A

SERCA1a	900 a.a.	ALSVLVTIEMCN
SERCA1b	900 a.a.	ALSVLVTIEMCN
SERCA1c	775 a.a.	ALSVLVTIEMCN
SERCA2a	899 a.a.	ALSVLVTIEMCN
SERCA2b	899 a.a.	ALSVLVTIEMCN
SERCA3a	900 a.a.	ALSVLVTIEMCN
SERCA3b	900 a.a.	ALSVLVTIEMCN
SERCA3c	900 a.a.	ALSVLVTIEMCN
SERCA3d	900 a.a.	ALSVLVTIEMCN
SERCA3e	900 a.a.	ALSVLVTIEMCN
SERCA3f	900 a.a.	ALSVLVTIEMCN
Homo sapiens	900 a.a.	ALSVLVTIEMCN
Rattus norwegicus	900 a.a.	ALSVLVTIEMCN
Mus musculus	900 a.a.	ALSVLVTIEMCN

B

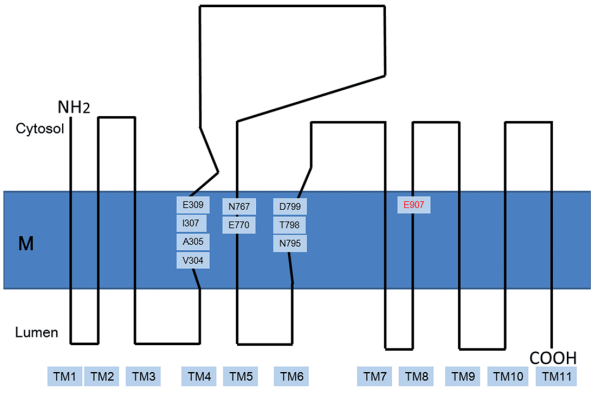

Fig. S1. Sequence alignments around the missense mutation, and the structure of SERCA2b. The sequence alignment of the SERCA family of *Homo sapiens* and the SERCA2b of mammals (A). Glu907 is in red. The glutamic acid is conserved among the SERCA family and diverse species. The structure of SERCA2b (B). There are 11 transmembrane domains (TM). Calcium-binding residues V304, A305, I307, E309 (TM4), N767, E770 (TM5), N795, T798, D799 (TM6) and E907 (TM8), located approximately in the middle of the TM. The novel mutation alters E907, indicated in red font. M indicates the membrane.