Supplementary material

Table S1. Primer sequences used for RT-qPCR analysis.

Gene	Forward primer	Reverse primer
Myh6	GGCACAGAAACACCTGAAGA	CATTGGCATGGACAGCATCATC
Myh7	ATGTGCCGGACCTTGGAA	CCTCGGGTTAGCTGAGAGATCA
Nppb	TTTGGGCTGTAACGCACTGA	TTGTGGCAAGTTTGTGCTCC
Nppa	TGTACAGTGCGGTGTCCAACA	AGAGCCCTCAGTTTGCTTTTC
Scd1	TACCGCTGGCACATCAACTTC	AACAGGAACTCAGAAGCCCAAAGC
Scd2	CACTGGGGAGCAGATGTTCG	CAAATACGCGAAGAGACAGGTG
Scd4	GTTCCAGAGGAGGTACTACAAG	GAGACGCATAAGCTGTGTTG
Ndufv2	TGGATGGCTACCTATCTCCGCT	GGTACTTCCCAACTGGCTTTCG
Rpl32	AGTTCCTGGTCCACAATGTCA	GCACACAAGCCATCTACTCATT

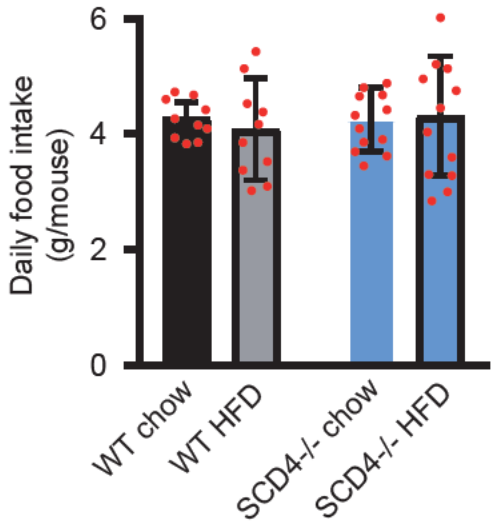

Fig. S1. Food intake during the eight weeks of the experiment. The data are expressed as mean ± SD, n = 10-12 mice/group.

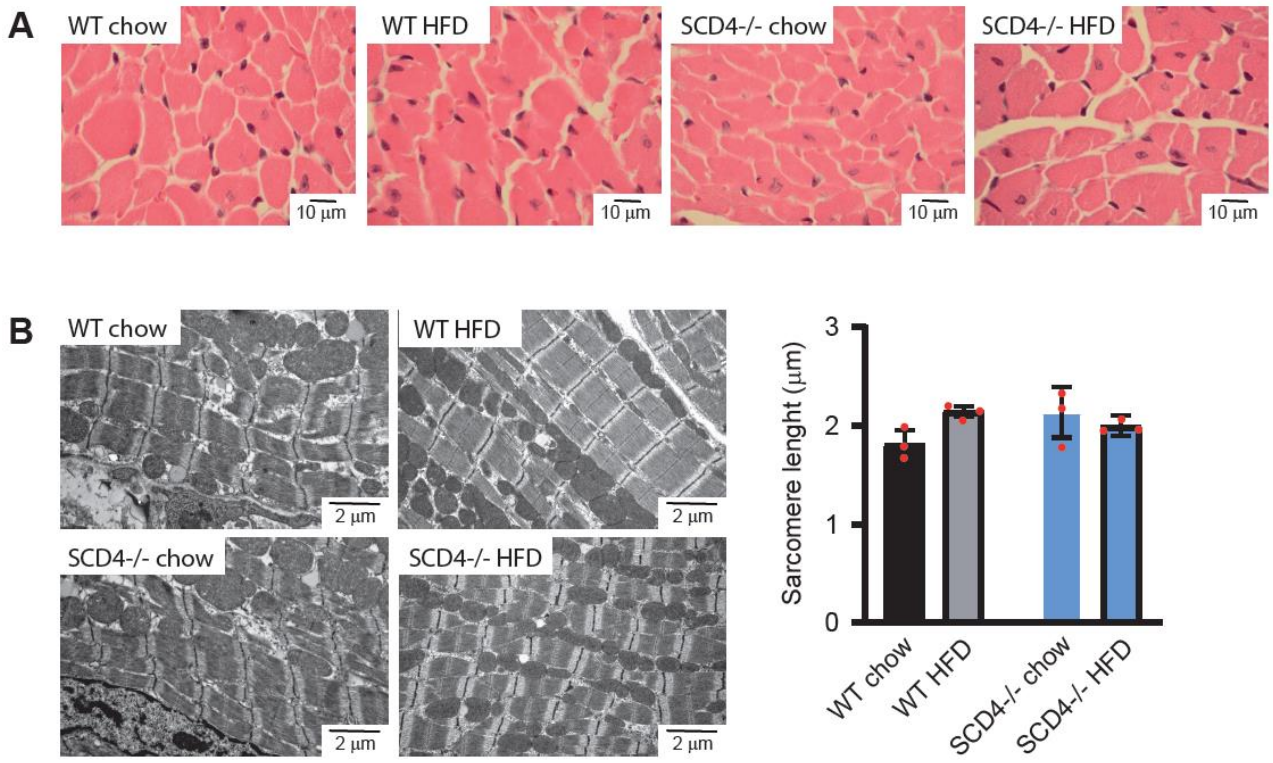

Fig. S2. (A) Hematoxylin and eosin staining of mouse left ventricle. Magnification 60 x, scale bar indicates 10 µm. **(B)** Representative electron microscopy images of left ventricular sarcomeres. Magnification 15,000 x, scale bar indicates 2 µm. Sarcomere length ($n > 40$) was measured at 6,000 x magnification electron microscopy images. The data are expressed as mean ± SD, n = 3 mice/group.

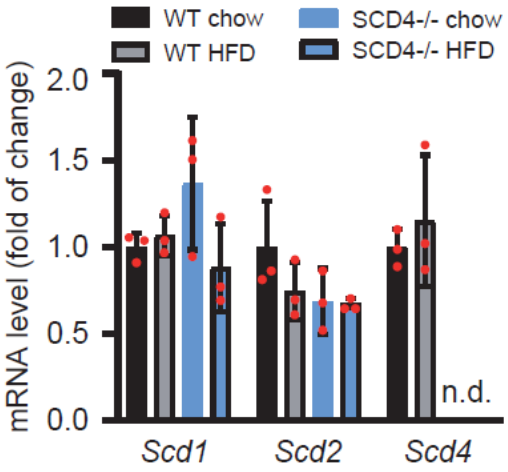

Fig. S3. Effect of SCD4 deficiency and HFD on the mRNA levels of individual SCD isoforms expressed in the heart. mRNA level was analyzed using quantitative real–time PCR and $2^{-\Delta\Delta Ct}$ method. The data are expressed as mean ± SD, n = 10–12 mice/group. No significant changes were found.