

Supplemental Figure 1

Legend of supplemental Figure 1. Mapping and modeling of A8V and C84Y HCM mutations in HcTnC in Ca²⁺ saturated state. HcTnC-HCM mutations A8V and C84Y modeled into the cTn complex crystal structure PDB 1J1E by Takeda (2004) A) Location of A8 and hydrophobic contacts between A8 in N-helix and the adjacent D-helix residue V82. Red dotted line is a measurement between closest portions of side chains and reported as Angstroms. B) Modeled structure showing V8 and the closest residue in D-helix V82. C) Structure indicating position of C84 and the hydrogen bond (red dotted line) between cTnI-A151 and the carbonyl-O of C84. Red dotted lines and numerical values indicate distance in Angstroms between cTnC-C84 and cTnI-149. D) Modeled structure with mutation Y84 indicated that shows H bond between cTnI-A151 and Y84 and distance between 84Y side chain and cTnI-A151. Helices in cTnC are blue and labeled. TnI is indicated in green.