

Table S1. Predicted CaMK phosphorylation sites of MyBP-C N-terminal fragments identified using GPS 3.0 (medium threshold).

Fragment	Amino Acid						
ssC1C2	S55	T92	T125	S252 ^a	S296	S316	S333
fsC1C2	N/D*	T81	T110	S250	S294	N/D	N/D
C0C2	N/D	N/D	N/D	S358	S402	S423	S440

^a Predicted CaMK phosphorylation site maps to region corresponding to the linker between the M-motif and C2 domain in cMyBP-C as reported by Michie *et al* 2016. This residue has also been identified in the NCBI ClinVar Database as likely to be pathogenic; *N/D – phosphorylation sites were not predicted at these positions.

Table S2. Amino acid sequences show conservation between mouse and human M-motif regions.

Type	Amino acid sequence
Slow Skeletal Mouse	IDVWEL LKNANP NEYEKIAFQYG ITD LRGMLKRLK
Cardiac Mouse	EDVWEI LRQAPP SEYERIAFQHGVTD LRGMLKRLK
Cardiac Human	EDVWEI LRQAPP SEYE RIAFQYGVTD LRGMLKRLK