

Neonatal-lethal dilated cardiomyopathy due to a homozygous *LMOD2* donor splice-site variant.

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Introduction

Inherited dilated cardiomyopathy is characterised by enlargement of the heart, ventricular dilation and normal or reduced thickness of the left ventricular wall (**Figure 1**). Patients display impaired ventricular contractility and commonly progressive heart disease which may result in heart failure if left untreated.¹ Inherited dilated cardiomyopathy has been associated with mutations in >50 genes, many genes encode for structural proteins of the cardiac sarcomere (e.g. *TTN*, *MYH7*, *TNNT2*, *MYBPC3*).^{2,3}

LMOD2 encodes leiomodins-2 (*LMOD2*), an actin filament associated protein. *LMOD2* binds the pointed-end of the sarcomeric thin filament and regulates thin filament length in chicken, mouse and human cardiomyocytes.⁴⁻⁷

Recently, a single patient with homozygous nonsense variant in *LMOD2* (c.1193G>A, p.Trp398*) has been identified, suggesting *LMOD2* may be a novel dilated cardiomyopathy disease gene.⁴

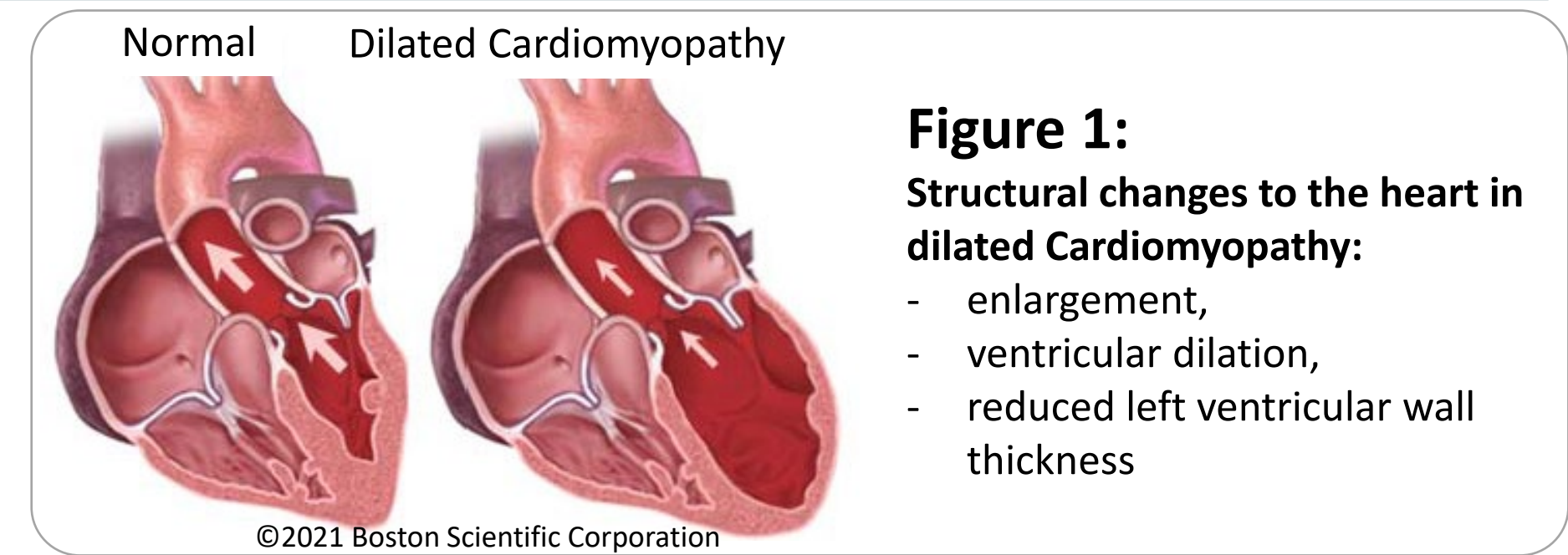


Figure 1:
Structural changes to the heart in dilated cardiomyopathy:
- enlargement,
- ventricular dilation,
- reduced left ventricular wall thickness

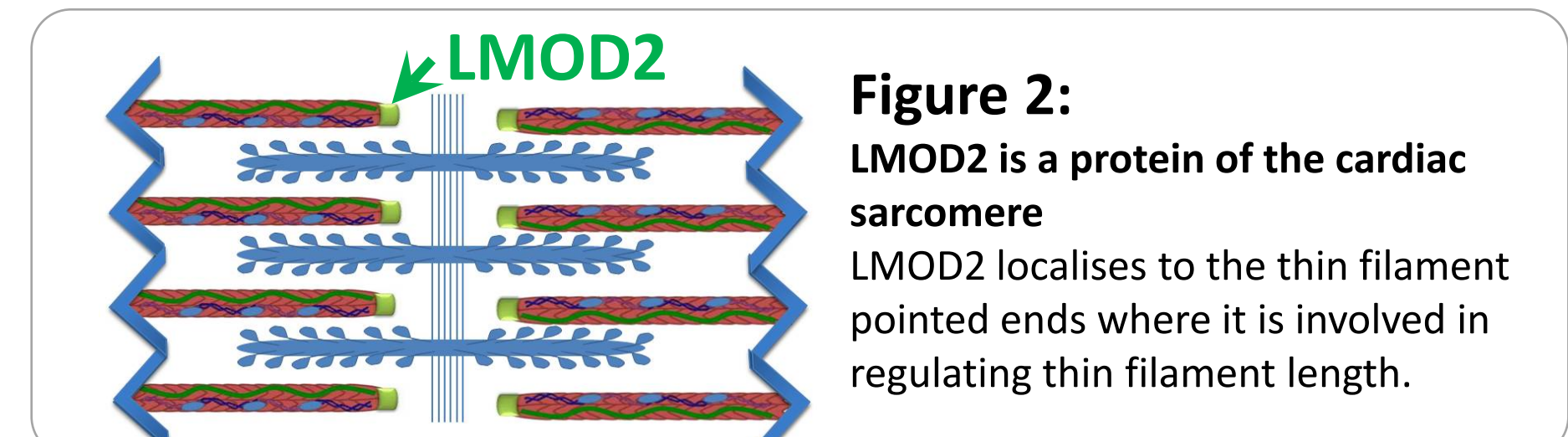


Figure 2:
LMOD2 is a protein of the cardiac sarcomere
LMOD2 localises to the thin filament pointed ends where it is involved in regulating thin filament length.

An *LMOD2* splice-site variant associated with neonatal heart failure

Here we report two siblings (III:3 and 4) which died shortly after birth due to heart failure (Pedigree in **Figure 3**).

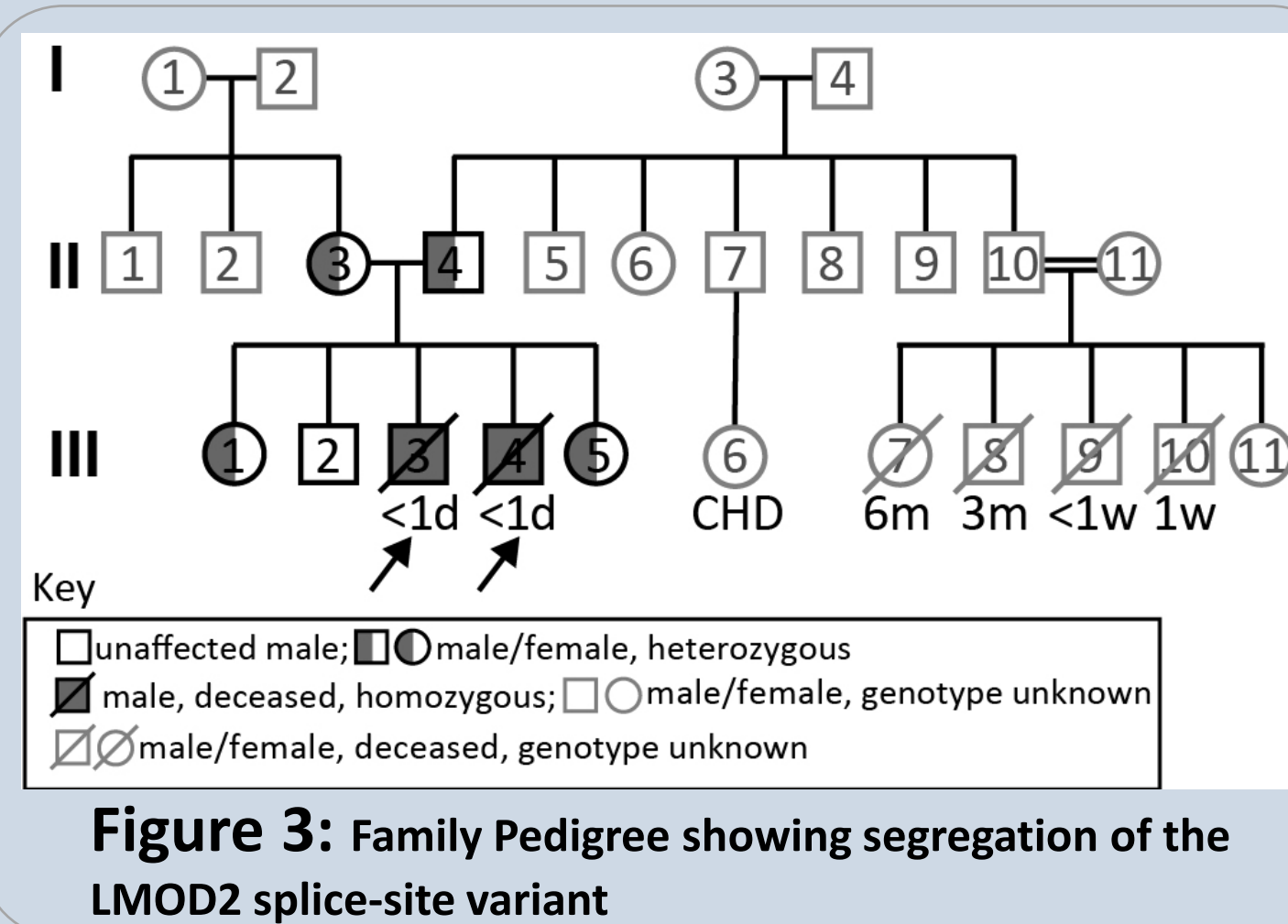


Figure 3: Family Pedigree showing segregation of the *LMOD2* splice-site variant

Cardiac ultrasound and autopsy (proband III:4) were consistent with dilated cardiomyopathy (showing bi-ventricular dilation and cardiac enlargement, **Figure 4**).

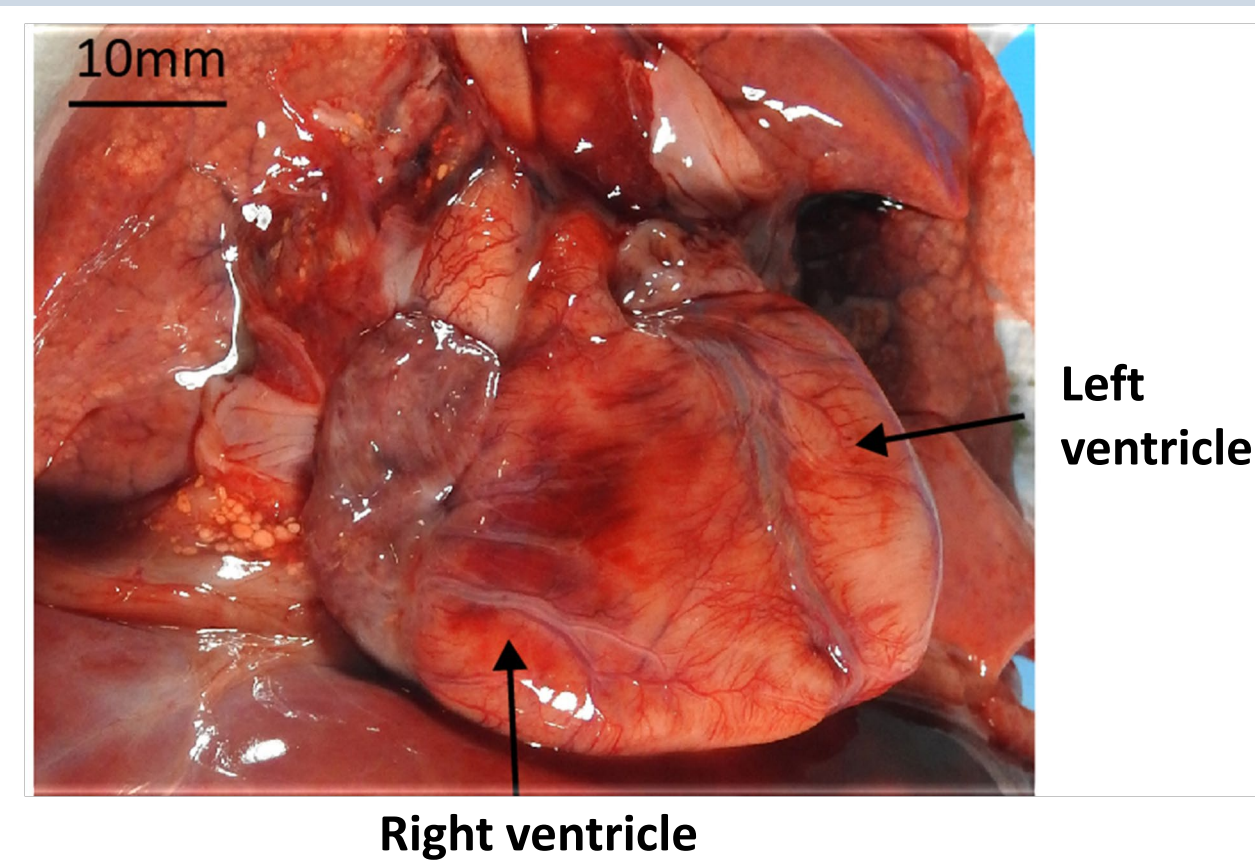


Figure 4: Anterior view of the heart of proband III:4 in situ demonstrates enlargement of the heart

Exome sequencing identified a segregating homozygous *LMOD2* variant ablating the donor 5' splice-site of intron 1

((GRCh37)chr7:g.123296291G>A; NM_207163.2:c.273+1G>A).

In silico splicing analysis (Alamut Visual® and SpliceAI) suggests this variant abolishes the 5' splice-site of intron 1 (**Figure 5**).

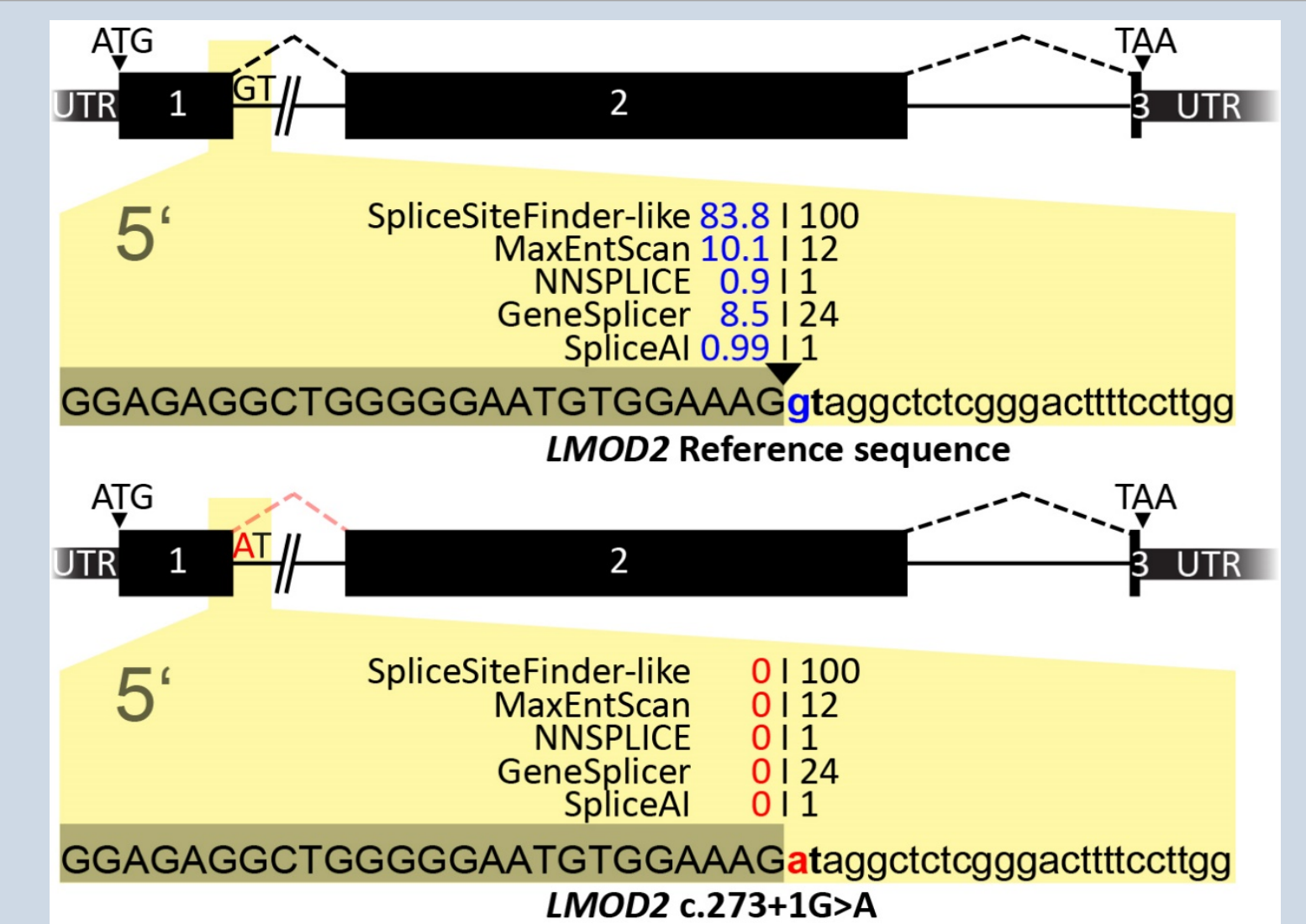


Figure 5: *LMOD2* c.273+1G>A abolishes the 5' splice-site of intron 1
A splice-site is located before the affected nucleotide (reference sequence splicing scores in blue, maximum score in black). The *LMOD2* c.273+1G>A variant abolishes this 5' splice-site (variant shown in red at bottom, along with prediction scores of 0 in red).

Consistent with previous reports of *LMOD2*s role as a regulator of thin filament length, thin filaments were significantly shortened in cardiac muscle of proband III:4 (**Figure 6**).

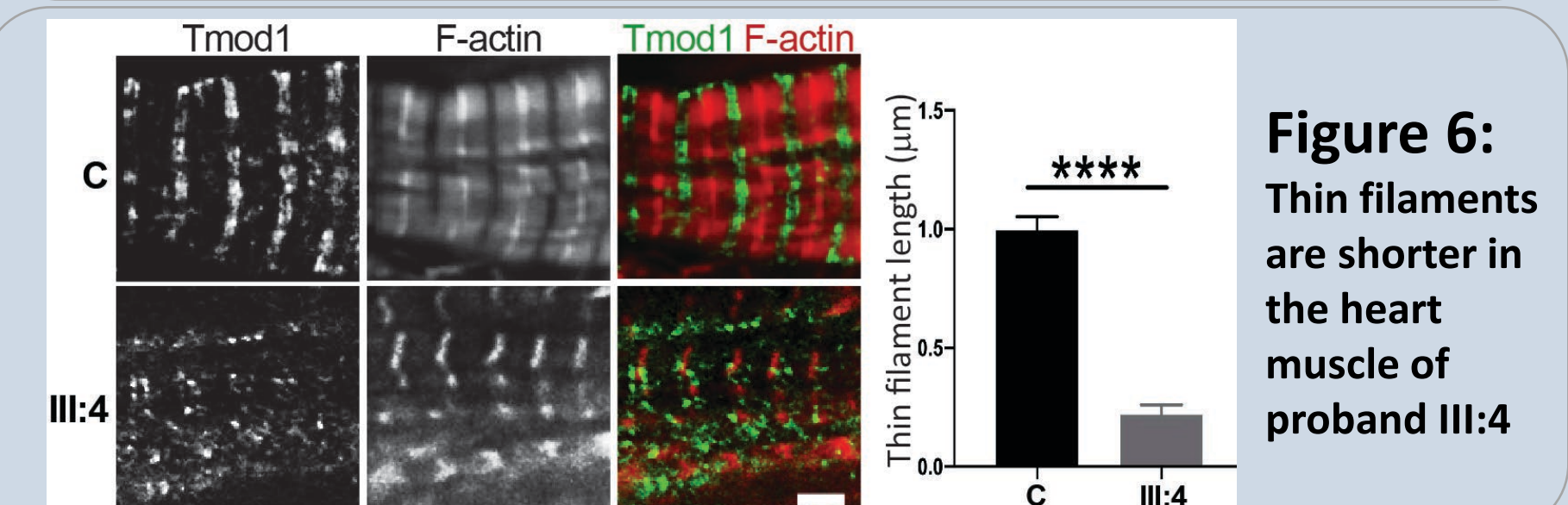


Figure 6:
Thin filaments are shorter in the heart muscle of proband III:4

LMOD2 c.273+1G>A - loss of correctly spliced *LMOD2* transcript and *LMOD2* protein

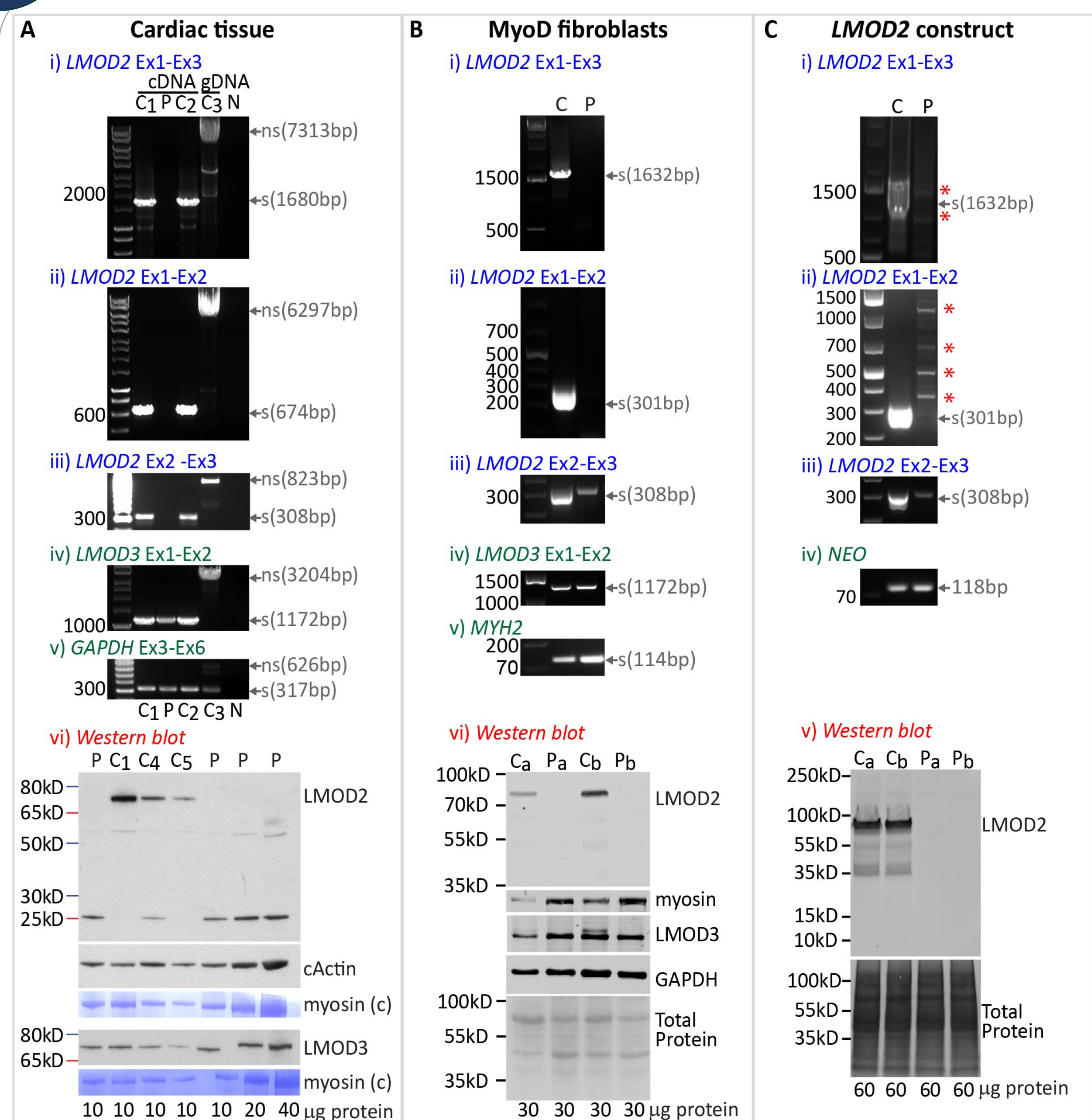


Figure 7: Reverse-transcription PCR and Western blot show *LMOD2* c.273+1G>A a lack of transcripts or mis-spliced transcripts in proband III:4 cardiac tissue, proband III:4 MyoD-transdifferentiated skin fibroblasts and *LMOD2* gene-construct transfected HEK293 cells.

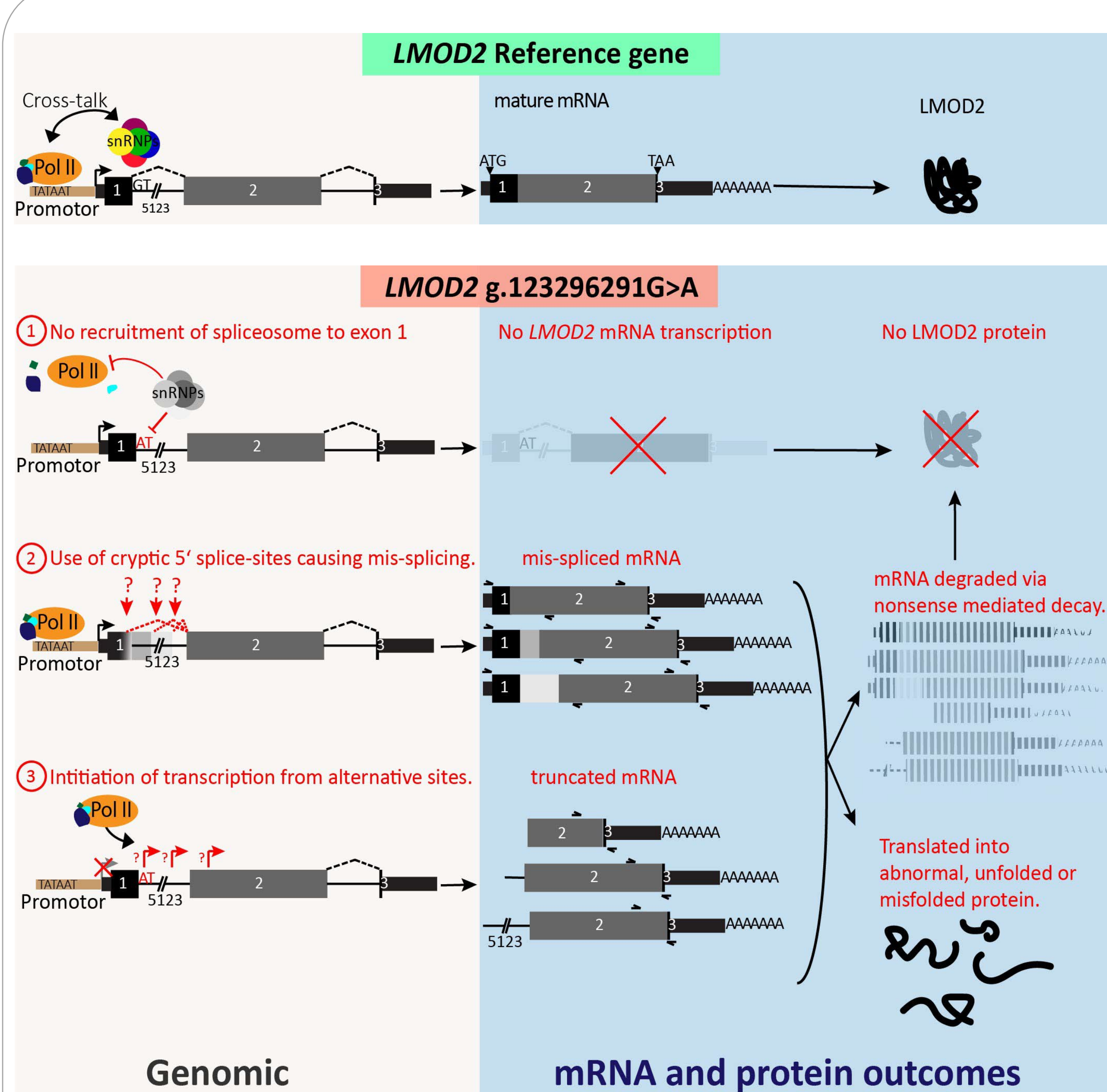


Figure 8: Proposed pathogenic mechanism resulting in loss of transcripts and protein from *LMOD2* g.123296291 G>A

Potential effects of Intron 1 5' splice-site mutagenesis are:

(1) The spliceosome does not recognise and assemble on the mutated splice-site resulting in loss of recruitment of the transcription machinery and no *LMOD2* transcripts.

(2) Transcription machinery transcribes *LMOD2* pre-mRNA and transcripts are spliced at alternative (cryptic) splice-sites (indicated by ?). Mis-spliced mRNA transcripts are either removed via nonsense-mediated decay or result in frame-shift/truncated or otherwise abnormal protein.

(3) The transcription machinery is recruited to an alternative transcription start site. This results in start-loss transcripts which are either targeted by nonsense-mediated decay or result in aberrant protein similar to mechanism (2).

Conclusion: *LMOD2* c.273+1G>A splice-site variant causes dilated cardiomyopathy by abolishing *LMOD2* protein expression resulting in thin filament shortening and contractile dysfunction.

ACKNOWLEDGMENTS

This research was funded by an NHMRC Early Career Fellowship.
Thank you to the team at Kids Neuroscience Center, in particular, Adam Bournazos, Samantha Bryen and Shobhana Bommireddipalli for their input and support.

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