

Supporting information:

The intrinsically disordered carboxy-terminus of troponin-T binds to troponin-C to modulate myocardial force generation

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Table S1. In silico prediction tools applied to *TNNC1*-p.Ile4Met

	MutPred2	PolyPhen-2	MutationTaster	SIFT
Prediction	Pathogenic	Benign	Disease-causing	Tolerated

Predictions were performed on MutPred2 (1), PolyPhen-2 (2), MutationTaster (3), and SIFT (4) using the FASTA sequence (with Ile4Met substitution) for human *TNNC1* (UniProt P63316) or Ensemble transcript ID (ENST00000232975). MutPred2 score: 0.569. MutationTaster probability: 0.999.

Table S2. cTnT-cTnI intersubunit cross-linked residues

cTnT	cTnI
K197	K117
K197	K120
K200	K117
K207	K117
K207	K120
K255	K117
K258	K117
K258	K120
K273	K138

Verified cTnT and cTnI intersubunit BS3 cross-links identified in the “dark band” (Fig. 5A).

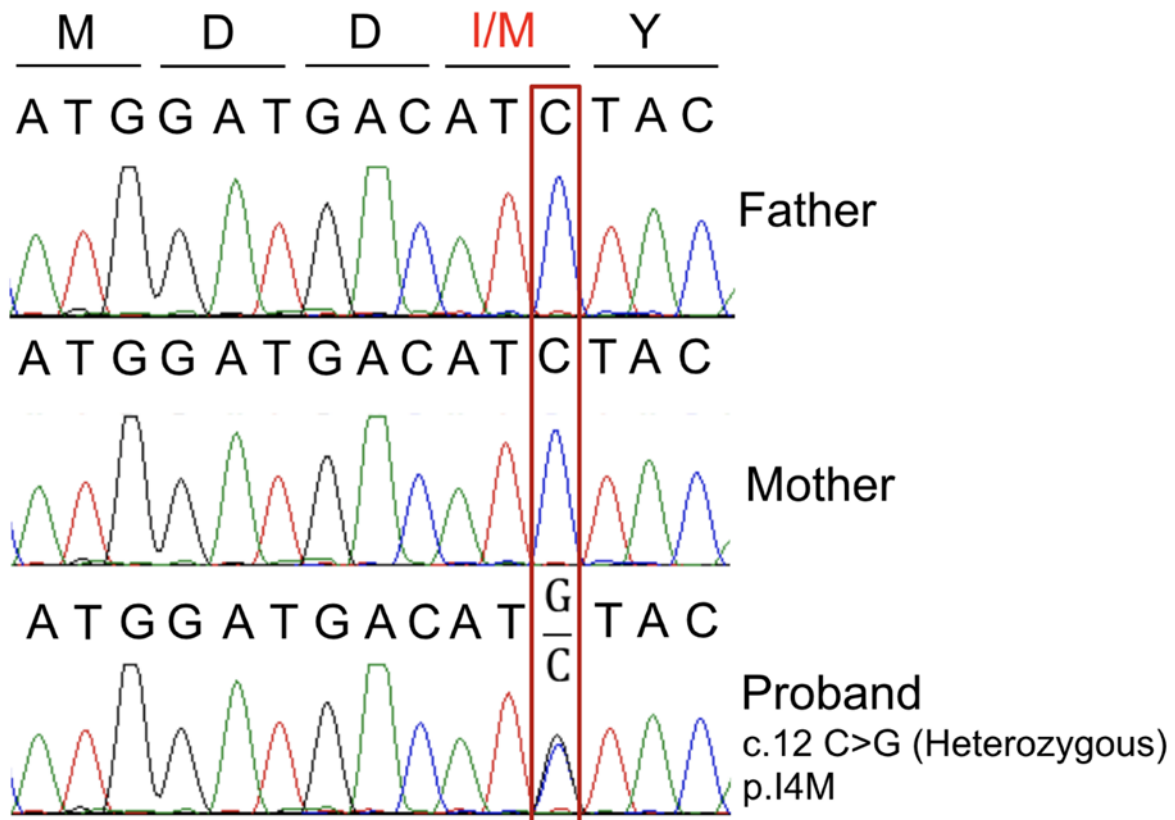


Fig. S1. Trio whole exome sequencing chromatograms. The first 5 codons in exon 1 of *TNNC1* are shown with their respective amino acid residues (single letter notation). Red box indicates the position at which the substitution occurred in the proband. Tracings: green, adenine (A); red, thymine (T); black, guanine (G); blue, cytosine (C). Note the presence of signals from both G and C at the 12th nucleotide position (12 C>G) in the proband, indicating heterozygosity.

Modulation of Contractile Force by Cardiac Troponin-T and Troponin-C Interactions

Zebrafish	MNDIYKAAAEQLTDEQKNEFRAAFDIFVQDAEDGCISTKELGKVMRMLGQNPTPEELQEM
Chicken	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Bovine	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Pig	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Sheep	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Human	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Chimpanzee	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Rabbit	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Mouse	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Rat	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Dog	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
Cat	MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEM
	*:*****.****:*****:*****.*****

Fig. S2. Multiple protein sequence alignment of *TNNC1* across various species. Red box indicates the conserved isoleucine (I) at position 4 in the primary amino acid sequence.

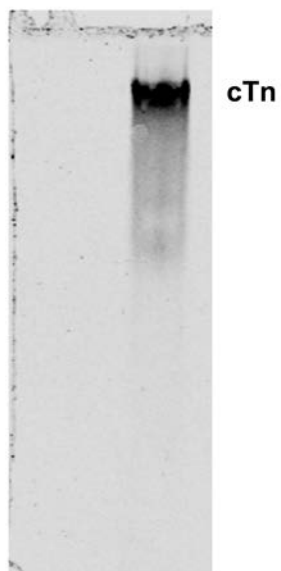


Fig. S3. Coomassie-stained native gel (4% stacking, 8% resolving) analysis of wild-type cTn.

Modulation of Contractile Force by Cardiac Troponin-T and Troponin-C Interactions

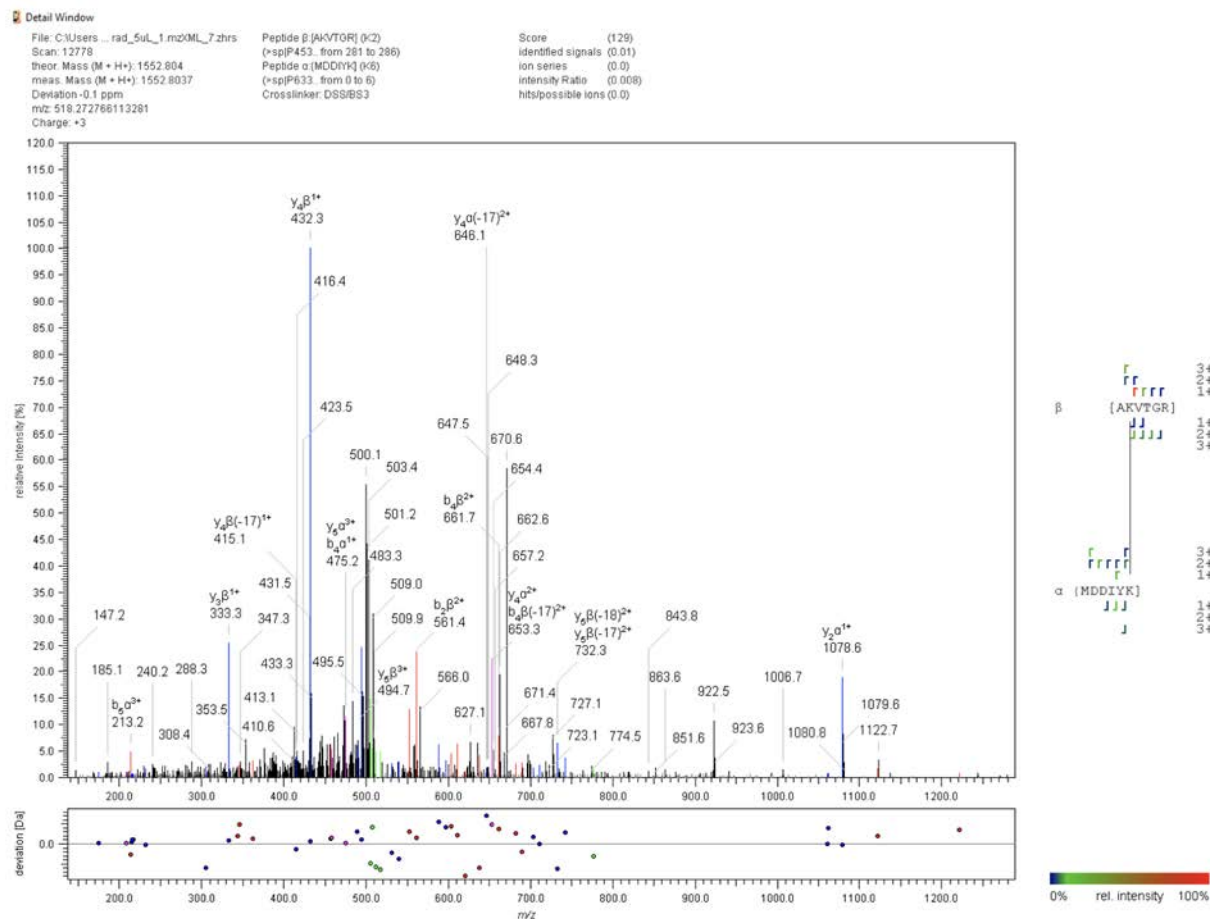


Fig. S4. Observed MS2 of the precursor ion m/z of 518.2721 corresponding to the cross-linked peptides between cTnT-K282 and cTnC-K6. Complete sequence coverage allows for localization of the cross-linking sites.

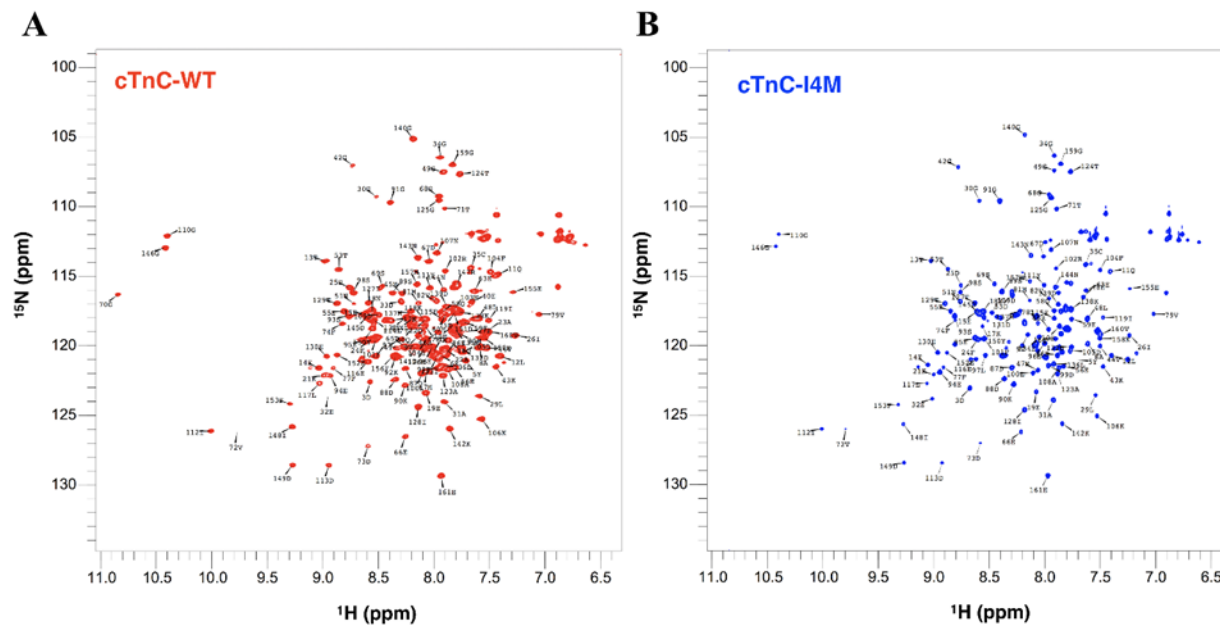


Fig. S5. Individual ^1H - ^{15}N HSQC spectra for (A) cTnC-WT and (B) cTnC-I4M. The ^1H - ^{15}N assignment for cTnC-I4M was obtained by cross-peak transferring from our previous cTnC-WT assignment. For further details please see Experimental Procedures.

1. Pejaver, V., Urresti, J., Lugo-Martinez, J., Pagel, K. A., Lin, G. N., Nam, H.-J., Mort, M., Cooper, D. N., Sebat, J., Iakoucheva, L. M., Mooney, S. D., and Radivojac, P. (2017) MutPred2: inferring the molecular and phenotypic impact of amino acid variants. *bioRxiv*, 134981
2. Adzhubei, I. A., Schmidt, S., Peshkin, L., Ramensky, V. E., Gerasimova, A., Bork, P., Kondrashov, A. S., and Sunyaev, S. R. (2010) A method and server for predicting damaging missense mutations. *Nat Methods* **7**, 248-249
3. Schwarz, J. M., Cooper, D. N., Schuelke, M., and Seelow, D. (2014) MutationTaster2: mutation prediction for the deep-sequencing age. *Nat Methods* **11**, 361-362
4. Kumar, P., Henikoff, S., and Ng, P. C. (2009) Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. *Nat Protoc* **4**, 1073-1081