617232, 615696	3q13.33
POMGNT1	Ar	253280, 613151, 613157, 617123	1p34.1
POMK	Ar	616094, 615249	8p11.21
POMT1	Ar	236670, 613155, 609308	9q34.13
POMT2	Ar	613150, 613156, 613158	14q24.3
POPDC3	Ar	618848	6q21
PYROXD1	Ar	617258	12p12.1
RYR1	AD, Ar	117000, 619542, 255320, 145600	19q13.2
SCN4A	AD, Ar	170500, 613345, 614198, 608390, 168300	17q23.3
SGCA	Ar	608099	17q21.33
SGCB	Ar	604286,	4q12
SGCD	Ar	606685, 601287	5q33.2-q33.3
SGCG	Ar	253700	13q12.12
SMPX	XLD, XLR	300066, 301075	Xp22.12
TCAP	AD, Ar	607487, 601954	17q12
RXYLT1	Ar	615041	12q14.2
TNPO3	AD	608423	7q32.1
TOR1AIP1	Ar	617072	1q25.2

Table S1: Genes included in our NGS-panel.